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The Peopling of the Bahamas: A Phylogeographical Perspective

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FLORIDA INTERNATIONAL UNIVERSITY

Miami, Florida

THE PEOPLING OF THE BAHAMAS: A PHYLOGEOGRAPHICAL PERSPECTIVE

A dissertation submitted in partial fulfillment of the

requirements for the degree of

DOCTOR OF PHILOSOPHY

in

BIOLOGY

by

Tanya M. Simms

2011

To: Dean Kenneth G. Furton
College of Arts and Sciences

This dissertation, written by Tanya M. Simms, and entitled The Peopling of the Bahamas: A Phylogeographical Perspective, having been approved in respect to style and intellectual content, is referred to you for judgment.

We have read this dissertation and recommend that it be approved.

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Date of Defense: March 30, 2011

The dissertation of Tanya M. Simms is approved.

Dean Kenneth G. Furton
College of Arts and Sciences

Interim Dean Kevin O'Shea
University Graduate School

Florida International University, 2011

DEDICATION

This dissertation is dedicated to my parents, Michael L. Simms and Sheila A. Simms, whose support, understanding and belief in me helped me successfully complete this project.

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ABSTRACT OF THE DISSERTATION

THE PEOPLING OF THE BAHAMAS: A PHYLOGEOGRAPHICAL PERSPECTIVE

by

Tanya M. Simms

Florida International University, 2011

Miami, Florida

Professor Rene J. Herrera, Major Professor

During the past 500 years, the Bahamas has been influenced by a wide array of settlers, including but not limited to, the Arawak Indians, Eleutherian Adventurers, British Loyalists, Creole slaves, liberated Africans as well as Chinese, Greek, Jewish, Lebanese, Jamaican and Haitian migrants. To date, however, only a few reports analyzing the genetic makeup and population dynamics of the Bahamas have been published, making this work pivotal in the endeavor to ascertain the genetic ancestry of these groups. As such, the current investigation was undertaken to genetically characterize six of the more densely populated islands throughout the Northwest (Grand Bahama and Abaco) and Central (Eleuthera, Exuma, Long Island and New Providence) Bahamas using different forensic marker systems. When autosomal STR markers are employed, the Bahamian collections were all found to receive differential contributions from the African, European, East Asian and Native American collections utilized in the analyses. Similar findings were also observed for two other Afro-Caribbean populations, Haiti and Jamaica, although the latter populace was found to share a greater proportion of its autosomal component with non-African sources than the former. On the contrary, analysis of the six Bahamian collections using high-resolution Y-chromosome markers

identifies genetic signals emanating exclusively from Africans and Europeans, but this is likely the result of smaller sample sizes collected from each island and/or sex-biased gene flow from East Asian and Native American groups.

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I. INTRODUCTION

The Bahamas is a low lying archipelago that extends from the southeastern tip of Florida to Cape Haitien, the northernmost part of Haiti. Geographically, the island chain is subdivided into three regions: the Northwest (NW), Central and Southeast (SE) Bahamas (Albury, 1975) (Fig. 1). While only Grand Bahama, Abaco, Bimini and the Berry Islands comprise the NW portion of the archipelago, the more populous Central Bahamas consists of (from north to south) Andros, New Providence, Eleuthera (including Harbor Island and Spanish Wells), Exuma and its cays, Cat Island, Long Island, San Salvador, Rum Cay and Ragged Island. Like the NW Bahamas, the SE Bahamas is formed by a smaller subset of islands (Crooked Island, Acklins, Mayagua and Inagua) but in contrast to the other two regions, the population size is substantially lower, totaling a mere 2,006 individuals (Department of Statistics of the Bahamas, 2000).

Historical records indicate that the indigenous people of the Bahamas, *i.e.*, the Arawak (Lucayan) Indians (Bahamas Dept. of Archives, 1996; Johnson 1996), settled throughout the archipelago during the Ostionoid expansion (600-1100 AD). This group of Amerindians is believed to have traveled north from the Amazon River Basin into the Lesser and then Greater Antilles, arriving in the Bahamas around 800 AD (Keegan, 1992; Keegen, 2000). The Lucayans resided on the island of Guanahani (believed to be present-day San Salvador) until the invasion of the Spanish, who deported them to Hispaniola and Cuba where they were enslaved (Bahamas Dept. of Archives, 1996; Wilkie and Farnsworth, 2005). By the mid 1500s, most of the Lucayans had perished (Granberry, 1981; Johnson, 1996) and the Bahamas became virtually uninhabited (Miller, 1945; Lawlor, 1998).

Although claimed by the British Empire in 1629 (Turner, 2003), the first permanent settlement of the islands did not occur until 1648 by the Eleutherian Adventurers, a group of Puritan pilgrims (Lawlor, 1998). The pilgrims fled England to escape religious persecution and after continued religious turmoil in Bermuda (the first place where they sought refuge), the Adventurers landed on Cigatoo (present-day Eleuthera) with the hope of establishing a truly independent colony in the Bahamas (Miller, 1945; Saunders, 1991). They were subsequently joined by other exiled Bermudian colonists that would not take oath to the new king, Charles II (Craton, 1986; Lawlor, 1998). The Bermudian period (1648-1670) in the Bahamas ended with most Puritans returning to Bermuda as conditions improved, leaving a few hundred individuals behind (Wilkie and Farnsworth, 2005).

In the following century, the Bahamas was raided over thirty times by French and Spanish pirates (Saunders, 1990), and in the course of power struggles among the European conquerors (*i.e.*, France, Spain, Britain and the Netherlands) for domination of the West Indies, was finally recaptured by Spain in 1782 (Williams, 1990). The signing of the Treaty of Versailles in 1783, however, brought an end to the American Revolutionary War and granted Florida to Spain and the Bahamas to the British Empire (Williams, 1983). As a result, thousands of British Loyalists fled continental North America for the Bahamas between 1783 and 1785 (“the Bahamian Revolution”) (Craton, 1986). The Bahamas was chosen as a suitable refuge since the islands remained under British rule and, as an additional incentive, each Loyalist was promised several acres of unoccupied land by the Crown (Saunders, 1978).

The migration of the Loyalists into the island chain greatly impacted Bahamian society. Prior to their arrival, only New Providence, Eleuthera, Harbour Island, Exuma and Cat Island were permanently settled and individuals of African and European descent were almost equally represented in number (Saunders, 1985). Yet, by 1788 the population had doubled, with Africans outnumbering Europeans 2:1, and the number of inhabited islands had expanded to include Abaco, Andros, Crooked Island and Long Island (Sharer, 1955). The escalation in the African component resulted from the slaves of Creole descent [an individual of African ancestry that is born in the New World (Saunders, 1985)] that accompanied the Loyalists and the importation of African born individuals in the following years to meet the increased demand for plantation laborers (Albury, 1975; Johnson, 1996). Additionally, large numbers of liberated African slaves captured by the British Royal Navy were resettled in the Bahamas following the abolition of the slave trade in 1807. Thereafter, the island chain was influenced by various ethnic groups, including Greeks, Chinese, Lebanese, Eastern European Jews (Johnson, 1991; McCartney, 2004), Jamaicans, Turks and Caicos islanders, Guyanese, Barbadians and Haitians (Tinker, 1998), who further contributed to the diverse collage-like populace of the archipelago.

On the basis of those historical accounts, it is not surprising that the deepest roots set within the Bahamas are attributed to African and European sources. Junkanoo, for example, is a festival that is believed to have originated from a West African slave leader by the name of “John Canoe.” Several elements derived from his culture, including the masks, which are similar to those worn by the Egunguns (a Yoruba tribe), and goombay music, a melodic mixture of rhythmic drumming [the goat skin drum used resembles the

West African djembe drum (Thompson, 2010)] and folk songs (Baker, 2001), are the basis of this important cultural celebration. In addition to Junkanoo, obeah (black and white magic), religion, dance (Ring play), ‘bush’ medicine, folklore and the ‘Asue’ (the communal practices of money management) are other predominantly African customs that are still widespread throughout the archipelago (Saunders, 1995). On the contrary, European traditions (*e.g.*, Plaiting of the Maypole) are less commonly practiced and, in most instances, are amalgamated with those derived from Africa. One of the most well-known examples is Rake ‘n’ Scrape music, a unique sound produced by an accordion (of European origin) in concert with a carpenter’s saw and a goombay drum (of African origin) (Ingraham, 2007).

Despite the wealth in historical and anthropological data, the amount of genetic information currently available on the Bahamas is limited. In the earliest report, Halberstein and colleagues (1981) characterized abnormal hemoglobin variants (Hb S, C and F) among the people residing in Bimini, suggesting that their presence is likely attributed to African influx into the island. In another study based on the D1S80 polymorphism, the Bahamas clustered with three African American groups from the United States (US) in an unweighted pair group method with arithmetic mean (UPGMA) tree, indicating that the Bahamian population is indeed of African origin (Duncan et al., 1996). Similar findings were also reported by Herrera and collaborators (2004), however, in their study, the Bahamian populace not only clustered with the collection from Haiti but also with the those from Benin, Cameroon, Congo, Kenya, Nigeria, Rwanda and Zimbabwe in both global principal component (PC) and maximum likelihood (ML) phylogenies. In addition to the D1S80 locus, Budowle et al. (1999) reported allele

frequencies for the 13 Combined DNA Index System (CODIS) Short Tandem Repeat (STR) loci in the general Bahamian population, amongst five other groups from the New World, in order to establish a genetic database for forensic purposes. Unfortunately, in these studies, no attempt has been made to genetically characterize any of the Bahamian islands (outside of Bimini) independently.

The work in Chapter II was undertaken to ascertain the genetic composition and phylogeny of the current population in New Providence since the majority of the Bahamian populace (69.4%) resides on this island (Department of Statistics of the Bahamas, 2000). In this study, the 15 autosomal STR loci included in the AmpF/STR[®] Identifiler kit (Applied Biosystems, Foster City, CA) were analyzed in the collection from New Providence and subsequently compared to published reference populations available from the literature. The results suggest a strong genetic affinity between the New Providence collection and two African American groups from the US, most likely attributed to the migration of the Loyalists and their slaves from continental North America. All three populations also appear to be genetically more similar to the reference West African collections (particularly Equatorial Guinea and Angola) than to the East African groups, possibly because of high degrees of gene flow from West Africa into the New World during the Transatlantic Slave Trade (Simms et al., 2008)

Given the lack of Caribbean reference populations available for phylogenetic comparisons to the Bahamian collections, autosomal STR datasets for two other Afro-Caribbean populations (Haiti and Jamaica) were compiled in Chapter III. Using the allelic frequency data generated across the 15 Identifiler loci, the Haitian and Jamaican collections were subsequently compared to worldwide geographically targeted reference

populations to survey the genetic diversity present in each island. In this study, I have found that although both Haiti and Jamaica display genetic affinities with the continental African collections, a much stronger African signal is detected in Haiti. Jamaica, on the other hand, exhibits an admixture profile similar to other New World collections of African descent analyzed in this report, with comparable levels of genetic input from European and East Asian sources. The divergent genetic signatures present in these populations allude to the different migratory events of Africans, Europeans, and East Asians into the New World (Simms et al., 2010).

Chapter IV focuses on the establishment of anthropologically well-characterized forensic databases for several of northwestern (Grand Bahama and Abaco) and central (Eleuthera, Exuma and Long Island) Bahamian islands across the 15 Identifiler loci. A second aim of the study is to ascertain the genetic distribution and phylogenetic relationships of each island population as well as their genealogies within the context of diverging migratory scenarios, settlement patterns, ethnic influences and present social structuring (Bethel, 2002), which are all postulated to have contributed to the highly diverse, collage-like populace of the island chain. Altogether, my findings suggest that Bahamians are a highly heterogeneous group, with each island sampled receiving differential contributions from African, European, East Asian and Native American sources. Even though the strongest genetic signal in all five collections emanates from continental Africa, inter-island differentiation is apparent in the MDS, *Structure* and admixture analyses (Simms et al., 2011).

In Chapter V, high-resolution Y-chromosome analyses were performed to delineate the patriarchal ancestry of the six Bahamian islands sampled (*i.e.*, Abaco, Eleuthera, Exuma, Grand Bahama, Long Island and New Providence) and their genetic relationships with previously published reference populations. The results identify genetic signals emanating exclusively from African and European sources, with haplogroups E-M96 and R-M306 accounting for greater than 85% of all Bahamian patrilineages. The major difference among the islands lies in the opposing distribution of sub-haplogroups E1b1a-M2 and R1b1b1-M269, with the former predominating Y-lineages in the collections from Abaco, Exuma, Eleuthera, Grand Bahama and New Providence while the latter is found at elevated levels in the Long Island populace. Substantial inter-island variation is also noted in the Y-STR based analyses, especially with respect to E1b1a7a-U174 and E1b1ba8-U175 sub-lineages. This Chapter is written in the format required by the American Journal of Physical Anthropology.

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Appendix I

Fig. 1: Map of the Bahamas illustrating the islands comprising the northwest, central and southeast portions of the archipelago

II. THE GENETIC LEGACY OF THE TRANSATLANTIC SLAVE TRADE IN THE ISLAND OF NEW PROVIDENCE

A. Introduction

The number of genetic studies characterizing the populations of the Bahamas is limited. For instance, Halberstein et al. [1] examined abnormal hemoglobin variants among the people residing on the island of Bimini while Duncan et al. [2] reported D1S80 polymorphisms in the general populace of the Bahamas. A more recent study by Budowle et al. [3], reported the allelic frequencies of the 13 CODIS STR loci in a collection of individuals from different Bahamian islands, in an attempt to establish a genetic database for forensic purposes. Considering the complex demographic landscape generated by unique ancestral populations that have contributed genetically to the island chain, the need for insular-specific population studies and datasets for forensic casework is paramount.

The present work was undertaken to ascertain the genetic diversity in the current population of the island of New Providence in the Bahamian archipelago and the discrimination provided by 15 autosomal STR markers routinely employed in forensic analyses. Autosomal STRs provide for the high resolution required for assessing individual identity in forensic cases for inclusion and exclusion determination [4]. The increased number of loci analyzed and larger number of anthropologically well-characterized individuals examined in this study, allow for robust probability determinations and greater scientific certainty in forensic testing than previously achieved.

B. Materials and Methods

Sample Collection and DNA Extraction

Buccal swabs were collected with informed consent from 221 individuals residing in the island of New Providence, Bahamas (Fig. 1A). All ethical guidelines were followed as set by the Florida International University Institutional Review Board (IRB). DNA was extracted according to the manufacturers' instructions (Qiagen Inc., Valencia, CA; Puregene, Gentra Systems, Minneapolis, MN) and stored at -80°C.

Published Data

A total of 29 data sets from published geographically targeted collections [5–30] (Table 1) were included as reference populations for comparisons to the New Providence group. The geographical origins of the reference African populations as well as known ports of embarkation are provided in Fig. 1B.

DNA Amplification and STR Genotyping

PCR amplification of the 15 autosomal STRs (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA) was performed utilizing the AmpF/STR[®] Identifiler kit (Applied Biosystems, Foster City, CA) according to the manufacturer's specifications. Amplified products were separated and scored as previously published [6,31].

Statistical and Phylogenetic Analyses

Allelic frequencies, several parameters of forensic and population genetics interest [Matching Probability (MP), Power of Discrimination (PD), Polymorphic Information Content (PIC), Power of Exclusion (PE), Gene Diversity Index (GDI) and Typical Paternity Index (TPI)], expected and observed heterozygosities (H_e and H_o , respectively), and Hardy-Weinberg equilibrium (HWE) P -values were assessed as previously reported [6,31]. Inter-, intra- and total population variance (G_{st} , H_s and H_t , respectively) were estimated with the DISPAN program [6,31]. The collections examined in this analysis were assembled according to bio-geographical origin as shown in Table 1.

The Carmody's G-test program and Bonferroni adjustment ($\alpha = 0.05/378 = 0.0001323$) were utilized to ascertain whether pair-wise population comparisons yield statistically significant differences through 100,000 simulations [6,31]. In addition, correspondence analysis (CA) [6,31] and neighbor-joining (NJ) [31] dendrograms were generated as previously indicated. Ancestry informative markers (AIMs) were also assessed as described in earlier studies [6,31].

Admixture analyses were performed with the Statistical Package for the Social Sciences (SPSS) 14.0 software [6,31]. Parental groups were constructed according to bio-geographic origin (Table 1) and for the Afro-American populations, the parental African reference collections were partitioned into West (Angola and Equatorial Guinea) and East (Kenya, Madagascar, Mozambique, Rwanda Hutu and Rwanda Tutsi) African groups.

C. Results

Intra-Population Diversity

Genotype assignment and allelic frequencies for the 15 autosomal STR loci typed in the New Providence population are listed in Supplementary Tables 1 and 2, respectively, while H_o , H_e and HWE P -values are provided in Supplementary Table 3 along with the parameters of population genetics and forensic interest. Four loci, CSF1PO, D2S1338, D19S433 and TPOX, were found to deviate from HWE expectations, however, these departures became statistically insignificant after applying the Bonferroni correction ($\alpha = 0.05/15 = 0.0033$). GDI values illustrate that the D13S317 locus (0.7251) exhibits the lowest variability out of the 15 loci tested while D2S1338 (0.8885) possesses the highest within the population. Furthermore, the locus with the highest PD was D2S1338 (0.9723) whereas the FGA locus was found to be the most informative for PE (0.8242) analyses. Overall, the combined matching probability is 1 in 6.99×10^{17} and the Combined PE is 0.999998696.

Although present at low frequencies in the New Providence collection, alleles D16S539-6 and FGA-44.2 are shared exclusively with the West African population of Angola as well as allele FGA-16.1 with the Madagascar populace. New Providence and the general US African American collection (US2) share allele 30.2 at the FGA locus with Angola, Equatorial Guinea, Mozambique and the Rwanda Hutus. The same US African American group was also found to exhibit alleles D21S11-38 and D18S51-16.2 characteristic of the East African groups, *i.e.*, Mozambique and the Rwanda Hutus,

respectively. All three Afro-American populations also carry allele 19.2 at the FGA locus, present in Kenya, Mozambique and the Rwanda Hutus.

Intra-population variance (H_s) values are provided in Supplementary Table 4. The Afro-American assemblage (0.80205) exhibits the highest intra population variance while the lowest H_s levels are observed in the Asian collections (0.78103).

Inter-Population Diversity

Assessment of the phylogenetic relationships among populations was accomplished by performing a G-test, CA, NJ and admixture analyses. Three well-delineated groupings are evident in the CA plot (Fig. 2): an African group in the lower right quadrant, a European/Latin American partition in the upper left section of the graph and an Asian cluster in the lower left portion. The New Providence and US African American populations fall within the African cluster and map closer to each other than to the rest of the African collections (Fig. 2).

The topology of the NJ phylogram (Fig. 3) reveals a tight clustering of populations according to bio-geographic origin. An African branch is situated at the upper portion of the dendrogram while the other three clades (Asian, Latin American and European) are located toward the bottom of the projection. Also evident from the tree is the intermediate partitioning of the New Providence, US African American 1 and 2, Madagascar, Brazil and Puerto Rican American populations between the African groups and the other three clusters.

The highest inter-population variance (G_{st}) is observed in the All populations (0.02403) group and lowest in the Afro-American collections (0.00208) while total variance (H_t) is highest within the Afro-American group (0.80372), with the exception of the All populations group (0.80987), and lowest in the European populations (0.78737). Statistically insignificant genetic differences in the pair-wise analyses (G-test, See Supplementary Table 5) are shown in italics before and in bold after applying the Bonferonni correction.

Admixture proportions (Table 2) for the New Providence population, when analyzed against grouped parentals, reveal that 83.6% of its gene pool is contributed by the African groups while the remaining genetic influences are from the Europeans (16.3%). Similar results were also obtained for both the US African American 1 (Minnesota) and US African American 2 (general) populations (Table 2): African (84.1%, 83.8%) and European (15.9%, 14.6%), respectively. With regard to the African reference populations, the admixture proportions (Table 2) demonstrate that the West African collections (Angola and Equatorial Guinea) make a greater contribution (46.8%, 56.1% and 48.5%, respectively) to all three Afro-American populations than do the East African groups (Kenya, Madagascar, Mozambique, Rwanda Hutu and Tutsi) (36.8%, 28.0% and 35.3%, respectively). Furthermore, admixture estimations performed for each of the individual Latin American collections (Table 3) reveal that European contributions to each group's gene pool reach levels greater than 48% while the remaining influences are of African and to a lesser extent Asian descent.

Assessment of AIMs delineates TH01, TPOX and D18S51 as particularly informative loci for African ancestry while D8S1179, D2S1338 and D19S433 are elucidative for both African and European descent (Table 4).

D. Discussion

In the present study, 15 autosomal STR loci, routinely employed in forensic analyses, were typed in order to examine the genetic diversity and assess the genetic ancestry of the New Providence population. The increased number of hypervariable markers analyzed along with a larger number of individuals typed improves upon earlier studies by providing a higher resolution for defining phylogenetic relationships and an anthropologically well-characterized database for forensic purposes including exclusion and inclusion determinations.

The New Providence and US African American 1 and 2 collections exhibit 173, 162 and 168 alleles, respectively, while on average, the mainland sub-Saharan African populations included in this study possess 147 alleles. This high diversity level is likely the result of the combined contributions of European and African DNA known to have occurred in these populations [32,33]. These results are corroborated by the average heterozygosity values of the three Afro-American collections (Table 1) which are comparable to the collective average heterozygosity of the continental African groups (0.7974) (excluding South Africa since H_o values were not provided in the original report) examined in this study (Table 1). Of the three Afro-American populations, the Minnesota US African American collection exhibits the highest average heterozygosity value (0.80380) while New Providence possesses the lowest (0.78311). The relatively

lower average heterozygosity seen in the New Providence collection, in combination with the 3.87% (Average) heterozygote deficiency based on 12 loci (Supplementary Table 3) may reflect inbreeding given its insular geographical isolation.

The comparability in the level of genetic diversity between the Afro-American populations and the mainland African collections is also apparent upon examination of the intrapopulation diversity values (H_s). At the intra-population level, the Afro-American assemblage harbors the highest H_s value (0.80205) of all groups examined, even higher than the African populations, including (0.79543) and excluding (0.79474) Madagascar (Madagascar was excluded in one of the African sets to ascertain the effect, if any, of Austronesian gene flow [6]), possibly the result of admixture of several founder populations, for example the Loyalists and Africans [32,34]. Moreover, comparison of the Afro-American assemblage with the reference collections in this study reveals that these groups possess certain specific signature alleles at the D16S539 (allele 6), D18S51 (allele 16.2), D21S11 (allele 38) and the FGA (alleles 16.1, 19.2, 30.2 and 44.2) loci characteristic of sub-Saharan African groups, suggesting a connection between the two.

Additionally, AIM analysis reveals diagnostic loci (TPOX, D18S51, D8S1179, D2S1338, D19S433 and TH01) for all populations of African descent, including the three Afro-American populations. These loci set the African collections apart from other worldwide bio-geographic groups and therefore represent pharos of gene flow from Africa into the New World.

The G-test results also indicate genetic similarities between New Providence and both US African American populations consistent with an earlier study based on the D1S80 locus in which a general collection from the Bahamas was found to cluster in a UPGMA tree with four African American populations [2]. The New Providence and US African American collections also display insignificant genetic differences with sub-Saharan African groups (Supplementary Table 5). The high degree of homogeneity among the Afro-American populations is also reflected at the inter-population variance level, with the assemblage exhibiting the lowest G_{st} value of all groups examined (Supplementary Table 4).

The partitioning of the two US African American and New Providence collections together at the periphery of the African cluster and in the direction of the European/Latin American assemblage in the CA graph suggests European genetic contributions to these New World populations while still advocating close genetic ties to mainland African groups. The intermediate positions of New Providence and US African American 1 and 2 close to the sub-Saharan populations as well as the segregation of Brazil and Puerto Rican Americans further away from the African populations in the NJ tree argues for various degrees of African genetic influence to these ethnic groups. In the present study, utilizing bi-parental hypervariable markers, the African mainland was found to contribute 41.0% and 34.4% to the Brazil and Puerto Rican American collections, respectively, while contributing on average only 18.5% (ranging from 10.3% to 27.3%) to the other Latin American groups (Table 3).

The admixture proportions (Table 2) generated when West and East African groups were used separately as parents for the New Providence population indicate that the majority of the influence to the collection's gene pool is from West Africa (46.8%) followed by East Africa (36.8%) and Europe (16.3%). The greater impact made by the West African populations most likely is indicative of the proportion of slaves captured from the various West African regions and shipped to the Bahamas, as reported in Pepin [35]. Most of the slaves that entered the Bahamas are believed to have been transported from West African ports (Fig. 1B). Duncan et al. [2] report that the majority of slaves shipped to the Bahamas were specifically from Nigeria, Ghana and Congo. Other sources indicate that the Africans settling in the New World were from Angola, the Bight of Biafra [33] and the East Coast of Africa [36]. The West African influences in the island chain are supported by a D1S80 study in which the Bahamas was found to cluster with West African groups but further away from the East African collections in a principal component (PC) plot of 33 worldwide populations [37].

Also noteworthy are the contributions detected from East Africa (36.8%) to the New Providence populace in the admixture studies (Table 2). It is likely that the influences from this region are the result of the genetic imprints left by the Bantu diaspora (from West Africa) throughout sub-Saharan Africa [38,39]. In addition, it is possible that a portion of the contribution from South East Africans stems from the transportation of approximately 7.69% of the total African captives from the Mozambique/Madagascar region to the West African ports and from there to the New World [40,41].

West Africa also provides a sizeable contribution to the gene pools of US African American collections 1 and 2, 56.1% and 48.5%, respectively (Table 2). Hammer et al. [42] demonstrated the presence of African derived Y-chromosomes (haplogroups A, B and E) within a general US African American population, with haplogroup E (sub-haplogroup E3a being a Bantu marker) exhibiting the highest frequency (62%). A more recent study by Lind et al. [43] examining mtDNA markers corroborates the Y chromosome data indicating the presence of sub-Saharan African mtDNA haplogroup L (sub-haplogroups L0, L1, L2 and L3) at frequencies as high as 86% in US African Americans. The L1b sub-haplogroup (abundant throughout West Africa), for instance, is particularly prominent in US African Americans, thus supporting West African ancestry [44-46].

The New Providence and both US African American populations share similar admixture proportions (16.3%, 15.9% and 14.6%, respectively) from Europeans (Table 2). European influences on New Providence most likely derive, for the most part, from the influx of British Loyalists to the Bahamas during the American Revolutionary War [47]. European Y haplogroups I and R [42,43] and mtDNA haplogroups M and N [43] have been detected in US African American populations. In addition, only the General US African American (US2) collection exhibits contributions from the Asian groups (Table 2). Asian-specific mtDNA haplogroups A, B, C and D have been observed at low frequencies in US African American collections [33,48]. It is likely that this is partly due to admixture between US African American groups and Native Americans [33]. Also, these signals of Asian gene flow may stem from, to some extent, mainland Asian migrants ubiquitous to many New World locations.

Although the analyses point to a strong African influence on the three Afro-American populations examined, differences are observed, most likely due to admixture involving different sub-Saharan African source populations as well as with non-African groups [49]. African Americans from the United States are reported as having genetic contributions from African and European ancestral populations [33], like Bahamians, but may have greater contributions from Native American populations due to the prominence of Amerindians in continental America and their early demise in the Caribbean. The Native American impact on the General US African American population (US2) may be reflected in the 1.7% contribution by Asians in the admixture analyses performed in this study. These differences are also observed when comparing each of the Afro-American populations, which reveals alleles unique to each, namely D21S11-27.1, TH01-6.3, D19S433-14.1, FGA-34.2 and FGA-46.2 present in the New Providence populace, FGA-24.3 in the US Minnesota population, and D21S11-39, FGA-16.2 and FGA-22.3 in the US general African American collection. These allelic incongruencies between the New Providence and the US African American collections as well as between the two US African American populations themselves could impact on the probability of inclusion estimations when utilizing the different datasets. In turn, these allelic differences may incriminate further defendants whose STR profiles possess variants absent in non-authentic databases from geographical regions outside the source of the crime [50]. Therefore, the presence of these rare alleles in combination with the varied ethnic distributions throughout the Bahamian islands may justify the creation of island-specific forensic datasets for these 15 autosomal STR loci.

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Appendix II

Fig. 1A: Map of the Bahamian archipelago indicating the island of New Providence

Fig. 1B: Map of Africa illustrating ports of departure (arrows) of African slaves during the Transatlantic Slave Trade and also the location of reference African collections used in the analyses

Fig. 2: Correspondence Analysis

Fig. 3: Neighbor-Joining Dendrogram

Population	Abbreviation	# alleles present	Avg. Heterozygosity	Reference
AFRO-AMERICAN				
US African American 1 (Minnesota)	US1	162	0.80380	Gross and Budowle, 2006
US African American 2 (General)	US2	168	0.79573	Butler <i>et al.</i> , 2003
New Providence (Bahamas)	NWP	173	0.78312	<i>present study</i>
AFRICAN				
Cabinda (Angola)	ANG	151	0.79698	Beleza <i>et al.</i> , 2004
Cape Town (South Africa)	SAF	144	-	Kido <i>et al.</i> , 2007
Equatorial Guinea	EGU	153	0.89193	Alves <i>et al.</i> , 2005
Hutu (Rwanda)	HUT	154	0.81193	Shepard and Herrera, 2006
Kenya	KEN	139	0.81436	Shepard and Herrera, 2006
Madagascar	MAD	129	0.80350	Regueiro <i>et al.</i> , 2007
Maputo (Mozambique)	MOZ	148	0.79580	Alves <i>et al.</i> , 2004
Tutsi (Rwanda)	TUT	143	0.77818	Regueiro <i>et al.</i> , 2004
ASIAN				
Chao Shan (South China)	CCS	147	0.77793	Hu <i>et al.</i> , 2005
Japan	JAP	152	0.77127	Hashiyada <i>et al.</i> , 2003
Korea	KOR	140	0.77087	Kim <i>et al.</i> , 2003
Malaysia	MAL	156	0.78127	Seah <i>et al.</i> , 2003
Philippines	PHI	129	0.77793	De Ungria <i>et al.</i> , 2005
Shaanxi Han (NW China)	CSH	160	0.78232	Wang <i>et al.</i> , 2005
LATIN AMERICAN				
Caracas (Central Venezuela)	CAR	161	0.79267	Chiurillo <i>et al.</i> , 2003
Central Mexico	MEX	177	0.82827	Hernández-Gutiérrez <i>et al.</i> , 2005
Costa Rica	CSR	190	0.85353	Rodríguez <i>et al.</i> , 2007
Hispanic (US -Minnesota)	HIS	143	0.80120	Gross and Budowle, 2006
Maracaibo (Venezuela)	MAR	148	0.77896	Bernal <i>et al.</i> , 2006
Metztitlán (Mexico)	MET	138	0.75067	Gorostiza <i>et al.</i> , 2007
Puerto Rico American (Massachusetts)	PRA	149	0.79113	Zúñiga <i>et al.</i> , 2006
Rio de Janeiro (Brazil)	BRA	161	0.85533	de Souza Góes <i>et al.</i> , 2004
EUROPEAN				
Andalusia (South Spain)	SPA	129	0.77600	Coudray <i>et al.</i> , 2007
Belaruse	BLR	142	0.77160	Rebala <i>et al.</i> , 2007
Caucasian (US - General)	CAU	153	0.78173	Butler <i>et al.</i> , 2003
Flemish (North Belgium)	FLE	147	0.79533	Mertens <i>et al.</i> , 2006
North and Central Poland	POL	155	0.79447	Czarny <i>et al.</i> , 2005

Avg. Heterozygosity is not included for South Africa since observed heterozygosity (H_o) values were not included by the authors

Table 1: Populations Analyzed

Parental Groups	Hybrid Population		
	NWP	US1	US2
West Africans	0.468 ± 0.048	0.561 ± 0.051	0.485 ± 0.043
East Africans	0.368 ± 0.050	0.280 ± 0.053	0.353 ± 0.045
Asian	0.000 ± 0.018	0.000 ± 0.019	0.017 ± 0.017
European	0.163 ± 0.020	0.159 ± 0.021	0.146 ± 0.018

Refer to Table 1 for key to abbreviations

Table 2: Admixture analysis for New Providence and two African American groups from the US

Parental Groups	Hybrid Population							
	BRA	PRA	CAR	HIS	CSR	MAR	MEX	MET
African	0.410 ± 0.016	0.344 ± 0.026	0.273 ± 0.026	0.206 ± 0.032	0.190 ± 0.035	0.187 ± 0.027	0.152 ± 0.037	0.103 ± 0.061
Asian	0.037 ± 0.016	0.170 ± 0.025	0.175 ± 0.025	0.281 ± 0.031	0.235 ± 0.034	0.166 ± 0.026	0.285 ± 0.036	0.412 ± 0.059
European	0.553 ± 0.018	0.486 ± 0.027	0.551 ± 0.028	0.513 ± 0.035	0.575 ± 0.037	0.647 ± 0.028	0.563 ± 0.040	0.484 ± 0.066

Refer to Table 1 for key to abbreviations

Table 3: Admixture analysis of Latin American populations

		Average F_{st} Distances						
Locus	Informative For	AF	AS	LA	EU	AF/AS	AF/LA	AF/EU
D8S1179	African and European Ancestry	0.00152	0.00392	0.00155	0.00203	0.02396	0.01928	0.02894
D21S11	European & Asian and African & Asian populations	-0.00124	0.00546	0.00015	-0.00100	0.04097	0.02397	0.00949
D7S820	Asian Ancestry	0.00036	0.00622	0.00411	0.00060	0.05352	0.01855	0.00823
CSF1PO	Not informative on the basis of ethnicity	0.00604	0.00506	-0.00060	0.00242	0.02016	0.01455	0.01338
D3S1358	Asian and European populations	0.00041	0.00893	0.00937	0.00017	0.00525	0.00902	0.01601
TH01	African from Asian, Latin American and European populations	0.00247	0.01177	0.01214	0.01128	0.07956	0.04914	0.09368
D13S317	African, Asian and European ancestry	-0.00282	0.00236	0.00790	0.00126	0.09371	0.03024	0.02383
D16S539	European ancestry	-0.00042	0.00603	0.00421	0.00118	0.00744	0.00919	0.02252
D2S1338	African and European Ancestry	-0.00016	0.00299	0.00580	0.00133	0.01820	0.01565	0.02243
D19S433	African and European Ancestry	-0.00064	0.01127	0.00438	0.00090	0.02070	0.01496	0.02527
vWA	Not informative on the basis of ethnicity	-0.00129	0.01089	0.00416	0.00128	0.04757	0.01166	0.01457
TPOX	African Ancestry	0.00360	0.00116	0.00638	0.00421	0.05177	0.04658	0.07029
D18S51	African Ancestry	-0.00118	0.00349	-0.00047	0.00058	0.03470	0.01635	0.01824
D5S818	African and European Ancestry	-0.00379	0.00398	0.00935	0.00061	0.04009	0.03141	0.01698
FGA	European ancestry	-0.00117	0.00026	0.00261	0.00090	0.00415	0.00268	0.01199

AF = African, AS = Asian, LA = Latin American and EU = European

Table 4: Ancestry Informative Markers (AIMs)

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp001	14	18	31.2	33.2	10	10	7	11	15	17	6	7	13	13	10	12	19	22	12	14	16	19	8	9	13	17	X	Y	11	13	20	25
Nwp002	13	14	30	31.2	8	8	12	12	14	18	7	7	12	12	11	12	17	17	14	14.2	16	17	10	11	16	16	X	Y	11	13	21	25
Nwp003	14	14	34	37	10	10	10	12	15	16	8	8	11	13	12	12	21	23	12	13.2	17	18	11	11	13	15	X	Y	11	12	23	31.2
Nwp004	13	15	29	30	10	10	11	12	15	15	7	8	12	12	11	13	20	22	14.2	15	16	17	9	11	16	21	X	Y	13	13	22	26
Nwp005	13	14	29	29	7	8	11	12	16	18	8	9.3	13	14	12	13	17	20	11	13	16	18	8	8	12	16	X	Y	12	12	21	22
Nwp006	14	15	27	30	8	10	10	11	15	16	7	7	11	14	10	13	19	21	14	14.2	15	17	9	10	15	18	X	Y	11	12	18.2	21
Nwp007	12	13	29	31.2	10	11	11	12	16	17	8	9	11	13	10	12	17	18	13	14	16	16	11	12	14	14	X	Y	11	11	19	27
Nwp008	11	14	30	32.2	11	11	7	10	15	17	6	6	11	12	11	12	19	22	11	16.2	15	17	8	8	15	17	X	X	11	12	22	23
Nwp009	13	16	28	32.2	10	12	11	12	16	17	7	7	12	13	9	9	17	23	13	14	15	18	6	10	18	18	X	Y	11	12	24	24
Nwp010	11	14	28	28	8	9	9	12	14	18	6	9.3	10	11	11	14	20	21	12	13	15	17	9	10	15	22	X	Y	11	12	20	21
Nwp011	10	14	27	35	8	11	7	7	15	16	7	7	12	13	9	12	18	20	11	14.2	16	18	11	11	17	17	X	Y	8	12	23	23
Nwp012	12	16	29	31.2	10	13	7	7	15	16	9	9.3	12	13	11	13	17	18	11	13	15	18	6	10	16	20	X	Y	11	12	22	23
Nwp013	14	14	28	29	9	11	12	12	14	17	7	8	12	13	11	11	17	23	14	15	16	18	9	9	13	14	X	Y	8	12	23	26
Nwp014	14	14	31	33.2	10	12	10	12	15	16	6	8	12	13	10	12	21	22	12	13	18	19	9	9	12	18	X	Y	12	13	21	24
Nwp015	13	14	29	29	9	11	11	12	17	18	6	8	8	12	11	12	22	23	13	15	15	18	9	11	13	19	X	Y	13	13	22	23
Nwp016	13	15	30	35	8	9	11	12	16	17	8	8	12	12	11	13	16	25	13	14	15	19	8	9	18	18	X	Y	13	13	19	24
Nwp017	13	14	29	29	9	11	11	12	17	18	6	8	8	12	11	12	22	23	13	15	15	18	9	11	13	19	X	Y	13	13	22	23
Nwp018	12	12	30	30	8	12	8	10	15	17	7	7	12	12	12	19	23	15.2	15.2	15	15	9	11	16	17	X	Y	11	13	22	23	
Nwp019	11	14	29	32.2	8	11	10	11	12	18	7	9	12	13	11	14	16	23	9	13.2	16	18	9	9	13	16	X	X	10	13	25	26
Nwp020	13	15	30	35	10	11	7	12	15	16	7	8	10	11	13	13	16	16	14	15	15	15	8	9	15	17	X	Y	9	12	23	24
Nwp021	14	15	28	28	10	13	10	12	16	17	7	9.3	12	13	10	14	21	25	12.2	12.2	14	18	8	9	12	18	X	Y	8	12	19	23
Nwp022	12	14	30	35	8	10	8	10	16	17	6	7	13	13	11	12	19	19	11	14	15	19	8	11	16	17	X	X	11	12	22	23
Nwp023	13	15	30	35	9	11	8	10	15	16	6	9.3	12	13	11	12	16	27	12.2	13.2	15	15	6	9	15	18	X	Y	11	13	23	24
Nwp024	13	15	30	31	12	12	8	8	14	15	7	9	11	11	9	10	17	19	11.2	13	15	16	8	11	17	19	X	Y	12	13	24	25
Nwp025	15	15	30	30	9	10	10	12	14	17	6	7	11	11	10	11	21	24	13	14.2	16	18	8	9	15	20	X	Y	12	12	22	23
Nwp026	10	15	28	30	10	11	10	11	16	18	9	9	14	14	13	13	19	19	11	11	14	17	7	9	19	20	X	Y	11	11	21	29
Nwp027	13	16	28	30	10	10	9	13	15	16	8	9	11	11	11	12	21	22	13	13	16	16	8	9	15	17	X	Y	12	13	23	25
Nwp028	11	13	28	30.2	10	11	7	12	15	16	7	8	12	14	11	13	19	23	13	13	15	15	10	10	17	18	X	Y	12	13	19	23
Nwp029	12	15	28	28	8	10	11	13	15	15.2	7	7	11	12	9	12	19	22	11	14	17	18	8	11	16	20	X	Y	8	11	24	25
Nwp030	14	15	28	30	10	11	10	11	15	16	7	9	11	12	9	11	17	21	13	15.2	15	19	9	11	14	15	X	Y	12	12	20	21
Nwp031	11	12	30	30	9	10	10	11	16	17	7	9	12	14	11	12	17	24	13	15.2	15	16	9	9	12	15	X	Y	12	12	23	25
Nwp032	14	14	28	30	8	8	10	12	15	15	7	9.3	10	13	9	14	20	22	13	13	16	17	8	9	17	17	X	Y	11	12	22	24
Nwp033	11	13	30	31	8	8	10	10	15	18	6	7	12	12	11	12	18	21	13	13	15	15	8	9	14	22	X	Y	10	13	22	23
Nwp034	12	12	31	34	10	13	12	12	14	15	6	7	12	12	6	11	22	24	13	15.2	13	15	11	11	15	16	X	Y	8	11	22	27
Nwp035	14	14	31	31	8	9	10	11	15	15	6	8	11	12	12	12	17	21	14	14	14	16	10	11	16	17	X	Y	13	14	20	21
Nwp036	13	14	28	28	8	10	11	11	15	17	7	8	11	12	11	12	21	22	11	13.2	17	17	8	11	19	20	X	Y	12	13	22	25
Nwp037	12	14	30	34	10	11	8	8	16	17	7	8	12	14	9	11	17	21	13	13	15	16	10	11	14	19	X	Y	13	15	22	23
Nwp038	15	17	29	30	10	12	9	9	14	15	7	8	13	13	9	9	16	24	12	15	17	17	8	10	17	18	X	X	12	12	24	26
Nwp039	11	14	28	30	8	12	11	11	16	16	7	9	9	11	10	13	18	18	13	14	16	18	9	11	16	16	X	Y	8	13	34.2	34.2
Nwp040	13	15	27	29	11	11	9	10	14	15	7	8	11	14	11	11	19	22	12	13	13	14	8	10	16	16	X	Y	8	13	21	24

Supplementary Table 1: Genotype Assignment

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp041	13	15	28	29	10	12	7	12	17	17	8	8	11	12	10	13	20	23	13	14.2	17	18	8	11	12	15	X	X	12	12	25	27
Nwp042	14	15	27	32	8	9	11	11	16	16	7	9	11	12	10	14	23	23	12.2	13.2	15	16	8	11	18	18	X	X	8	13	21	23
Nwp043	12	15	29	34	8	9	10	13	15	16	8	9	14	15	10	10	19	25	12	14	15	17	8	12	12	17	X	Y	11	12	21	23
Nwp044	15	17	30	30	9	10	12	12	15	16	7	8	9	12	10	10	17	25	13	13	14	14	8	11	16	18	X	Y	12	13	21	23
Nwp045	13	16	29	29	8	10	7	7	14	17	6	7	12	12	11	11	16	19	12	13	16	19	8	8	15	18	X	Y	11	13	23	27
Nwp046	14	15	29	31.2	8	11	10	12	16	17	7	7	11	13	9	12	21	22	13	13	15	20	8	11	15	18	X	Y	13	13	22	24
Nwp047	12	13	30	32	10	11	11	12	15	16	7	8	11	13	11	12	20	22	13.2	14	13	16	8	11	15	17	X	X	12	12	21	27
Nwp048	11	13	29	32.2	8	11	8	11	14	18	7	8	8	11	12	13	16	21	12	13	16	16	10	11	15	16	X	Y	12	13	22	24
Nwp049	14	14	28	32.2	9	10	11	12	15	18	7	7	12	12	9	12	19	21	12	13	13	18	8	8	13	19	X	Y	11	13	22	22
Nwp050	13	14	27	33.2	10	12	11	12	15	16	8	8	11	12	9	11	19	19	13	15	14	16	9	10	15	18	X	Y	8	13	23	24
Nwp051	13	14	28	30	8	8	12	13	16	16	6	7	12	13	11	12	17	21	13	13	17	17	8	10	15	16	X	Y	8	11	24	25
Nwp052	13	13	30	30.2	12	12	8	10	15	17	6	9	7	13	9	10	17	19	14	14	16	17	8	8	15	16	X	Y	11	11	20	27
Nwp053	13	15	31	35	8	9	11	12	16	18	7	7	11	11	11	11	22	25	13	13	15	17	6	8	18	19	X	Y	12	12	19	22
Nwp054	12	14	32.2	32.2	9	12	12	12	15	17	8	9	11	12	10	11	19	22	12.2	14	16	17	9	9	17	18	X	Y	11	13	16.1	23
Nwp055	12	13	28	28	8	10	11	11	15	16	7	7	11	12	11	13	19	19	12.2	14	16	18	11	11	13	18	X	Y	10	12	19	25
Nwp056	14	14	31	35	10	10	12	13	14	16	6	7	12	13	9	9	16	19	13	13	15	18	9	10	13	16	X	Y	11	12	20	22
Nwp057	13	15	28	28	10	11	10	11	15	15	7	7	11	12	11	11	24	24	13	14	15	18	8	8	12	17	X	X	11	12	20	22
Nwp058	15	16	29	29	8	12	7	8	12	15	6	6	12	12	10	12	16	19	10	13	14	19	8	8	18	19	X	Y	12	13	22	29
Nwp059	11	13	30	32	9	10	10	11	17	19	8	9	12	12	11	12	20	22	15	15.2	17	19	6	8	14	18	X	Y	8	13	22	22
Nwp060	14	15	28	28	10	10	10	12	15	18	7	9.3	11	13	10	12	19	24	13	14	15	17	10	11	13	17	X	Y	11	13	21	22
Nwp061	11	14	31	35	8	12	10	12	15	17	7	7	11	12	10	11	17	19	15	15	17	18	6	9	12	13	X	X	10	12	22	22
Nwp062	14	15	28	31.2	10	11	7	7	14	16	7	9	11	12	13	13	21	24	14	14	16	17	9	9	13	19	X	X	12	12	23	24
Nwp063	11	14	28	30	8	9	6	11	14	16	8	9.3	12	12	11	11	17	17	14	14	17	19	11	11	14	17	X	Y	10	13	21	24
Nwp064	13	16	28	29	8	8	7	10	15	15	6	7	11	12	9	11	20	25	11	14	15	15	10	11	12	16	X	X	11	12	23	27
Nwp065	11	16	28	37	10	11	11	12	15	15	7	9.3	11	12	9	10	16	23	12.2	14	15	18	9	9	13	18	X	Y	11	13	28	28
Nwp066	12	16	31	32.2	11	12	9	10	16	17	6	8	11	11	9	11	20	21	13.2	16	16	20	9	11	16	17	X	X	8	12	19	23
Nwp067	11	14	30	33.2	11	11	10	12	15	16	9	9	13	13	10	11	21	23	15	15.2	16	16	7	11	15	20	X	Y	7	12	21	24
Nwp068	12	15	29	31.2	10	12	10	12	15	15	7	9.3	11	12	11	13	22	25	12	12	11	15	8	11	15	18	X	Y	11	12	17.2	21
Nwp069	13	15	29	30	10	10	8	12	14	17	6	7	11	12	12	13	19	21	12	12	17	17	7	9	15	16	X	Y	11	11	22	22
Nwp070	11	16	29	29	8	11	10	12	15	16	7	8	12	14	11	13	19	26	11	12	17	17	6	8	15	17	X	Y	11	12	19	26
Nwp071	11	14	28	28	9	10	11	11	15	17	7	7	12	12	9	12	19	21	12	13	16	16	6	11	12	20	X	X	10	13	24	27
Nwp072	14	15	31.2	35	11	12	11	12	16	17	8	9.3	12	13	10	11	18	19	13	14	14	15	8	12	15	15	X	Y	10	10	22	24
Nwp073	11	14	27	29	9	10	10	11	16	16	7	8	11	12	12	13	17	19	11	14	17	20	8	9	12	16	X	Y	8	11	22	24
Nwp074	13	16	28	31	10	11	10	11	15	17	6.3	9	10	14	9	11	17	24	13	15.2	16	16	8	11	17	18	X	Y	8	10	25	26
Nwp075	14	15	29	31	10	11	10	11	15	15.2	8	9	12	14	10	10	21	23	13	14	16	16	8	8	15	16	X	Y	12	13	22	22
Nwp076	13	14	29	29	10	11	11	11	15	16	7	8	13	14	12	12	20	20	12	13	14	16	6	8	13	15	X	Y	12	12	21	22
Nwp077	15	16	29	37	8	8	11	12	15	16	6	7	11	11	11	13	17	18	10	14	15	19	8	8	15	15	X	X	12	12	23	23
Nwp078	14	15	28	28	8	10	11	12	16	17	7	7	11	12	10	12	21	26	13.2	14	16	17	8	11	17	19	X	Y	11	12	23	24
Nwp079	13	13	32.2	32.2	9	12	11	12	16	17	7	8	11	12	11	13	19	23	13	13	15	16	6	9	19	22	X	X	12	12	18.2	26
Nwp080	12	15	29	32.2	9	11	12	12	15	17	7	9	11	12	11	13	19	19	13	14	17	19	10	11	13	15	X	X	12	12	24	25

Supplementary Table 1: Genotype Assignment (Cont'd)

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp081	13	16	28	33.2	10	10	10	12	15	16	6	7	12	12	9	10	21	24	13	14.2	12	17	11	12	13	14	X	X	13	14	20	25
Nwp082	11	14	29	31.2	8	10	11	12	15	17	8	9.3	11	13	11	12	17	17	13	14	16	18	9	11	15	17	X	Y	10	12	21	22
Nwp083	13	13	29	34	10	13	10	12	16	16	7	8	11	12	10	12	20	21	13	14	16	17	8	10	12	18	X	X	11	12	22	22
Nwp084	14	15	28	32.2	9	10	10	10	15	15	7	8	12	13	13	14	17	19	13.2	14	15	15	8	10	13	17	X	Y	11	13	19	22
Nwp085	14	15	28	30	10	12	11	12	15	15	6	7	9	12	9	9	21	24	12	13	17	17	11	11	14	19	X	X	10	10	23	26
Nwp086	15	15	30	33.2	10	12	8	10	16	16	7	9	10	11	11	12	17	26	13	15	16	17	9	10	15	15	X	Y	13	15	20	46.2
Nwp087	13	14	28	29	9	12	12	12	15	16	7	8	11	12	11	14	17	17	13	16.2	16	17	6	7	17	18	X	Y	12	13	22	23
Nwp088	11	14	28	29	8	8	10	11	15	18	7	8	11	12	12	12	17	22	13	13	17	17	11	11	16	17	X	X	8	13	19	20
Nwp089	12	15	28	30	8	9	7	10	16	17	7	9	12	13	12	13	21	25	14	15	15	17	11	11	15	21	X	X	12	13	25	27
Nwp090	13	15	27	32.2	9	10	10	10	15	16	6	9.3	12	12	12	13	21	24	12	13	15	17	7	8	16	17	X	X	8	12	23	29
Nwp091	13	13	29	32.2	8	8	12	12	14	15	7	7	12	12	9	13	17	21	12	13	15	18	11	11	16	18	X	X	12	13	24	24
Nwp092	12	13	31	31	8	8	12	12	14	18	6	9.3	11	12	8	10	17	24	14.2	15	16	16	9	11	12	19	X	X	11	11	18.2	25
Nwp093	11	14	30	30	11	11	11	12	16	16	6	8	12	14	8	13	21	21	12	13	16	17	8	8	15	16	X	Y	8	11	23	23
Nwp094	14	18	31	35	11	12	12	12	14	15	7	8	11	12	11	11	19	23	14	14	15	15	10	12	16	17	X	Y	12	13	19	22
Nwp095	14	14	29	29	8	13	11	12	15	17	7	9.3	12	14	11	11	17	24	12	13	16	19	8	8	13	19	X	X	12	12	24	24
Nwp096	14	15	28	31	8	10	12	12	16	18	9	9	8	13	10	12	20	22	10	12	14	18	6	7	15	18	X	X	11	12	22	23
Nwp097	11	13	31	32.2	9	9	10	11	15	16	6	7	8	8	11	13	20	20	13	13	16	17	8	8	13	17	X	X	11	13	20	25
Nwp098	12	15	28	29	9	12	10	12	16	18	7	9.3	8	11	11	14	17	17	14	14	16	16	8	8	16	18	X	Y	11	13	19	25
Nwp099	11	13	27	30	8	8	11	12	15	15	6	7	10	11	11	13	22	23	12	12	14	17	11	12	13	17	X	Y	8	12	19	23
Nwp100	14	14	29	32.2	9	11	11	12	15	17	7	7	11	13	11	13	17	25	12	13	12	17	6	9	18	19	X	Y	7	12	21	24
Nwp101	12	13	28	29	12	12	10	11	18	18	8	9.3	11	11	12	13	18	25	13	13	16	18	8	8	15	17	X	Y	11	12	20	22
Nwp102	11	15	30	31	8	10	11	14	15	16	7	8	12	12	11	13	20	25	15	17	16	17	8	10	14	15	X	Y	11	13	22	26
Nwp103	10	14	29	31	9	12	12	13	15	17	6	6	11	12	11	13	19	19	13	14	17	18	8	11	14	18	X	X	11	12	20	25
Nwp104	12	14	28	30	10	11	11	11	15	17	8	9.3	8	9	10	11	18	26	14	14	17	17	8	10	13	22	X	Y	11	11	22	25
Nwp105	11	14	29	30	10	12	9	12	16	16	9.3	9.3	10	12	12	13	19	22	14	15.2	18	21	9	9	13	13	X	X	11	12	19	23
Nwp106	13	15	29	31.2	8	10	7	10	16	17	8	9.3	10	12	8	12	20	20	14	15	17	18	9	11	15	18	X	Y	11	11	22	22.2
Nwp107	12	14	29	30	8	10	10	11	16	16	7	8	12	13	9	9	19	21	13	13.2	17	18	9	10	15	18	X	X	11	13	20	23
Nwp108	14	14	28	32.2	8	10	11	13	16	17	7	8	12	12	12	13	18	23	14	15	15	18	6	11	14	15	X	X	11	13	21	28
Nwp110	14	15	35	35	12	12	10	15	14	15	7	8	12	13	9	10	17	26	11	15	15	17	6	9	12	17	X	X	11	11	18.2	27
Nwp111	12	13	28	30	8	10	10	12	16	17	9	9.3	11	14	12	13	25	25	13	13	13	17	8	11	16	18	X	Y	8	11	23	23
Nwp112	15	17	29	32	9	12	7	12	16	16	8	8	11	13	9	11	20	22	12	12	15	16	8	8	15	20	X	Y	11	13	23	24
Nwp113	15	16	28	29	8	8	7	10	17	18	7	7	11	12	10	11	22	22	13	14	15	17	8	9	15	17	X	Y	11	12	20	22
Nwp114	14	15	30	31.2	10	11	10	13	12	15	7	9.3	11	13	10	13	18	19	12	14	17	18	9	10	17	17	X	X	10	13	24	27
Nwp115	12	13	28	30	10	11	10	12	15	18	6	8	11	11	8	14	21	24	14	14	16	19	8	8	15	18	X	X	11	12	23	27
Nwp116	15	15	29	31	8	11	10	11	16	17	7	9.3	12	12	9	15	19	24	13.2	14.2	17	18	11	11	17	22	X	X	11	13	20	24
Nwp117	13	14	28	28	8	11	7	11	16	18	6	8	12	12	8	13	16	20	12	14	16	19	8	8	15	15	X	X	11	13	18.2	24
Nwp118	14	15	28	29	9	10	12	12	16	16	7	10	12	12	11	13	19	24	12.2	12.2	17	21	10	10	19	20	X	X	12	13	22	27
Nwp119	15	16	30	35	9	11	10	13	14	16	8	9	11	13	9	12	20	22	12	12	15	18	9	9	16	17	X	Y	12	13	24	25
Nwp120	10	15	30	31	9	10	10	11	16	17	6	9.3	12	13	11	13	17	20	14	14	17	19	8	11	12	19	X	X	11	12	20	22.2

Supplementary Table 1: Genotype Assignments (Cont'd)

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp121	11	14	27	28	10	10	7	10	17	17	6	7	12	13	12	14	20	22	12	13	14	17	9	11	13	13	X	X	13	13	21	22
Nwp122	11	17	29	32	8	10	10	11	14	16	8	8	11	12	9	11	16	18	13	13	16	17	8	9	14	16	X	X	12	13	22	23
Nwp123	14	15	29	30	9	11	10	12	16	17	8	9	10	11	10	12	21	23	13	14.1	15	16	9	10	16	17	X	X	11	12	23	26
Nwp124	12	16	28	31	9	10	7	11	15	18	6	7	11	11	9	9	17	22	13	15	16	19	8	12	17	18	X	X	12	13	24	24
Nwp125	11	13	28	28	9	10	7	11	15	16	8	8	11	14	10	11	17	19	12	13	16	17	6	11	12	15	X	Y	11	13	21	24
Nwp126	12	14	28	29	9	12	12	12	14	16	7	9.3	11	12	9	12	21	23	13	14	18	19	11	11	16	18	X	X	12	12	18.2	27
Nwp127	13	15	28	30	8	12	10	12	16	16	9	9.3	8	11	11	13	17	17	13	15	15	17	8	8	13	18	X	X	11	12	23	25
Nwp128	14	14	29	29	9	11	8	12	14	16	6	8	12	12	9	9	16	19	12	13	14	16	9	10	13	16	X	X	13	13	18.2	21
Nwp129	13	15	28	29	10	10	12	12	15	16	7	7	11	12	9	11	16	22	13	14	15	15	11	12	17	19	X	Y	11	11	23	26
Nwp130	8	15	28	29	10	10	11	12	16	16	6	6	11	12	10	13	22	23	10	13	17	18	8	8	18	21	X	Y	11	14	26	27
Nwp131	12	14	28	28	10	13	11	12	15	16	7	7	12	12	11	11	21	24	14	16.2	18	18	8	8	12	17	X	Y	10	13	22	25
Nwp132	14	15	29	34	10	11	10	10	17	17	7	9	11	13	9	11	17	22	14	15	15	16	8	11	15	19	X	X	11	13	23	25
Nwp133	12	15	29	29	8	9	10	11	15	16	8	9.3	12	12	10	11	17	26	13	14	15	16	8	9	16	18	X	Y	11	12	23	24
Nwp134	10	14	30	31	8	10	8	13	16	16	7	9	12	12	11	11	19	22	11	13	16	16	10	11	16	22	X	Y	11	13	24	28
Nwp135	11	15	32.2	32.2	8	10	8	8	16	17	6	7	12	13	9	13	20	21	12.2	13	14	16	9	10	16	16	X	X	11	13	19	21
Nwp136	12	13	28	30	8	10	12	13	16	16	7	7	11	12	11	12	17	18	12	14	16	18	9	12	17	18	X	X	11	13	23	24
Nwp137	13	14	27	29	11	12	7	7	15	15	9.3	9.3	11	12	12	12	16	25	14	14	14	16	6	8	13	18	X	X	11	12	22	27
Nwp138	13	14	30	30	10	10	11	12	15	16	7	7	11	13	9	11	19	24	13	14.2	15	16	10	11	11	16	X	Y	8	12	23	25
Nwp139	13	15	30	33.2	10	11	7	12	15	16	6	9.3	13	13	10	11	20	21	13	16.2	18	19	8	9	16	18	X	Y	8	12	23	24
Nwp140	14	14	27	27	9	12	10	10	16	17	8	10	11	11	11	13	16	24	12	12.2	16	16	6	8	18	19	X	X	12	13	25	44.2
Nwp141	12	13	28	28	11	12	7	7	15	15	7	7	11	11	9	11	18	24	13	15	15	17	8	10	17	18	X	X	13	13	19.2	22
Nwp142	15	15	28	31	7	11	10	12	16	17	6	9.3	12	12	10	11	19	21	13	14	19	20	10	11	13	14	X	X	11	12	22	24
Nwp143	12	14	30	30	10	11	10	11	14	16	8	9	12	13	9	9	19	22	12	16	16	18	8	10	14	18	X	X	12	12	19	22
Nwp144	12	12	28	32.2	8	11	10	10	15	16	8	8	11	12	11	13	22	25	12	14	17	17	8	10	12	17	X	Y	8	12	18.2	19
Nwp145	15	16	27.1	28	9	11	10	12	16	16	7	7	11	12	10	12	21	24	12	14.2	16	16	6	9	13	15	X	X	11	11	23	25
Nwp146	12	14	28	28	10	10	10	12	16	16	7	8	8	12	11	12	16	21	14.2	15	15	18	8	10	15	20	X	Y	10	11	24	27
Nwp147	11	13	31	32	8	8	11	11	15	17	7	8	11	11	13	14	24	25	13	13.2	14	16	9	9	17	18	X	X	11	12	20	23
Nwp148	14	15	29	32.2	9	10	10	12	14	15	6	8	12	13	9	12	16	25	12	14	14	15	9	9	13	15	X	Y	12	13	18.2	21
Nwp149	12	14	30	32.2	10	10	10	11	14	15	6	7	11	12	9	12	19	25	11	15	15	18	9	10	16	17	X	X	12	12	21	22
Nwp150	12	13	28	29	9	9	10	13	15	18	6	9.3	11	13	11	12	23	25	14	14	14	17	8	10	12	12	X	X	12	14	22	24
Nwp151	14	15	29	30	8	12	13	13	15	16	7	7	11	14	11	12	19	24	13.2	15.2	17	17	6	11	16	18	X	X	8	13	20	23
Nwp152	12	15	28	30.2	9	12	10	11	15	16	7	8	13	13	11	12	19	21	14	15	16	17	8	12	17	19	X	Y	13	14	19	24
Nwp153	14	16	28	29	8	8	11	11	17	17	7	8	11	11	9	10	19	19	12	14	15	15	8	8	15	21	X	Y	11	13	24	26
Nwp154	12	13	29	30	9	12	10	10	14	18	6	7	11	11	11	13	21	25	14	14	14	17	8	8	13	15	X	X	12	13	22	27
Nwp155	14	15	30	31.2	9	11	10	10	16	17	7	9.3	11	12	11	12	16	21	13	14	16	16	7	9	15	16	X	Y	11	11	17	24
Nwp156	15	15	30	30	10	12	10	12	14	14	6	7	11	13	12	12	19	21	11	11	14	15	9	11	13	16	X	Y	11	13	21	22
Nwp157	12	13	30	31	8	9	11	12	16	16	6	7	11	12	10	13	17	18	13	14.2	15	18	9	11	16	17	X	Y	13	13	17.2	20
Nwp158	13	13	27	28	9	10	10	12	16	17	6	7	11	14	11	13	21	25	13	13	16	17	8	8	14	15	X	Y	8	11	22	26
Nwp159	14	15	28	32.2	8	11	7	8	16	17	6	7	12	12	12	13	17	23	13	15	14	17	8	11	15	19	X	X	11	13	22	26
Nwp160	14	15	28	28	8	8	12	12	15	15	6	7	11	12	9	11	17	21	11	12	17	18	9	12	12	17	X	Y	12	13	25	26

Supplementary Table 1: Genotype Assignment (Cont'd)

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp161	13	14	30	32.2	10	12	11	12	16	16	7	8	11	13	11	11	19	24	13	13	16	17	9	11	13	18	X	X	12	13	19	21
Nwp162	13	15	29	30	8	10	11	13	17	18	9	9.3	11	11	13	14	17	23	13	14.2	16	19	8	8	14	16	X	X	13	13	22	25
Nwp165	14	15	29	30	10	12	9	12	16	17	6	9	11	15	9	11	16	22	11	17.2	17	19	6	6	18	19	X	X	12	13	18.2	25
Nwp166	13	15	29	30	10	12	8	12	15	17	7	8	12	12	10	11	21	23	14	15.2	14	15	11	11	12	22	X	X	9	12	25	25
Nwp167	14	14	29	30	10	11	11	12	16	16	6	8	11	13	12	14	20	21	14	16.2	14	16	7	9	17	17	X	X	11	13	22	22
Nwp168	14	15	29	30.2	9	12	11	11	15	17	7	9	12	13	11	12	19	19	13	14.2	16	18	9	11	18	18	X	X	12	12	20	25
Nwp170	16	16	29	31	10	10	12	14	15	17	7	8	10	12	9	12	17	20	11	15	16	18	8	11	15	17	X	X	13	13	21	22
Nwp171	14	15	29	30.2	8	11	10	10	15	16	7	9.3	11	12	10	12	19	19	12	14.2	15	19	8	8	13	20	X	X	12	13	21	22
Nwp172	14	14	28	31.2	8	11	10	11	17	18	6	9.3	10	11	8	11	19	21	12	13	16	18	8	10	14	15	X	Y	8	11	23	23
Nwp173	13	14	28	33.2	7	10	10	11	15	15	7	8	12	13	9	11	17	23	13	14	16	17	8	9	15	20	X	Y	12	12	20	23
Nwp174	15	18	31	33.2	8	9	8	11	14	15	7	7	11	12	9	12	21	22	12	12.2	15	16	6	9	12	20	X	Y	11	11	18	19
Nwp175	13	16	27	29	10	10	8	11	16	16	9	9.3	8	9	12	13	16	19	12.2	15.2	17	18	9	9	17	18	X	Y	12	13	22	25
Nwp178	12	14	29	30	10	14	8	12	15	15	7	8	12	13	11	12	19	23	13	14	16	18	8	11	15	16	X	Y	11	11	20	25
Nwp180	12	14	28	30	8	9	12	13	14	15	8	9	11	13	8	9	17	18	12	15.2	15	16	10	11	16	17	X	X	10	12	19	22
Nwp181	12	15	30	32	8	10	11	12	15	17	7	9	11	12	11	11	17	26	13	13	16	16	10	11	16	20	X	Y	11	11	20	21
Nwp182	13	14	30	31	8	10	7	12	16	17	7	9	11	12	8	8	19	19	14	14.2	17	17	10	10	19	22	X	X	12	12	20	27
Nwp183	11	11	28	29	9	9	12	12	16	18	7	7	12	13	12	12	21	25	10	13	17	19	9	9	15	17	X	X	8	13	23	29
Nwp184	14	16	28	34	9	11	10	12	15	17	7	8	11	12	12	13	17	19	14	16.2	15	16	8	11	17	19	X	X	10	12	21	22
Nwp185	11	14	28	30.2	9	10	11	11	14	18	7	8	11	12	9	10	22	23	11.2	15	16	19	10	10	12	15	X	X	13	13	21	22
Nwp186	12	15	28	29	10	10	11	12	15	16	8	9	11	13	10	13	19	23	13	13	15	18	11	11	15	16	X	Y	13	13	18.2	22
Nwp187	12	14	28	29	8	9	12	12	16	17	7	9	12	13	9	12	24	25	13	14	16	17	8	12	14	16	X	X	13	13	22	24
Nwp188	14	15	32.2	32.2	9	10	11	13	16	17	9	9.3	11	11	10	12	16	19	13	14.2	15	19	8	11	16	19	X	Y	12	13	21	24
Nwp189	12	13	30	33.2	10	11	7	12	14	16	6	9	11	12	12	12	16	19	12	13	16	18	6	9	16	17	X	X	12	12	22	26
Nwp190	15	15	28	29	10	12	11	12	17	17	7	9.3	10	11	11	11	21	24	11	13.2	15	20	6	11	16	17	X	Y	11	12	23	26
Nwp191	13	14	29	30	8	10	11	11	15	15	7	8	11	11	11	12	19	24	12	14.2	16	18	7	10	18	19	X	X	10	11	22	24
Nwp193	14	14	30	30	10	10	12	12	15	15	7	9.3	11	13	11	11	17	17	12.2	13	15	17	8	11	15	18	X	Y	11	13	22	23
Nwp194	13	14	28	29.2	10	10	7	8	15	15	7	8	10	12	9	12	19	20	13	14	17	19	8	8	13	17	X	X	11	13	24	25
Nwp195	12	14	28	30	10	10	12	12	15	17	9.3	9.3	12	12	9	12	19	19	12	13	14	17	9	10	13	16	X	Y	8	12	24	26
Nwp196	15	16	31.2	32.2	8	11	11	12	15	16	6	9	10	11	9	13	17	23	13	14	16	18	6	8	13	15	X	X	11	12	21	26
Nwp197	14	15	28	28	10	10	10	13	15	15	6	8	12	13	11	11	20	24	15	15	16	17	8	9	15	15	X	Y	12	13	20	24
Nwp198	10	15	32.2	32.2	9	10	8	10	15	16	9	9.3	9	12	11	11	24	26	13	13	16	17	9	9	15	21	X	X	8	12	23	24
Nwp199	13	15	28	33.2	8	9	10	11	17	17	8	9	12	13	9	11	21	23	14	15.2	15	17	6	11	14	21	X	Y	11	13	23	24
Nwp200	14	14	28	28	8	9	10	12	16	17	7	8	9	14	13	13	17	22	11.2	16	17	17	8	8	14	17	X	Y	11	12	18	24
Nwp201	13	14	28	28	8	8	12	12	14	16	7	8	12	14	9	12	17	21	13	14.2	14	18	11	11	18	19	X	Y	11	11	22	25
Nwp202	14	14	27	28	10	10	11	12	15	15	8	9.3	12	14	12	13	17	21	13	16.2	15	19	8	11	13	17	X	Y	11	12	20	24
Nwp203	14	15	30	32.2	10	10	13	13	14	15	6	9.3	11	14	11	13	17	19	11	13	16	17	8	11	18	19	X	Y	10	10	23	24
Nwp204	13	13	28	30	10	10	11	11	16	17	7	7	12	12	9	13	19	22	14	15.2	14	19	8	11	15	19	X	X	12	13	21	23
Nwp206	13	15	29	31	10	12	8	11	15	16	7	7	12	12	11	12	19	21	11	14.2	17	19	6	11	15	20	X	Y	12	13	21	23
Nwp208	14	15	27	30	10	10	11	12	16	17	7	8	12	12	11	13	25	25	12	12.2	16	17	9	11	16	20	X	Y	11	13	22	24

Supplementary Table 1: Genotype Assignment (Cont'd)

Sample #	D8S1179		D21S11		D7S820		CSF1PO		D3S1358		TH01		D13S317		D16S539		D2S1338		D19S433		vWA		TPOX		D18S51		AMEL		D5S818		FGA	
	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Nwp209	13	15	29	29	12	12	7	8	14	16	7	9	9	12	10	11	22	23	13	13.2	16	18	11	11	15	16	X	Y	12	13	18	27
Nwp210	11	15	30	31	10	10	10	10	17	18	7	7	11	11	9	11	19	19	13	13	15	15	6	8	16	18	X	Y	11	11	21	25
Nwp211	14	15	29	30.3	8	10	10	11	13	17	8	8	11	14	10	13	17	21	11	15	17	18	11	11	16	18	X	Y	10	12	22	23
Nwp212	13	14	30	31	11	12	11	13	15	16	9	9	11	13	9	11	16	23	13	15.2	15	17	6	6	16	17	X	Y	11	13	21	23
Nwp214	12	15	29	30	10	11	11	11	15	16	9	9.3	11	12	11	12	17	18	13	14	15	18	8	12	15	18	X	Y	11	12	20	24
Nwp215	11	14	28	29	10	11	9	11	15	17	7	8	11	11	9	10	22	24	12	13	15	15	8	11	17	18	X	Y	12	13	23	24
Nwp216	11	13	31	32.2	12	12	10	11	14	16	8	8	11	12	13	13	17	19	11	14	15	15	6	11	18	19	X	Y	12	12	19	25
Nwp218	14	14	30	30.2	10	12	10	12	14	15	6	7	13	14	11	13	22	22	14	14.2	15	17	9	11	15	17	X	X	12	12	19	22
Nwp219	11	12	27	28	9	10	10	11	14	18	6	8	12	12	9	11	20	21	12	12.2	15	16	8	11	11	16	X	Y	12	13	21	25
Nwp220	11	15	31.2	35	8	9	10	11	15	17	7	8	12	13	11	12	20	23	13	14	15	18	8	8	15	16	X	Y	9	13	22	23.3
Nwp221	12	13	28	29	9	11	8	12	16	16	7	7	10	11	9	11	23	23	13	15.2	16	17	9	11	16	17	X	Y	8	14	21	24
Nwp223	13	14	28	30	8	9	8	12	15	17	7	9	11	12	11	13	21	24	13	13	16	17	8	11	15	17	X	Y	8	11	22	24
Nwp224	14	16	28	32.2	10	10	8	12	14	17	7	9	12	13	9	12	21	25	13	13.2	17	19	6	9	15	17	X	Y	12	13	20	22
Nwp225	14	15	28	28	10	11	10	12	15	17	7	7	11	11	12	12	22	23	14.2	15	15	19	8	8	14	16	X	Y	11	12	19	22
Nwp226	14	14	29	31	8	10	10	10	16	17	7	8	11	12	9	12	19	24	12	13	15	17	9	9	17	18	X	Y	10	13	25	30.2
Nwp611	11	14	29	31.2	8	11	10	10	15	15	6	6	11	12	11	12	18	19	13	14	16	17	8	10	18	19	X	X	11	11	18.2	22
Nwp612	13	15	29	30	10	10	11	11	18	18	9.3	9.3	12	12	12	12	23	25	14	16.2	16	18	8	8	16	17	X	X	12	13	22	25
Nwp613	12	15	29	32.2	11	12	10	10	18	18	7	9.3	8	11	11	13	18	20	13	14	17	17	8	11	12	18	X	X	13	13	20	21
Nwp614	13	14	29	30	8	9	11	12	16	18	7	9	8	8	10	13	19	23	13	14	16	17	8	8	13	15	X	X	12	13	22	23
Nwp615	15	16	31.2	31.2	10	11	11	12	17	18	7	9.3	11	11	9	12	17	20	13	14	18	18	8	8	15	17	X	Y	12	12	23	24
Nwp616	14	14	28	29	9	11	10	10	15	17	7	8	11	12	11	11	16	20	14.2	16.2	16	16	8	11	15	15	X	X	10	13	23	24
Nwp617	14	15	29	31	11	11	8	12	15	17	7	9.3	12	12	12	12	20	24	14.2	15	14	18	9	12	14	17	X	X	11	12	22	25
Nwp618	11	14	30	31.2	10	10	11	11	15	15	7	9.3	12	13	10	11	20	24	12	12.2	16	16	11	11	16	16	X	X	8	12	20	22

Supplementary Table 1: Genotype Assignment (Cont'd)

allele	6	6.3	7	8	9	9.3	10	11	11.2	12	12.2	13	13.2	14
D8S1179				0.0023			0.0136	0.0860		0.1154		0.1900		0.3032
D21S11														
D7S820			0.0068	0.2104	0.1538		0.3371	0.1584		0.1176		0.0136		0.0023
CSF1PO	0.0023		0.0747	0.0656	0.0204		0.2376	0.2557		0.2896		0.0475		0.0045
D3S1358										0.0068		0.0023		0.0882
TH01	0.1425	0.0023	0.3869	0.2240	0.1199	0.1199	0.0045							
D13S317			0.0023	0.0317	0.0181		0.0339	0.3122		0.3869		0.1538		0.0566
D16S539	0.0023			0.0204	0.1561		0.1176	0.2919		0.2240		0.1561		0.0294
D2S1338														
D19S433					0.0023		0.0113	0.0566	0.0068	0.1244	0.0385	0.3122	0.0362	0.2081
vWA								0.0023		0.0045		0.0113		0.0633
TPOX	0.0747		0.0204	0.3122	0.2059		0.1131	0.2421		0.0317				
D18S51								0.0045		0.0566		0.0814	0.0090	0.0475
D5S818			0.0045	0.0701	0.0068		0.0520	0.2557		0.3235		0.2692		0.0136
FGA														

allele	14.1	14.2	15	15.2	16	16.1	16.2	17	17.2	18	18.2	19	19.2	20
D8S1179			0.2195		0.0543			0.0090		0.0068				
D21S11														
D7S820														
CSF1PO			0.0023											
D3S1358			0.3077	0.0045	0.3100			0.1968		0.0814		0.0023		
TH01														
D13S317			0.0045											
D16S539			0.0023											
D2S1338					0.0588			0.1425		0.0452		0.1833		0.0837
D19S433	0.0023	0.0566	0.0747	0.0385	0.0068		0.0204	0.0023	0.0023					
vWA			0.2014		0.2534			0.2376		0.1403		0.0701		0.0113
TPOX														
D18S51		0.0068	0.1742	0.0068	0.1584			0.1652		0.1471		0.0747		0.0362
D5S818			0.0045											
FGA						0.0023		0.0023	0.0045	0.0068	0.0271	0.0543	0.0023	0.0701

Supplementary Table 2: New Providence Allelic Frequencies (n=221)

allele	21	22	22.2	23	23.3	24	25	26	27	27.1	28	29	29.2	30
D8S1179														
D21S11									0.0385	0.0023	0.2353	0.2127	0.0023	0.1991
D7S820														
CSF1PO														
D3S1358														
TH01														
D13S317														
D16S539														
D2S1338	0.1380	0.0995		0.0882		0.0792	0.0611	0.0181	0.0023					
D19S433														
vWA	0.0045													
TPOX														
D18S51	0.0136	0.0181												
D5S818														
FGA	0.0973	0.1968	0.0045	0.1652	0.0023	0.1448	0.0973	0.0452	0.0452		0.0090	0.0090		

allele	30.2	30.3	31	31.2	32	32.2	33.2	34	34.2	35	37	44.2	46.2
D8S1179													
D21S11	0.0158	0.0023	0.0792	0.0430	0.0158	0.0747	0.0249	0.0158		0.0317	0.0068		
D7S820													
CSF1PO													
D3S1358													
TH01													
D13S317													
D16S539													
D2S1338													
D19S433													
vWA													
TPOX													
D18S51													
D5S818													
FGA	0.0023			0.0023					0.0045			0.0023	0.0023

Supplementary Table 2: New Providence Allelic Frequencies (n=221) (Cont'd)

	H_o	H_e	HWE	GDI	MP	PD	PIC	PE	TPI
D8S1179	0.8326	0.8017	0.2387	0.8017	0.0731	0.9269	0.7721	0.6608	2.9865
D21S11	0.7783	0.8441	0.1121	0.8441	0.0442	0.9558	0.8240	0.5594	2.2551
D7S820	0.7376	0.8287	0.2612	0.7810	0.0794	0.9206	0.7468	0.4887	1.9052
CSF1PO	0.7195	0.8057	0.0149	0.7835	0.0850	0.9150	0.7487	0.4590	1.7823
D3S1358	0.7557	0.7577	0.2439	0.7577	0.1033	0.8967	0.7163	0.5195	2.0463
TH01	0.7557	0.7619	0.8187	0.7528	0.1030	0.8970	0.7148	0.5195	2.0463
D13S317	0.7104	0.7767	0.0832	0.7251	0.1239	0.8761	0.6795	0.4445	1.7266
D16S539	0.7919	0.8076	0.5014	0.8026	0.0719	0.9281	0.7722	0.5840	2.4022
D2S1338	0.8552	0.8925	0.0225	0.8885	0.0277	0.9723	0.8758	0.7051	3.4531
D19S433	0.7873	0.8292	0.0421	0.8287	0.0530	0.9470	0.8085	0.5757	2.3511
vWA	0.7964	0.8117	0.8150	0.8117	0.0630	0.9370	0.7831	0.5923	2.4556
TPOX	0.6833	0.7835	0.0459	0.7835	0.0776	0.9224	0.7490	0.4028	1.5786
D18S51	0.8959	0.8815	0.5869	0.8780	0.0321	0.9679	0.8635	0.7871	4.8043
D5S818	0.7330	0.7513	0.5011	0.7513	0.1038	0.8962	0.7074	0.4812	1.8729
FGA	0.9140	0.8856	0.8808	0.8831	0.0289	0.9711	0.8698	0.8242	5.8158

Supplementary Table 3: Forensic parameters for the New Providence population across the 15 Identifiler loci

	Afro-American			African w/o Madagascar			African with Madagascar			Asian		
Locus	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t
D8S1179	0.00348	0.79481	0.79758	0.00911	0.77616	0.78329	0.01144	0.77841	0.78742	0.00762	0.84274	0.84921
D21S11	0.00132	0.84440	0.84551	0.00749	0.85154	0.85797	0.00893	0.85366	0.86134	0.00872	0.81684	0.82403
D7S820	0.00229	0.78374	0.78554	0.00882	0.75652	0.76325	0.01014	0.75987	0.76765	0.00944	0.75890	0.76614
CSF1PO	0.00066	0.77993	0.78044	0.01508	0.77298	0.78481	0.01396	0.77162	0.78255	0.00874	0.72284	0.72921
D3S1358	0.00353	0.75652	0.75920	0.00910	0.73288	0.73960	0.00975	0.72939	0.73657	0.01190	0.71940	0.72807
TH01	0.00135	0.74817	0.74918	0.00889	0.73109	0.73765	0.00805	0.73330	0.73925	0.01458	0.69915	0.70949
D13S317	0.00096	0.71751	0.71820	0.00554	0.72035	0.72436	0.01121	0.72826	0.73652	0.00607	0.80012	0.80501
D16S539	0.00231	0.79199	0.79382	0.00810	0.78449	0.79090	0.00935	0.78460	0.79200	0.00959	0.77473	0.78223
D2S1338	0.00231	0.88917	0.89123	0.00903	0.88566	0.89373	0.00907	0.88447	0.89256	0.00707	0.86775	0.87392
D19S433	0.00217	0.83525	0.83706	0.00892	0.82476	0.83219	0.01084	0.82766	0.83673	0.01381	0.79937	0.81056
vWA	0.00147	0.81372	0.81492	0.00701	0.81647	0.82223	0.00808	0.81412	0.82075	0.01370	0.79304	0.80405
TPOX	0.00187	0.77164	0.77308	0.01072	0.77671	0.78512	0.01833	0.76488	0.77916	0.00569	0.62611	0.62969
D18S51	0.00179	0.87818	0.87975	0.00723	0.86463	0.87093	0.00776	0.86543	0.87220	0.00741	0.85317	0.85954
D5S818	0.00216	0.75284	0.75447	0.00380	0.74904	0.75190	0.00910	0.75812	0.76508	0.00760	0.78443	0.79044
FGA	0.00330	0.87295	0.87584	0.00619	0.87787	0.88334	0.00761	0.87767	0.88440	0.00466	0.85686	0.86087
All Loci	0.00208	0.80205	0.80372	0.00833	0.79474	0.80142	0.01018	0.79543	0.80361	0.00905	0.78103	0.78816

Supplementary Table 4: Total, inter- and intra-population genetic variance

	Latin American			European			All populations		
Locus	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t
D8S1179	0.00533	0.79687	0.80114	0.00479	0.80173	0.80559	0.02000	0.80171	0.81808
D21S11	0.00407	0.83425	0.83765	0.00229	0.84684	0.84878	0.01964	0.83904	0.85585
D7S820	0.00753	0.79103	0.79703	0.00386	0.80061	0.80371	0.02224	0.77715	0.79482
CSF1PO	0.00330	0.71758	0.71996	0.00606	0.72614	0.73057	0.01487	0.74070	0.75188
D3S1358	0.01200	0.75931	0.76853	0.00304	0.79534	0.79776	0.01611	0.74906	0.76132
TH01	0.01458	0.77061	0.78201	0.00865	0.77137	0.77810	0.05989	0.74425	0.79166
D13S317	0.01072	0.80817	0.81693	0.00297	0.77649	0.77881	0.03620	0.77090	0.79986
D16S539	0.00764	0.77955	0.78555	0.00175	0.75457	0.75590	0.01883	0.77702	0.79193
D2S1338	0.00894	0.86449	0.87229	0.00381	0.87090	0.87423	0.01925	0.87400	0.89115
D19S433	0.00778	0.82664	0.83312	0.00299	0.76087	0.76316	0.02152	0.81134	0.82919
vWA	0.00751	0.79042	0.79640	0.00419	0.80765	0.81104	0.02298	0.80244	0.82132
TPOX	0.00926	0.67460	0.68091	0.00561	0.61168	0.61513	0.03559	0.68819	0.71358
D18S51	0.00356	0.87685	0.87998	0.00474	0.87157	0.87572	0.01745	0.86831	0.88373
D5S818	0.01213	0.71663	0.72543	0.00421	0.71256	0.71557	0.02878	0.74418	0.76622
FGA	0.00614	0.87368	0.87908	0.00375	0.85336	0.85657	0.01094	0.86791	0.87752
All Loci	0.00796	0.79204	0.79840	0.00414	0.78411	0.78737	0.02403	0.79041	0.80987

Supplementary Table 4: Total, inter- and intra-population genetic variance (Cont'd)

	US1	US2	ANG	SAF	EGU	HUT	KEN	MAD	MOZ	NWP	TUT	CCS	JAP	KOR	MAL	PHI
US1		231.37	274.24	401.03	231.16	290.16	202.69	351.59	372.76	211.53	487.75	1144.96	1917.27	1707.98	1149.36	953.06
US2	<i>0.0524</i>		294.30	404.33	244.94	342.16	217.64	390.81	338.15	260.99	524.11	1354.70	2606.87	2136.76	1480.48	1149.23
ANG	0.0000	0.0000		315.24	224.30	266.23	202.20	380.37	343.92	295.92	391.04	1152.36	1814.77	1641.26	1227.65	987.45
SAF	0.0000	0.0000	0.0000		335.73	358.40	245.45	395.38	250.34	419.22	447.51	1244.97	1880.16	1711.28	1309.26	1095.10
EGU	0.0302	0.0103	0.0169	0.0000		299.34	194.76	372.47	320.27	239.05	413.61	1233.01	1999.51	1835.54	1268.44	1041.81
HUT	0.0000	0.0000	0.0000	0.0000	0.0000		210.35	384.45	358.15	344.63	363.93	1131.69	1652.72	1521.73	1140.98	1007.69
KEN	<i>0.1020</i>	0.0247	<i>0.0648</i>	0.0001	<i>0.1681</i>	<i>0.0507</i>		312.61	225.57	213.95	294.42	857.00	1168.80	1221.49	888.55	782.11
MAD	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		379.17	431.85	473.88	697.44	907.37	947.66	638.76	530.65
MOZ	0.0000	0.0000	0.0000	0.0003	0.0000	0.0000	0.0033	0.0000		410.61	532.59	1345.85	2081.23	1937.59	1467.47	1167.28
NWP	<i>0.3446</i>	0.0136	0.0000	0.0000	0.0423	0.0000	<i>0.0757</i>	0.0000	0.0000		489.02	1441.89	2566.75	2199.37	1510.60	1223.42
TUT	0.0440	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		1423.28	2103.06	1934.98	1492.11	1174.46
CCS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		418.85	420.65	394.87	339.75
JAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		501.19	795.81	511.80
KOR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		759.62	523.08
MAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		286.89
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations.

Pair-wise population comparisons yielding statistically insignificant differences both before (in italics) and after (in bold) applying the Bonferroni correction.

Supplementary Table 5: G-test

	CSH	CAR	MEX	CSR	HIS	MAR	MET	PRA	BRA	SPA	BLR	CAU	FLE	POL
US1	1581.20	720.66	1018.05	1093.93	681.27	717.26	1314.02	618.46	491.73	681.61	949.85	1044.45	1018.15	1360.81
US2	1991.02	924.57	1335.51	1557.23	863.07	943.29	1650.64	830.74	664.20	873.97	1193.36	1413.50	1345.87	1652.15
ANG	1532.26	890.91	1168.84	1277.39	852.96	902.47	1414.07	779.70	646.26	879.73	1113.61	1268.78	1225.88	1283.22
SAF	1567.01	963.69	1268.69	1297.72	944.55	1027.20	1431.59	891.04	792.60	955.18	1271.24	1361.44	1326.07	1643.72
EGU	1666.15	853.74	1166.74	1308.00	842.06	892.42	1452.48	754.50	643.90	831.19	1117.48	1275.58	1177.84	1533.86
HUT	1434.93	803.44	1042.83	1128.60	805.63	805.24	1316.93	691.05	639.72	803.92	982.72	1098.88	1081.38	1278.09
KEN	1083.50	577.64	754.55	761.60	576.37	587.27	931.81	535.91	423.91	619.43	823.00	835.15	827.17	1003.52
MAD	808.88	566.62	694.29	768.77	539.70	592.92	819.59	568.89	539.10	667.22	812.53	878.73	865.21	806.89
MOZ	1793.59	994.20	1349.94	1433.90	957.00	1030.06	1574.63	910.20	825.18	974.17	1309.76	1449.83	1426.98	1794.12
NWP	2001.73	916.26	1304.43	1514.85	834.96	918.82	1625.91	753.80	647.19	871.08	1150.30	1319.93	1277.35	1601.97
TUT	1824.54	1086.84	1376.41	1570.52	1021.23	1059.94	1574.57	992.01	926.14	987.93	1262.52	1511.79	1429.41	1530.42
CCS	293.10	921.84	845.27	1095.84	676.42	815.87	1042.22	880.48	815.87	760.04	1017.96	1127.43	1100.27	1394.66
JAP	584.83	1565.68	1607.56	1694.37	1016.61	1317.08	1656.62	1523.31	2001.13	1069.78	1627.64	2085.00	1912.00	2254.12
KOR	559.27	1384.09	1368.58	1747.26	1004.39	1235.32	1540.45	1299.03	1632.93	1028.00	1376.46	1605.97	1542.45	1654.50
MAL	534.30	924.39	882.91	1320.41	622.01	808.52	1135.47	872.75	1119.01	697.78	976.75	1198.61	1135.91	983.58
PHI	411.77	873.03	849.70	1066.98	670.54	781.88	1108.11	825.71	948.26	708.70	914.08	1038.82	985.92	943.67
CSH		1843.37	1299.69	1843.37	1006.27	1221.03	1441.53	1342.99	1632.24	1036.67	1416.82	1696.83	1568.04	1702.61
CAR	0.0000		434.58	316.44	206.20	194.90	757.13	323.23	312.82	351.60	551.61	503.35	533.76	455.77
MEX	0.0000	0.0000		590.90	261.76	378.39	583.88	574.17	676.46	493.61	726.54	783.96	740.42	1136.39
CSR	0.0000	0.0000	0.0000		260.49	336.72	828.49	558.15	627.05	512.32	762.56	789.12	816.17	1130.95
HIS	0.0000	<i>0.1027</i>	0.0025	0.0000		220.76	442.05	304.36	336.70	378.29	507.03	451.80	484.11	479.11
MAR	0.0000	<i>0.4600</i>	0.0000	0.0000	0.0106		611.75	369.83	321.21	303.97	479.34	423.37	457.74	644.09
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		941.78	1122.83	910.93	1208.44	1256.30	1165.76	1419.81
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		338.29	376.59	593.38	509.84	543.58	481.19
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		365.67	556.06	508.96	548.30	469.52
SPA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		259.40	254.35	240.61	283.53
BLR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		286.89	272.83	206.69
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		229.52	265.03
FLE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0030		340.50
POL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0336	0.0000	0.0000	

Refer to Table 1 for key to abbreviations.

Pair-wise population comparisons yielding statistically insignificant differences both before (in italics) and after (in bold) applying the Bonferroni correction.

Supplementary Table 5: G-test (Cont'd)

III. THE GENETIC STRUCTURE OF POPULATIONS FROM HAITI AND JAMAICA REFLECT DIVERGENT DEMOGRAPHIC HISTORIES

A. Introduction

The West Indian archipelago is bordered on the north by the southeastern United States, on the west by Central America, and on the south by the northern coast of South America. This island chain is classified into two groups: the Greater (northern) and Lesser (southeastern) Antilles, the two encompassing a broad arc 4,000 km long (Watts, 1987). The Antilles was first settled by Amerindians about 2,500-3,000 years before the present (YBP) (Keegan, 1995) who then served as slave laborers for the Spanish Crown. Overwork, malnourishment, and exposure to European diseases, concomitantly, led to the drastic reduction of the native population and consequently, a major deficit in the workforce (Rogoziński, 1999). As a result, enslaved migrants from the West African coast were imported into the New World beginning from the early 1500s until the late 1800s (Knight and Crahan, 1979). At the same time, struggles ensued among the European powerhouses, namely Britain, Spain, France, and the Netherlands, for control of the West Indian islands. Because of the different European influences, the islands have experienced diverging cultural, economical, political, and demographic histories. In this study, I attempt to characterize the genetic input from European, African, and East Asian colonizations into the Greater Antillean islands of Haiti and Jamaica.

Haiti was the largest and most profitable of the French colonies in the New World during the 18th century, monopolizing the world's sugar (40%) and coffee (>50%) production (Knight, 2000). The rise in prosperity was accompanied by the importation of

an estimated 860,000 African slaves into the island (Curtin, 1975; Coupeau, 2008) and, as a direct consequence, the number of *Affranchis* or *gens de couleur* (free coloreds and mulattoes) increased (Coupeau, 2008). Slave rebellions culminated in the Haitian Revolution (1789-1804) and ultimately resulted in the emigration of large numbers of French colonists and their slaves (Pamphile, 2001; Treco, 2002), which reduced the population to half of its original size (Ott, 1973). In 1804, Haiti was declared a republic (Knight, 2000; Coupeau, 2008), and under the newly established constitutions of the “world’s first Black Republic” (Heinl and Heinl, 2005), whites were prohibited from purchasing land in the island until the American occupation (1915–1934) (Coupeau, 2008). Consequently, a schism was generated between the European and African populations, most likely resulting in endogamy, *i.e.*, marriage within one’s own race.

During the early 19th century, Jamaica surpassed Haiti as the principal sugar-producing island in the Antilles (Rogoziński, 1999). Along with this affluence came increased demands for plantation laborers that were satisfied originally by European (Irish, Scottish, and Welsh) white bond servants and later on, by the introduction of approximately 914,902 African slaves (Pepin, 2005) who, by the early 1800s, outnumbered the Caucasians 20:1 (Mordecai and Mordecai, 2001). According to Pepin (2005), 90.4% of the total slave population in Jamaica disembarked from West African ports while the remaining 9.6% were transported from Southeast Africa (Mozambique, Madagascar, and Tanzania) although a smaller proportion [7.7% (Thomas, 1998; Pereira et al., 2001)] from the same region has been reported for the New World. Specifically, the Madagass, those native to Madagascar, were known to be present in Jamaica (Henriques, 1964). With the abolition of slavery and the culmination of the

Apprenticeship period (1834-1838) throughout the British West Indies, massive labor shortages arose again, motivating the Jamaican government to contract more than 4,000 West European [British and German] and approximately 1,000 Chinese indentured servants to work on plantations between 1838 and 1918 (Lai, 1990, 1998). In addition to these two groups, a limited number of African laborers from Sierra Leone and Central Africa was also recruited (Roberts, 1954; Mordecai and Mordecai, 2001). The extent to which the aforementioned groups contributed to the current population's gene pool is uncertain since many returned to their native land upon expiration of their contracts (Roberts, 1954; Lai, 1990, 1998).

West African influences have become ingrained into both Haitian and Jamaican societies because of the large proportion of enslaved Africans transported from continental Africa to these New World destinations. The Yoruba speakers (natives of Nigeria and Benin), although not the most prominent group, seem to have had the greatest impact on Haitian society. The most practiced Yoruba customs include Haitian Vodou, an amalgamation of the religious beliefs of the Dahomey (present-day Benin) people and Roman Catholics (de Heusch, 1995; Brown, 1997), and its associated festival, Rara (Tselos, 1996). Yoruba imprints have also been detected in Haitian art (Okediji, 2003; Roberts, 2004), music, dance (Tselos, 1996) and folklore (Roberts, 2004). Jamaica, on the other hand, has not been impacted to such an extent by one particular ethnic group, but instead displays influences from various West African sources including the Akan (Mordecai and Mordecai, 2001), Coromantee, Ibo, Fula, Mandingo, and Yoruba peoples (Mason, 2000). Important cultural traditions derived from West Africa include obeah [magic] (Curtin, 1955), myalism [religion] (Curtin, 1955; Schuler, 1979), Jonkonnu

[music and dance] (Curtin, 1955; Bettelheim, 1979), “jerk,” [a method of food preparation] and elements of the Jamaican dialect (Mordecai and Mordecai, 2001).

Studies delineating the genetic ancestry of the Haitian populace are limited. On the basis of the D1S80 polymorphic locus, Haiti was found to cluster with the continental African groups in both principal component (PC) and maximum likelihood (ML) analyses of worldwide populations (Herrera et al., 2004). In addition, using the polymarker system (PM) [lipoprotein receptor (LDLR), glycophorin A (GYPA), hemoglobin G gamma globin (HBGG), group specific component (GC), and D7S8], genetic affinities between Haiti and other African derived New World populations (French Antilles, Costa Rica, and Brazilian Mulattoes) were observed in a neighbor-joining (NJ) tree (Hidalgo et al., 2005). Haitian women were also subjects in a clinical study examining the frequency of Duffy antigen receptor for chemokines (DARC) single-nucleotide polymorphisms (SNPs) in populations from the Caribbean, Europe, and the US. Seventy-five percent of the Haitian samples examined exhibited the CC genotype (absent among women of European ancestry) at levels comparable to females of African descent from the US (73%) (Grann et al., 2008).

In contrast to Haiti, the genetic structure of the Jamaican population has been better characterized. In the aforementioned study by Grann et al. (2008), the frequency of the CC genotype among Jamaican females (63%) is less than the levels present in either Haitian (75%) or US African American (73%) women. Close genetic ties between Jamaicans and continental Africans have been detected through analysis of β -globin gene polymorphisms (Antonarakis et al., 1984), autosomal SNP and insertion/deletion (INDEL) frequency data (Parra et al., 1998), mtDNA (Parra et al., 1998; McLean et al.,

2003, 2005), Y-chromosome markers (Bergen et al., 1999; Benn Torres et al., 2007), as well as 28 ancestry informative markers (AIMs) generated from autosomal SNP and INDEL loci (Benn-Torres et al., 2008). African genetic influences detected in Jamaica include the insertion allele in the Y-chromosome *Alu* polymorphism (YAP), the marker defining Y-haplogroups D-M174 and E-M96 (sub-Saharan African-specific), and the presence of mtDNA haplogroup L, prevalent throughout sub-Saharan Africa (Parra et al., 1998). European genetic contributions, on the other hand, are generally much lower, ranging from virtually no genetic influence (McLean et al., 2003) up to 18.1% (Gibbs et al., 1972) and vary depending on the marker system used (Parra et al., 1998; McLean et al., 2005; Benn-Torres et al., 2008). Furthermore, in addition to the presence of DNA from these two sources, Benn-Torres and colleagues (2008) have also reported limited Native American contributions (3.2%) in Jamaica.

Reports surveying the genetic diversity present throughout the remainder of the West Indian archipelago also indicate strong genetic binds with continental Africans, although varying degrees of genetic input from other sources have been observed. In the Greater Antilles, for example, the Cuban population was found to share the majority (45.3%) of its maternal component, but only a limited portion (19.7%) of its Y-chromosome lineages, with African sources (Mendizabal et al., 2008). Also, in an earlier study, in which HLA class I polymorphisms were examined, genetic contributions from Africa were detected in Cuban-Mulattoes at a comparable level (45.32%) while the frequency in Cuban-Whites (21.46%) was generally much lower (Ferrer et al., 2007). In addition, admixture estimates for the Puerto Rican population reveal signals of gene flow from mainland Africa [26% when JC virus strains were examined (Fernández-Cobo et al.,

2001) and 27.2% based on mtDNA haplogroup data (Martínez-Cruzado et al., 2005)], but in contrast to Cuba, Native Americans serve as the major contributor to this island's maternal gene pool.

Admixture profiles published for the Lesser Antillean populations also indicate significant gene flow from the African continent into the region. When Y-chromosome markers are used, collections from Grenada, St. Kitts, St. Vincent, St. Thomas, and Trinidad were all found to receive greater than 75% of their paternal contributions from African sources, whereas lower proportions were exhibited by the Dominican (34.1%) and St. Lucian (45.8%) samples. In the same group of populations, with the exception of St. Thomas, the mtDNA was also primarily African-specific (haplogroups L0, L1, L2, and L3), although Native American (A, C, and D, ranging from 0.63% to 2.87%) and Eurasian (H, K, M, and N, ranging from 0.32% to 1.91%) haplogroups were detected at low frequencies (Benn Torres et al., 2007). Furthermore, in two additional studies, commensurate levels of African influences (94%, 89.6%, and 86.8%) were reported for Tobago (Miljkovic-Gacic et al., 2005), Barbados, and St. Thomas (Benn-Torres et al., 2008), respectively, when AIMs were employed. The authors also identify European and Native American influences at frequencies ranging from 4.6% to 10.6% and 0.2% to 2.6%, respectively (Miljkovic-Gacic et al., 2005; Benn-Torres et al., 2008).

In the present study, allelic frequency data for 15 hypervariable autosomal STR loci are reported for the first time for the current populations of Haiti and Jamaica. Although the Jamaican populace has been examined previously across the 13 Combined DNA Index System (CODIS) STR loci (Budowle et al., 1999), the increased number of markers analyzed in this report allows for added resolution, thereby strengthening the

statistical analyses. Phylogenetic comparisons to worldwide geographically targeted reference populations reveal strong genetic affinities between Haitians, Jamaicans, the other New World groups of African descent [New Providence (Bahamas) and African Americans from the US], and the continental African collections. Even though both Haiti and Jamaica exhibit their most substantial genetic input from Africa, Jamaica, in contrast to Haiti, also displays greater genetic contributions from Europe and East Asia.

B. Materials and Methods

Sample collection and DNA extraction

Buccal swabs, along with genealogical information for at least two generations, were collected at random from unrelated individuals belonging to the general populations of Haiti (n=111) and Jamaica (n=119). All ethical guidelines were followed as set forth by the Florida International University Institutional Review Board (IRB). DNA extractions were performed using the Gentra Buccal Cell Kit according to the manufacturer's specifications (Puregene, Gentra Systems, Minneapolis, MN) and stored at -80°C.

Published data

A total of 35 geographically targeted reference populations reporting 15 loci and 36 collections genotyped at 13 loci were included for comparison to the Haitian and Jamaican groups presented in this study. The African (East, West, and South) populations were chosen to assess their impact on Haiti and Jamaica, since both islands are known to

have received genetic contributions from this region during slave trade and post-slave trade events. Inclusion of the Latin American collections is warranted because of the substantial African component detected by Simms et al. (2008). In addition, the East Asian collections were included to survey the extent to which this group influenced the Jamaican populace during the indentured labor system. All collections, their abbreviations, biogeographical origin, and average heterozygosity values are listed in Table 1.

DNA amplification and STR genotyping

The complete set of 15 autosomal STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA) was amplified simultaneously using the AmpF/STR Identifiler PCR Amplification Kit (Applied Biosystems, Foster City, CA) according to the manufacturer's instructions (Applied Biosystems, 2001). Amplified products were separated and detected by high performance multicapillary electrophoresis in an ABI 3130xl Genetic Analyzer with POP 7TM separation medium. ABI GeneScanTM 500 LIZTM was used as the internal size standard. The fragment analysis files generated were examined using the GeneMapper[®] software v3.2 which allows for sample comparisons to the commercially available allelic ladder and subsequent genotype assignment (Butler et al., 2004).

Statistical and phylogenetic analyses

Allelic frequencies for the general populations of Haiti and Jamaica were estimated using the GenePop v 3.4 program (Raymond and Rousset, 1995). Using this data, histograms comparing the distribution of alleles in both collections per STR locus were constructed with Microsoft Excel. The Arlequin version 2.000 software (Schneider et al., 2000) was used to generate observed and expected heterozygosities (H_o and H_e , respectively) along with Hardy-Weinberg equilibrium (HWE) P values and gene diversity indices (GDI). The Bonferroni adjustment ($\alpha = 0.05/15 = 0.00333$ for 15 loci) was applied to minimize possible type I errors. In addition, to assess the effects of topogeographical barriers (*e.g.*, the Caribbean Sea and the Atlantic Ocean) on gene flow and possible inbreeding in the three Afro-Caribbean collections, heterozygote deficiencies (F_{IS} and corresponding P values) were computed for each of the 15 loci with GenePop v 3.4 (Raymond and Rousset, 1995).

Intra-, inter-, and total population (H_s , G_{st} , and H_t , respectively) genetic variance values were calculated with the DISPAN program (Ota, 1993). The groups examined were assembled according to biogeographic origin as shown in Table 1. Delta (δ) values for each of the 15 STR loci were also computed (Listman et al., 2007) for the grouped East versus West African collections to ascertain marker information content, *i.e.*, the ability of the Identifiler loci to differentiate between the two groups of populations. Any locus yielding a δ value ≥ 0.30 (Vergara et al., 2009) is considered informative for discriminating between the two sources.

The Carmody's G-test program (Carmody, 1990) was used to assess the statistical significance of pair-wise population comparisons through 100,000 simulations, both before and after application of the Bonferroni correction ($\alpha = 0.05/666 = 0.000075$). Comparisons yielding P values greater than α indicate genetic homogeneity among the populations.

Multidimensional scaling (MDS) plots (with associated stress values) were constructed with the statistical package SPSS version 14.0 (SPSS, 2001) using Nei's genetic distances (F_{st}) generated with the PHYLIP 3.52c software (Felsenstein, 2002). Phylogenetic comparisons of the Haitian and Jamaican collections with pertinent available reference populations were performed across the complete set of 15 loci and were repeated using 13 of the loci included in the set of 15 to allow inclusion of the Dominican Republic in the analysis. In addition, the New World (Haiti, Jamaica, New Providence, and the two US African American populations) and continental African groups [Madagascar was not included given its known Austronesian ancestry (Hurles et al., 2005; Regueiro et al., 2008)] were analyzed by themselves to better assess phylogenetic relationships among them. The aforementioned US African American collections, which represent a Minnesotan (US1) and a general population from the United States (US2), were included as additional representatives of New World Africans.

Admixture analyses were conducted to determine the genetic contributions made to the gene pools of the Haitian and Jamaican populations by three parental groups encompassing the geographical regions of Africa, East Asia and Europe [the Latin American collections were not included as a parental source because of the substantial proportion of their autosomal component shared with continental Africans and European

(Simms et al., 2008)]. The Bahamian population of New Providence and the two US African American collections (US1 and US2) previously investigated by Simms et al. (2008) were also reexamined for their source populations in light of additional African data sets now available and employed in the present study.

To calculate admixture proportions (m), three different approaches were taken. Using the SPSS version 14.0 software (SPSS, 2001), genetic contributions from the parental sources were generated using the weighted least squares (WLS) method proposed by Long et al. (1991). Admixture was also quantified with the ADMIX 2.0 program, which employs the coalescent-based approach described by Bertorelle and Excoffier (1998). Standard deviations were computed with bootstrapping implementing 1,000 reiterations. Additionally, with the LEADMIX program (Wang, 2003), admixture proportions were calculated using the least square regression method of Roberts and Hiorns (1965). Each of the aforementioned admixture estimators are referred to throughout the remainder of the article as m_L , m_Y , and m_{RH} , respectively.

The admixture tests (Long et al., 1991) as well average heterozygosity calculations were repeated for the five New World African groups following the segregation of the 15 STR markers into slow (≥ 0.001 mutations/meioses) vs. fast (≥ 0.01 mutations/meioses) mutating loci. The analyses were performed to examine the effects of mutation rate on admixture proportions and genetic diversity indices. Mutation rates for the Identifiler loci were provided by the NIST STR database at <http://www.cstl.nist.gov/div831/strbase/mutation.htm>.

The *Structure* software v. 2.3.1, available at <http://pritch.bsd.uchicago.edu/structure/html>, was used to infer population substructure for both the Haitian and Jamaican collections (Pritchard et al., 2000). After uploading the genotypic data into the program, a length of burn-in period of 20,000 was selected and the number of Markov chain Monte Carlo (MCMC) repetitions after burn-in was also set to 20,000. When updating the ancestry model specifications, the admixture model that performs clustering without using population of origin information and that assumes the allele frequencies in the population to be independent, was chosen. In the current study, the *Structure* analyses were performed with the number of ancestral population fixed at $K = 3$ and $K = 4$.

C. Results

Intra-population Diversity

Allelic frequencies for the 15 autosomal STR loci are listed in Tables 2 and 3 for Haiti and Jamaica, respectively, while H_o , H_e , HWE P values and GDI for both populations are provided in Table 4. Histograms generated from the allele-frequency data generally reveal no differences in the distribution of alleles between the two collections but do illustrate variation in the frequencies of alleles across loci (Supporting Information Figure 1). In Jamaica, two loci (D16S539 and D2S1338) deviate from HWE expectations ($\alpha = 0.05$) but were found to be statistically insignificant after application of the Bonferroni adjustment. Interestingly, in the Haitian population, ten loci (D8S1179, D21S11, CSF1PO, D16S539, D2S1338, D19S433, vWA, TPOX, D5S818, and FGA)

possess H_o values exceeding H_e , whereas only three loci (D8S1179, D18S51, and FGA) in the Jamaican collection have higher than expected heterozygosities. Haiti and Jamaica both exhibit the highest genetic variability at locus D2S1338, with a GDI of 0.8887 and 0.8877, respectively, while D13S317, with values of 0.6717 for Haiti and 0.7132 for Jamaica, was found to be least variable in both populations. The combined power of exclusion (CPE) was > 99.9% for both collections; however, noticeable differences between the two populations were detected when comparing the combined power of discrimination (CPD), 0.733211 for Haiti versus 0.69732 for Jamaica, and average heterozygosities, 0.80300 versus 0.77647, with Jamaica exhibiting the lower of the two values.

The number of alleles present in the Haitian population (160) and the Jamaican collection (158) outnumber the average allele count (149) for the continental African populations and are comparable in number to the other New World collections of African descent [New Providence (173), US African American 1 (162) and US African American 2 (168) (Simms et al., 2008)]. The Jamaican populace shares alleles D7S820-6 and FGA-45.2 with Tanzania, whereas the Haitian collection possesses allele D16S539-6 characteristic of Angola. Both Haiti and Jamaica, along with New Providence, exhibit FGA-16.1 present in the East African nations of Madagascar and Tanzania. In addition, only two of the five New World African groups, Haiti and US African American 1 (US1), carry allele FGA-24.3, which is not present in any continental African collection examined in this report. Other alleles shared between these island populations and the mainland African groups include FGA-19.2 and 30.2.

The highest intrapopulation variances (H_s) are observed in the New World African populations (0.79889) and the Afro-Caribbean collections (0.79712), both of which exceed the values seen in the continental Africans including (0.79411) and excluding Madagascar (0.79356). The lowest H_s levels are observed among the European (0.78461) and East Asian (0.78131) groups of populations (Table 5). Despite the high-diversity levels observed for the Afro-Caribbean group, F_{IS} calculations and associated P values (Table 6) reveal two loci in Haiti (D7S820 and TH01), two loci in Jamaica (TH01 and D2S1338), and five loci in New Providence (D21S11, CSF1PO, D19S433, TPOX, and FGA) that exhibit lower than the statistically expected number of heterozygotes.

Inter-population Diversity

Phylogenetic relationships among all populations examined in this study were investigated using MDS projections, pair-wise population comparisons (G-test) and admixture analyses. In addition, G_{st} and H_t values were computed to assess inter- and total population variance, respectively, whereas δ values were calculated to evaluate the ability of the 15 Identifiler loci to statistically differentiate between the grouped East and West African populations.

In the MDS plot of all populations (Fig. 1A), three groupings according to biogeographical origin are evident: an East Asian cluster in the lower left quadrant, a Latin American/European assemblage in the upper left section (although a clear partitioning between the two is apparent), and an African group occupying the right half of the graph. At the periphery of the African cluster, Jamaica, along with the two US African-American collections (US1 and US2), New Providence and Angola, segregate

away from the mainland African populations in the direction of the Latin American/European conglomerate. However, when only the African and African derived collections are employed (Fig. 1B), Jamaica plots on the outskirts of the central cluster at a considerable distance from Angola and the New World African populations. In contrast, Haiti maps among the continental Africans in both dendrograms (Fig. 1A,B) but lies closest to two of the West African collections (Guinea-Bissau and Equatorial Guinea) when all the populations are examined (Fig. 1A) and displays greater genetic affinities with Angola (Dimension 1), US2, and Equatorial Guinea (Dimension 2) when only the African and African derived groups are considered (Fig. 1B). At 13 loci, Haiti plots distantly from the general populace of the Dominican Republic (Supporting Information Figure 2), thereby suggesting a differential contribution of source populations as well as limited gene flow between the two portions of the island. Although the Latin American collections plot close to the European groups (Fig. 1A), they clearly segregate in two directions: the Hispanics from Minnesota in the direction of the East Asian cluster while the Brazilians and Puerto Rican Americans head toward the African collections. The tendency of some Latin American groups to segregate toward the East Asian collections is possibly the result of the Amerindian component in those New World populations. The stress value for the all population projection was 0.10202, whereas estimates for the African and African derived groups alone led to an output of 0.19149.

Inter- and total population diversity indices (G_{st} and H_t , respectively) are presented in Table 5. The highest G_{st} values are recorded for the All populations group (0.02400) and are lowest among the New World African collections (0.00330), likely attributed to the genetic contributions made to the populations in the group by similar

sources. Total population variance (H_t) is also highest in the All populations assemblage (0.81014) and is followed in decreasing order by the Africans including (0.80320) and excluding (0.80169) Madagascar, New World Africans (0.80154), Afro-Caribbeans (0.79984), Latin Americans (0.79840), East Asians (0.78807), and Europeans (0.78789).

Delta (δ) values calculated for the grouped East versus West African collections are provided in Table 7. The average δ across the entire set of 15 loci was 0.088, and values at each locus for the pair ranged from 0.045 to 0.117. Since no locus attained a value ≥ 0.30 , these markers are not considered informative for statistically differentiating between the two groups of populations.

In the G-test pair-wise analyses (Table 8), statistically insignificant genetic differences are observed between several of the New World and continental African collections, indicating a close genetic relationship between the two groups of populations. Specifically, all five New World African populations were not found to differ significantly from Kenya or Equatorial Guinea. G-test results also indicate genetic similarities between the Afro-Caribbean collections and Guinea-Bissau as well as between Haiti, Jamaica, US1, and Angola. Given the genetic affinities displayed by the New World and continental African collections, in combination with the large proportion of enslaved Africans transported to the New World, it is not surprising that results from the pair-wise population comparisons reflect genetic homogeneity between the Afro-Caribbean and Afro-American collections.

Admixture estimates for the New World African collections employing grouped African, East Asian, and European populations as parentals are provided in Table 9. The results generated from each of the three methods used, as well as for the admixture tests

involving the segregated loci (Supporting Information Table 1), collectively indicate that the most significant genetic contributions made to the gene pools of all five hybrid populations originate from Africans. In particular, m_L and m_{RH} estimates demonstrate that of all the New World collections, the Haitian populace receives the largest African genetic component, sharing greater than 95% of its DNA with this group, while comparable levels of genetic input (ranging from 69.7% to 83.7%, depending on the approach taken to quantify admixture) from African sources are detected in the other hybrid populations. The remaining genetic influences observed in New World Africans, with the exception of New Providence, arise from both the European and East Asian collections. In Jamaica, genetic contributions from the European ($m_L = 16\%$, $m_Y = 17.9\%$ and $m_{RH} = 14.2\%$) and East Asian ($m_L = 5.7\%$, $m_Y = 5.65\%$ and $m_{RH} = 3.73\%$) sources are commensurate among the methods employed, whereas in Haiti and the two Afro-American populations, the degree of European and East Asian admixture varies according to the method employed. Interestingly, of the New World African groups, Jamaica is the only collection to exhibit significant variation in admixture proportions between slow and fast mutating loci.

The divergent genetic signals observed in the admixture profiles for Haiti and Jamaica are not reflected in the output of the *Structure* analyses. The bar plots generated for both groups (Supporting Information Figure 3), assuming either three ($K = 3$) or four ($K = 4$) ancestral populations, reveal no population substructure in either collection. The graphs also indicate that both groups receive equivalent contributions from the same ancestral source populations. The general lack of population substructure observed in Haiti and Jamaica is likely attributed to the limited number of loci (15) employed in the

analyses (Listman et al., 2007), which according to Ardlie and colleagues (2002) should be much larger (>100) to reliably differentiate between highly admixed populations sharing close genetic ties.

D. Discussion

The Antilles is recognized as a “great melting pot,” (Knight and Crahan, 1979) with influences that stem from Africa, Europe, and East Asia; however, the extent to which these ancestral source populations have contributed genetically to the island chain remains relatively unexplored. Thus, in this study, 15 autosomal STR loci were typed in the general populations of Haiti and Jamaica to assess the genetic implications of their known divergent colonial histories and associated migratory events. This investigation represents the first time that Haitian STR allelic frequency data are presented, whereas the Jamaican population is examined across the full set of 15 STR loci since D2S1338 and D19S433 were not previously reported (Budowle et al., 1999). Inclusion of additional loci in the dataset not only increases the phylogenetic resolution between closely related populations, but also generates more robust probability calculations important in forensic and/or paternity testing.

Genetic diversity in the New World is expected to be high because of genetic contributions from various founder populations and subsequent admixture events over the last 500 years. Historical accounts for the West Indies indicate extensive gene flow from continental Africa during the period of the Transatlantic slave trade in addition to varying degrees of genetic input from European, Asian, and/or other sources (Parra et al., 1998; Saunders, 2003; Herrera et al., 2004; Pepin, 2005; Benn Torres et al., 2007; Benn-Torres

et al., 2008). For instance, Jamaica, whose motto is “Out of many one people,” has been settled by a wide array of sources including enslaved Africans, Portuguese Jews, Scottish and Irish bond servants, German and Chinese indentured laborers, and later on Syrian (Henriques, 1964), Cuban and Haitian (Thomas-Hope, 2003) nationals, whereas Haiti, the “world’s first Black Republic,” has received gene flow, for the most part, exclusively from Africa. Given the high level of diversity anticipated for the region, it is not surprising that average heterozygosity values for all five New World collections (Table 1) are comparable to the combined average heterozygosity of the mainland African populations (0.79778) included in the present study. With respect to Haiti (0.80300) and Jamaica (0.77647), notable differences in average heterozygosities are observed for each collection upon segregation of the STR markers into slow versus fast mutating loci [0.74325 versus 0.66387 (slow) and 0.81200 versus 0.79380 (fast) for Haiti and Jamaica, respectively], but this disparity should be tempered considering the unequal distribution of loci within the two categories. The New World Africans also exhibit the highest intra-population variance level of any group examined (Table 5).

Although δ values generated for the 15 Identifiler loci (Table 7) do not support the segregation of the African collections into East and West, noticeable differences between the two groups of populations are observed in both the MDS analysis (Fig. 1B) and the G-test (Table 8). In the MDS plot of African and African derived populations, noteworthy is the partitioning of the East African collections. Although the East African collections from Mozambique, Tanzania, and Kenya were found to group with the West African (Angola, Equatorial Guinea, and Guinea-Bissau) and New World populations in the central cluster, the Uganda, Hutu, and Tutsi collections lie on the fringes of this

assemblage. A plausible explanation for the lack of discrimination observed between the East and West African populations is the Bantu expansion, which is known to have been a venue for the demic diffusion of a number of West African markers, including Y-haplogroups E1b1a, E2, and B2a (Berniell-Lee et al., 2009), as well as mtDNA haplogroup L subclades (specifically L1a and L2a), into East Africa (Salas et al., 2002). Moreover, the Bantu diaspora is also likely the cause for genetic similarities observed in the G-test between Kenya and the West African groups (with the exception of Namibia).

Admixture proportions generated for the five New World African populations (Table 9), regardless of the method employed, indicate that their strongest genetic signal derives from the African continent. Given the large number of African laborers [estimates ranging from about 6,000 (Dominican Republic) to greater than one million (Brazil) slaves (Pepin, 2005)] transported to the region during the period of the Transatlantic slave trade, these findings are not surprising. In Jamaica, the relatively high rate of the YAP insertion [ranging from 17.89% (Parra et al., 1998) to 59.09% (Benn Torres et al., 2007)] in combination with elevated levels of Y-haplogroup E1b1a-M2 (about 43%) (Athey, 2006; Benn Torres et al., 2007) and mtDNA haplogroup L (25.86%) (Parra et al., 1998), corroborate the large African component detected in this population in the present study. Africa's prominent contribution to the Haitian gene pool is supported by an earlier D1S80 study in which Haiti was found to cluster with continental Africans in PC and ML analyses of worldwide populations (Herrera et al., 2004). In addition, phylogenetic assessments performed by Simms and colleagues (2008) reveal strong genetic affinities between New Providence in the Bahamas, the two US African American groups and the continental Africans.

Of the five New World African groups, the percent contribution from continental Africa is greatest in Haiti for two of three admixture tests performed. The larger percentage of African DNA present in the Haitian gene pool is supported by Haiti's position amidst the African collections in the MDS plot of all populations (Fig. 1A). Within this cluster, Haiti maps in closest proximity to Guinea-Bissau and Equatorial Guinea in both Dimensions. Likewise, when only the African and African derived populations are considered, the Haitian populace still exhibits genetic affinities with the West Africans. In addition, pair-wise population comparisons (Table 8) performed also indicate genetic homogeneity between Haiti/Angola, Haiti/Equatorial Guinea, and Haiti/Guinea-Bissau. These findings are supported by a previous study, based on the D1S80 polymorphic locus, in which Haiti was found to map equidistant from Benin and a general collection from the Bahamas in the PC plot of African and New World African populations (Herrera et al., 2004).

Admixture data for the Jamaican collection reveals commensurate contributions from Africa (ranging from 76.5% to 82.1%), regardless of the method employed to quantify admixture. Genetic ties with the African continent are not only observed in the clustering of Jamaica, along with the other New World African groups, on the fringes of the African assemblage in Figure 1A, but are also detected in the results of the pair-wise comparisons (Table 8), which indicate genetic similarities between Jamaica, the West African collections (Angola, Equatorial Guinea, and Guinea-Bissau), and Kenya. Within the assembly of New World populations (Fig. 1A), noteworthy is the position of Angola, which maps distantly from the remaining continental African groups. The close proximity of Jamaica and Angola in Figures 1A (Dimensions 1 and 2) and 1B (Dimension 2) most

likely derives from the large proportion of enslaved Africans [approximately 142,725 persons according to Pepin (2005)] transported to the island from West-Central Africa, the region encompassing Angola and the Congos. Genetic influences in Jamaica from West Africa have also been detected in earlier studies in which elevated levels (approximately 70%) of the Benin β^S -haplotype, prevalent throughout West-Central Africa [Cameroon, Nigeria, and Benin], have been reported (Wainscoat et al., 1983; Antonarakis et al., 1984; Nagel et al., 1984; Pante-de-Sousa, 1998). Also, in a more recent study examining mtDNA haplotypes, the Jamaican population was found to branch together with samples native to Sierra Leone in NJ trees (McLean et al., 2005). This clustering is expected since indentured servants from this region of West Africa were transported to Jamaica during the postslavery period.

The comparable African admixture proportions exhibited by the New Providence and US African American collections (US1 and US2) echoes data published by Simms et al. (2008). However, with the introduction of additional African populations in the present study (Guinea-Bissau, Namibia, Tanzania, and Uganda), the contributions from Africa have decreased on average by 0.93%, 5.76%, and 10.8% when the Roberts and Hirons (1965), Long (1991), and Bertorelle and Excoffier (1998) approaches were employed, respectively. Despite this decrease, genetic affinities between these collections and the continental African groups are still the most prominent.

The remaining influences present in each of the New World African population's gene pool are contributed by the European groups and, except for the New Providence collection, the East Asian populations as well. The genetic input from Europeans is minimal in Haiti (with the exception of the m_Y estimator) when compared with the other

New World African populations that exhibit much larger contributions (ranging from 14.2% to 36.3%). These findings are corroborated by the MDS plot of all populations (Fig. 1A), which illustrates the latter populations plotting closely together on the outskirts of the African assemblage but in the direction toward the European/Latin American group while the Haitian collection maps amidst the mainland African populations within the African cluster.

European gene flow into Jamaica is supported by previous studies which report admixture profiles portraying from as little as no apparent contributions up to 2% when mtDNA haplotypes were analyzed (McLean et al., 2003, 2005), 6.8% when autosomal SNP and INDEL frequency distributions were employed (Parra et al., 1998), 12.4% when a panel of 28 AIMs generated from SNP and INDEL frequency data was utilized (Benn-Torres et al., 2008) and 18.1% when glucose-6-phosphate dehydrogenase (G6PD) deficiency alleles were examined (Gibbs et al., 1972). Genetic contributions from Europe most likely derive from the influx of British soldiers, white bond servants and, later, as a result of the immigration of Western European indentured laborers. In contrast to the other New World African collections, the admixture proportions for Haiti, with the exception of the coalescent based approach, indicate only minor contributions from European sources. The limited presence of European DNA in the current population is likely due to ramifications of the Haitian Revolution in which the French colonists were either killed or coerced out of the island.

Signals of East Asian gene flow into the Jamaican population most likely stem from the influx of indentured servants contracted from China between 1852 and 1884 to replace the dwindling African sources (Lai, 1990). Demographic data reports that the

Chinese comprise 0.2% of the total Jamaican populace (Mordecai and Mordecai, 2001), supporting the minor East Asian component detected in the present study. Although less likely, genetic input from East Asia may have also arisen from remnants of the indigenous Arawak Indian population still present in Jamaica before the British occupation of the island (Henriques, 1964). Genetic imprints (SNP and INDEL AIMs) of this group have been reported by Benn-Torres and collaborators (2008) who observed minor Native American genetic influences (3.2%) in the island. In contrast, Haiti exhibits minimal East Asian contributions (0.3%) only when the Long (1991) method is employed. Genetic influences from this region may be attributed to residual Native American input or to gene flow from East Asian migrants ubiquitous to the New World.

Overall, my results substantiate greater genetic contributions to Haiti from Africa than to Jamaica, which shares larger portions of its autosomal component with the European and East Asian groups. The prominent presence of African DNA in the Haitian and Jamaican populations is likely the result of the transportation of hundreds of thousands of enslaved Africans to the colony from ports along Africa's West coast. My data clearly demonstrates that among the New World African collections, the contributions of different ancestral groups of populations, namely Africans, Europeans, and East Asians, varies and corroborates information from historical accounts of migratory events.

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Appendix III

Fig. 1A: Multidimensional Scaling plot (Stress = 0.10202) of all populations at 15 loci

Fig. 1B: Multidimensional Scaling plot (Stress = 0.19149) of the African derived collections

Population	Abbreviation	n	Avg H _e	Reference
AFRO-CARIBBEAN^a				
Haiti	HAT	111	0.80300	<i>present study</i>
Jamaica	JAM	119	0.77647	<i>present study</i>
New Providence (Bahamas)	NWP	221	0.78312	Simms <i>et al.</i> , 2008
AFRO-AMERICAN^a				
US African American 1 (Minnesota)	US1	157	0.80380	Gross and Budowle, 2006
US African American 2 (General)	US2	258	0.79573	Butler <i>et al.</i> , 2003
WEST AFRICAN				
Cabinda (Angola)	ANG	110	0.79698	Beleza <i>et al.</i> , 2004
Guinea-Bissau	GUB	92	0.80249	Pereira <i>et al.</i> , 2005
Equatorial Guinea	EGU	134	0.89193	Alves <i>et al.</i> , 2005
Namibia	NAM	195	0.78293	Muro <i>et al.</i> , 2008
EAST AFRICAN				
Hutu (Rwanda)	HUT	95	0.81193	Shepard and Herrera, 2006
Kenya	KEN	65	0.81436	Shepard and Herrera, 2006
Madagascar	MAD	67	0.80350	Regueiro <i>et al.</i> , 2008
Maputo (Mozambique)	MOZ	144	0.79580	Alves <i>et al.</i> , 2004
Tanzania	TAN	272	0.81062	Forward <i>et al.</i> , 2008
Tutsi (Rwanda)	TUT	126	0.77818	Regueiro <i>et al.</i> , 2004
Uganda	UGA	90	-	Gusmão <i>et al.</i> , 2006
SOUTH AFRICAN				
Cape Town (South Africa)	SAF	98	-	Kido <i>et al.</i> , 2007
EAST ASIAN				
Chao Shan (South China)	CCS	144	0.77793	Hu <i>et al.</i> , 2005
Japan	JAP	526	0.77127	Hashiyada <i>et al.</i> , 2003
Korea	KOR	231	0.77087	Kim <i>et al.</i> , 2003
Malaysia	MAL	210	0.78127	Seah <i>et al.</i> , 2003
Philippines	PHI	106	0.77793	De Ungria <i>et al.</i> , 2005
Shaanxi Han (NW China)	CSH	203	0.78232	Wang <i>et al.</i> , 2005
LATIN AMERICAN				
Caracas (Central Venezuela)	CAR	255	0.79267	Chiurillo <i>et al.</i> , 2003
Central Mexico	MEX	211	0.82827	Hernández-Gutiérrez <i>et al.</i> , 2005
Costa Rica	CSR	500	0.85353	Rodríguez <i>et al.</i> , 2007
Dominican Republic ^b	DMR	2565	0.89677	Díaz <i>et al.</i> , 2008
Hispanic (US -Minnesota)	HIS	151	0.80120	Gross and Budowle, 2006
Maracaibo (Venezuela)	MAR	203	0.77896	Bernal <i>et al.</i> , 2006
Metztitlán (Mexico)	MET	180	0.75067	Gorostiza <i>et al.</i> , 2007
Puerto Rico American (Massachusetts)	PRA	205	0.79113	Zúñiga <i>et al.</i> , 2006
Rio de Janeiro (Brazil)	BRA	300	0.85533	de Souza Góes <i>et al.</i> , 2004
EUROPEAN				
Andalusia (South Spain)	AND	114	0.77600	Coudray <i>et al.</i> , 2007
Belaruse	BLR	176	0.77160	Rebala <i>et al.</i> , 2007
Caucasian (US - General)	CAU	302	0.78173	Butler <i>et al.</i> , 2003
Flemish (North Belgium)	FLE	231	0.79533	Mertens <i>et al.</i> , 2006
North and Central Poland	POL	412	0.79447	Czarny <i>et al.</i> , 2005
Spain	SPN	342	0.76666	Camacho <i>et al.</i> , 2007

^aThese groups are combined in some analyses as New World Africans. For specific analyses see Materials & Methods.

^bThe Average Heterozygosity (Avg H_e) for this group was calculated at the level of 13 loci.

Table 1: Populations Analyzed

allele	5	6	7	8	9	9.3	10	10.1	10.2	11	12	12.2	13
D8S1179				0.0045			0.0090			0.0495	0.0586		0.1847
D21S11													
D7S820			0.0045	0.2297	0.1532		0.3018	0.0045		0.1667	0.1036		0.0315
CSF1PO			0.0360	0.0676	0.0225		0.2613			0.2523	0.2883		0.0586
D3S1358													
TH01	0.0090	0.1036	0.4775	0.2207	0.1486	0.0315	0.0090						
D13S317				0.0045	0.0090		0.0270			0.2928	0.4730		0.1306
D16S539	0.0090	0.0045		0.0495	0.1937		0.0856			0.2793	0.2027		0.1351
D2S1338													
D19S433							0.0180			0.0450	0.1081	0.0495	0.2838
vWA										0.0045	0.0045		0.0045
TPOX		0.0946	0.0135	0.2928	0.2117		0.0811			0.2748	0.0270		0.0045
D18S51					0.0045		0.0045		0.0045		0.0586		0.0405
D5S818				0.0631	0.0180		0.0721			0.1937	0.3784		0.2387
FGA													

allele	13.2	14	14.2	15	15.2	16	16.1	16.2	17	17.2	18	18.2	19
D8S1179		0.3874		0.2432		0.0541			0.0090				
D21S11													
D7S820		0.0045											
CSF1PO		0.0090		0.0045									
D3S1358		0.1261		0.3063		0.3108			0.2117		0.0360		0.0090
TH01													
D13S317		0.0631											
D16S539		0.0360		0.0045									
D2S1338						0.0676			0.1081		0.0405		0.1712
D19S433	0.0495	0.1937	0.0676	0.0856	0.0586	0.0135		0.0180	0.0045	0.0045			
vWA		0.0991		0.1937		0.3108			0.1757		0.1261		0.0721
TPOX													
D18S51	0.0045	0.0586	0.0090	0.1261	0.0045	0.2162			0.1532		0.1036		0.0991
D5S818		0.0270				0.0045			0.0045				
FGA							0.0045				0.0045	0.0045	0.0450

Table 2: Haiti allelic frequencies (n=111)

allele	20	20.2	21	21.2	22	23	24	24.3	25	26	27	28	29
D8S1179													
D21S11										0.0045	0.0315	0.3018	0.1532
D7S820													
CSF1PO													
D3S1358													
TH01													
D13S317													
D16S539													
D2S1338	0.0676		0.1396		0.1396	0.1261	0.0676		0.0631	0.0090			
D19S433													
vWA			0.0045		0.0045								
TPOX													
D18S51	0.0856		0.0180	0.0045	0.0045								
D5S818													
FGA	0.0586	0.0045	0.0991		0.1847	0.1802	0.1667	0.0045	0.1486	0.0495	0.0315		

allele	30	30.2	31	31.2	32	32.2	33	33.2	34	34.2	35	36
D8S1179												
D21S11	0.2072	0.0180	0.0721	0.0631	0.0225	0.0495	0.0045	0.0090	0.0135	0.0045	0.0405	0.0045
D7S820												
CSF1PO												
D3S1358												
TH01												
D13S317												
D16S539												
D2S1338												
D19S433												
vWA												
TPOX												
D18S51												
D5S818												
FGA		0.0045		0.0090								

Table 2: Haiti allelic frequencies (n=111) (Cont'd)

allele	6	7	8	9	9.3	10	10.2	11	11.2	12	12.2	13	13.2
D8S1179				0.0126		0.0378		0.0714		0.1134		0.1513	
D21S11													
D7S820	0.0084	0.0084	0.1639	0.0798		0.3992		0.2101		0.1176		0.0084	
CSFIPO		0.0546	0.0672	0.0420		0.2941		0.2017		0.2647		0.0630	
D3S1358										0.0042			
TH01	0.1429	0.3655	0.2311	0.1555	0.0840	0.0210							
D13S317			0.0336	0.0294		0.0336		0.2731		0.4244		0.1765	
D16S539			0.0168	0.2521		0.1134		0.2983		0.2101		0.0924	
D2S1338													
D19S433				0.0042		0.0084		0.0546	0.0084	0.1218	0.0546	0.2563	0.0462
vWA								0.0084				0.0084	
TPOX	0.0336	0.0210	0.4286	0.1807		0.0714		0.2437		0.0210			
D18S51							0.0042	0.0084		0.0714		0.0630	0.0042
D5S818			0.0588	0.0210		0.0420		0.2689		0.3445		0.2479	
FGA													

allele	14	14.2	15	15.2	16	16.1	16.2	17	17.2	18	18.2	19	19.2
D8S1179	0.2857		0.2227		0.0882			0.0168					
D21S11													
D7S820	0.0042												
CSFIPO	0.0126												
D3S1358	0.0630		0.2983	0.0042	0.3109			0.2521		0.0588		0.0084	
TH01													
D13S317	0.0294												
D16S539	0.0168												
D2S1338					0.0378			0.0966		0.0630		0.2017	
D19S433	0.2185	0.0588	0.0798	0.0252	0.0168		0.0378	0.0042	0.0042				
vWA	0.0630		0.2437		0.2479			0.1681		0.1345		0.0882	
TPOX													
D18S51	0.0798	0.0084	0.1429		0.1975			0.1513		0.1092		0.1050	
D5S818	0.0084		0.0042		0.0042								
FGA						0.0042					0.0252	0.0588	0.0042

allele	20	20.2	21	21.2	22	23	24	25	26	27	28	29	30
D8S1179													
D21S11									0.0042	0.0336	0.2521	0.2101	0.1849
D7S820													
CSFIPO													
D3S1358													
TH01													
D13S317													
D16S539													
D2S1338	0.1176		0.1218		0.1092	0.0966	0.0840	0.0588	0.0084	0.0042			
D19S433													
vWA	0.0252		0.0042		0.0084								
TPOX													
D18S51	0.0336		0.0084		0.0084	0.0042							
D5S818													
FGA	0.0336	0.0042	0.1050	0.0084	0.1597	0.1891	0.2017	0.1008	0.0420	0.0336	0.0168	0.0042	0.0042

Table 3: Jamaica allelic frequencies (n=119)

allele	30.2	31	31.2	32	32.2	33	33.2	34.2	35	36	45.2
D8S1179											
D21S11	0.0042	0.0630	0.0546	0.0294	0.0630	0.0084	0.0378	0.0084	0.0336	0.0126	
D7S820											
CSF1PO											
D3S1358											
TH01											
D13S317											
D16S539											
D2S1338											
D19S433											
vWA											
TPOX											
D18S51											
D5S818											
FGA											0.0042

Table 3: Jamaica allelic frequencies (n=119) (Cont'd)

Locus	Haiti				Jamaica			
	H _o	H _e	HWE	GDI	H _o	H _e	HWE	GDI
D8S1179	0.8198	0.7511	0.3208	0.7511	0.8740	0.8217	0.5772	0.8217
D21S11	0.8559	0.8308	0.3520	0.8308	0.7983	0.8459	0.3424	0.8459
D7S820	0.7387	0.7967	0.3609	0.7967	0.7143	0.7524	0.9637	0.7524
CSF1PO	0.8378	0.7786	0.4647	0.7786	0.7899	0.7927	0.9435	0.7927
D3S1358	0.7207	0.7509	0.6197	0.7508	0.7227	0.7464	0.7683	0.7464
TH01	0.6757	0.6924	0.0740	0.6924	0.6555	0.7641	0.1598	0.7641
D13S317	0.6306	0.6717	0.7018	0.6717	0.6807	0.7132	0.1949	0.7132
D16S539	0.8198	0.8176	0.9226	0.8176	0.7563	0.7846	0.0178	0.7846
D2S1338	0.8919	0.8887	0.4855	0.8887	0.8235	0.8877	0.0040	0.8877
D19S433	0.8829	0.8510	0.2813	0.8510	0.8319	0.8548	0.3589	0.8548
vWA	0.8469	0.8076	0.9874	0.8076	0.8151	0.8237	0.4727	0.8237
TPOX	0.8108	0.7810	0.3768	0.7810	0.6723	0.7202	0.6787	0.7202
D18S51	0.8649	0.8809	0.9021	0.8809	0.8908	0.8815	0.6876	0.8815
D5S818	0.7568	0.7555	0.8624	0.7555	0.7311	0.7449	0.9691	0.7449
FGA	0.8919	0.8685	0.6072	0.8685	0.8908	0.8720	0.4080	0.8720

Table 4: Observed (H_o) and Expected Heterozygosity (H_e), Hardy-Weinberg Equilibrium (HWE) *P*-values and Gene Diversity indices (GDI) for the Haitian and Jamaican populations across the 15 Identifiler loci

Locus	Afro-Caribbean			New World African ¹			African w/o Madagascar			African with Madagascar		
	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t
D8S1179	0.00476	0.78859	0.79236	0.00493	0.79008	0.79399	0.01146	0.77362	0.78259	0.01253	0.77533	0.78517
D21S11	0.00262	0.83717	0.83937	0.00249	0.84052	0.84262	0.00937	0.85160	0.85966	0.01000	0.85301	0.86162
D7S820	0.00549	0.77387	0.77814	0.00461	0.77871	0.78231	0.00811	0.76163	0.76786	0.00910	0.76344	0.77045
CSF1PO	0.00214	0.78204	0.78372	0.00187	0.78084	0.78230	0.01527	0.77695	0.78899	0.01457	0.77571	0.78718
D3S1358	0.00213	0.74892	0.75052	0.00349	0.75207	0.75470	0.01227	0.73200	0.74109	0.01231	0.72975	0.73884
TH01	0.00588	0.73376	0.73810	0.00472	0.73893	0.74243	0.01389	0.72753	0.73778	0.01299	0.72930	0.73889
D13S317	0.00331	0.70077	0.70309	0.00247	0.70627	0.70802	0.00704	0.70777	0.71278	0.01095	0.71409	0.72199
D16S539	0.00363	0.79869	0.80159	0.00348	0.79425	0.79702	0.00870	0.78878	0.79570	0.00967	0.78850	0.79619
D2S1338	0.00216	0.88510	0.88702	0.00247	0.88726	0.88945	0.01061	0.88152	0.89097	0.01043	0.88107	0.89036
D19S433	0.00135	0.84174	0.84288	0.00214	0.84083	0.84263	0.01017	0.82757	0.83607	0.01120	0.82926	0.83865
vWA	0.00342	0.81135	0.81414	0.00317	0.81307	0.81565	0.00947	0.81916	0.82700	0.00980	0.81737	0.82546
TPOX	0.00655	0.75879	0.76379	0.00491	0.76191	0.76567	0.01585	0.76994	0.78234	0.02124	0.76262	0.77917
D18S51	0.00310	0.87691	0.87964	0.00262	0.87786	0.88017	0.00658	0.86494	0.87067	0.00708	0.86545	0.87162
D5S818	0.00273	0.74781	0.74986	0.00259	0.75047	0.75242	0.00627	0.74582	0.75053	0.01009	0.75214	0.75980
FGA	0.00229	0.87133	0.87333	0.00378	0.87035	0.87366	0.00776	0.87454	0.88138	0.00897	0.87468	0.88260
All Loci	0.00339	0.79712	0.79984	0.00330	0.79889	0.80154	0.01015	0.79356	0.80169	0.01131	0.79411	0.80320

¹ The New World African assemblage includes the Afro-Caribbean populations along with the two US Afro-American collections

Table 5: Inter-, intra- and total population genetic variance

	East Asian			Latin American			European			All populations		
Locus	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t
D8S1179	0.00762	0.84279	0.84926	0.00533	0.79687	0.80114	0.00469	0.80477	0.80856	0.02144	0.79769	0.81517
D21S11	0.00871	0.81690	0.82408	0.00407	0.83425	0.83765	0.00263	0.84413	0.84636	0.01917	0.83997	0.85639
D7S820	0.00944	0.75886	0.76608	0.00753	0.79102	0.79702	0.00428	0.80119	0.80463	0.02157	0.77684	0.79397
CSF1PO	0.00874	0.72283	0.72920	0.00330	0.71758	0.71996	0.00529	0.72430	0.72815	0.01486	0.74692	0.75819
D3S1358	0.01191	0.71936	0.72803	0.01200	0.75931	0.76853	0.00319	0.79479	0.79733	0.01623	0.74802	0.76036
TH01	0.01452	0.69914	0.70944	0.01458	0.77066	0.78206	0.00847	0.77510	0.78172	0.05882	0.74208	0.78845
D13S317	0.00608	0.80024	0.80513	0.01072	0.80819	0.81695	0.00354	0.77766	0.78042	0.03782	0.75766	0.78744
D16S539	0.00957	0.77487	0.78235	0.00764	0.77957	0.78557	0.00244	0.75587	0.75772	0.01811	0.77984	0.79423
D2S1338	0.00706	0.86761	0.87377	0.00894	0.86449	0.87229	0.00414	0.86760	0.87121	0.02051	0.87396	0.89225
D19S433	0.01380	0.79961	0.81079	0.00778	0.82661	0.83310	0.00290	0.76447	0.76670	0.02022	0.81494	0.83175
vWA	0.00681	0.79667	0.80213	0.00751	0.79039	0.79637	0.00403	0.80725	0.81051	0.01900	0.80596	0.82156
TPOX	0.00567	0.62619	0.62976	0.00926	0.67459	0.68089	0.00481	0.61521	0.61818	0.03776	0.69746	0.72483
D18S51	0.00742	0.85343	0.85981	0.00356	0.87685	0.87998	0.00457	0.87159	0.87559	0.01820	0.86864	0.88474
D5S818	0.00761	0.78432	0.79033	0.01213	0.71660	0.72540	0.00400	0.71021	0.71306	0.02917	0.74265	0.76496
FGA	0.00468	0.85688	0.86091	0.00614	0.87367	0.87907	0.00358	0.85508	0.85814	0.01136	0.86781	0.87778
All Loci	0.00858	0.78131	0.78807	0.00796	0.79204	0.79840	0.00415	0.78461	0.78789	0.02400	0.79070	0.81014

Table 5: Inter-, intra- and total population genetic variance (Cont'd)

Locus	Haiti				Jamaica				New Providence			
	H _o	H _e	F _{IS}	P	H _o	H _e	F _{IS}	P	H _o	H _e	F _{IS}	P
D8S1179	0.8198	0.7511	-0.0920	0.9934	0.8740	0.8217	-0.0640	0.9383	0.8326	0.8017	-0.0390	0.8563
D21S11	0.8559	0.8308	-0.0300	0.1716	0.7983	0.8459	0.0560	0.1832	0.7783	0.8441	0.0780	0.0019
D7S820	0.7387	0.7967	0.0730	0.0270	0.7143	0.7524	0.0510	0.3209	0.7376	0.8287	0.0560	0.0792
CSF1PO	0.8378	0.7786	-0.0760	0.7320	0.7899	0.7927	0.0040	0.5900	0.7195	0.8057	0.0820	0.0016
D3S1358	0.7207	0.7509	0.0400	0.4083	0.7227	0.7464	0.0320	0.5445	0.7557	0.7577	0.0030	0.4488
TH01	0.6757	0.6924	0.0240	0.0162	0.6555	0.7641	0.1430	0.0163	0.7557	0.7619	-0.0040	0.4157
D13S317	0.6306	0.6717	0.0610	0.4027	0.6807	0.7132	0.0460	0.4918	0.7104	0.7767	0.0200	0.0597
D16S539	0.8198	0.8176	-0.0030	0.5326	0.7563	0.7846	0.0360	0.1389	0.7919	0.8076	0.0130	0.0946
D2S1338	0.8919	0.8887	-0.0040	0.6875	0.8235	0.8877	0.0730	0.0147	0.8552	0.8925	0.0380	0.0580
D19S433	0.8829	0.8510	-0.0380	0.8002	0.8319	0.8548	0.0270	0.3725	0.7873	0.8292	0.0500	0.0491
vWA	0.8469	0.8076	-0.0490	0.9187	0.8151	0.8237	0.0100	0.3964	0.7964	0.8117	0.0190	0.5672
TPOX	0.8108	0.7810	-0.0380	0.7439	0.6723	0.7202	0.0670	0.3706	0.6833	0.7835	0.1280	0.0150
D18S51	0.8649	0.8809	0.0180	0.2617	0.8908	0.8815	-0.0110	0.6247	0.8959	0.8815	-0.0200	0.7320
D5S818	0.7568	0.7555	-0.0020	0.2589	0.7311	0.7449	0.0190	0.5483	0.7330	0.7513	0.0240	0.0949
FGA	0.8919	0.8685	-0.0270	0.8145	0.8908	0.8720	-0.0220	0.9037	0.9140	0.8856	-0.0350	0.0000

P values < 0.05 are in bold

Table 6: Heterozygote deficiencies for the Afro-Caribbean populations

Locus	WA/EA
D8S1179	0.107
D21S11	0.095
D7S820	0.063
CSF1P0	0.117
D3S1358	0.045
TH01	0.104
D13S317	0.080
D16S539	0.110
D2S1338	0.063
D19S433	0.078
vWA	0.063
TPOX	0.105
D18S51	0.086
D5S818	0.097
FGA	0.105
Average	0.088

WA: West African
EA: East African

Table 7: Delta (δ) values for the grouped East vs. West African populations

	US1	US2	ANG	SAF	EGU	GUB	HAT	HUT	JAM	KEN	MAD
US1		231.3660	272.1790	396.6248	231.1540	284.6625	232.8402	290.1581	186.0889	202.7056	345.3930
US2	0.0506		292.7030	399.4874	244.9366	282.1639	227.0359	342.1582	216.0961	217.6445	382.9854
ANG	<i>0.0001</i>	0.0000		310.2818	221.7053	282.4472	239.2100	260.0201	262.8510	198.6299	371.3746
SAF	0.0000	0.0000	0.0000		333.2830	326.4199	279.4336	355.1657	348.8613	243.6538	385.7041
EGU	<i>0.0309</i>	<i>0.0099</i>	<i>0.0238</i>	0.0000		251.2966	169.9370	299.3431	235.1849	194.7626	364.9853
GUB	0.0000	0.0000	0.0000	0.0000	<i>0.0005</i>		238.6009	323.5085	251.3156	213.7887	354.1472
HAT	<i>0.0440</i>	0.0886	<i>0.0120</i>	0.0000	0.9480	<i>0.0109</i>		335.4467	230.7371	198.6350	332.5014
HUT	0.0000	0.0000	<i>0.0001</i>	0.0000	0.0000	0.0000	0.0000		301.1588	210.3549	376.5460
JAM	0.7290	0.1866	<i>0.0002</i>	0.0000	<i>0.0122</i>	<i>0.0006</i>	<i>0.0462</i>	0.0000		195.1255	333.7593
KEN	0.1050	<i>0.0247</i>	0.0916	<i>0.0003</i>	0.1682	<i>0.0193</i>	0.2982	0.0516	0.2052		306.9289
MAD	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
MOZ	0.0000	0.0000	0.0000	<i>0.0005</i>	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0035</i>	0.0000
NAM	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
NWP	0.3478	<i>0.0142</i>	0.0000	0.0000	<i>0.0440</i>	<i>0.0009</i>	0.0847	0.0000	0.1261	0.0754	0.0000
TAN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0365</i>	0.0000
TUT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UGA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0003</i>	0.0000
CCS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
JAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KOR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
AND	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Table 8: G-test

	MOZ	NAM	NWP	TAN	TUT	UGA	CCS	JAP	KOR	MAL	PHI
US1	369.3774	504.0229	211.5335	370.5138	487.7301	436.9200	1321.3734	1815.1772	1571.8273	1145.4186	956.6950
US2	336.3618	544.4847	260.9949	400.2196	523.5327	483.2588	1612.5165	2444.9363	1978.6023	1474.4789	1150.3481
ANG	334.9184	290.9848	297.1790	327.6299	378.0364	468.1497	1319.5687	1743.0122	1547.0536	1230.0575	994.3469
SAF	246.7927	419.0391	414.8787	330.5381	440.1677	510.8528	1347.2368	1787.0132	1613.6172	1294.1763	1088.1547
EGU	317.1875	352.9726	239.0506	334.4801	407.6942	456.9542	1410.5985	1908.0112	1703.4598	1264.7218	1045.0815
GUB	312.9706	394.3167	265.0812	321.6954	440.6943	416.2239	1101.0726	1417.4559	1327.3401	1044.8998	898.3178
HAT	297.7143	337.0298	236.7576	308.1873	414.9631	416.9154	1258.7485	1702.6776	1540.2103	1153.0020	987.1977
HUT	352.6128	462.6141	344.6294	333.5834	361.3040	328.6649	1243.8484	1588.8331	1444.2677	1138.2894	1010.2482
JAM	305.3622	419.8413	228.4719	299.7603	405.2145	367.2077	1105.7494	1451.3796	1325.4003	987.2772	861.8778
KEN	225.2373	299.9806	213.9525	227.2508	297.4595	241.7360	965.3720	1132.9982	1112.2170	886.5229	784.0193
MAD	371.9299	506.4148	421.1929	437.2512	461.2226	501.2495	708.5034	868.1801	857.8117	625.9515	527.1189
MOZ		486.0583	408.3094	283.4961	523.5334	519.5912	1516.8990	1978.8864	1779.2944	1456.1948	1166.9080
NAM	0.0000		548.6736	534.3686	634.0131	622.8959	1964.9546	2927.8337	2514.9470	1966.7240	1467.2649
NWP	0.0000	0.0000		450.5210	484.4134	462.1212	1640.0826	2419.7532	2044.1027	1505.4727	1227.9337
TAN	0.0001	0.0000	0.0000		481.9146	527.5989	1851.1737	2691.5598	2241.6169	1783.1946	1353.2587
TUT	0.0000	0.0000	0.0000	0.0000		537.8627	1533.4893	1974.8872	1805.7122	1471.2946	1165.1117
UGA	0.0000	0.0000	0.0000	0.0000	0.0000		1159.6693	1464.1675	1357.8638	1083.6028	974.2226
CCS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		431.2647	353.6910	432.0402	356.7864
JAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		293.7658	741.7219	497.2908
KOR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		636.6891	459.4520
MAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		289.0813
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
AND	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Table 8: G-test (Cont'd)

	CSH	CAR	MEX	CSR	HIS	MAR	MET	PRA	BRA
US1	1366.2150	720.6636	1018.0546	1026.5992	681.2700	717.2574	1314.0172	618.4646	503.5044
US2	1668.1620	924.5727	1335.5060	1435.1771	863.0743	943.2885	1650.6353	830.7430	673.8070
ANG	1340.3058	893.2872	1170.4983	1226.6724	855.5585	906.1671	1417.8441	785.2439	656.7479
SAF	1417.8231	951.1696	1255.0952	1228.6013	935.6351	1016.5126	1419.9254	881.2035	788.1117
EGU	1449.3634	853.7404	1166.7423	1237.9307	842.0637	892.4207	1452.4832	754.5046	653.2888
GUB	1120.6151	669.1605	942.4453	929.3496	685.0397	746.6887	1180.8689	649.6805	563.4520
HAT	1291.3613	781.3412	1056.8923	1114.7231	778.7883	821.7631	1295.0150	726.1169	589.4932
HUT	1298.2859	803.4444	1042.8290	1083.9535	805.6285	805.2376	1316.9272	691.0500	647.6494
JAM	1130.8444	616.8490	880.0184	918.5863	637.9739	668.6646	1130.4785	577.1983	482.6524
KEN	959.9223	577.6357	754.5463	736.7450	576.3684	587.2698	931.8091	535.9065	430.8232
MAD	775.9848	553.3486	678.7587	725.1730	529.5678	579.8524	803.1285	558.0521	532.5978
MOZ	1575.8204	989.1948	1346.6300	1351.3932	956.1947	1024.2223	1573.4152	905.7759	824.1256
NAM	2218.7803	1549.8578	1926.5803	2248.2058	1367.1688	1593.1064	2180.9568	1340.3010	1211.3700
NWP	1753.9027	916.2577	1304.4275	1401.6000	834.9598	918.8211	1625.9066	753.7961	658.0684
TAN	1953.3273	1328.6235	1714.4022	1863.9269	1228.1897	1356.3922	2000.8979	1146.5701	1061.1766
TUT	1633.0477	1071.8092	1358.7449	1459.8461	1011.6371	1045.1583	1561.3545	976.0688	926.4795
UGA	1209.6449	863.1320	1019.6701	1109.8484	778.4283	827.5852	1233.6215	809.3176	715.9099
CCS	279.7270	1125.1412	1056.0265	1340.8743	849.0118	1002.9550	1209.4363	1094.1124	1297.0906
JAP	487.8763	1469.3901	1516.2504	1839.5123	972.6217	1249.6879	1583.5695	1436.7079	1865.7714
KOR	344.5786	1187.6215	1165.9557	1402.4498	844.1308	1037.3330	1330.2899	1180.2168	1468.2697
MAL	472.2081	918.8443	877.5515	1212.1229	618.0319	803.8587	1130.5956	867.9807	1118.8350
PHI	377.1124	877.9362	854.0881	1016.2513	674.0782	786.16370	1106.5436	830.0125	957.3215
CSH		1131.8489	1023.6318	1295.5643	789.0430	979.0354	1224.3311	1062.3735	1312.8925
CAR	0.0000		434.5750	291.5373	206.2046	194.9020	757.1349	323.2320	335.2340
MEX	0.0000	0.0000		545.4443	261.7632	378.3874	583.8787	574.1693	686.5186
CSR	0.0000	0.0000	0.0000		248.0351	317.3796	779.3468	519.6517	604.9189
HIS	0.0000	0.1002	<i>0.0023</i>	<i>0.0001</i>		220.7598	442.0474	304.3576	352.9807
MAR	0.0000	0.4610	0.0000	0.0000	<i>0.0103</i>		611.7493	369.8294	340.7615
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		941.7846	1130.1987
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		353.1628
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
AND	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Table 8: G-test (Cont'd)

	AND	BLR	CAU	FLE	POL	SPN
US1	681.6089	949.8528	1044.4484	1018.1482	1313.8867	1147.5273
US2	873.9698	1193.3600	1413.5024	1345.8695	1775.0813	1548.8081
ANG	883.2368	1118.5775	1275.2731	1231.9263	1470.5598	1355.2976
SAF	946.0394	1259.1360	1347.4409	1312.3367	1584.3025	1425.7090
EGU	831.1876	1117.4847	1275.5774	1177.8361	1488.0153	1311.7319
GUB	760.4780	960.4456	1036.7103	1000.3499	1215.0681	1098.9459
HAT	806.1568	1076.9105	1138.1791	1094.1213	1371.2069	1187.7039
HUT	803.9218	982.7222	1098.8838	1081.3782	1249.1531	1185.1730
JAM	666.4562	912.5247	978.4950	948.8259	1174.8984	1039.3077
KEN	619.4303	823.0012	835.1530	827.1734	983.0800	891.3480
MAD	656.8502	799.5281	863.2474	849.9046	943.9898	908.0583
MOZ	970.4476	1301.5133	1439.9630	1420.3245	1726.0402	1557.8480
NAM	1316.3779	1716.7960	2128.6575	1949.6779	2491.4854	2229.7070
NWP	871.0754	1150.2979	1319.9277	1277.3502	1710.0082	1462.1938
TAN	1203.8531	1595.0778	1900.5359	1805.7930	2265.0481	2074.0374
TUT	976.5187	1242.6163	1480.4247	1403.4790	1682.7332	1564.5051
UGA	845.9526	1026.6661	1078.6869	1088.3894	1281.5101	1225.9478
CCS	889.4481	1176.4991	1356.3972	1272.7761	1577.0469	1384.5605
JAP	1030.0175	1547.7587	1952.4344	1806.0680	2485.0547	2096.0361
KOR	891.8792	1247.3016	1462.3920	1391.4364	1799.3508	1547.2969
MAL	695.2513	972.6280	1192.6473	1130.7333	1423.9149	1216.8807
PHI	711.6191	914.1631	1044.2216	990.5612	1174.5063	1085.7383
CSH	874.6797	1201.5341	1388.6058	1331.6224	1709.8162	1476.5314
CAR	351.6024	551.6054	503.3499	533.7566	753.9863	527.7271
MEX	493.6120	726.5411	783.9633	740.4211	1093.4510	840.4451
CSR	491.1570	716.8347	726.0587	752.0983	1151.3206	829.2176
HIS	378.2934	507.0346	451.7975	484.1142	674.2834	510.1093
MAR	303.9688	479.3408	423.3698	457.7372	618.5443	461.2663
MET	910.9257	1208.4436	1256.2998	1165.7612	1651.3641	1436.8680
PRA	376.5916	593.3844	509.8419	543.5773	734.4340	528.5404
BRA	379.7395	570.6100	528.9551	564.9875	784.5393	570.0999
AND		259.4031	254.3532	240.6117	295.3663	191.7305
BLR	0.0000		286.8939	272.8293	202.3072	336.5193
CAU	0.0000	0.0000		229.5211	276.5790	287.8519
FLE	0.0000	0.0000	<i>0.0030</i>		330.2069	319.8255
POL	0.0000	0.0602	0.0000	0.0000		387.8344
SPN	<i>0.0329</i>	0.0000	0.0000	0.0000	0.0000	

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Table 8: G-test (Cont'd)

Haiti			
	m_L	m_Y	m_{RH}
Parental Groups			
African	0.955 ± 0.022^a	0.778177 ± 0.122908^b	1.0021 ± 0.0359^b
East Asian	0.003 ± 0.025^a	$-0.0758699 \pm 0.193892^b$	-0.0219 ± 0.0347^b
European	0.043 ± 0.027^a	0.297693 ± 0.252631^b	0.0198 ± 0.0527^b
Jamaica			
	m_L	m_Y	m_{RH}
Parental Groups			
African	0.783 ± 0.020^a	0.764788 ± 0.126145^b	0.8212 ± 0.0657^b
East Asian	0.057 ± 0.022^a	0.0564919 ± 0.179226^b	0.0373 ± 0.0423^b
European	0.160 ± 0.024^a	0.17872 ± 0.239307^b	0.1415 ± 0.0657^b
New Providence (Bahamas)			
	m_L	m_Y	m_{RH}
Parental Groups			
African	0.780 ± 0.017^a	0.783536 ± 0.105421^b	0.8366 ± 0.0243^b
East Asian	0.000 ± 0.019^a	-0.0707197 ± 0.148^b	-0.0547 ± 0.0315^b
European	0.220 ± 0.021^a	0.287184 ± 0.186574^b	0.2181 ± 0.0379^b
US African American 1 (Minnesota)			
	m_L	m_Y	m_{RH}
Parental Groups			
African	0.780 ± 0.019^a	0.697312 ± 0.0705579^b	0.8276 ± 0.0440^b
East Asian	0.004 ± 0.022^a	$-0.0609425 \pm 0.217413^b$	-0.0215 ± 0.0443^b
European	0.216 ± 0.024^a	0.36363 ± 0.230357^b	0.1939 ± 0.0550^b
US African American 2 (General)			
	m_L	m_Y	m_{RH}
Parental Groups			
African	0.782 ± 0.016^a	0.711886 ± 0.0651698^b	0.8228 ± 0.0297^b
East Asian	0.030 ± 0.018^a	$-0.0178861 \pm 0.158548^b$	0.0101 ± 0.0210^b
European	0.188 ± 0.019^a	0.306 ± 0.188193^b	0.1671 ± 0.0360^b

Table 9: Admixture analyses for the New World African populations

Supporting Information Figure 1: Histograms comparing allele frequency data for Haiti and Jamaica per STR locus

Supporting Information Figure 2: Multidimensional Scaling Plot (Stress = 0.13124) of all populations at 13 loci

Supporting Information Figure 3: *Structure* bar plots assuming three and four ancestral populations ($K=3$ and $K=4$)

Haiti

Parental Groups	Slow	Fast	All loci
African	0.994 ± 0.064	0.921 ± 0.025	0.955 ± 0.022
East Asian	0.006 ± 0.079	0.000 ± 0.027	0.003 ± 0.025
European	0.000 ± 0.067	0.079 ± 0.032	0.043 ± 0.027

Jamaica

Parental Groups	Slow	Fast	All loci
African	0.677 ± 0.056	0.845 ± 0.022	0.783 ± 0.020
East Asian	0.038 ± 0.068	0.081 ± 0.024	0.057 ± 0.022
European	0.285 ± 0.058	0.074 ± 0.029	0.160 ± 0.024

New Providence
(Bahamas)

Parental Groups	Slow	Fast	All loci
African	0.809 ± 0.057	0.762 ± 0.020	0.780 ± 0.017
East Asian	0.000 ± 0.069	0.004 ± 0.021	0.000 ± 0.019
European	0.191 ± 0.059	0.234 ± 0.025	0.220 ± 0.021

US African American 1

Parental Groups	Slow	Fast	All loci
African	0.793 ± 0.048	0.766 ± 0.023	0.780 ± 0.019
East Asian	0.000 ± 0.059	0.041 ± 0.024	0.004 ± 0.022
European	0.207 ± 0.050	0.193 ± 0.029	0.216 ± 0.024

US African American 2

Parental Groups	Slow	Fast	All loci
African	0.774 ± 0.072	0.791 ± 0.016	0.782 ± 0.016
East Asian	0.000 ± 0.088	0.048 ± 0.017	0.030 ± 0.018
European	0.226 ± 0.074	0.160 ± 0.021	0.188 ± 0.019

Supporting Information Table 1: Admixture estimates generated for slow vs. fast mutating loci

IV. DIVERGENT GENETIC STRATA IN FIVE BAHAMIAN ISLANDS

A. Introduction

Depicted as “one of the Atlantic’s most geographically [complex] nations” [1], the Bahamas, a chain of 29 islands, 661 cays and 2,387 rocks [2], spans approximately 550 miles from southeastern continental Florida to the northernmost part of Haiti (Cape Haitien). Over the past 500 years, this archipelago has witnessed a series of migratory events emanating from several different sources including, but not limited to, the Arawak Indians, Eleutherian Adventurers, Loyalists, Creole slaves, liberated Africans as well as Chinese, Greek, Jew, Lebanese [3], Jamaican and Haitian [4] migrants. However, the extent that each group contributed to the Bahamian gene pool remains unclear and the degree of genetic admixture between groups is relatively unexplored.

In an early study designed to characterize the genetic composition of the Bahamian population, elevated levels of Hemoglobin (Hb) S, C and F variants were detected in residents of Bimini and are suggested by the authors to result from the influx of Africans into the island [5]. Genetic ties with continental and/or New World Africans were also observed in investigations performed by Duncan et al. [6] and Herrera et al. [7] utilizing the D1S80 hypervariable marker. More recent reports from my group [8, 9] also corroborate the phylogenetic relationships between Bahamians and Africans (from the mainland as well as the New World) detected in the aforementioned studies. Unfortunately, no study to the authors’ knowledge has attempted to characterize any of the Bahamian islands (outside of New Providence and Bimini) independently despite the

high possibility of asymmetrical gene flow from varied sources to each insular population.

Despite the archipelago's minute landmass (13,943 km²) and relatively low population density (22/km²) [10], the Bahamas exhibits some of the highest murder, assault and rape rates per capita [11], reinforcing the importance of Bahamian-specific DNA databanks. Although STR datasets are available for the general (All) Bahamian population [12] as well as for a collection from New Providence [8], differences observed between the two may signal statistically significant heterogeneity among the islands of the archipelago. Therefore, the current investigation was undertaken to establish anthropologically well-characterized datasets across the 15 Identifiler forensic loci for several of the more densely populated islands in the Bahamian chain, namely Abaco, Eleuthera, Exuma, Grand Bahama and Long Island. Also, the genetic profiles of the five Bahamian islands under scrutiny were employed to assess their phylogenetic relationships to pertinent geographically targeted reference collections.

B. Materials and Methods

Sample Collection and DNA Isolation

Buccal swabs were collected from 535 unrelated individuals residing in the islands of Abaco (n=111), Eleuthera (n=112), Exuma (n=92), Grand Bahama (n=133) and Long Island (n=87) (Fig. 1) with informed consent. Genealogical information for every donor was recorded for at least two generations to establish local descent. All samples were procured according to the ethical guidelines stipulated by the institutions

involved. Genomic DNA was extracted using the Gentra Buccal Cell Kit (Puregene, Gentra Systems, Minneapolis, MN) according to the manufacturers' instructions and stored at -80°C in the Puregene™ DNA hydration solution (10mM Tris, 1mM EDTA, pH 8.0). DNA quantification was performed with a NanoDrop 2000 spectrophotometer (NanoDrop products, Wilmington, DE) and each sample was diluted to a final concentration of 0.75ng/μl prior to PCR amplification.

STR Genotyping

All samples were amplified across the 15 autosomal STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA) included in the commercially available AmpF/STR® Identifiler kit (Applied Biosystems, Foster City, CA). Amplification reactions were performed in an Eppendorf Mastercycler® gradient (Eppendorf, Hamburg, Germany) according to the manufacturer's recommended protocols [13]. Following amplification, PCR products were separated by multicapillary electrophoresis in an ABI 3130xl Genetic Analyzer using POP 7™ as the separation medium and ABI GeneScan™ 500 LIZ® as the internal size standard. The resulting STR fragments were genotyped with the GeneMapper® software v3.2, which determines allele size and designation through comparisons to the internal size standard and allelic ladder, respectively. Off-ladder alleles are those characterized by incomplete repeat sequences [14].

Statistical and phylogenetic analyses

Allelic frequencies for the 15 STR loci typed in the collections from Abaco, Eleuthera, Exuma, Grand Bahama and Long Island were determined with the GenePop v 3.4 program [15]. To compare the distribution of alleles among these populations, histograms for each STR locus were constructed with Microsoft Excel. The Arlequin version 3.11 software package [16] was utilized to compute observed and expected heterozygosities (H_o and H_e , respectively) as well as gene diversity indices (GDI) and Hardy-Weinberg equilibrium (HWE) P values. Possible inbreeding in these island populations was assessed through calculation of F_{IS} values for each of the 15 STR markers with GenePop v 3.4 [15]. Additionally, several parameters of forensic and population genetics interest, including matching probability (MP), power of discrimination (PD), polymorphic information content (PIC), power of exclusion (PE) and typical paternity index (TPI) were estimated employing the PowerStats 1.2 software [17, 18].

Genetic distances (F_{st}) among the five Bahamian populations studied and the 43 geographically targeted reference collections [8, 9, 19-53] were computed using the GeneDist option of the PHYLIP 3.52c software [54]. Utilizing the F_{st} distances generated, multidimensional scaling (MDS) plots were constructed with the Statistical Package for the Social Sciences (SPSS) version 14.0 [55]. The analysis was performed at the all populations level and was repeated to include only the African and African-derived (Bahamian, Afro-American and Afro-Caribbean) populations to better assess phylogenetic associations between them. Because of its sizeable Austronesian genetic component [27], Madagascar was excluded from the latter analysis.

To determine the African, East Asian, European and Native American genetic contributions made to the gene pools of the Bahamian populations under study, admixture determinations employing the Weighted Least Square (WLS) method described in Long et al. [56] were performed using SPSS version 14.0 [55]. In addition to quantifying admixture proportions for Abaco, Eleuthera, Exuma, Grand Bahama and Long Island, the impact of parental populations on New Providence was reevaluated to assess potential influences from the Native American collections, which were not included in my earlier studies [8, 9]

Inter-, intra- and total population (G_{st} , H_s and H_t , respectively) genetic variance values were calculated with the DISPAN program [57]. The collections examined were assembled into population groups representing the different biogeographic areas demarcated in Table 1. In addition, G-tests [58] were conducted to determine the statistical significance of genetic differences among all 48 populations examined. The significance of each pair-wise comparison was assessed through 100,000 simulations, both before (in bold) and after (in italics) application of a conservative Bonferroni adjustment ($\alpha = 0.05/1128 = 0.000044326$).

Population substructure was ascertained using the *Structure* software v. 2.3.3 [59] available at <http://pritch.bsd.uchicago.edu/structure/html>. For this test, the autosomal profiles of individuals residing in Abaco, Eleuthera, Exuma, Grand Bahama, Long Island and New Providence were analyzed alongside the reference African (Kenya, Madagascar, Rwanda Hutu and Tutsi), East Asian (Atayal and Ami from Formosa, and Java [60]), Native American (Kakchikel, K'iche and Yucatan Mayan populations) and European (Spain, Sweden and Greece) populations for which genotypic data has been provided by

the authors. Prior to analysis, incomplete alleles were replaced with integers (outside of the normal allele range) and missing and/or null alleles were assigned a value of -9 as indicated by the *Structure* program. Clustering was performed at $K=3$ and $K=4$ using the admixture model that does not require population of origin information and assumes allele frequencies in the populations under study to be correlated to each other. For each K value, a burn-in period of 20,000 generations followed by 20,000 Markov chain Monte Carlo (MCMC) simulations was employed.

C. Results

Intra-population Diversity

Allelic frequencies generated for the collections from Abaco, Eleuthera, Exuma, Grand Bahama and Long Island are listed in Supplementary Tables 1 through 5, respectively. Also provided in Supplementary Table 6 are several indices of forensics and population genetics interest. Examination of allelic distributions among these populations reveals no substantial differentiation in allelic counts, which range from 144 in Exuma to 154 in Abaco (Table 2), but does illustrate that each collection is characterized by the presence of unique alleles in relation to the other Bahamian islands surveyed (Supplementary Figure 1); Abaco was found to possess the greatest number of distinct alleles (12) while both Grand Bahama and Long Island exhibit the least (3). These findings are not surprising given that Abaco harbors the highest observed average heterozygosity value (0.80187) and Long Island, the lowest (0.78084) (Table 2). Interestingly, each Bahamian population possesses seven or more loci with lower than

expected H_0 values, yet departures from HWE expectations (Table 3) were detected only in the collections from Abaco (D2S1338), Exuma (D8S1179) and Long Island (D8S1119, D19S433 and FGA). These deviations, however, did not persist after application of the Bonferroni correction ($\alpha = 0.05/15 = 0.0033$).

The highest GDI values are noted for D2S1338 in Abaco and Grand Bahama, D18S51 in Eleuthera, and FGA in both Long Island and Exuma. The D13S317 locus, in contrast, exhibits the lowest genetic variability in all populations examined, with the exception of Long Island. Of the 15 STR markers, D2S1338 (Abaco, Eleuthera and Grand Bahama), D18S51 (Abaco and Long Island) and FGA (Exuma) possess the strongest discriminative power while D5S818 (Long Island), D3S1358 (Abaco) and D13S317 (Eleuthera, Exuma and Grand Bahama) were found to be the least discriminatory (Supplementary Table 6). Although the combined power of exclusion (CPE) is >99.9% for all five collections, the combined power of discrimination (CPD) values differ, ranging from 67.3% for Abaco to 73.0% for Exuma (Table 2).

The 15 Identifiler loci in the Bahamian (0.80162) and New World African (0.79785) assemblages exhibit the highest average intra-population variance values of all groups examined, including the continental African conglomerate (0.79404), while the lowest overall H_s levels were observed among the Native American (0.72701) and Asian (0.78131) groups of populations (Table 4). Even though the Bahamian group displays the highest intra-population diversity, three islands, Exuma, Long Island and Grand Bahama, were found to possess either one or two loci with statistically significant heterozygote deficiencies (Table 3).

Inter-population Diversity

The G-test results (Supplementary Table 7) reveal statistically insignificant genetic differences between the Bahamian collections and several of the continental African populations (*i.e.*, Angola, Equatorial Guinea, Guinea-Bissau and the Bantu group from Kenya) either before or after application of the Bonferroni correction. In addition, Abaco, Eleuthera, Exuma, Grand Bahama and New Providence were not found to differ significantly from the other New World groups of African descent (Haiti, Jamaica and the two US African American collections), likely attributed to genetic contributions from similar ancestral sources and/or gene flow among these populations. Interestingly, Long Island was the only Bahamian collection to exhibit genetic heterogeneity with all 47 populations examined in the pair-wise analyses.

In the global MDS plot (Fig. 2A), five clusters are distinctly delineated according to biogeographic origin. In the upper left quadrant, a tightly packed European group lies proximal to the more loosely associated conglomerate of East Asian populations while the Native American collections occupy the extreme lower left portion of the graph. The Latin American groups form an assemblage at the center of the projection with Brazilians and Puerto Rican Americans occupying the right half of the plot close to the African collections. Within the African cluster, a clear demarcation between the New World (with the exemption of Haiti) and continental Africans (excluding Angola, Madagascar and Mozambique) is apparent; Abaco, Eleuthera, Exuma, Grand Bahama, Long Island, New Providence, Jamaica and the two US Afro-American collections (US1 and US2) segregate together with Angola, Mozambique and Madagascar at the periphery of the continental African conglomerate, occupying a transitional position between this group of

populations and the Latin American and European clusters. Specifically, within the New World/Angola/Madagascar/Mozambique assemblage, Abaco partitions centrally with Jamaica, New Providence, Angola and the two US African American populations while Eleuthera, Grand Bahama, Exuma and Long Island plot peripherally. Also noteworthy is Long Island's position nearest to Madagascar, an island off the East African coast, which shares approximately 33.9% of its autosomal component with Austronesians [27].

Phylogenetic relationships among the Bahamian, Afro-Caribbean, Afro-American and continental African populations apparent in the global projection are also noted in the MDS analysis employing only the African and African-derived groups (Fig 2B). In both graphs, Abaco partitions along with New Providence and the two US African American (US1 and US2) collections. In Figure 2B, however, the above mentioned New World populations cluster not only with Angola but also with Equatorial Guinea and Nigeria, two additional, historically known West African sources of slaves. Genetic ties between Bahamians and West Africans are also evident in the segregation of Exuma with Guinea-Bissau and Grand Bahama with the Bantu group from Kenya as well as in the positioning of Eleuthera intermediate to the collections from Angola and Guinea-Bissau. Long Island, in contrast, plots as an outlier, displaying a considerable degree of genetic separation from the other Bahamian populations as well as the continental and New World African collections.

When G_{st} values (Table 4) are compared, the Bahamian populations exhibit one of the lowest average inter-population diversity levels (0.00583) while the Native American group possesses the highest (0.02412). The Bahamian assemblage was also found to

exhibit the highest total population (H_t) variance (0.80633), followed by the continental (0.80287) and New World (0.80053) African conglomerates.

Results of the admixture analyses (Table 5) indicate that the largest genetic contributor to the Bahamian gene pool is continental Africa, with Long Island, Abaco, Eleuthera, Grand Bahama and Exuma sharing approximately 65.4%, 75.0%, 80.3%, 86.7% and 90.4% of their autosomal component with the African collections, respectively. Influences from the European populations are the second largest for all hybrid collections but are most prominent in Long Island (26.9%). East Asian genetic signals were only present in Long Island (7.7%), Abaco (1.5%) and Grand Bahama (0.5%) while Native American influences were detected in Grand Bahama (3.9%), Exuma (5.9%) and Eleuthera (6.0%). Recalculation of admixture estimates for New Providence identifies proportions similar to those observed in my earlier reports [8, 9] with only minimal (0.06%) genetic contributions from Native Americans.

In the *Structure* bar plots (Supplementary Figure 2), assessment of the African (red and yellow colors at $K=3$ and $K=4$, respectively) and European (blue and red colors at $K=3$ and $K=4$, respectively) ancestral components in the Bahamian populations was possible at $K=3$ and $K=4$. At both K values, the Bahamian groups exhibit patterns mirroring those of the continental African collections, although Long Island, Abaco, Eleuthera and New Providence also possess distinct groups of individuals whose profile is consistent with the one observed in the European populations. Membership proportions (Table 6) indicate that the majority of samples in each Bahamian collection share membership within the African cluster, with the highest percentages being observed in Exuma (80.1% for $K=3$ and 75.3 % for $K=4$) and the lowest in Long Island (59.4% for

$K=3$ and 53.2 % for $K=4$). European membership proportions, which range from 11.5% to 28.5% when $K=3$ and from 9.3% to 20.6% when $K=4$, are comparable to those obtained from this parental group in the admixture tests (Table 5), with Long Island receiving the strongest European genetic signals and Exuma the weakest. Native American proportions (with the exception of New Providence, which exhibits larger genetic contributions from Native Americans) generated by both the SPSS (uses Long's WLS approach) and *Structure* programs are commensurate yet, the percentage of East Asian DNA in each population's gene pool is substantially higher in the membership proportion results (Table 6). The relatively stronger genetic signals from the East Asian group are likely the result of their shared genetic profiles with the European collections.

D. Discussion

In the present study, allelic frequencies for the 15 Identifiler loci routinely employed in forensic applications are reported for five Bahamian collections representing the more populous northwest (Grand Bahama and Abaco) and central (Eleuthera, Exuma and Long Island) portions of the archipelago. Although several published reports [5-9] have established genetic links between Bahamians and Africans, the current investigation represents the first to delineate phylogenetic relationships and identify differential genetic stratification among the Bahamian islands.

As a group, the Bahamian populations exhibit an average of 152 allelic types, however, when considered on an individual basis, total allele numbers vary, ranging from 144 in Exuma (Table 2) to 173 in New Providence [8]. This average, although comparable to that of the continental African collections (151), is lower than the allelic

counts for the other New World groups of African descent [Afro-Caribbean (159) and Afro-American (165)]. The reduced number of alleles present in each of the Bahama Island populations (with the exception of New Providence), in combination with the seven or more loci that display lower than expected H_o values, is likely the result of genetic isolation, bottlenecks and/or inbreeding. Another plausible explanation is that the Bahamas has not witnessed the degree of genetic admixture experienced by other nations within the Caribbean basin [61, 62]. Despite expectations of decreased genetic variability, the Bahamian islands examined actually exhibit the highest intra-population variance (H_s) of all groups examined (Table 4), suggesting that each population's gene pool represents a mosaic of several different groups. This high level of diversity is supported by the *Structure* analyses which reflect several degrees of sub-population structure in the populations of the five Bahamian islands. Furthermore, Abaco (0.81441), Grand Bahama (0.80187) and Eleuthera (0.79986) possess average heterozygosities that exceed the mean values for the mainland African collections (0.79777) as well as both New World African groups [Afro-Caribbean (0.78974) and Afro-American (0.79977)], reflecting a high level of diversity throughout the island chain.

When inter-population diversity (Table 4) is examined, Bahamians possess the third to lowest value (0.00583) after New World Africans (0.00334) and Europeans (0.00337). The higher average G_{st} in the populations from the Bahamas, as compared to that among the New World African collections, may result from genetic drift, geographical isolation and/or differential gene flow. Genetic stratification among the islands is also evident in the widespread segregation of the Bahamian collections in both MDS projections (Fig. 2A,B) as well as in the sub-population structure patterns observed

in the *Structure* bar graphs (Supplementary Figure 2). Of particular interest is the Long Island population, which displays a considerable degree of heterogeneity from the other Bahamian collections, not only in the aforementioned analyses but also in the G-test (Supplementary Table 7) where it exhibits statistically significant genetic differences with all populations in the pair-wise comparisons, even after application of the Bonferroni adjustment.

Admixture (Table 5) as well as membership proportions (Table 6) for Abaco, Eleuthera, Exuma, Grand Bahama, Long Island and New Providence identify continental Africa as the primary genetic contributor to Bahamian gene pool. These findings are anticipated given the large number of Creole slaves and liberated Africans transported to the colony during the slave trade [63] and post-slave trade [2] eras, respectively. In addition, migrants from several other African-derived populations in the West Indies, including Turks and Caicos, Haiti, Jamaica and Barbados, are known to have been incorporated into Bahamian society [4, 64]. The high percentage of African DNA present is also reflected in the *Structure* bar plots (Supplementary Figure 2), where each Bahama Island population was found to share membership in the same cluster of similar profiles with the continental Africans collections, likely inferring a common genetic ancestry [65]. Furthermore, several alleles representative of the continental and New World Africans collections examined in the current report are observed in Abaco (D21S11-24.3 and FGA-30.2), Exuma (D21S11-33.1, D21S11-37 (also present in Mexico [42]), D7S820-6 (also detected in Honduras [45]) and vWA-12), and Long Island (FGA-31.2 (also exhibited by Caracas [41])).

Although each hybrid shares the majority of its autosomal component with the African collections, substantial variation in admixture (Table 5) as well as membership proportions (Table 6) exists among the islands. The relatively lower percent contribution (65.4% in the admixture tests; 59.4% ($K=3$) and 53.2% ($K=4$) in the membership proportion results) detected in Long Island is supported by the segregation of this population away from the New World and continental African collections (excluding Madagascar) in both MDS projections (Fig. 2A,B). Long Island also exhibits significant heterogeneity with all populations in the G-test (Supplementary Table 7). Meanwhile, the positioning of Abaco, New Providence and Eleuthera near the center of Figure 2B corroborates the intermediate level of African genetic input (Tables 5 and 6) detected in these islands while Grand Bahama and Exuma, which receive larger African contributions (Tables 5 and 6), lie on the periphery of the graph proximal to Guinea-Bissau and Namibia, respectively. Additionally, the Bahamian populations (with the exception of Long Island) were not found to differ significantly from Angola, Guinea-Bissau, Equatorial Guinea and/or Kenya in the G-test pair-wise analyses.

A contrasting distribution pattern of European genetic influences is noted throughout the archipelago, with Long Island displaying the strongest genetic signal and Exuma, the weakest (Tables 5 and 6). Genetic input from Europeans stems from two main sources: (1) British Independents from Bermuda [66] and (2) the Loyalists. Sharer [2], in his work on Bahamian population growth, reports “a peculiar distribution of Europeans” in the Bahamas, noting that those islands permanently settled by the Bermudian colonists (*i.e.*, Eleuthera, New Providence and Abaco) possessed the highest proportions of Europeans in 1943, a trend that is observed not only in the admixture

analyses (Table 5) but also in the bar graphs (Supplementary Figure 2) and membership proportions (Table 6) generated by *Structure*. Additional sources of European gene flow include Greeks, Eastern European Jews [3], Canadians, Americans and migrants from the United Kingdom [64].

Genetic signals from the East Asian populations are restricted to the collections from Long Island (7.7%), Abaco (1.5%) and Grand Bahama (0.05%) in the admixture tests (Table 5) but are detected in all six populations (ranging from 10.1% to 21.4% at $K=4$) in the membership proportion results (Table 6), with the most notable contribution in both analyses being observed in Long Island. Genetic influences from East Asia are most likely attributed to the two waves of Chinese immigration that took place during the late nineteenth (1879) and early twentieth (1920s) centuries [67]. Unfortunately, records regarding the number of Chinese migrants entering the colony and the island(s) on which they settled are scanty. Native American contributions, on the other hand, are detected in New Providence (0.6%), Grand Bahama (3.9%), Exuma (5.9%), and Eleuthera (6.0%) in the admixture analyses (Table 5) and in all six collections (ranging from 4.4% to 13.8% at $K=4$) in the membership proportion results (Table 6). Genetic input from this group, although minimal, may represent genetic signatures of the indigenous Arawak Indian population. A more plausible explanation is through immigration from Turks and Caicos, a group of islands to the southeast of the Bahamas, which over the years has received a number of migrants from the Dominican Republic [68]. According to Torroni et al. [69], the Dominican maternal gene pool is characterized by an Amerindian-specific component.

Considering the genetic differences among the five Bahamian islands examined in this study, it is not surprising to uncover dissimilarities among the previously published All Bahamian dataset [12], the database for New Providence [8] and the insular-specific datasets generated. These differences include the absence of frequency data for loci D2S1338 and D19S433 which were not typed for the general Bahamian population. The incorporation of these two additional hypervariable markers provides greater discriminatory resolution to this battery of autosomal STR markers. Also, in the All Bahamian dataset small and large alleles are grouped together (*e.g.*, alleles 8, 9, 10 and 11 are designated as <11 at D18S51) at several loci. The clustering of the smaller and/or larger alleles (*e.g.*, <11 at D18S51 and <18 and >30 at FGA) prevents assessment of the specific allele in question when utilizing this database for forensic statistical calculations. Furthermore, an 11 year old database, considering the population dynamics (*e.g.*, recent migrations from neighboring countries, including Haiti and Jamaica) of the islands, may not accurately represent present-day allelic frequencies.

E. Conclusion

Overall, my data reflects a high level of diversity throughout the Bahamian chain indicating that Bahamians are a heterogeneous group, receiving genetic contributions from a wide array of sources. Although all five populations surveyed display a closer genetic relationship with Africans than with any other group examined, differential genetic stratification among them is noted in the MDS and admixture analyses as well as in the membership proportion results. In addition, the *Structure* bar plots reveal collage-like profiles signaling the presence of sub-population structure in the islands of Abaco,

Eleuthera, Long Island and New Providence. These genetic differences, in combination with the presence of alleles not in common among the five Bahamian islands, indicate island-specific heterogeneity within the archipelago. This is especially the case when considering the Long Island population, where the G-test indicates statistically significant genetic differences in all pair-wise analyses (both before and after application of the Bonferroni correction) including those with the other four Bahamian populations studied as well with the New Providence and New World African (Afro-American and Afro-Caribbean) collections.

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Appendix IV

Fig. 1: Geographic locations of Abaco (ABA), Eleuthera (ELU), Exuma (EXU), Grand Bahama (GRB) and Long Island (LNG) within the Bahamian archipelago

Fig. 2A: Multidimensional Scaling plot (Stress = 0.10286) of all populations

Fig. 2B: Multidimensional Scaling plot (Stress = 0.22533) of African and African-derived collections

Biogeographical origin	Population	Abbreviation	Sample Size	Reference
Bahamian	Abaco	ABA	111	<i>Present study</i>
	Eleuthera	ELU	112	<i>Present study</i>
	Exuma	EXU	92	<i>Present study</i>
	Grand Bahama	GRB	133	<i>Present study</i>
	Long Island	LNG	87	<i>Present study</i>
	New Providence	NWP	221	[8]
Afro-Caribbean†	Haiti	HAT	111	[9]
	Jamaica	JAM	119	[9]
Afro-American†	US African American 1 (Minnesota)	US1	157	[19]
	US African American 2 (General)	US2	258	[20]
West African	Cabinda (Angola)	ANG	110	[21]
	Guinea-Bissau	GUB	92	[22]
	Equatorial Guinea	EGU	134	[23]
	Namibia	NAM	195	[24]
	Nigeria	NIG	337	[25]
East African	Hutu (Rwanda)	HUT	95	[26]
	Kenya	KEN	65	[26]
	Madagascar	MAD	67	[27]
	Maputo (Mozambique)	MOZ	144	[28]
	Tanzania	TAN	272	[29]
	Tutsi (Rwanda)	TUT	126	[30]
	Uganda	UGA	90	[31]
South African	Cape Town (South Africa)	SAF	98	[32]
East Asian	Chao Shan (South China)	CCS	144	[33]
	Japan	JAP	526	[34]
	Korea	KOR	231	[35]
	Malaysia	MAL	210	[36]
	Philippines	PHI	106	[37]
	Shaanxi Han (NW China)	CSH	203	[38]
Native American	Guarani	GUA	50	[39]
	Kakchikel	KAK	59	[40]
	K'iche	KIC	27	[40]
	Yucatan	YUC	121	[40]
Latin American	Caracas (Central Venezuela)	CAR	255	[41]
	Central Mexico	MEX	211	[42]
	Costa Rica	CSR	500	[43]
	El Salvador	ELS	228	[44]
	Hispanic (US -Minnesota)	HIS	151	[19]
	Honduras	HON	198	[45]
	Maracaibo (Venezuela)	MAR	203	[46]
	Metztitlán (Mexico)	MET	180	[47]
	Puerto Rico American (Massachusetts)	PRA	205	[48]
	Rio de Janeiro (Brazil)	BRA	300	[49]
European	Caucasian (US - General)	CAU	302	[50]
	Greece	GRE	300	[51]
	Portugal	POR	2125	[52]
	Spain	SPN	342	[53]
	Sweden	SWE	311	[54]

† These groups are combined in some analyses as New World Africans. For specific analyses see Materials & Methods.

Table 1: Populations analyzed

Population	No. of Alleles	Avg H_e	CMP	CPD	CPE
Abaco	154	0.81441	6.0957E+17	0.6725596555	0.999999803
Eleuthera	148	0.79986	1.114E+17	0.719034632	0.999999408
Exuma	144	0.79131	7.2498E+16	0.7302691485	0.999999554
Grand Bahama	149	0.80187	4.0009E+17	0.6819381436	0.999999535
Long Island	145	0.78084	3.2122E+17	0.6960417459	0.999998200

Table 2: Parameters of forensic and population genetics interest

Locus	Abaco				Eleuthera				Exuma			
	H _o	H _e	HWE	F _{IS}	H _o	H _e	HWE	F _{IS}	H _o	H _e	HWE	F _{IS}
D8S1179	0.76577	0.81301	0.80445	0.0584	0.77679	0.75857	0.96226	-0.0241	0.72826	0.75944	<i>0.03445</i>	0.0413
D21S11	0.90991	0.86776	0.93121	-0.0488	0.89286	0.84910	0.09641	-0.0518	0.84783	0.84058	0.92516	-0.0087
D7S820	0.83784	0.79475	0.72825	-0.0545	0.76786	0.77386	0.99972	0.0078	0.83696	0.78908	0.43687	-0.0610
CSF1PO	0.82883	0.77689	0.80345	-0.0672	0.74107	0.74135	0.16399	0.0004	0.80435	0.75493	0.71746	-0.0658
D3S1358	0.75676	0.75692	0.06352	0.0002	0.80357	0.77002	0.14962	-0.0438	0.73913	0.72054	0.41334	-0.0259
TH01	0.78378	0.76870	0.51328	-0.0197	0.79464	0.78303	0.14210	-0.0149	0.73913	0.76746	0.41596	0.0371
D13S317	0.78378	0.75541	0.07326	-0.0377	0.71429	0.70992	0.14828	-0.0062	0.67391	0.69779	0.91552	0.0344
D16S539	0.73874	0.80995	0.36917	0.0883	0.76786	0.81538	0.78695	0.0585	0.65217	0.77251	0.14300	0.1565
D2S1338	0.86486	0.89434	<i>0.01319</i>	0.0331	0.87500	0.88625	0.78298	0.0128	0.85870	0.88673	0.60520	0.0318
D19S433	0.85586	0.84379	0.95210	-0.0144	0.81250	0.83836	0.12827	0.0310	0.85870	0.82294	0.52092	-0.0437
vWA	0.83784	0.82165	0.40457	-0.0198	0.81250	0.79056	0.50154	-0.0279	0.70652	0.81159	0.07931	0.1301
TPOX	0.77477	0.77869	0.76354	0.0050	0.75676	0.77726	0.72729	0.0265	0.84783	0.79205	0.65367	-0.0708
D18S51	0.88288	0.88158	0.86188	-0.0015	0.89286	0.88837	0.24703	-0.0051	0.85870	0.86636	0.66511	0.0089
D5S818	0.75676	0.76503	0.74637	0.0109	0.78571	0.74752	0.47691	-0.0513	0.77174	0.77798	0.33374	0.0081
FGA	0.83784	0.86727	0.10227	0.0341	0.80357	0.87748	0.16620	0.0846	0.94565	0.88952	0.99769	-0.0635

HWE P values in italics are $< \alpha = 0.05$; F_{IS} values in bold represent associated P values $< \alpha = 0.05$

Table 3: Intra-population diversity indices for the Bahamian populations

Locus	Grand Bahama				Long Island			
	H _o	H _e	HWE	F _{IS}	H _o	H _e	HWE	F _{IS}
D8S1179	0.80451	0.79671	0.87995	-0.0098	0.71264	0.82001	<i>0.02718</i>	0.1316
D21S11	0.84962	0.84091	0.32556	-0.0104	0.78161	0.82971	0.62111	0.0583
D7S820	0.80451	0.79765	0.36357	-0.0086	0.85057	0.79158	0.95176	-0.0750
CSF1PO	0.77444	0.78539	0.66134	0.0140	0.74713	0.75497	0.32754	0.0104
D3S1358	0.71429	0.73993	0.56191	0.0348	0.60920	0.72912	0.05238	0.1653
TH01	0.80451	0.76164	0.20138	-0.0565	0.74713	0.77889	0.12645	0.0410
D13S317	0.66165	0.72799	0.11995	0.0914	0.77011	0.77782	0.48606	0.0100
D16S539	0.80451	0.79665	0.75466	-0.0099	0.83908	0.79682	0.67838	-0.0534
D2S1338	0.89474	0.89604	0.80579	0.0015	0.82759	0.88958	0.76268	0.0701
D19S433	0.86466	0.87093	0.30027	0.0072	0.83908	0.86639	<i>0.02676</i>	0.0317
vWA	0.84962	0.82241	0.30851	-0.0332	0.79310	0.82440	0.36944	0.0382
TPOX	0.78195	0.77568	0.34062	-0.0081	0.75862	0.76766	0.26181	0.0118
D18S51	0.81203	0.87090	0.16695	0.0678	0.85057	0.89529	0.26791	0.0502
D5S818	0.74242	0.75029	0.98880	0.0105	0.71264	0.72693	0.54526	0.0198
FGA	0.86466	0.85816	0.26612	-0.0076	0.87356	0.89649	<i>0.04548</i>	0.0257

HWE *P* values in italics are $< \alpha = 0.05$; F_{IS} values in bold represent associated *P* values $< \alpha = 0.05$

Table 3: Intra-population diversity indices for the Bahamian populations (Cont'd)

	Bahamian			New World African †			African			Asian		
Locus	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t	G _{st}	H _s	H _t
D8S1179	0.00616	0.78811	0.79299	0.00552	0.78764	0.79201	0.01168	0.77586	0.78503	0.00762	0.84279	0.84926
D21S11	0.00654	0.84166	0.84720	0.00243	0.84011	0.84216	0.01012	0.85178	0.86048	0.00871	0.81690	0.82408
D7S820	0.00622	0.78457	0.78948	0.00501	0.77856	0.78248	0.00853	0.76342	0.76999	0.00944	0.75886	0.76608
CSF1PO	0.00613	0.76285	0.76756	0.00192	0.78062	0.78212	0.01376	0.77664	0.78748	0.00874	0.72283	0.72920
D3S1358	0.00904	0.74247	0.74924	0.00378	0.75108	0.75393	0.01152	0.73082	0.73934	0.01191	0.71936	0.72803
TH01	0.00286	0.76538	0.76758	0.00521	0.73590	0.73975	0.01320	0.72643	0.73614	0.01452	0.69914	0.70944
D13S317	0.00534	0.72914	0.73306	0.00229	0.70197	0.70358	0.01077	0.71109	0.71883	0.00608	0.80024	0.80513
D16S539	0.00856	0.79550	0.80237	0.00295	0.79262	0.79497	0.00925	0.78909	0.79645	0.00957	0.77487	0.78235
D2S1338	0.00596	0.88636	0.89167	0.00242	0.88744	0.88959	0.01026	0.88062	0.88975	0.00706	0.86761	0.87377
D19S433	0.00423	0.84150	0.84507	0.00209	0.84433	0.84609	0.01130	0.83199	0.84150	0.01380	0.79961	0.81079
vWA	0.00496	0.81016	0.81420	0.00335	0.81387	0.81661	0.00967	0.81619	0.82416	0.00681	0.79667	0.80213
TPOX	0.00471	0.77575	0.77941	0.00538	0.75695	0.76105	0.02079	0.76301	0.77921	0.00567	0.62619	0.62976
D18S51	0.00640	0.87624	0.88188	0.00197	0.87834	0.88007	0.00690	0.86610	0.87211	0.00742	0.85343	0.85981
D5S818	0.00438	0.74986	0.75316	0.00220	0.75069	0.75234	0.00974	0.75268	0.76008	0.00761	0.78432	0.79033
FGA	0.00590	0.87483	0.88003	0.00400	0.86767	0.87115	0.00859	0.87488	0.88246	0.00468	0.85688	0.86091
All Loci	0.00583	0.80162	0.80633	0.00334	0.79785	0.80053	0.01100	0.79404	0.80287	0.00858	0.78131	0.78807

† The New World African assemblage includes the Afro-Caribbean and Afro-American groups of populations

Table 4: Inter-, intra- and total population genetic variance

Locus	European			Latin American			Native American			All populations		
	G_{st}	H_s	H_t	G_{st}	H_s	H_t	G_{st}	H_s	H_t	G_{st}	H_s	H_t
D8S1179	0.00258	0.81289	0.81499	0.00480	0.79695	0.80079	0.04425	0.72114	0.75453	0.02339	0.79043	0.80936
D21S11	0.00410	0.83263	0.83606	0.00377	0.83353	0.83669	0.02130	0.78235	0.79937	0.02398	0.83360	0.85408
D7S820	0.00253	0.80819	0.81024	0.00771	0.78777	0.79389	0.02102	0.69099	0.70583	0.03066	0.77045	0.79482
CSF1PO	0.00213	0.71876	0.72029	0.00312	0.72011	0.72236	0.00543	0.69694	0.70075	0.01495	0.74407	0.75536
D3S1358	0.00198	0.78931	0.79088	0.01391	0.74930	0.75987	0.00406	0.64577	0.64841	0.02005	0.73539	0.75044
TH01	0.00842	0.77844	0.78505	0.01688	0.76321	0.77631	0.00940	0.59100	0.59660	0.06824	0.73047	0.78397
D13S317	0.00301	0.78118	0.78353	0.01044	0.81336	0.82195	0.02490	0.79415	0.81443	0.04547	0.75926	0.79543
D16S539	0.00569	0.77226	0.77668	0.00741	0.78106	0.78689	0.06529	0.72020	0.77051	0.02227	0.77924	0.79699
D2S1338	0.00324	0.86862	0.87145	0.00897	0.86660	0.87444	0.02276	0.80745	0.82625	0.02256	0.87001	0.89009
D19S433	0.00340	0.78286	0.78553	0.00799	0.82660	0.83326	0.01867	0.81190	0.82735	0.02240	0.82224	0.84109
vWA	0.00187	0.80861	0.81012	0.00790	0.78317	0.78941	0.01685	0.71646	0.72874	0.02207	0.79682	0.81481
TPOX	0.00465	0.61984	0.62273	0.00875	0.67422	0.68017	0.06050	0.61551	0.65514	0.04403	0.70129	0.73359
D18S51	0.00244	0.87438	0.87652	0.00344	0.87671	0.87974	0.01180	0.83139	0.84132	0.01961	0.86698	0.88432
D5S818	0.00293	0.70337	0.70544	0.01129	0.71450	0.72266	0.02495	0.62816	0.64423	0.04563	0.73265	0.76768
FGA	0.00206	0.85976	0.86154	0.00592	0.87427	0.87948	0.01096	0.85179	0.86123	0.01470	0.86840	0.88135
All Loci	0.00337	0.78741	0.79007	0.00807	0.79076	0.79719	0.02412	0.72701	0.74498	0.02897	0.78675	0.81023

Table 4: Inter-, intra- and total population genetic variance (Cont'd)

Parental Groups	Hybrid population					
	Long Island	Abaco	New Providence	Eleuthera	Grand Bahama	Exuma
African	0.654± 0.029	0.750 ± 0.019	0.797± 0.016	0.803 ± 0.022	0.867 ± 0.023	0.904± 0.025
East Asian	0.077 ± 0.033	0.015 ± 0.022	0.000 ± 0.018	0.000 ± 0.025	0.005 ± 0.026	0.000 ± 0.029
European	0.269 ± 0.036	0.235 ± 0.024	0.196 ± 0.019	0.137 ± 0.027	0.089 ± 0.028	0.037 ± 0.031
Native American	0.000 ± 0.023	0.000 ± 0.015	0.006 ± 0.012	0.060 ± 0.017	0.039 ± 0.018	0.059 ± 0.020

Table 5: Admixture proportions generated using grouped parental sources

$K=3$		Long Island	Abaco	New Providence	Eleuthera	Grand Bahama	Exuma
	Inferred Cluster						
	African	0.594	0.625	0.747	0.724	0.771	0.801
	European	0.285	0.245	0.172	0.176	0.156	0.115
	East Asian/Native American	0.121	0.103	0.081	0.100	0.073	0.084
$K=4$		Long Island	Abaco	New Providence	Eleuthera	Grand Bahama	Exuma
	Inferred Cluster						
	African	0.532	0.611	0.702	0.677	0.722	0.753
	European	0.206	0.168	0.138	0.140	0.114	0.093
	East Asian	0.214	0.170	0.109	0.125	0.120	0.101
	Native American	0.048	0.051	0.138	0.058	0.044	0.053

Table 6: Membership proportions generated by *Structure*

Supplementary Figure 1: Histograms comparing allelic distributions in the five Bahamian populations surveyed

Supplementary Figure 2: *Structure* bar plots assuming three ($K=3$) and four ($K=4$) ancestral populations

Locus	n	Allele												
		6	7	8	9	9.3	10	10.2	11	11.2	12	12.2	13	13.2
D8S1179	111				0.0090		0.0315		0.0901		0.1216		0.2252	
D21S11	111													
D7S820	111		0.0180	0.1847	0.1667		0.3153		0.1937		0.0946		0.0270	
CSF1PO	111		0.0541	0.0676	0.0360		0.2568		0.2387		0.3063		0.0315	
D3S1358	111										0.0045		0.0045	
TH01	111	0.1712	0.3604	0.2027	0.1441	0.1171	0.0045							
D13S317	111		0.0045	0.0360	0.0315		0.0676		0.2928		0.3604		0.1486	
D16S539	111			0.0315	0.1667		0.1036		0.2432		0.2387		0.1937	
D2S1338	111													
D19S433	111						0.0045		0.0450	0.0090	0.0901	0.0360	0.2838	0.0225
vWA	111								0.0135				0.0270	
TPOX	111	0.0901	0.0090	0.3423	0.2117		0.0856		0.2117		0.0495			
D18S51	111							0.0045	0.0045		0.0676		0.0586	
D5S818	111			0.0811	0.0270		0.0676		0.1802		0.3243		0.2973	
FGA	111													

Locus	n	Allele												
		14	14.2	15	15.2	16	16.2	17	17.2	18	18.2	19	20	21
D8S1179	111	0.2838		0.1802		0.0541		0.0045						
D21S11	111													
D7S820	111													
CSF1PO	111			0.0090										
D3S1358	111	0.0901		0.2973		0.3018		0.2342		0.0631			0.0045	
TH01	111													
D13S317	111	0.0586												
D16S539	111	0.0225												
D2S1338	111					0.0586		0.0856		0.0495		0.1712	0.1126	0.1306
D19S433	111	0.2252	0.0721	0.0811	0.0405	0.0270	0.0495	0.0045	0.0090					
vWA	111	0.0315		0.2072		0.2703		0.1892		0.1486		0.0721	0.0315	0.0090
TPOX	111													
D18S51	111	0.1036	0.0045	0.1441		0.2072		0.1396		0.1081		0.0766	0.0495	0.0180
D5S818	111	0.0225												
FGA	111									0.0225	0.0045	0.0901	0.0811	0.1036

Locus	n	Allele												
		22	23	23.2	24	24.2	24.3	25	26	27	28	29	30	30.2
D8S1179	111													
D21S11	111					0.0045	0.0045			0.0405	0.1982	0.1757	0.1892	0.0135
D7S820	111													
CSF1PO	111													
D3S1358	111													
TH01	111													
D13S317	111													
D16S539	111													
D2S1338	111	0.1126	0.1216		0.0856			0.0405	0.0315					
D19S433	111													
vWA	111													
TPOX	111													
D18S51	111	0.0045	0.0045					0.0045						
D5S818	111													
FGA	111	0.2252	0.1892	0.0045	0.1441			0.0450	0.0225	0.0135	0.0180	0.0090		0.0045

Supplementary Table 1: Allelic Frequencies for Abaco

Locus	n	Allele											
		31	31.2	32	32.2	33	33.2	34	34.2	35	36	44.2	46.2
D8S1179	111												
D21S11	111	0.1306	0.0721	0.0541	0.0450	0.0090	0.0225	0.0135	0.0045	0.0180	0.0045		
D7S820	111												
CSF1PO	111												
D3S1358	111												
TH01	111												
D13S317	111												
D16S539	111												
D2S1338	111												
D19S433	111												
vWA	111												
TPOX	111												
D18S51	111												
D5S818	111												
FGA	111						0.0045					0.0135	0.0045

Supplementary Table 1: Allelic Frequencies for Abaco (Cont'd)

		Allele												
	n	6	7	8	9	9.3	10	10.2	11	11.2	12	12.2	13	13.2
D8S1179	112				0.0045				0.0357		0.0893		0.1964	
D21S11	112													
D7S820	112			0.1786	0.1116		0.3214		0.2634		0.1116		0.0089	
CSF1PO	112		0.0268	0.0268	0.0357		0.2991		0.3080		0.2723		0.0268	
D3S1358	112												0.0089	
TH01	112	0.1384	0.3348	0.2232	0.1250	0.1518	0.0268							
D13S317	112			0.0179	0.0134		0.0223		0.2500		0.4286		0.2054	
D16S539	112	0.0179		0.0446	0.2321		0.1920		0.2500		0.1384		0.1161	
D2S1338	112													
D19S433	112						0.0045	0.0045	0.0670		0.0893	0.0536	0.2991	0.0268
vWA	112													
TPOX	111	0.0676	0.0586	0.3063	0.1667		0.0676		0.3018		0.0315			
D18S51	112				0.0045		0.0134		0.0089		0.0670		0.0625	0.0045
D5S818	112			0.0670	0.0223		0.0670		0.2500		0.3661		0.2232	
FGA	112													

Supplementary Table 2: Allelic Frequencies for Eleuthera

		Allele												
	n	14	14.2	15	15.2	16	16.2	17	17.2	18	18.2	19	19.2	20
D8S1179	112	0.3750		0.2277		0.0670		0.0045						
D21S11	112													
D7S820	112	0.0045												
CSF1PO	112	0.0045												
D3S1358	112	0.0982		0.2902		0.2991		0.2009		0.0982		0.0045		
TH01	112													
D13S317	112	0.0625												
D16S539	112	0.0089												
D2S1338	112					0.0536		0.1205		0.0491		0.2009		0.0893
D19S433	112	0.2143	0.0804	0.0536	0.0491	0.0134	0.0446							
vWA	112	0.0446		0.2009		0.3036		0.2411		0.1295		0.0580		0.0045
TPOX	111													
D18S51	112	0.0759		0.1652		0.1473		0.1786		0.1071		0.0804		0.0357
D5S818	112	0.0045												
FGA	112							0.0045		0.0045	0.0089	0.0491	0.0045	0.0625

		Allele												
	n	21	22	22.2	23	24	25	26	27	28	29	30	30.2	30.3
D8S1179	112													
D21S11	112								0.0357	0.2500	0.2188	0.1607	0.0312	0.0089
D7S820	112													
CSF1PO	112													
D3S1358	112													
TH01	112													
D13S317	112													
D16S539	112													
D2S1338	112	0.1295	0.1027		0.1116	0.0938	0.0223	0.0223	0.0045					
D19S433	112													
vWA	112	0.0134	0.0045											
TPOX	111													
D18S51	112	0.0179	0.0268		0.0045									
D5S818	112													
FGA	112	0.1696	0.1607	0.0089	0.1429	0.1830	0.0804	0.0625	0.0268	0.0089	0.0134	0.0045		

		Allele									
	n	31	31.2	32	32.2	33	33.2	34	35	36	43.2
D8S1179	112										
D21S11	112	0.1027	0.0223	0.0223	0.0357	0.0089	0.0357	0.0179	0.0402	0.0089	
D7S820	112										
CSF1PO	112										
D3S1358	112										
TH01	112										
D13S317	112										
D16S539	112										
D2S1338	112										
D19S433	112										
vWA	112										
TPOX	111										
D18S51	112										
D5S818	112										
FGA	112										0.0045

Supplementary Table 2: Allelic Frequencies for Eleuthera (Cont'd)

		Allele											
	n	6	7	8	9	9.3	10	11	12	12.2	13	13.2	14
D8S1179	92						0.0109	0.0489	0.1087		0.1848		0.3859
D21S11	92												
D7S820	92	0.0054	0.0163	0.2717	0.1250		0.2935	0.1793	0.0815		0.0217		0.0054
CSF1PO	92		0.0435	0.0435	0.0272		0.3098	0.2337	0.3043		0.0380		
D3S1358	92								0.0109				0.1087
TH01	92	0.1739	0.3587	0.2065	0.1630	0.0924	0.0054						
D13S317	92			0.0109	0.0163		0.0163	0.3261	0.4130		0.1576		0.0598
D16S539	92				0.1359		0.1739	0.3533	0.2174		0.1033		0.0163
D2S1338	92												
D19S433	92						0.0163	0.0761	0.1467	0.0380	0.3152	0.0435	0.2120
vWA	92							0.0109			0.0163		0.0707
TPOX	92	0.0435	0.0435	0.2935	0.2228		0.1304	0.2337	0.0326				
D18S51	92							0.0109	0.0380		0.0435	0.0163	0.0380
D5S818	92		0.0054	0.1033	0.0109		0.0598	0.1957	0.3098		0.2772		0.0272
FGA	92												

		Allele											
	n	14.2	15	15.2	16	16.2	17	17.2	18	18.2	19	20	21
D8S1179	92		0.2120		0.0489								
D21S11	92												
D7S820	92												
CSF1PO	92												
D3S1358	92		0.3859		0.3261		0.1196		0.0435		0.0054		
TH01	92												
D13S317	92												
D16S539	92												
D2S1338	92				0.0761		0.0598		0.0598		0.1522	0.0598	0.1957
D19S433	92	0.0489	0.0326	0.0489		0.0217							
vWA	92		0.2065		0.2500		0.2663		0.0761		0.0707	0.0217	0.0109
TPOX	92												
D18S51	92		0.1957		0.1576		0.2065		0.1141		0.1141	0.0272	0.0217
D5S818	92		0.0054						0.0054				
FGA	92							0.0054	0.0054	0.0326	0.0598	0.0598	0.0870

		Allele											
	n	21.2	22	22.2	23	23.2	24	25	26	27	28	29	30
D8S1179	92												
D21S11	92									0.0326	0.1957	0.2065	0.2554
D7S820	92												
CSF1PO	92												
D3S1358	92												
TH01	92												
D13S317	92												
D16S539	92												
D2S1338	92		0.1359		0.0707	0.0054	0.1196	0.0435	0.0217				
D19S433	92												
vWA	92												
TPOX	92												
D18S51	92	0.0054	0.0109										
D5S818	92												
FGA	92	0.0054	0.1739	0.0054	0.1685		0.1467	0.1087	0.0761	0.0380	0.0054	0.0054	

Supplementary Table 3: Allelic Frequencies for Exuma

		Allele										
	n	30.2	31	31.2	32	32.2	33.1	33.2	35	37	43.2	44.2
D8S1179	92											
D21S11	92	0.0326	0.0707	0.0489	0.0109	0.0815	0.0054	0.0272	0.0272	0.0054		
D7S820	92											
CSF1PO	92											
D3S1358	92											
TH01	92											
D13S317	92											
D16S539	92											
D2S1338	92											
D19S433	92											
vWA	92											
TPOX	92											
D18S51	92											
D5S818	92											
FGA	92										0.0054	0.0109

Supplementary Table 3: Allelic Frequencies for Exuma (Cont'd)

		Allele											
	n	6	7	8	9	9.3	10	10.2	11	12	12.2	13	13.2
D8S1179	133			0.0038			0.0113		0.0677	0.1353		0.1729	
D21S11	133												
D7S820	133		0.0075	0.2594	0.1053		0.2707		0.1842	0.1353		0.0376	
CSF1PO	133	0.0038	0.0602	0.0827	0.0376		0.3045		0.1955	0.2707		0.0376	
D3S1358	133											0.0038	
TH01	133	0.1429	0.3534	0.2632	0.1353	0.0902	0.0150						
D13S317	133			0.0414	0.0188		0.0301		0.2406	0.4135		0.1992	
D16S539	133			0.0489	0.1917		0.0940		0.3271	0.1805		0.1353	
D2S1338	133												
D19S433	133						0.0113		0.0451	0.1241	0.0489	0.2368	0.0526
vWA	133								0.0113			0.0188	
TPOX	133	0.0639	0.0301	0.3421	0.2444		0.1165		0.1767	0.0263			
D18S51	133							0.0038		0.0489		0.0714	0.0038
D5S818	132			0.0682	0.0114		0.0492		0.2273	0.2955		0.3258	
FGA	133												

Supplementary Table 4: Allelic Frequencies for Grand Bahama

		Allele											
	n	14	14.1	14.2	15	15.2	16	16.2	17	17.2	18	18.2	19
D8S1179	133	0.3383			0.1805		0.0789		0.0075		0.0038		
D21S11	133												
D7S820	133												
CSF1PO	133	0.0075											
D3S1358	133	0.1165			0.3684		0.2707		0.1955		0.0451		
TH01	133												
D13S317	133	0.0564											
D16S539	133	0.0226											
D2S1338	133				0.0038		0.0526		0.0977		0.0451		0.1842
D19S433	133	0.1842	0.0038	0.0940	0.0602	0.0639	0.0075	0.0526		0.0150			
vWA	133	0.0489			0.1654		0.2820		0.2143		0.1278		0.0865
TPOX	133												
D18S51	133	0.0564			0.1579	0.0075	0.2180		0.1541		0.1203		0.0940
D5S818	132	0.0152			0.0076								
FGA	133									0.0075	0.0038	0.0038	0.0677

		Allele											
	n	19.2	20	21	22	22.2	23	24	25	26	27	28	29
D8S1179	133												
D21S11	133										0.0639	0.2256	0.2068
D7S820	133												
CSF1PO	133												
D3S1358	133												
TH01	133												
D13S317	133												
D16S539	133												
D2S1338	133		0.0940	0.1165	0.1090		0.0902	0.0940	0.0827	0.0301			
D19S433	133												
vWA	133		0.0338	0.0038	0.0075								
TPOX	133												
D18S51	133		0.0414	0.0188	0.0038								
D5S818	132												
FGA	133	0.0075	0.0301	0.0827	0.1955	0.0075	0.2256	0.1579	0.1278	0.0338	0.0301	0.0075	0.0038

		Allele										
	n	30	30.2	31	31.2	32	32.2	33	33.2	34	34.2	35
D8S1179	133											
D21S11	133	0.2218	0.0150	0.0564	0.0414	0.0075	0.0940	0.0075	0.0263	0.0075	0.0038	0.0226
D7S820	133											
CSFIPO	133											
D3S1358	133											
TH01	133											
D13S317	133											
D16S539	133											
D2S1338	133											
D19S433	133											
vWA	133											
TPOX	133											
D18S51	133											
D5S818	132											
FGA	133	0.0075										

Supplementary Table 4: Allelic Frequencies for Grand Bahama (Cont'd)

		Allele											
	n	6	7	8	9	9.3	10	11	11.1	12	12.2	13	13.2
D8S1179	87			0.0057	0.0172		0.0402	0.0977		0.1264		0.1092	
D21S11	87												
D7S820	87		0.0057	0.1494	0.1379		0.3448	0.2011	0.0057	0.0862		0.0690	
CSF1PO	87		0.0345	0.0115	0.0115		0.3448	0.2069		0.2701		0.1149	
D3S1358	87									0.0115		0.0057	
TH01	87	0.1724	0.3103	0.2414	0.1782	0.0977							
D13S317	87			0.0862	0.0287		0.0690	0.2816		0.3391		0.1207	
D16S539	87			0.0460	0.1379		0.0920	0.3046		0.2356		0.1724	
D2S1338	87												
D19S433	87							0.0747		0.1034	0.0747	0.2414	0.0460
vWA	87							0.0115				0.0230	
TPOX	87	0.0460	0.0287	0.3678	0.1897		0.1034	0.2241		0.0402			
D18S51	87						0.0230	0.0057		0.0517		0.1379	0.0057
D5S818	87			0.0402			0.0575	0.2759		0.3161		0.3103	
FGA	87												

		Allele											
	n	14	14.2	15	15.2	16	16.2	17	17.2	18	19	20	21
D8S1179	87	0.282		0.2529		0.035		0.0287		0.0057			
D21S11	87												
D7S820	87												
CSF1PO	87			0.0057									
D3S1358	87	0.058		0.2241		0.402		0.2356		0.0632			
TH01	87												
D13S317	87	0.0690		0.0057									
D16S539	87	0.0115											
D2S1338	87					0.0287		0.1437		0.0460	0.1494	0.0632	0.0862
D19S433	87	0.1954	0.0230	0.0977	0.0805	0.0115	0.0345		0.0172				
vWA	87	0.1149		0.1782		0.2184		0.2241		0.1897	0.0230	0.0172	
TPOX	87												
D18S51	87	0.1379		0.1379	0.0057	0.0862		0.1552		0.1034	0.0690	0.0460	0.0172
D5S818	87												
FGA	87									0.0057	0.0862	0.1149	0.1092

		Allele											
	n	21.2	22	22.2	23	24	25	26	27	28	29	30	30.2
D8S1179	87												
D21S11	87								0.0345	0.2414	0.1149	0.2931	0.0402
D7S820	87												
CSF1PO	87												
D3S1358	87												
TH01	87												
D13S317	87												
D16S539	87												
D2S1338	87		0.1149		0.1782	0.0517	0.0920	0.0460					
D19S433	87												
vWA	87												
TPOX	87												
D18S51	87	0.0057	0.0057		0.0057								
D5S818	87												
FGA	87		0.1667	0.0287	0.1437	0.1264	0.0862	0.0172	0.0172	0.0287		0.0057	

Supplementary Table 5: Allelic Frequencies for Long Island

		Allele										
	n	31	31.2	32	32.2	33	33.2	34	35	36	43.2	44.2
D8S1179	87											
D21S11	87	0.0805	0.0345	0.0115	0.0747	0.0057	0.0172	0.0057	0.0287	0.0172		
D7S820	87											
CSF1PO	87											
D3S1358	87											
TH01	87											
D13S317	87											
D16S539	87											
D2S1338	87											
D19S433	87											
vWA	87											
TPOX	87											
D18S51	87											
D5S818	87											
FGA	87		0.0172								0.0057	0.0402

Supplementary Table 5: Allelic Frequencies for Long Island (Cont'd)

	Abaco						Eleuthera						Exuma					
Locus	GDI	MP	PD	PIC	PE	TPI	GDI	MP	PD	PIC	PE	TPI	GDI	MP	PD	PIC	PE	TPI
D8S1179	0.81301	0.06176	0.93824	0.78341	0.53712	2.13	0.75857	0.09853	0.90147	0.71928	0.55669	2.24	0.75944	0.10681	0.89319	0.72095	0.47332	1.84
D21S11	0.86776	0.04099	0.95901	0.84942	0.81571	5.55	0.84910	0.05931	0.94069	0.82836	0.78085	4.67	0.84058	0.04891	0.95109	0.81674	0.69058	3.29
D7S820	0.79475	0.08027	0.91973	0.76087	0.67104	3.08	0.77386	0.08721	0.91279	0.73451	0.54081	2.15	0.78908	0.09310	0.90690	0.75268	0.66933	3.07
CSF1PO	0.77690	0.09796	0.90204	0.73847	0.65359	2.92	0.74135	0.11767	0.88233	0.69193	0.49461	1.93	0.75493	0.11484	0.88516	0.70952	0.60713	2.56
D3S1358	0.75692	0.11436	0.88564	0.71195	0.52140	2.06	0.77002	0.11049	0.88951	0.72901	0.60569	2.55	0.72054	0.13705	0.86295	0.67015	0.49135	1.92
TH01	0.76870	0.09926	0.90074	0.73016	0.56930	2.31	0.78303	0.08769	0.91231	0.74712	0.58914	2.43	0.76746	0.09617	0.90383	0.72733	0.49135	1.92
D13S317	0.75541	0.11257	0.88743	0.71525	0.56930	2.31	0.70992	0.13600	0.86400	0.66019	0.45071	1.75	0.69779	0.13729	0.86271	0.64140	0.38907	1.53
D16S539	0.80996	0.06728	0.93272	0.77783	0.49070	1.91	0.81538	0.06234	0.93766	0.78502	0.54081	2.15	0.77251	0.08932	0.91068	0.73381	0.35821	1.44
D2S1338	0.89434	0.03222	0.96778	0.88010	0.72436	3.70	0.88625	0.03109	0.96891	0.87098	0.74469	4.00	0.88673	0.03214	0.96786	0.87061	0.71207	3.54
D19S433	0.84379	0.04342	0.95658	0.82360	0.70644	3.47	0.83837	0.05580	0.94420	0.81754	0.62244	2.67	0.82294	0.06191	0.93809	0.79792	0.71207	3.54
vWA	0.82165	0.06323	0.93677	0.79379	0.67104	3.08	0.79056	0.08498	0.91502	0.75547	0.62244	2.67	0.81159	0.06616	0.93384	0.78084	0.43842	1.70
TPOX	0.77869	0.08855	0.91145	0.74252	0.55309	2.22	0.77726	0.09163	0.90837	0.74050	0.52140	2.06	0.79205	0.09074	0.90926	0.75586	0.69058	3.29
D18S51	0.88158	0.03222	0.96778	0.86561	0.76060	4.27	0.88837	0.03412	0.96588	0.87352	0.78085	4.67	0.86636	0.04182	0.95818	0.84676	0.71207	3.54
D5S818	0.76503	0.09569	0.90431	0.72474	0.52140	2.06	0.74752	0.11862	0.88138	0.70312	0.57280	2.33	0.77798	0.09806	0.90194	0.73926	0.54768	2.19
FGA	0.86727	0.03969	0.96031	0.84921	0.67104	3.08	0.87748	0.03332	0.96668	0.86069	0.60569	2.55	0.88952	0.03119	0.96881	0.87383	0.88926	9.20

Supplementary Table 6: Forensic parameters for Abaco, Eleuthera, Exuma, Grand Bahama and Long Island across the 15 Identifiler loci

Locus	Grand Bahama						Long Island					
	GDI	MP	PD	PIC	PE	TPI	GDI	MP	PD	PIC	PE	TPI
D8S1179	0.79671	0.07298	0.92702	0.76661	0.60744	2.56	0.82001	0.06355	0.93645	0.79206	0.44809	1.74
D21S11	0.84091	0.04980	0.95020	0.81837	0.69412	3.33	0.82971	0.05351	0.94649	0.80533	0.56537	2.29
D7S820	0.79765	0.08305	0.91695	0.76398	0.60744	2.56	0.79158	0.08257	0.91743	0.75838	0.69600	3.35
CSF1PO	0.78539	0.08361	0.91639	0.75059	0.55249	2.22	0.75497	0.11560	0.88440	0.70991	0.50486	1.98
D3S1358	0.73994	0.11267	0.88733	0.69351	0.45071	1.75	0.72912	0.12010	0.87990	0.68109	0.30206	1.28
TH01	0.76164	0.10295	0.89705	0.72180	0.60744	2.56	0.77889	0.09711	0.90289	0.73817	0.50486	1.98
D13S317	0.72799	0.11369	0.88631	0.68395	0.37147	1.48	0.77782	0.08786	0.91214	0.74180	0.54480	2.18
D16S539	0.79665	0.07321	0.92679	0.76535	0.60744	2.56	0.79682	0.08416	0.91584	0.76209	0.67346	3.11
D2S1338	0.89604	0.02697	0.97303	0.88300	0.78468	4.75	0.88958	0.02946	0.97054	0.87338	0.65120	2.90
D19S433	0.87093	0.03986	0.96014	0.85481	0.72396	3.69	0.86639	0.04664	0.95336	0.84737	0.67346	3.11
vWA	0.82242	0.06676	0.93324	0.79619	0.69412	3.33	0.82440	0.06355	0.93645	0.79441	0.58630	2.42
TPOX	0.77568	0.08915	0.91085	0.73957	0.56599	2.29	0.76766	0.09658	0.90342	0.72943	0.52463	2.07
D18S51	0.87090	0.03533	0.96467	0.85389	0.62156	2.66	0.89529	0.03025	0.96975	0.87995	0.69600	3.35
D5S818	0.75029	0.10227	0.89773	0.70524	0.49689	1.94	0.72693	0.13251	0.86749	0.67095	0.44809	1.74
FGA	0.85816	0.04438	0.95562	0.83890	0.72396	3.69	0.89649	0.03290	0.96710	0.88141	0.74180	3.95

Supplementary Table 6: Forensic parameters for Abaco, Eleuthera, Exuma, Grand Bahama and Long Island across the 15 Identifiler loci (Cont'd)

	ABA	ELU	EXU	GRB	LNG	NWP	HAT	JAM	US1	US2
ABA		255.5159	257.4368	208.0772	262.4739	217.1170	246.8775	208.3699	212.2777	258.4031
ELU	<i>0.0004</i>		232.3493	255.7313	341.4149	248.6331	249.9456	222.2641	224.9921	248.9695
EXU	<i>0.0002</i>	<i>0.0038</i>		201.0366	342.4225	178.6515	236.5814	239.4758	239.6547	236.6326
GRB	0.1061	<i>0.0001</i>	0.1301		311.0807	199.8735	216.8389	190.3541	221.6427	210.3668
LNG	0.0000	0.0000	0.0000	0.0000		332.3794	341.7630	315.0483	317.1819	369.1798
NWP	0.2210	<i>0.0079</i>	0.8231	0.4211	0.0000		236.7342	228.4719	211.5335	260.9949
HAT	<i>0.0073</i>	<i>0.0027</i>	<i>0.0246</i>	0.1006	0.0000	0.0851		230.7371	232.8402	227.0359
JAM	0.1668	<i>0.0327</i>	<i>0.0043</i>	0.4090	0.0000	0.1246	<i>0.0454</i>		186.0889	216.0961
US1	0.1884	<i>0.0357</i>	<i>0.0041</i>	<i>0.0292</i>	0.0000	0.3462	<i>0.0441</i>	0.7311		231.3660
US2	<i>0.0016</i>	<i>0.0014</i>	<i>0.0080</i>	0.1525	0.0000	<i>0.0134</i>	0.0887	0.1879	0.0516	
ANG	0.0000	0.0000	<i>0.0053</i>	<i>0.0001</i>	0.0000	0.0000	<i>0.0129</i>	<i>0.0003</i>	<i>0.0001</i>	0.0000
GUB	0.0000	<i>0.0001</i>	0.0743	<i>0.0183</i>	0.0000	<i>0.0007</i>	<i>0.0106</i>	<i>0.0007</i>	0.0000	0.0000
EGU	<i>0.0186</i>	0.0000	<i>0.0125</i>	0.0670	0.0000	<i>0.0428</i>	0.9483	<i>0.0122</i>	<i>0.0312</i>	<i>0.0112</i>
NAM	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
NIG	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HUT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KEN	0.0363	<i>0.0289</i>	0.0541	0.1101	0.0000	0.0749	0.2962	0.2032	0.1046	<i>0.0246</i>
MAD	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MOZ	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TAN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TUT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UGA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SAF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CCS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
JAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KOR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GUA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KAK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KIC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
YUC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ELS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HON	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GRE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SWE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Supplementary Table 7: G-test

	ANG	GUB	EGU	NAM	NIG	HUT	KEN	MAD	MOZ	TAN	TUT
ABA	297.2374	272.1868	228.8550	476.3658	519.3773	314.9507	209.4983	359.6303	341.9447	367.0154	434.3069
ELU	267.2055	261.4782	271.5772	458.4311	521.8970	325.4992	206.3521	336.2793	348.6951	337.8375	426.5738
EXU	231.6894	212.4731	229.8473	398.9417	431.8459	281.0202	201.1246	343.2468	288.4355	322.3360	359.2256
GRB	262.3734	219.9234	210.5812	411.2646	486.5968	307.4404	190.7949	387.6601	338.3468	366.4198	452.0832
LNG	402.8164	354.8444	369.9366	568.4601	641.6237	355.9456	297.2808	408.7142	482.6778	507.1758	530.6234
NWP	297.1790	265.0812	239.0506	548.6736	648.9391	344.6294	213.9525	421.1929	408.3094	450.5210	484.4134
HAT	239.2100	238.6009	169.9370	337.0298	428.7914	335.4467	198.6350	332.5014	297.7143	308.1873	414.9631
JAM	262.8510	251.3156	235.1849	419.8413	454.9703	301.1588	195.1255	333.7593	305.3622	299.7603	405.2145
US1	272.1790	284.6586	231.1618	504.0307	583.7384	290.1581	202.6939	345.3930	369.3774	370.5138	487.7301
US2	292.7030	282.1795	244.9366	544.4769	644.8873	342.1582	217.6445	382.9854	336.3618	400.2274	523.5483
ANG		282.4472	221.7092	290.9848	506.0028	260.0201	198.6299	371.3746	334.9184	327.6299	378.0364
GUB	0.0000		251.2966	394.3167	515.3693	323.5085	213.7887	354.1472	312.9706	321.6954	440.6943
EGU	<i>0.0236</i>	<i>0.0005</i>		352.9726	443.1427	299.3392	194.7626	364.9931	317.1875	334.4801	407.6942
NAM	0.0000	0.0000	0.0000		805.2330	462.6141	299.9806	506.4148	486.0583	534.3686	634.0131
NIG	0.0000	0.0000	0.0000	0.0000		524.0104	336.9669	603.3051	594.8241	570.8818	734.8482
HUT	<i>0.0001</i>	0.0000	0.0000	0.0000	0.0000		210.3549	376.5460	352.6128	333.5834	361.3040
KEN	0.0924	<i>0.0204</i>	0.1700	0.0000	0.0000	0.0511		306.9289	225.2373	227.2508	297.4595
MAD	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		371.9299	437.2512	461.2226
MOZ	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0038</i>	0.0000		283.4961	523.5334
TAN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0373</i>	0.0000	<i>0.0001</i>		481.9146
TUT	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
UGA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0002</i>	0.0000	0.0000	0.0000	0.0000
SAF	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0003</i>	0.0000	<i>0.0007</i>	0.0000	0.0000
CCS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
JAP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KOR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAL	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GUA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KAK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
KIC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
YUC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ELS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HON	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GRE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SWE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Supplementary Table 7: G-test (Cont'd)

	UGA	SAF	CCS	JAP	KOR	MAL	PHI	CSH	GUA	KAK	KIC
ABA	353.1068	385.4726	1124.9126	1474.3500	1283.3197	967.7285	845.1508	1136.1504	1162.8175	1063.3929	618.9303
ELU	466.6238	341.0126	1198.8967	1622.3893	1408.1648	1087.0167	935.8827	1256.2819	1116.3730	1051.5525	626.4266
EXU	408.4935	307.4785	1160.9515	1484.1227	1334.0588	1045.5013	947.4545	1203.3729	1105.9020	1015.7192	632.3660
GRB	380.2610	387.3344	1303.5280	1845.0591	1572.8790	1202.7966	1009.8267	1304.8824	1219.4445	1144.1353	668.3839
LNG	435.1848	450.6429	949.6135	1221.7439	1070.1912	838.0112	788.5061	956.1392	1037.1217	976.2270	593.6605
NWP	462.1212	414.8787	1640.0826	2567.4902	2044.1027	1505.4727	1227.9337	1753.9027	1347.5922	1277.1736	706.2735
HAT	416.9154	279.4336	1258.7485	1775.1469	1540.2103	1153.0020	987.1977	1291.3613	1198.3019	1157.5844	689.5162
JAM	367.2077	348.8613	1105.7494	1517.8855	1325.4003	987.2772	861.8778	1130.8444	1116.5532	1048.3948	613.2034
US1	436.9200	396.6248	1321.3734	1913.9091	1571.8273	1145.4186	956.6950	1366.2150	1197.0146	1140.5813	652.3872
US2	483.2510	399.4874	1612.5165	2607.3901	1978.6023	1474.4789	1150.3481	1668.1620	1335.1168	1301.6584	686.3676
ANG	468.1497	310.2818	1319.5687	1819.9849	1547.0536	1230.0575	994.3469	1340.3058	1246.9574	1221.3892	736.8767
GUB	416.2239	326.4199	1101.0726	1473.7946	1327.3401	1044.8998	898.3178	1120.6151	1073.9020	1037.8618	660.8270
EGU	456.9542	333.283	1410.5985	1999.6361	1703.4598	1264.7218	1045.0815	1449.3634	1274.7736	1241.0842	709.8235
NAM	622.8959	419.0391	1964.9546	3091.0125	2514.9470	1966.7240	1467.2649	2218.7803	1575.6923	1673.7672	947.6314
NIG	716.3812	543.8169	2314.3889	3950.7646	2972.3582	2351.0574	1680.2054	2583.8701	1642.0138	1667.4712	892.8112
HUT	328.6649	355.1657	1243.8484	1652.9045	1444.2677	1138.2894	1010.2482	1298.2859	1239.0825	1115.5770	692.9352
KEN	241.7360	243.6538	965.3720	1168.9825	1112.2170	886.5229	784.0193	959.9223	997.4241	886.2337	580.9343
MAD	501.2495	385.7041	708.5034	896.1970	857.8117	625.9515	527.1189	775.9848	843.7770	788.8383	538.3190
MOZ	519.5912	246.7927	1516.899	2071.0671	1779.2944	1456.1948	1166.9080	1575.8204	1271.2258	1225.5809	712.3813
TAN	527.5989	330.5381	1851.1737	2849.9404	2241.6169	1783.1946	1353.2587	1953.3273	1484.1809	1426.6024	787.9786
TUT	537.8627	440.1677	1533.4893	2063.9529	1805.7122	1471.2946	1165.1117	1633.0477	1364.9073	1238.0286	725.4368
UGA		510.8528	1159.6693	1520.1287	1357.8638	1083.6028	974.2226	1209.6449	1242.2509	1069.8838	638.9430
SAF	0.0000		1347.2368	1861.0095	1613.6172	1294.1763	1088.1547	1417.8231	1237.6667	1186.8896	740.8685
CCS	0.0000	0.0000		450.1981	353.6910	432.0402	356.7864	279.7270	1063.6783	960.7687	561.3939
JAP	0.0000	0.0000	0.0000		307.2385	789.6036	512.5523	518.3922	1140.1155	1072.4084	554.2070
KOR	0.0000	0.0000	0.0000	0.0000		636.6891	459.4520	344.5786	1043.5566	962.5594	530.4380
MAL	0.0000	0.0000	0.0000	0.0000	0.0000		289.0813	472.2081	1056.2954	934.7960	539.4123
PHI	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		377.1124	948.9913	929.8623	573.2806
CSH	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		1043.9146	915.2687	517.5212
GUA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		435.1290	342.1435
KAK	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		117.3686
KIC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.7793	
YUC	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	<i>0.0418</i>	0.3783
CAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MEX	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CSR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ELS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HIS	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HON	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MAR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GRE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SWE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Supplementary Table 7: G-test (Cont'd)

	YUC	CAR	MEX	CSR	ELS	HIS	HON	MAR	MET	PRA	BRA
ABA	1353.0326	579.2944	875.0407	820.0099	916.2750	593.2062	725.7686	639.6459	1161.6478	526.9998	420.4385
ELU	1309.6718	659.7865	923.4464	852.1955	969.9579	660.9830	735.3638	702.7872	1159.7047	615.9531	521.0963
EXU	1281.6718	691.1995	958.0234	905.9418	914.7685	674.7468	763.1531	721.2356	1122.4939	620.6492	586.5692
GRB	1508.5903	806.0059	1110.681	1060.9438	1098.458	765.9351	888.8896	821.0711	1327.1202	686.5521	579.8114
LNG	1186.8391	529.3632	771.5473	722.8311	829.3315	542.2606	605.2902	560.6844	1050.6177	494.9232	423.7663
NWP	1773.7449	916.2577	1304.4275	1326.8551	1369.7275	834.9598	1050.2084	918.8211	1625.9066	753.7961	658.0684
HAT	1477.6381	781.3412	1056.8923	1077.0100	1102.7203	778.7883	884.1358	821.7631	1295.0150	726.1169	589.4932
JAM	1346.7625	616.8490	880.0184	880.1427	916.9183	637.9739	723.2188	668.6646	1130.4785	577.1983	482.6524
US1	1518.0441	720.6636	1018.0546	981.1761	1082.5024	681.2700	840.9960	717.2574	1314.0172	618.4646	503.5044
US2	1823.5214	924.5727	1335.5060	1355.6930	1372.6104	863.0743	1067.8580	943.2885	1650.6353	830.7430	673.8070
ANG	1558.0151	893.2638	1170.4983	1182.0731	1222.3256	855.5546	1008.7388	906.1593	1417.8519	785.2361	656.7401
GUB	1313.6796	669.1605	942.4453	899.1371	974.1279	685.0397	788.3484	746.6809	1180.8689	649.6805	563.4754
EGU	1635.1782	853.7247	1166.7345	1186.9500	1249.6600	842.0480	1001.3279	892.4285	1452.4832	754.5124	653.2888
NAM	2304.2668	1549.8344	1926.5725	2135.2070	2039.6251	1367.1532	1675.1727	1593.1064	2180.9568	1340.3010	1211.3700
NIG	2488.7112	1811.4435	2201.2400	2504.2888	2274.3838	1558.8279	1928.0959	1775.2377	2439.0427	1609.4078	1399.4497
HUT	1454.3555	803.4522	1042.8290	1045.6145	1096.0526	805.6285	912.1329	805.2376	1316.9272	691.0344	647.6494
KEN	1087.4355	577.6357	754.5463	717.4965	766.8672	576.3567	637.4384	587.2816	931.8091	535.9026	430.8232
MAD	971.6964	553.3408	678.7587	703.9114	693.7454	529.5678	622.7135	579.8524	803.1363	558.0521	532.5900
MOZ	1646.1967	989.1791	1346.6300	1292.2472	1262.3871	956.1791	1090.8823	1024.2301	1573.4073	905.7759	824.1334
TAN	2023.4288	1328.6235	1714.4022	1769.5472	1749.7040	1228.1897	1425.6716	1356.3922	2000.8979	1146.5701	1061.1844
TUT	1673.3124	1071.8170	1358.7527	1402.1351	1398.4064	1011.6332	1150.2482	1045.1583	1561.3545	976.0688	926.4951
UGA	1325.5048	863.1320	1019.6857	1070.6263	1039.0920	778.4244	896.9662	827.6086	1233.6410	809.3254	715.9099
SAF	1517.7279	951.1462	1255.0874	1186.9851	1211.3289	935.6351	1038.3463	1016.5126	1419.9254	881.2035	788.1117
CCS	1282.3461	1125.1412	1056.0265	1295.3372	1154.4877	849.0040	1061.2214	1002.9550	1209.4363	1094.0968	1297.0906
JAP	1602.8132	1566.3851	1608.1471	1845.0237	1544.7782	1017.1887	1390.7443	1317.6730	1657.5911	1524.1836	1994.3584
KOR	1327.4171	1187.6215	1165.9557	1333.3911	1208.3761	844.1308	1115.5143	1037.3252	1330.2821	1180.2168	1468.2697
MAL	1264.3585	918.8443	877.5515	1148.2570	1071.1489	618.0397	938.5854	803.8509	1130.5956	867.9650	1118.8350
PHI	1179.9622	877.9362	854.0881	983.8277	1035.2817	674.0821	914.7985	786.1715	1106.5436	830.0203	957.3449
CSH	1249.6803	1131.8567	1023.6318	1242.4084	1144.3292	789.0430	1035.3973	979.0354	1224.3311	1062.3579	1312.8768
GUA	475.6041	833.7254	819.9080	860.1639	718.1748	743.9924	715.8883	835.0385	669.2868	955.7305	1078.0349
KAK	180.9592	736.3215	603.5414	616.2818	381.8049	560.7665	456.6211	699.0212	378.0226	864.5172	1018.7928
KIC	142.4620	386.5930	330.0640	338.3410	227.1561	326.2403	270.8716	365.0222	218.6322	498.1128	522.9999
YUC		916.5757	677.5196	809.8257	396.9612	622.4636	527.5845	837.645	396.3743	1093.6871	1359.9556
CAR	0.0000		434.5750	274.2459	468.5515	206.2046	302.2975	194.9020	757.1349	323.2320	335.2340
MEX	0.0000	0.0000		512.9736	432.9026	261.7632	384.6056	378.3874	583.8787	574.1693	686.5186
CSR	0.0000	0.0000	0.0000		396.42790	236.06460	247.61630	299.10020	743.95430	490.14500	566.00690
ELS	0.0000	0.0000	0.0000	0.0000		291.6533	211.1138	438.3164	389.0716	704.0356	848.7307
HIS	0.0000	0.1007	<i>0.0023</i>	<i>0.0013</i>	0.0000		247.1386	220.7598	442.0474	304.3576	352.9807
HON	0.0000	0.0000	0.0000	<i>0.0008</i>	<i>0.0427</i>	<i>0.0003</i>		270.1303	460.7533	479.1521	560.8553
MAR	0.0000	0.4590	0.0000	0.0000	0.0000	<i>0.0106</i>	0.0000		611.7493	369.8294	340.7615
MET	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		941.7846	1130.1987
PRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		353.1628
BRA	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
CAU	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
GRE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POR	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SPN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SWE	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Supplementary Table 7: G-test (Cont'd)

	CAU	GRE	POR	SPN	SWE
ABA	835.9993	829.8376	831.4743	915.6335	933.9509
ELU	1001.3349	944.7720	951.8909	1067.2238	1091.9521
EXU	998.6556	961.8715	996.8214	1090.2428	1105.3458
GRB	1159.6194	1076.8927	1129.9086	1238.5070	1246.4890
LNG	738.1310	708.7573	702.9459	770.1165	788.1989
NWP	1319.9277	1303.3640	1352.7836	1462.1938	1490.2942
HAT	1138.1791	1100.8298	1110.3181	1187.7039	1243.0212
JAM	978.4950	896.0058	976.6739	1039.3077	1088.1926
US1	1044.4484	1008.4053	1072.1235	1147.5273	1184.6985
US2	1413.5024	1340.9468	1439.9379	1548.8081	1564.6559
ANG	1275.2731	1230.3677	1293.5306	1355.2976	1345.2188
GUB	1036.7103	983.4028	1017.8761	1098.9459	1143.3224
EGU	1275.5774	1198.9954	1221.1036	1311.7319	1373.1744
NAM	2128.6575	1976.3612	2115.2041	2229.7070	2229.2861
NIG	2569.1582	2369.3403	2599.3826	2681.0117	2532.1086
HUT	1098.8838	1061.8978	1087.2113	1185.1730	1186.5238
KEN	835.1530	803.4288	814.1584	891.3480	922.3879
MAD	863.2474	733.5222	859.1796	908.0583	960.3611
MOZ	1439.9630	1357.5609	1440.5740	1557.8480	1609.4237
TAN	1900.5359	1829.0458	1953.1154	2074.0374	2029.2335
TUT	1480.4247	1444.9843	1482.8862	1564.5051	1584.5837
UGA	1078.6869	1083.7622	1120.7635	1225.9478	1160.2367
SAF	1347.4409	1285.5853	1322.6709	1425.7090	1507.3118
CCS	1356.3972	1175.9008	1421.0850	1384.5605	1449.6512
JAP	2086.0447	1828.4130	2348.3293	2244.5029	2302.3438
KOR	1462.3920	1306.5034	1630.5028	1547.2969	1592.0238
MAL	1192.6473	1006.2543	1250.0984	1216.8807	1347.4709
PHI	1044.2216	898.5118	1089.7184	1085.7383	1137.3915
CSH	1388.6058	1267.3691	1526.7745	1476.5314	1516.7231
GUA	1216.2964	1178.3501	1290.5380	1259.0676	1267.4799
KAK	1112.8190	1131.9576	1202.5743	1239.4248	1155.2915
KIC	562.7928	576.3088	596.9670	625.5599	566.8100
YUC	1517.5282	1538.1063	1663.1080	1710.7399	1549.4232
CAR	503.3499	507.6903	499.8065	527.7271	669.8088
MEX	783.9633	738.6413	846.1116	840.4451	873.8793
CSR	685.68180	702.45790	750.1179	785.60460	840.07780
ELS	1021.2999	1013.9773	1156.3560	1169.0570	1162.2632
HIS	451.7975	485.5252	481.1879	510.1093	567.4726
HON	727.9613	707.3621	767.3145	831.9730	814.4814
MAR	423.3698	457.9126	450.6965	461.2663	526.8037
MET	1256.2998	1235.3875	1403.1581	1436.8680	1314.5502
PRA	509.8419	533.2666	507.1979	528.5404	641.0922
BRA	528.9551	555.2408	505.0330	570.0999	556.5077
CAU		370.04950	286.5906	287.8519	288.3658
GRE	0.0000		312.2703	343.1823	483.5353
POR	0.0000	0.0000		220.5439	436.4818
SPN	0.0000	0.0000	<i>0.0092</i>		441.1469
SWE	0.0000	0.0000	0.0000	0.0000	

Refer to Table 1 for key to abbreviations

Pair-wise population comparisons yielding statistically insignificant differences both before (in bold) and after (in italics) applying the Bonferroni correction

Supplementary Table 7: G-test (Cont'd)

V. THE PATRIARCHAL GENETIC SUBSTRATA OF THE BAHAMIAN ARCHIPELAGO

A. Introduction

Historical records indicate that the indigenous people of the Bahamas were the Arawak (Lucayan) Indians (Bahamas Department of Archives, 1996), a group of Amerindians who traveled north from the Amazon River Basin and settled throughout the archipelago during the Ostionoid expansion (600-1100 AD) (Berman and Gnivecki, 1995; Keegan, 1995). Although this group resided in the island chain at the time of the discovery of the New World, most had perished by the early 1500s (Granberry, 1981; Johnson, 1996), leaving the Bahamas virtually uninhabited (Miller 1945, Lawlor 1998). The islands remained deserted until 1648 when a group of British independents from Bermuda migrated to the archipelago in search of religious freedom (Lawlor, 1998). The pilgrims, who were subsequently joined by other Bermudian colonists, of both African and European descent, established settlements on the island of Eleuthera and later on, in New Providence (Saunders, 1991).

In the following century, the Bahamas was raided over thirty times by French and Spanish pirates (Saunders, 1990), a period that would not end until the signing of the Treaty of Versailles in 1783, which granted the Bahamas to the British Empire (Williams, 1983). As a result, the Loyalists (a group of American colonists originating from Great Britain), fled continental North America for the Bahamas between 1783 and 1785 (the Bahamian Revolution). Prior to their arrival, African and European migrants were almost equally represented throughout the island chain (Saunders, 1985) yet, by 1788 the

population had doubled, with Africans outnumbering Europeans 2:1 (Sharer, 1955). The escalation of the African component resulted from the influx of Creole slaves [individuals of African ancestry born in the New World (Saunders, 1985)] that accompanied the Loyalists and the importation of African-born individuals prior to the abolition of the British slave trade (Tinker, 1998). In addition, ~6,000 enslaved Africans, most of whom were aboard Portuguese slavers en route to Cuba, were captured by the British Royal Navy in the post slavery era (1807-1860) and resettled in the Bahamas (Dalleo, 1984; Tinker 1998), further contributing to the growth of the African populace.

During the post-emancipation era, the Bahamas, in contrast to other British Caribbean societies, experienced a surplus rather than a deficit in the labor force due to the collapse of the cotton industry in the early 1800s and the importation of thousands of liberated Africans after 1807 (Saunders, 2003a). Consequently, the Bahamas, unlike the sugar-producing colonies (*e.g.*, British Guiana, Jamaica and Trinidad), was not reliant upon indentured servitude (1838-1918) for the recruitment of hundreds of thousands of Asian laborers (Richardson, 1989). The archipelago did, however, receive migrants belonging to several different ethnic groups, although the extent of their genetic contributions is not known. Of the non-West Indian immigrants incorporated into Bahamian society, the Chinese were the first to make their mark, followed by the Greeks who traveled to the island chain seeking employment in the prospering Bahamian sponge trade. The 1920's bore witness to the introduction of Eastern European Jews, a second wave of Chinese migrants (by way of Cuba), as well as a small group of Lebanese nationals seeking religious asylum in the New World (Johnson, 1991; McCartney, 2004). Significant numbers of West Indians from Turks and Caicos, Barbados, Jamaica, Cuba

and Guyana were also brought to the Bahamas from the 1920s onward to fulfill roles in law enforcement, education and construction. In addition to the aforementioned groups, Haitians have and continue to colonize the Bahama Islands as illegal immigrants (Tinker, 1998), comprising 7.1% of the total Bahamian population in the year 2000 (Department of Statistics of the Bahamas, 2000).

Studies characterizing the genetic structure of populations residing throughout the Caribbean basin have revealed differential African, European and Native American contributions to the maternal and/or paternal gene pools of each island sampled. In the recent report published by Benn-Torres and collaborators (2007), for example, high frequencies (72.0% - 97.9%) of the sub-Saharan African-specific mtDNA haplogroup L (sub-clades L0, L1, L2 and L3) were observed in Grenada, St. Kitts, St. Lucia, Dominica, St. Vincent and Trinidad, whereas the remaining influences in each collection's matrilineages originate from Eurasian (haplogroups H, K, M, N and U) and, in the case of the latter three populations, Native American (haplogroups A, C, and D) sources (Benn Torres et al., 2007). In the same study, Grenada, St. Kitts, St. Vincent, Trinidad, Jamaica and St. Thomas were found to share the majority (ranging from 58.3% to 88.3%) of their paternal component with continental Africans, however, these estimates were generated based exclusively on Y-STR haplotype data. The Cuban populace, in contrast, displays sex-biased gene flow, receiving much larger genetic contributions from European males (78.8%) than females (21.6%) (Mendizabal et al., 2008), while collections from Aruba (Toro-Labrador, Wever and Martínez-Cruzado, 2003) and Puerto Rico (Martínez-Cruzado et al., 2005) are characterized by a predominantly Amerindian-specific (81.3% and 61.1%, respectively) maternal component (*i.e.*, haplogroups A, B, C and D).

Despite the wealth of genetic data available for Caribbean and other New World populations, the islands of the Bahamas remain virtually unexplored genetically, with only a few phylogenetic and evolutionary studies on the island chain reported thus far. These investigations, which are based exclusively on classical (Halberstein et al., 1981) and autosomal STR (Duncan et al., 1996; Budowle et al, 1999; Herrera et al., 2004; Simms et al., 2008; 2010; 2011) polymorphisms, reveal substantial gene flow from continental Africa and varying degrees of genetic input from European, East Asian and Native American sources. However, given the high rate of recombination of autosomal STRs and the lack of resolution provided by classical markers, I explore here, for the first time, the paternal genetic histories of six geographically well-characterized Bahamian groups and their relationships with previously published reference collections using high-resolution Y-chromosome binary markers. Considering the unique biology of the human Y-chromosome (*i.e.*, selective neutrality, low mutation rate, stability and overall lack of recombination), it is a powerful tool for delineating genetic associations among closely related populations such as those examined in this report. In addition, I provide seventeen loci Y-STR haplotypes for three of the most prominent haplogroups (E1b1a7a-U174, E1b1a8-U175 and R1b1b1-M269) in order to assess the diversity within each of the six Bahamian islands and elucidate possible associations with specific source populations and/or migratory events.

B. Materials and Methods

Sample Collection and DNA Extraction

Buccal swabs were collected from 428 unrelated male donors residing in the central [Grand Bahama (58) and Abaco (66)] and northwest portions [New Providence (142), Eleuthera (60), Exuma (59) and Long Island (43)] of the Bahamian archipelago. Genealogical information from each sampled individual was recorded for a minimum of two generations to establish paternal ancestry. All samples were procured with informed consent following the ethical guidelines stipulated by the Institutional Review Board of Florida International University. DNA was extracted using the Gentra Buccal Cell Kit (Puregene, Gentra Systems, Minneapolis, MN) according to the manufacturer's recommended protocols and quantitated with a NanoDrop 2000 spectrophotometer (NanoDrop products, Wilmington, DE) prior to PCR amplification.

Y-chromosome haplogrouping

A total of 136 binary markers were examined in hierarchical order by standard methods, including PCR-RFLP (Luis et al., 2004), allele-specific PCR (Gayden et al., 2008), size detection of the Y polymorphic *Alu* (YAP) insertional element (Hammer and Horai, 1995) or direct sequencing (Underhill et al., 2000). Y-haplogroup nomenclature is in accordance with Karafet et al. (2008) and recent updating by Myres et al. (2011).

For comparative purposes, sample collections from West [Benin (Fon) and Cameroon (Bantu)], Central [Rwanda (Hutu)] and East [Kenya (Bantu)] Africa analyzed in a previously published report (Luis et al., 2004) were also included in the present study. The M191 derived individuals were tested for U174, P9.2, P115 and P116, while those reported as E3a*-M2 were typed for U175 and its downstream mutations (P278, U290, P59 and U181).

Population Comparisons

The Y-chromosome haplogroup variation among the six Bahamian populations and the 55 geographically targeted reference collections gathered from the literature (Table 1) was assessed through calculation of pairwise F_{st} distances using Arlequin version 3.11 (Excoffier et al., 2005). The F_{st} distances generated were represented in a multidimensional scaling (MDS) graph with the aid of PASW Statistics version 18 (SPSS, Inc., Chicago, IL, 2009). The same analysis software was also employed to quantify admixture for the Bahamian and other New World collections (*i.e.*, Cuba, Nicaragua, South Argentina as well as Hispanic Americans, European Americans and African Americans from the United States) using the grouped African, European, East Asian and Native American populations as parental sources (Table 1). All analyses performed were based on the observed haplogroup frequencies at the resolution of the major haplogroups (A-T) of the Y-chromosome phylogram.

Y-STR genotyping

Samples under the SNP backgrounds of E1b1a7a-U174, E1b1a8-U175 and R1b1b1-M269 were typed for 17 Y-STR loci (DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, and Y-GATA H4) in a multiplex reaction using the AmpF/STR[®] Yfiler Amplification Kit (Applied Biosystems, Foster City, CA). PCR products were electrophoresed on an ABI 3130xl Genetic Analyzer utilizing ABI GeneScan[™] 500 LIZ as the internal size standard. The GeneMapper[®] software v3.2 was employed to analyze the resulting Y-STR profiles through comparisons to the allelic ladder supplied by the manufacturer. Seventeen loci Y-STR haplotypes for individuals under the background of E1b1a7a, E1b1a8 and R1b1b1 are provided in Supplementary Tables 1-3, respectively.

Phylogenetic and Statistical Analyses

Haplotype diversity (HD), the number of haplotypes, the number of unique haplotypes and the mean number of pairwise differences were calculated using the Arlequin package version 3.11. The diversity indices generated were based on the 10 STR markers (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439) common to all collections included in the analyses. The same dataset was also utilized in the construction of multi-population networks with the aid of NETWORK version 4.5.1.6. Networks based on the Y-STR profiles of E1b1a7a, E1b1a8 and R1b1b1 individuals were calculated using the RM-MJ technique described in the program's user guide, available at <http://www.fluxus-engineering.com>. The Y-STR markers employed in the analyses were assigned weights as described previously

(Berniell-Lee et al., 2009), ϵ was set to zero and the “frequency>1” criterion was activated. To further reduce network complexity, the postprocessing option, which employs a maximum parsimony (MP) calculation, was selected. MDS plots based on Y-STR frequency distributions were also generated as described earlier.

For all Y-STR based analyses, the allele repeat length for DYS389b was computed by subtracting the number of repeats at DYS389II from the number at DYS389I and samples exhibiting duplicated loci, microvariant and/or null alleles were excluded. Also, to allow inclusion of pertinent European reference collections, the Athey’s Haplogroup Predictor 23-Haplogroup Beta program (Athey, 2006) was employed to infer haplogroup assignments. Only those samples yielding confidence estimates $\geq 90\%$ were utilized for phylogenetic comparisons. Supplementary Tables 4-6 provide a list of SNP-STR references for haplogroups E1b1a7a, E1b1a8 and R1b1b1, respectively, along with the number of individuals utilized in the analyses.

C. Results

Y-haplogroup distribution

A total of 44 paternal lineages (Fig. 1) distributed throughout haplogroups A, B, DE*, E, G, I, J, Q, R and T were identified among the 428 Bahamian males analyzed in the present study. Of these, E-M96 (65.7%), a clade detected at elevated levels in sub-Saharan Africa, is the most frequently observed haplogroup and is trailed by two European-specific lineages, R1b1b1-M269 (19%) and I-M258 (6.5%). Cumulatively, these three haplogroups constitute greater than 90% of the Y-chromosomes in the

Bahamian gene pool. The geographic distribution of the major haplogroups (A-T) is illustrated in Figure 2A.

Haplogroup E1b1a-M2 is the most common of the E-M96 lineages in my dataset, accounting for greater than 50% of Bahamian Y-chromosomes. Although E1b1a-M2 lineages are shared across all six studied populations, they are detected at substantially lower levels (23.3%) in the Long Island populace than in the collections from New Providence (60.6%), Abaco (60.6%), Exuma (62.7%), Grand Bahama (63.8%) and Eleuthera (68.3%). It is interesting to note that haplogroups E1b1a7-M191 and E1b1a8-U175, the two most abundant E1b1a sub-lineages in Africa (Karafet et al., 2008), are almost equally represented in the latter five populations while in Long Island, the vast majority of M2 chromosomes (13.95%) carry U175 derivatives (Fig. 2B). Appreciable frequencies of E1b1a* are also observed in all six collections, ranging from 7% in Long Island to 25% in Eleuthera.

Within the E1b1a7 sub-clade, the majority of Bahamian males are characterized by the U174 mutation, a trend that is also observed in the East and West African populations typed in the current report (Table 2). Interestingly, the sole Central African representative (Rwanda Hutus) was found to exhibit the highest proportion (23.2%) of undifferentiated M191 Y-chromosomes, *i.e.*, E1b1a7* lineages. The same group, along with the Bantu speakers from Cameroon, also displays the highest frequencies of the P116 derivative (13% and 7.1%, respectively). The E1b1a8 derived chromosomes, on the other hand, are predominated by the U290 mutation (haplogroup E1b1a8a1) in both the Bahamian and continental African collections, with the exception of Benin, which possesses a greater frequency (15.7%) of E1b1a8a*-P278 lineages. Even though all U290

derived samples were tested for U181 (a downstream mutation), this marker was observed only in Exuma, Grand Bahama and New Providence. Finally, the E1b1a8a2 sub-clade, which is present in only one of the Bahamian collections examined (*i.e.*, New Providence, 2.1%), is exclusive to the Bantu population from Kenya (3.5%).

Haplogroups E1a, E2b and E1b1b (defined by the M33, M98 and M35 mutations, respectively), although not as abundant as E1b1a lineages, are also present (Fig. 2B). Of the three sub-clades, E2b is by far the most common, with the highest levels (7%) detected in the Exuma populace. Within this branch, M85* Y-chromosomes typically predominate over all other M98 patrilineages in the Bahamian gene pool, although two individuals (one in Exuma and one in New Providence) have also acquired the M200 mutation (Fig. 2B). This E2b derivative, to the authors' knowledge, has thus far been detected only in Mbuti Pygmies from the Democratic Republic of the Congo (Cruciani et al., 2002).

The B-M60 derived Y-chromosomes, on the other hand, which are reported at elevated levels in the Pygmy, Nilo-Saharan, Khoisan, and, to a lesser extent, Bantu populations of Africa (Wood et al., 2005; Gomes et al., 2010), are detected in the Bahamian gene pool at a frequency of 4%. In each population studied, the vast majority of B-M60 derived individuals are represented by the B2a-M150 sub-clade and its downstream derivatives (M218 and M109), whereas the paralogous branch (B1-M236) is restricted to the collections from Abaco (3%) and New Providence (2.1%). It is interesting to note that four of the six Bahamian populations are also characterized by one sample bearing only the defining M60 mutation (*i.e.*, B*-M60).

Another haplogroup shared across all six studied populations is R1b1b1-M269, a lineage present at elevated levels in Western Europe (Meyers et al., 2011). In the present study, the majority of these Bahamian Y-chromosomes belong to haplogroups R1b1b1a1a-M405 and R1b1b1a1b2-M529, which occur at an average frequency of 5.6% and 8.4%, respectively. However, when the distribution of these two branches are compared, greater frequencies of M529 lineages are noted in the sample collections from Exuma (5.1%), Eleuthera (6.7%), Grand Bahama (6.9%), New Providence (9.9%) and Long Island (18.6%), while higher proportions of M405/U106 derivatives are detected in Abaco (10.6%). Interestingly, the Long Island populace, which harbors the highest frequencies of the above mentioned sub-clades, is also characterized by relatively high percentages of R1b1b1a1b*-S116 (9.3%) and R1b1b1a1b1-U152 (14%) derived Y-chromosomes. Outside of haplogroup R1b1b1, the remaining R-M306 derived samples were assigned to the R1a1a*-M198 (2.3%) and R1b2*V88 (3%) sub-clades, which are present at elevated levels in South Asia (Underhill et al., 2010) and Cameroon (Cruciani et al., 2010), respectively.

The other important European haplogroup, I-M258, was detected in the combined Bahamian dataset at a frequency of 6.5%. Of this haplogroup's sub-clades, the I1 branch (typical of Northern Europeans (Rootsi et al., 2004)) was found to predominate I lineages in Eleuthera (6.7%), Grand Bahama (5.2%) and Long Island (4.7%) whereas the frequency of haplogroup I2 derivatives (characteristic of Southeast European/Balkan populations (Battaglia et al., 2009)) was higher in the collections from Abaco (6.1%) and Exuma (5.1%). It is noteworthy that all of the Y-chromosomes within the latter branch (except for one individual in Exuma and one in Abaco) have acquired the M223, and in

some cases, the M284 mutation, whereas those belonging to the former sub-clade bear only the M253 mutation and are therefore classified as I1*.

Genetic Structure

In the MDS plot (Fig. 3), the Bahamian (*i.e.*, Abaco, Eleuthera, Exuma, Grand Bahama and New Providence) and US African American collections segregate to the right half of the projection, forming a loosely associated aggregate with Kenya (Bantu) and several of the West [Cameroon (Bantu), Gabon and Angola] and Central [Democratic Republic of the Congo (Hema), Central African Republic (Pygmies) and Botswana] African populations (denoted by the dashed circle in Fig. 3). Long Island, in contrast, displays a considerable degree of genetic separation from the other five Bahamian groups, partitioning on the opposite side of the graph with the European, Northeast African (although the Nilotes from Uganda and the Khoisan from South Africa are also included) and New World populations. The positioning of Abaco, New Providence, Grand Bahama, Eleuthera and Exuma amidst the continental Africans is anticipated given the high frequencies of haplogroup E lineages (65.2%, 68.1%, 70.7%, 73.3% and 76.3%, respectively) in these collections whereas the separation of Long Island is likely driven by elevated levels of M269 derived Y-chromosomes (55.8%).

Admixture proportions for Abaco, Eleuthera, Exuma, Grand Bahama, Long Island and New Providence are provided in Table 3, along with those calculated for several other New World populations. The results indicate that five of the islands sampled have received the majority of their paternal lineages (89.7% - 100%) from African sources, while the remaining influences in each collection's gene pool emanate exclusively from

Europeans. The Long Island populace is the exception, sharing 75.2% of its paternal component with the latter group of populations. Commensurate levels of European influences (ranging from 67.3% in Hispanic Americans to 97.4% in European Americans) were also observed in the other New World collections examined, but, in contrast to Bahamians (excluding Long Island) and US African Americans, these populations also receive genetic input from East Asian (1.40% - 2.90%) and Native American (0.10% - 16.5%) sources.

Y-STR Distributions and Diversity

Haplotype diversity (HD) for the Bahamian populations is high (ranging from 0.9341-1.0000, 0.9455-1.0000 and 0.9565-1.0000 for haplogroups E1b1a7a, E1b1a8 and R1b1b1, respectively) and haplotype sharing within the islands is limited, with the largest number of shared haplotypes equaling 10 (Long Island, haplogroup R1b1b1). In most instances, the Bahamian collections exhibit HD levels comparable to or even higher than those of the reference populations. Diversity indices for all populations examined within haplogroups E1b1a7a, E1b1a8 and R1b1b1 are provided in Supplementary Tables 7-9, respectively.

Phylogenetic networks representing Y-STR haplotype variation within haplogroups E1b1a7a and E1b1a8 are presented in Figures 4A and 4B, respectively. Haplotype distributions in the six Bahamian populations are widespread throughout both projections, sharing clusters with all three African groups employed in the analysis. In the E1b1a7a network, 24 different Y-STR haplotypes are in common among the Bahamian and continental African collections, with 19 of these are shared exclusively with West

and/or Central Africans. Figure 4B, on the other hand, illustrates a greater number (32) of shared haplotypes, although the majority of these are also present in both the West and Central African populations. Several Bahamian-specific clades are also noted in both networks, further attesting to the high level of diversity observed in this group of populations.

Network analysis of the R1b1b1 samples (Fig. 5) demonstrates extensive haplotype sharing between the Bahamian and European populations, particularly with those from the United Kingdom, Ireland and the Iberian Peninsula. Although the Bahamian collections display stronger genetic affinities with West Europeans, they also possess Y-STR profiles in common with individuals from the Balkan Peninsula. In this projection, New Providence is the only Bahamian group to exhibit a cluster exclusively with Poland and the Balkan groups. Also, in comparison to the African-specific networks (Fig. 4A,B), a greater number of independent Bahamian clades are observed.

In the MDS projections based on the Y-STR allelic frequencies of individuals possessing haplogroup E1b1a7a (Fig. 6A) and E1b1a8 (Fig. 6B) derivatives, substantial variation among the six studied populations is apparent. When only the E1b1a7a derived samples are considered (Fig. 6A), Eleuthera and Exuma form a loosely associated cluster in the upper portion of the graph with the populations from Gabon, Cameroon (Bantu), Benin, Nigeria, Ivory Coast, Uganda and Central African Republic (Pygmy). In the lower half of the plot, Abaco lies adjacent to several of the Central [Democratic Republic of the Congo (Bantu) and Zambia (Bantu)] and East [Tanzania (Bantu) and Kenya (Nilo-Saharan)] African groups, while New Providence and Grand Bahama map in closest proximity to Burkina Faso and Tanzania (Khoisan). However, in the case of haplogroup

E1b1a8 (Fig. 6B), the MDS reveals genetic associations distinct from those for E1b1a7a. The collection from Eleuthera lies intermediate to Angola and the population pair consisting of Botswana and Tanzania (Khoisan) in the upper left quadrant, while Exuma maps in closest proximity to Kenya (Bantu) and Burkina Faso in the lower left section but also exhibits genetic affinities to the Bantu speakers from the Democratic Republic of the Congo. To the right of the projection, Long Island and Grand Bahama segregate together with Cameron (Bantu), occupying a transitional position between Uganda and the collection from Abaco, which plots as an outlier at the perimeter of the graph. Interestingly, the New Providence populace strays away from all other Bahamian groups, exhibiting genetic affinities with the Ivory Coast collection in the bottom-right quadrant.

D. Discussion

Genetic signatures of the Transatlantic slave trade

The considerable proportion (ranging from 71.2% to 79.7%) of haplogroup A-M91, B-M60, E1a-M33, E1b1a-M2 and E2b-M98 lineages in five of the Bahamian populations analyzed (*i.e.*, Abaco, Eleuthera, Exuma, Grand Bahama and New Providence) signals a direct genetic connection with continental Africa, consistent with earlier reports based on classical (Halberstein et al., 1981) and autosomal STR (Herrera et al., 2004; Simms et al., 2008; 2010; 2011) markers. Genetic affinities between the two regions, which are also observed in the MDS (Fig. 3) and admixture analyses (Table 3), further corroborate historical accounts of gene flow from African and Creole slaves prior

to the abolition of slavery in 1807 (Saunders, 1985; Johnson, 1996; Pepin, 2005) and from liberated Africans during the post-slavery era (Wood, 1974; Tinker 1998).

According to Pepin (2005), the largest proportion of slaves transported to the Bahamas during the period of the Transatlantic slave trade embarked from West-Central Africa (26.8%), although substantial numbers also departed from ports along the Gold Coast (20.2%), the Bight of Biafra (17.1%) and the Windward Coast (14.6%). Utilizing high-resolution Y-chromosome binary markers, I was able to uncover genetic associations between the Bahamian collections and those originating in West and Central Africa not only in MDS graph (Fig. 3) but also with respect to NRY haplogroup distributions. Particularly suggestive of this close genetic relationship is the observed prominence of sub-Saharan specific E1b1a7-M191 and E1b1a8-U175 lineages in the Bahamas, with sub-haplogroups E1b1a7a-U174 and E1b1a8a1-U290 accounting for the majority of Y-chromosomes (with the exemption of Rwanda and Benin, respectively) in the Bahamian, West and Central African populations (Table 2). P116, a downstream mutation of E1b1a7a-U174, provides additional support for this notion, with low frequencies of this marker being observed in the collections from Abaco, Eleuthera, Exuma and New Providence as well as those from Cameroon (Bantu) and Rwanda (Hutus) (Table 2). Moderate levels of undifferentiated M2* chromosomes throughout the archipelago also allude to genetic signatures from West Africa, with the Mande speakers from Senegal and Burkina Faso (de Filippo et al., 2011) displaying the highest frequencies and groups from Nigeria, Ghana and Cameroon exhibiting appreciable proportions (Veeramah et al., 2010).

The distribution of Y-STR haplotypes within haplogroups E1b1a7a-U174 and E1b1a8-U175, as illustrated in the Network (Fig. 4A and 4B, respectively) and MDS projections (Fig. 6A and 6B, respectively) as well as in the substantially high HD values (Supplementary Tables 7 and 8, respectively), is strikingly diverse, suggesting that the Bahamian archipelago has been influenced by a wide array of African source populations. This finding is not surprising given that the Africans settling in the Bahamas were members of various tribes, including, but not limited to, the Igbo/Ebo, Mandingo, Fulani, Hausa (Albury, 1975), Yoruba, Congo (Albury, 1975; Duncan et al. 1996), Akan (Wilkie, 1993), Kru, Ndongo and Mbundu (Saunders, 1996) peoples, originating throughout West and Central Africa. It is important to note that many cultural influences derived from these groups (*e.g.*, music (Goombay, Junkanoo), dance (Ring play), story-telling, obeah (black and white magic), ‘bush’ medicine and even the communal practice of money management, the ‘Asue’) still remain a part of Bahamian tradition (Saunders, 1995).

Genetic signals from East Africa, albeit not as prominent, are also noted in the current investigation. In both the U174 (Fig. 4A) and U175 (Fig. 4B) networks, a considerable number of Y-STR haplotypes are shared among the Bahamian, Central, West and East African populations, indicating a close genetic relationship among these four groups. Affinities with East Africans are also evident in the Y-STR based MDS plots (Fig. 6A, B) despite the fact that no Bahamian/East African specific clades are observed in either network projection. Genetic signatures linking the Bahamian and East African populations are likely relics of the Bantu expansion throughout sub-Saharan Africa (Plaza et al, 2004; Beleza et al, 2005), although several other explanations are plausible. These

include: (1) the apprehension and shipment of captives from Southeast Africa to West African ports prior to disembarking for the New World (Thomas, 1998; Pereira et al., 2001) and (2) the resettlement of Africans aboard slave ships transporting mixed cargoes [*i.e.*, slaves of Central, East and West African origins (Dalleo, 1984)] in the Bahamas (Tinker, 1998). According to the Collector of Customs' report in 1828, representatives of the Gamba and Hanga tribes of Sudan and Kenya, respectively, were present throughout the island chain (Dalleo, 1982).

Gene flow from Western Europe

Western European colonialism, although short-lived, has left marked genetic imprints throughout the Bahamian archipelago, with Long Island receiving the strongest European genetic signals and Exuma, the weakest; a distribution pattern consistent with my earlier reports utilizing autosomal STR markers (Simms et al., 2008; 2010; 2011). The relatively larger proportion of M269 derived Y-chromosomes in the Long Island population (55.8%), as compared to the other five Bahamian islands surveyed (ranging from 8.5% -18.3%), is likely attributed to higher rates of genetic admixture between European males and African females (Saunders, 2003b). According to the 1851 census, Long Island possessed one of the lowest European components (13.1%) yet, by 1953, almost 50% of this population was of 'mixed' ancestry (Craton, 1998). While this may simply be the result of lower numbers of M269 chromosomes in the other five islands sampled, it may also reflect genetic drift due to the small effective population size of the Long Island European colonial fraction during the eighteenth century. This notion is

further supported by Long Islands' low observed HD (0.9565 ± 0.0204) within haplogroup R1b1b1-M269.

Appreciable frequencies of haplogroups R1b1b1a1b2*-M529 [common in individuals of British or Irish ancestry (Myres et al., 2011)] and R1b1b1a1a*-M405 [typical of populations originating in Denmark, Germany (Cruciani et al., 2011), England, France and the Netherlands (Myres et al., 2011)] in the gene pools of the six Bahamian populations allude to genetic connections with Great Britain. Influences from this region, which are anticipated given the influx of British Independents from Bermuda in the mid 1600s and the thousands of British Loyalists from North America between 1783 and 1785, are also observed in the network of R1b1b1 individuals (Fig. 5). In this projection, 18 haplotypes are shared between the populations from the Bahamas and the United Kingdom (UK), with New Providence and Long Island forming a clade exclusively with this group. Considerable sharing of haplotypes (23) with the collections from the Iberian Peninsula is also noted, suggesting potential influences from Spain and/or Portugal. The presence of haplogroup R1b1b1a1b* in Abaco, Grand Bahama, Long Island and New Providence provides further support for this notion, as undifferentiated S116 Y-chromosome are almost exclusive to these two parts of Europe (Myres et al., 2011). Genetic affinities with populations originating in the Iberian Peninsula are likely the result of migratory events from Southern Europe, Latin America and/or the US (Department of Statistics of the Bahamas, 2000).

Interestingly, the distribution of European genetic influences in the Bahamian populations analyzed mirrors Loyalists settlement patterns throughout the archipelago. Saunders (1983) explains that two classes of Loyalists migrated into the island chain: (1) the ‘business men’ (officers, merchants and professionals) that settled in New Providence and the Northern Bahamas [excluding Grand Bahama since it was not permanently settled until 1806 (Dold, Folster and Vaitlingam, 2003)] and (2) the ‘farmers’ that ventured to the south. Those taking up residence in the north, particularly in Abaco and north Eleuthera, were more inclined to intermarry with the Old residents (the Conchs) than to genetically mix with the slaves. As a result of these endogamous practices, a larger proportion of European Y-chromosomes appear to have been preserved in both collections’ gene pool.

On the contrary, Loyalists settling in the Southern Bahamas (*e.g.*, Long Island and Exuma) implemented the plantation system, using slave labor to grow Sea Island cotton (Saunders, 1983). However, with the collapse of the cotton industry, most of these Loyalists abandoned their plantations granting the land to their slaves (Craton and Saunders, 1992). This is the most likely explanation for the strong African and relatively weak European genetic signals displayed by the Exuma populace regardless of which marker system [autosomal (Simms et al., 2011) or Y-chromosome (Table 3)] is employed. Long Island, on the other hand, possessed a large number of poor Loyalists who could not afford to leave when cotton failed. Instead this group remained in the island and, over time, genetically mixed with the slaves to form a community of “near-whites” (Craton, 1998). Therefore, it is not surprising that the admixture profile (Table 3) for Long Island identifies Europeans as the primary genetic contributor, although it is

interesting to note that influences from this region are substantially higher in this population's paternal vs. autosomal gene pool, possibly indicating asymmetric mating between European males and African females (Saunders, 2003b).

Comparisons with the other New World populations

In the present study, the NRY haplogroup distributions of Abaco, Eleuthera, Exuma, Grand Bahama and New Providence were not found to differ considerably from other African derived groups in the New World. E1b1a lineages, for example, are observed in the above mentioned islands (ranging from 60.6% to 68.3%) at frequencies comparable to those observed in African-Brazilian (Hünemeier et al., 2007; Gonçalves et al., 2008), Afro-Ecuadoran (González-Andrade et al., 2007), Barbadian (Harris et al., 2006) and US African American (Vallone and Butler, 2004; Sims, Garvey and Ballantyne, 2007) populations. Likewise, commensurate levels of E1b1a7-M191 (formerly classified as E3a7) derived chromosomes were detected in the Bahamian (at an average frequency of 20.3%), US African American (Sims, Garvey and Ballantyne, 2007) and African-Brazilian (Gonçalves et al., 2008) groups, however, Bahamians and US African Americans (Sims, Garvey and Ballantyne, 2007) were the only ones typed for the E1b1a8-U175 sub-clade. These latter three collections also exhibit similar levels of E1a-M33 and E2-M75, while M35 derived chromosomes, which are characteristic of Southeastern European as well as North and East African populations, are considerably more frequent in Afro-Brazilians than in the aforementioned groups.

The R1b1b1 lineages are also observed at commensurate levels in Bahamians (at an average frequency of 18.5%), US African Americans (Hammer et al., 2006; Sims, Garvey and Ballantyne, 2007), Afro-Ecuadorans (González-Andrade et al., 2007) and Barbadians (Harris et al., 2006), although when downstream markers are examined the collections from Abaco, Eleuthera, Exuma, Grand Bahama exhibit higher levels of M405 derived chromosomes than the US African American population. The comparability of distributions of the two most common haplogroups, E and R, in the Bahamian and other New World African populations, especially US African Americans (Table 3), may represent genetic signatures from similar ancestral sources and/or episodes of gene flow between the different countries within the region. The Long Island populace, on the other hand, which possesses a much lower frequency (23.3%) of M2 derived Y-chromosomes and a substantially higher proportion of R1b1b1 (58.1%) lineages, exhibits a genetic profile typical of several Latin American groups in the New World [*e.g.*, Brazilians (Porto Alegre) (Hünemeier et al., 2007) and Nicaraguans (Nuñez et al., 2010)].

Genetic signals from other ethnic groups

Over the last 150 years, the Bahamas has been witness to a rich and varied array of settlers, including Chinese immigrant workers, Greek spongers, Jewish businessmen and individuals of Lebanese descent fleeing religious persecution. The extent to which each group has contributed genetically to the Bahamian paternal gene pool, however, is unknown. My findings suggest that the Greeks, which exhibit relatively high frequencies of haplogroups E1b1a*-M78, J2a*-M410 and R1b1b1*-L23 (Myres et al., 2011; Semino et al., 2004), are a likely source of these lineages in the Bahamas, although the presence

of M78 derived chromosomes may also signal gene flow from Lebanon (Zalloua et al., 2008). J1e-P58 lineages, on the other hand, which are characteristic of Jewish (Hammer et al., 2009) and Arab speaking groups (Chiaroni et al., 2009), may represent genetic signatures of Eastern European Jews and/or Lebanese migrants entering the Bahamas in the early twentieth century. Interestingly, the Native American and East Asian genetic signals detected in my earlier study using autosomal STR makers (Simms et al., 2011) are completely absent from the paternal gene pool of each island analyzed (Table 3). The lack of genetic input from these groups may reflect smaller sample sizes and/or sex-biased gene flow.

E. Conclusion

My findings support a stronger genetic relationship between Bahamians (excluding Long Island) and continental Africans than with any other group examined. This close genetic affinity, particularly with the West and Central African populations, is most likely attributed to the immigration of African and Creole slaves into the archipelago by the Loyalists and the thousands of liberated Africans resettled in the Bahamas by the British during the post slavery era. The Long Island collection, in contrast to the other five Bahamian islands analyzed, derives the majority of its paternal component from Europeans, possibly the result of asymmetric mating between European males and African females on this island. Additional investigations of the six studied populations using mtDNA polymorphisms should provide further understanding of the genetic history of the Bahamas.

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Appendix V

Fig. 1: Hierarchical phylogenetic relationships and frequencies (%) of the 44 paternal haplogroups observed in the six Bahamian islands analyzed in the current investigation. M75, P147, P177, P123 and P143 (in italics) were not genotyped but were included for phylogenetic context.

Fig. 2A: Global Y-chromosome frequency distribution at the level of the major haplogroups (A-T)

Fig. 2B: Frequency distributions of Y-chromosome E sub-haplogroups within the Bahamian archipelago

Fig. 3: Multidimensional Scaling plot based on Y-haplogroup frequency data of the populations listed in Table 1

Fig. 4A: Network projection based on the Y-STR profiles within sub-haplogroup E1b1a7a-U174

Fig. 4B: Network projection based on the Y-STR profiles within sub-haplogroup E1b1a8-U175

Fig. 5: Network projection based on the Y-STR profiles within sub-haplogroup R1b1b1-M269

Fig. 6A: Multidimensional Scaling plot based on Y-STR allelic frequency data for individuals possessing haplogroup E1b1a7a-U174 derivatives

Fig. 6B: Multidimensional Scaling plot based on Y-STR allelic frequency data for individuals possessing haplogroup E1b1a8-U175 derivatives

Biogeographical origin	Population	Sample Size	Abbreviation	Reference
NEW WORLD				
	Bahamian			
	Abaco	66	ABA	<i>Present study</i>
	Eleuthera	60	ELU	<i>Present study</i>
	Exuma	59	EXU	<i>Present study</i>
	Grand Bahama	58	GRB	<i>Present study</i>
	Long Island	43	LIS	<i>Present study</i>
	New Providence	142	NWP	<i>Present study</i>
	Latin American			
	Cuba	132	CUB	Mendizabal et al., 2008
	Nicaragua	165	NIC	Núñez et al., 2010
	Argentina (South)	32	SOA	Corach et al., 2010
	United States			
	Hispanic Americans	479	HIS	Hammer et al., 2006
	European Americans	125	EUA	Sims et al., 2007
	African Americans	118	AFA	Sims et al., 2007
EUROPEAN				
	West			
	Cantabria	70	CAN	Flores et al, 2004
	Leon	60	LEO	Flores et al, 2004
	Galicia	292	GAL	Brion et al., 2004
	England	1344	ENG	Campbell et al., 2007
	Portugal	657	POR	Beleza et al., 2006
	Scotland	775	SCO	Campbell et al., 2007
	Wales	178	WAL	Campbell et al., 2007
	East			
	Croatia	90	CRO	Marjanovic et al., 2005
	Greece	92	GRE	Battaglia et al., 2009
	Romania	31	ROM	Bosch et al., 2006
	Slovakia	250	SLO	Petrejčková et al., 2010
EAST ASIAN				
	Bali (Indonesia)	641	BAL	Karafet et al., 2010
	China (Han)	165	CHI	Karafet et al., 2010
	Japan	259	JAP	Hammer et al., 2006
	Philippines	48	PHI	Karafet et al., 2010
	Taiwan	48	TAI	Karafet et al., 2010
	Vietnam	70	VIE	Karafet et al., 2010

Table 1: Populations utilized in Y-SNP analyses

Biogeographical origin	Population	Sample Size	Abbreviation	Reference
AFRICAN	West			
	Angola	74	ANG	Beleza et al., 2005
	Benin (Fon)	102	BEN	Luis et al., 2004
	Burkina Faso (Gur)	183	BFG	de Filippo et al., 2010
	Burkina Faso (Mande)	152	BFM	de Filippo et al., 2010
	Cameroon (Bantu)	14	CAB	Luis et al., 2004
	Cameroon (Bamelike)	79	BAM	Luis et al., 2004
	Guinea-Bissau (Fulbe)	59	FUL	Rosa et al., 2007
	Gabon	54	GAB	Berniel-Lee et al., 2007
	Namibia (Ambo)	22	AMB	Wood et al., 2005
	Nigeria (Yoruba)	12	NIG	de Filippo et al., 2010
	Senegal/Gambia (Mandinka)	39	MAN	Wood et al., 2005
	Senegal	15	SEN	de Filippo et al., 2010
	São Tomé e Príncipe	150	STP	Gonçalves, Spinola and Brehm, 2007
	East			
	Ethiopia	126	ETH	Semino et al., 2002
	Kenya (Bantu)	29	KEB	Luis et al., 2004
	Mozambique	130	MOZ	Brión et al., 2006
	Tanzania (Wairak)	41	TAN	Luis et al., 2004
	Sudan	445	SUD	Hassan et al., 2008
	Central			
	Botswana (Bantu)	40	BOT	de Filippo et al., 2010
	Central African Republic (Pygmy)	23	CAR	de Filippo et al., 2010
	Democratic Republic of the Congo (Hema)	18	HEM	Wood et al., 2005
	Democratic Republic of the Congo (Bantu)	58	DRC	de Filippo et al., 2010
	Rwanda (Hutu)	69	HUT	Luis et al., 2004
	Rwanda (Tutsi)	98	TUT	Luis et al., 2004
	Uganda (Nilotes)	118	UGA	Gomes et al., 2010
	Zambia East (Bantu)	69	ZAE	de Filippo et al., 2010
	South			
	Kung	64	KUN	Cruciani et al., 2004
	Khoisan	39	KHO	Underhill et al., 2001
	Xhosa	80	XHO	Wood et al., 2005
NATIVE AMERICAN				
	Apache	94	APA	Zegura et al., 2004
	Navajo	75	NAV	Zegura et al., 2004
	Pima	62	PIM	Malhi et al., 2008

Table 1: Populations utilized in Y-SNP analyses (Cont'd)

		Frequency of Haplogroup (%)													
		E1b1a7								E1b1a8					
		M191	U174	P9.2	P115	P116	P113	Total	U175	P278	U290	P59	U181	Total	
BAHAMAS	Population	N													
	Abaco	66	1.52	19.70	-	-	1.52	-	22.73	1.52	9.09	13.64	-	-	24.24
	Eleuthera	60	3.33	16.67	-	-	5.00	-	25.00	1.67	8.33	8.33	-	-	18.33
	Exuma	59	-	22.03	-	-	1.69	-	23.73	-	5.08	11.86	-	1.69	18.64
	Grand Bahama	58	-	24.14	-	-	-	-	24.14	1.72	6.90	6.90	-	3.45	18.97
	Long Island	43	-	2.33	-	-	-	-	2.33	-	2.33	11.63	-	-	13.95
	New Providence	142	2.11	16.90	-	-	0.70	-	19.72	0.70	7.04	9.15	2.11	0.70	19.72
AFRICA	West														
	Benin (Fon)	102	2.94	54.90	-	-	-	-	57.84	0.98	15.69	10.78	-	-	11.76
	Cameroon (Bantu)	14	-	14.29	-	-	7.14	-	21.43	-	-	42.86	-	-	42.86
	Central														
	Rwanda (Hutu)	69	23.19	14.49	-	-	13.04	-	50.72	-	1.45	1.45	-	-	2.90
	East														
Kenya (Bantu)	29	-	31.03	-	-	-	-	31.03	-	-	13.79	3.45	-	17.24	

- indicates that the haplogroup was not detected

Table 2: Frequencies of E1b1a7 and E1b1a8 sub-haplogroups in the Bahamian and continental African populations

BAHAMAS						
Parental Groups	Abaco	Eleuthera	Exuma	Grand Bahama	Long Island	New Providence
European	0.103 ± 0.077	0.004 ± 0.101	0.000 ± 0.075	0.054 ± 0.084	0.752 ± 0.074	0.081 ± 0.090
African	0.897 ± 0.084	0.996 ± 0.111	1.000 ± 0.082	0.946 ± 0.092	0.248 ± 0.081	0.919 ± 0.099
Native American	0.000 ± 0.060	0.000 ± 0.079	0.000 ± 0.058	0.000 ± 0.066	0.000 ± 0.058	0.000 ± 0.070
East Asian	0.000 ± 0.069	0.000 ± 0.091	0.000 ± 0.067	0.000 ± 0.076	0.000 ± 0.066	0.000 ± 0.081

NEW WORLD						
Parental Groups	Cuba	Nicaragua	South Argentina	European American	Hispanic American	African American
European	0.765 ± 0.041	0.686 ± 0.052	0.749 ± 0.073	0.974 ± 0.062	0.673 ± 0.032	0.084 ± 0.078
African	0.218 ± 0.045	0.131 ± 0.057	0.071 ± 0.080	0.000 ± 0.068	0.165 ± 0.035	0.916 ± 0.085
Native American	0.001 ± 0.032	0.165 ± 0.041	0.154 ± 0.057	0.012 ± 0.049	0.132 ± 0.025	0.000 ± 0.061
East Asian	0.017 ± 0.037	0.018 ± 0.047	0.026 ± 0.066	0.014 ± 0.056	0.029 ± 0.029	0.000 ± 0.070

Table 3: Admixture proportions generated for the Bahamian and New World populations

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA_H4	DYS437	DYS438	DYS448
NWP3	15	13	22	30	16	15	17	19	14	10	12	22	11	11	14	11	21
NWP4	15	13	21	30	16	17	18	19	14	10	12	21	11	11	14	11	21
NWP6	15	13	21	30	18	16	15	19	14	10	11	21	12	11	14	11	20
NWP11	16	14	21	31	15	17	18	19	15	10	11	21	11	11	14	11	21
NWP24	17	14	21	31	16	17	17	17	14	10	11	20	11	11	14	11	21
NWP29	16	12	21	29	15	16	17	19	15	10	12	21	11	11	14	11	21
NWP32	14	13	20	31	15	16	15	18	14	10	13	21	11	11	14	11	21
NWP39	16	12	21	29	15	16	17	19	15	10	12	21	11	11	14	11	20
NWP48	15	13	25	29	15	14	15	15	13	10	11	24	13	12	15	12	18
NWP51	16	13	21	30	16	16	17	17	15	11	12	22	11	11	14	11	21
NWP53	15	13	21	30	16	17	17	18	15	10	13	21	9	11	14	11	21
NWP68	16	13	21	31	19	16	16	18	14	10	11	21	11	11	13	11	21
NWP72	16	13	21	31	16	15	16	19	15	10	12	21	11	11	14	10	21
NWP75	15	13	21	29	17	16	17	17	13	12	11	22	11	11	14	11	21
NWP87	17	13	21	30	17	16	17	17	14	10	12	20	11	11	14	11	21
NWP93	16	13	21	30	17	17	15	17	15	10	11	21	11	11	14	11	21
NWP133	16	13	21	30	16	17	16	17	14	10	12	21	11	12	14	11	21
NWP134	15	13	20	31	17	17	18	18	15	10	11	21	11	11	14	11	21
NWP138	15	13	21	30	16	16	19	19	14	11	12	22	11	11	13	11	21
NWP181	16	13	21	30	16	16	16	18	13	10	11	21	11	11	14	11	22
NWP202	16	13	21	30	16	14	17	18	13	10	12	21	11	11	13	11	21
NWP212	16	13	22	30	16	16	17	18	16	10	12	21	11	11	14	11	21
NWP214	16	14	21	31	17	17	17	19	15	10	12	21	11	11	14	11	21
NWP216	16	13	21	30	16	17	16	18	14	10	11	22	11	11	14	11	21
NWP226	17	14	21	31	15	17	16	17	14	10	11	22	9	11	14	11	21
GRB266	15	14	21	31	16	17	17	20	15	10	12	20	11	11	14	11	21
GRB277	16	13	21	30	16	16	17	19	13	10	13	22	11	11	14	11	21
GRB306	16	12	21	29	16	17	17	20	15	10	13	21	11	11	13	11	21
GRB312	16	13	21	30	17	16	17	20	15	10	12	21	11	11	14	11	21
GRB314	16	13	21	30	17	15	17	18	14	11	11	22	11	12	14	11	21

Supplementary Table 1: Y-STR haplotypes for E1b1a7a individuals

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA_H4	DYS437	DYS438	DYS448
GRB318	14	13	21	30	16	17	17	17	14	10	12	21	11	11	14	11	21
GRB319	15	13	21	30	17	16	16	19	14	10	12	21	11	11	14	11	20
GRB324	16	13	21	30	16	15	16	18	13	10	11	21	11	11	14	11	22
GRB327	16	13	21	30	16	17	16	17	14	10	11	21	11	11	14	11	21
GRB328	14	13	21	31	17	15	16	18	16	10	12	21	11	12	14	11	21
GRB332	15	13	21	31	17	17	17	18	15	11	11	21	11	11	14	10	21
GRB344	15	13	21	31	17	17	17	17	15	11	11	21	11	11	14	11	21
GRB345	15	13	21	30	16	17	17	20	13	9	12	23	11	11	14	11	21
GRB352	16	13	21	30	16	16	14	17	13	10	12	23	11	11	14	11	21
ELU365	15	13	21	30	16	16	16	19	14	10	12	22	12	11	14	11	21
ELU387	15	13	21	30	16	17	18	18	14	10	12	21	11	11	14	11	21
ELU401	15	13	21	30	16	16	17	19	15	10	12	22	12	11	14	11	21
ELU408	17	13	21	30	17	16	17	17	14	10	12	20	11	11	14	11	21
ELU409	15	13	21	30	16	16	18	18	15	10	12	21	12	12	14	11	21
ELU437	15	13	21	30	17	15	17	19	15	10	12	21	11	11	14	11	21
ELU439	16	13	21	30	15	16	16	17	15	10	12	21	11	11	13	12	20
ELU446	16	14	21	31	17	17	17	20	15	10	13	21	11	11	14	11	21
ELU450	15	12	21	29	17	17	16	18	15	10	13	21	11	11	14	11	21
ELU458	14	13	21	30	16	17	18	18	14	9	13	21	11	11	14	11	21
ELU461	16	14	21	31	17	17	17	20	15	10	13	21	11	11	14	11	21
ELU488	17	14	21	31	16	17	17	19	15	10	12	21	11	11	14	11	21
ELU760	16	13	21	31	17	15	16	18	15	10	12	21	11	11	14	11	21
LIS501	15	13	21	29	16	15	17	20	15	10	12	21	11	11	14	11	21
EXU587	17	14	21	31	17	17	17	19	15	10	12	21	11	11	14	11	21
EXU590	16	14	21	31	16	16	17	17	15	10	13	21	11	11	14	11	21
EXU592	16	13	21	30	16	15	16	17	15	10	12	21	11	11	13	11	21
EXU596	16	14	21	31	16	16	17	17	15	10	13	21	11	11	14	11	20
EXU597	16	14	21	31	16	16	17	17	15	10	13	21	11	11	14	11	20
EXU598	16	14	21	31	16	16	17	17	15	10	13	21	11	11	14	11	20
EXU605	16	13	21	31	16	17	17	18	14	10	12	21	10	11	14	11	21

Supplementary Table 1: Y-STR haplotypes for E1b1a7a individuals (Cont'd)

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA_H4	DYS437	DYS438	DYS448
EXU630	16	13	21	30	16	16	16	18	15	11	11	21	11	11	14	11	21
EXU648	16	13	21	30	17	17	18	20	15	11	13	21	11	11	14	11	22
EXU650	16	13	21	30	17	16	17	18	15	10	12	21	11	11	13	11	21
EXU655	17	13	21	31	16	15	17	18	14	10	12	21	11	12	13	11	21
EXU656	15	13	21	30	16	17	18	19	14	10	12	21	11	11	14	11	21
EXU659	17	13	21	29	16	16	16	20	15	10	11	21	11	11	14	11	21
EXU661	15	13	21	29	17	17	18	18	15	10	12	21	11	11	14	11	19
ABA678	15	13	21	30	17	17	17	18	13	10	12	21	11	11	14	11	21
ABA695	16	13	21	30	17	16	17	20	15	10	12	21	11	11	14	11	21
ABA701	17	14	21	31	16	17	17	17	14	10	11	20	11	11	14	11	21
ABA709	17	13	21	30	16	17	16	17	14	10	12	21	11	11	14	11	21
ABA711	15	13	21	30	17	17	17	18	14	10	12	21	11	11	14	11	21
ABA718	16	13	21	30	17	17	16	18	15	10	12	21	11	11	14	11	21
ABA724	16	13	21	31	19	17	16	18	14	10	11	21	11	11	13	11	21
ABA735	15	13	21	30	16	15	17	18	14	10	11	21	11	11	14	11	21
ABA765	14	13	21	30	17	17	17	18	14	10	12	21	11	11	14	11	21
ABA768	16	14	21	31	16	17	18	20	15	10	12	21	11	11	13	11	21
ABA778	14	13	21	30	16	17	18	18	14	9	13	21	11	11	14	11	21
ABA782	17	13	21	30	16	16	19	20	14	10	12	21	11	11	14	11	22

Supplementary Table 1: Y-STR haplotypes for E1b1a7a individuals (Cont'd)

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA_H4	DYS437	DYS438	DYS448
NWP5	15	12	21	30	17	16	15	17	13	10	12	21	11	12	14	11	21
NWP9	15	13	21	31	17	15	16	17	13	10	12	22	11	12	14	12	21
NWP12	15	14	21	32	17	15	16	18	13	11	12	22	11	12	14	11	21
NWP16	15	13	21	32	16	15	17	17	13	10	12	21	12	12	14	11	21
NWP21	15	14	21	32	16	15	15	18	13	10	12	22	11	12	14	11	21
NWP28	15	13	21	31	17	15	16	17	13	10	12	21	11	12	14	11	21
NWP36	16	14	21	33	15	17	17	19	14	10	12	21	11	12	14	11	21
NWP50	15	12	21	30	15	15	14	18	13	10	12	21	11	12	14	11	20
NWP73	15	14	21	32	16	15	16	17	13	11	11	21	11	12	14	11	21
NWP76	15	12	21	30	17	16	15	17	13	10	12	21	11	12	14	11	21
NWP84	15	14	21	31	18	15	15	16	14	10	12	21	11	12	14	11	21
NWP86	15	13	21	30	18	15	15	15	13	10	12	21	11	12	14	11	20
NWP94	15	12	21	30	18	17	16	17	13	10	12	22	11	12	14	11	21
NWP100	16	13	21	31	19	15	16	16	13	10	12	21	7	12	14	11	21
NWP112	13	14	21	32	15	15	16	18	13	10	13	21	11	11	14	11	21
NWP113	15	13	21	31	17	15	16	17	13	10	12	21	11	11	14	11	21
NWP119	15	14	21	32	17	16	15	17	13	10	13	21	11	11	14	11	21
NWP152	15	13	21	31	16	16	16	17	13	10	12	20	11	12	14	12	21
NWP156	15	13	21	31	17	16	16	17	13	10	11	21	11	12	14	11	20
NWP160	14	14	21	33	17	16	16	16	13	10	12	21	11	11	14	11	21
NWP178	15	14	21	31	18	16	16	18	13	10	12	21	11	12	13	11	21
NWP188	14	13	21	31	17	15	16	17	13	10	12	21	11	12	14	12	21
NWP190	15	13	21	31	17	16	16	17	13	10	11	21	11	12	14	11	20
NWP206	15	13	21	30	18	15	15	15	13	10	12	21	11	12	14	11	20
NWP208	15	13	21	32	15	16	15	16	13	10	12	23	11	12	14	11	21
NWP213	14	12	21	30	17	15	15	19	13	10	12	21	11	12	14	11	21
NWP215	15	13	21	31	16	15	16	17	13	11	11	21	11	12	14	11	21
NWP217	14	13	21	31	16	15	16	17	13	11	11	21	11	12	14	11	21
GRB227	15	13	21	30	17	15	16	17	13	11	13	21	11	12	14	11	21
GRB228	15	13	21	30	19	15	14	18	14	10	12	21	11	11	14	11	21

Supplementary Table 2: Y-STR haplotypes for E1b1a8 individuals

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA H4	DYS437	DYS438	DYS448
GRB244	16	13	21	31	18	15	16	18	13	10	12	21	11	12	15	11	21
GRB271	15	14	21	31	18	15	15	16	14	10	12	21	11	12	14	11	21
GRB275	16	13	21	32	17	16	16	17	14	10	11	21	12	12	14	11	20
GRB322	15	13	21	31	16	17	16	17	13	10	12	21	11	12	14	11	21
GRB326	15	12	21	32	15	16	16	18	13	9	13	21	11	12	14	11	21
GRB334	15	13	21	31	17	15	15	16	13	10	12	21	11	11	14	12	21
GRB341	15	13	21	31	16	15	16	17	13	11	11	21	11	12	14	11	21
GRB343	15	12	21	29	17	15	16	18	13	10	12	22	11	12	14	11	21
GRB355	15	13	21	31	16	15	15	17	13	10	11	22	12	12	14	11	21
ELU376	16	13	21	32	19	16	17	17	14	10	11	21	11	12	14	11	21
ELU378	16	13	21	30	17	15	15	17	13	11	12	21	11	12	14	11	21
ELU380	14	13	21	31	16	15	16	16	13	10	12	21	11	12	14	11	21
ELU395	16	13	21	30	18	16	17	18	13	10	12	21	11	12	14	11	22
ELU397	16	13	21	30	17	15	15	17	13	11	12	21	11	12	14	11	21
ELU416	15	13	21	30	16	15	16	18	13	10	12	22	11	12	14	11	21
ELU421	15	13	21	31	15	15	16	18	13	10	12	21	11	12	14	11	22
ELU425	14	13	21	30	17	15	14	15	13	10	12	23	11	11	14	11	21
ELU426	15	13	21	31	17	16	16	17	13	10	11	21	11	12	14	11	20
ELU440	15	12	21	30	17	16	16	18	13	10	12	21	11	12	14	11	21
ELU454	15	13	21	31	16	15	16	18	13	11	12	21	11	12	14	11	21
LIS471	16	13	21	31	17	15	17	17	13	10	12	21	11	12	14	11	21
LIS472	15	13	21	31	16	15	16	17	13	10	11	22	11	12	14	12	21
LIS498	15	13	22	32	17	15	15	16	13	10	13	22	11	12	13	11	21
LIS516	14	13	21	30	17	15	14	15	13	10	12	23	11	11	14	11	21
LIS536	15	13	21	31	16	17	16	17	13	10	12	21	11	12	14	11	21
LIS547	15	13	21	30	17	15	17	18	13	10	11	21	11	12	14	11	21
EXU572	15	13	21	31	17	15	16	17	13	10	11	21	11	12	14	12	21
EXU573	15	12	21	32	15	16	16	18	13	9	13	21	11	12	14	11	21
EXU582	16	13	21	30	20	15	16	17	13	10	12	21	11	13	14	11	21
EXU586	15	12	21	32	15	16	16	18	13	9	14	21	11	12	14	11	21

Supplementary Table 2: Y-STR haplotypes for E1b1a8 individuals (Cont'd)

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA H4	DYS437	DYS438	DYS448
EXU591	16	13	21	31	20	15	16	17	13	10	12	21	11	13	14	11	21
EXU594	15	12	21	31	15	16	16	18	13	9	13	21	11	12	14	11	21
EXU595	15	13	21	31	18	15	14	15	13	10	12	21	11	14	14	11	21
EXU623	15	13	21	32	16	15	15	16	13	10	12	21	11	12	14	11	21
EXU632	15	14	21	32	17	13	17	20	13	10	12	21	11	12	14	11	22
EXU641	15	13	21	31	16	15	16	17	13	10	12	22	11	12	14	12	21
EXU645	15	13	21	31	16	15	17	18	13	10	12	21	11	12	14	11	21
ABA671	15	14	21	33	17	13	17	21	13	10	12	21	11	12	15	11	22
ABA672	15	12	21	32	15	16	16	18	13	9	14	21	11	12	14	11	21
ABA674	15	13	21	30	16	16	15	18	14	10	13	21	10	12	14	11	21
ABA676	15	13	21	30	16	16	15	18	14	10	13	21	10	12	14	11	21
ABA677	15	13	21	30	16	15	16	17	13	11	11	21	11	12	14	11	20
ABA680	15	12	21	30	15	15	14	18	13	10	12	21	11	12	14	11	21
ABA685	15	13	21	30	16	16	15	18	14	10	13	21	10	12	14	11	21
ABA696	15	13	20	30	17	16	14	20	14	10	13	22	11	12	14	11	21
ABA698	15	13	20	30	17	16	14	20	14	10	13	22	11	12	14	11	21
ABA702	15	12	21	32	15	16	15	18	13	9	14	21	11	12	14	11	21
ABA703	14	13	21	31	16	15	14	16	13	10	12	22	13	11	14	11	22
ABA706	15	13	21	32	17	15	15	17	13	10	12	21	11	11	14	11	21
ABA727	15	13	21	31	18	15	15	17	13	10	13	21	11	11	14	11	21
ABA728	15	13	21	31	17	15	16	17	13	10	12	21	11	12	14	11	21
ABA742	15	12	21	29	17	15	15	15	13	10	13	21	11	13	14	12	21
ABA747	16	14	21	31	18	16	16	17	14	10	12	22	11	11	14	11	21
ABA762	15	13	21	32	17	15	17	17	13	10	13	21	11	12	14	11	21

Supplementary Table 2: Y-STR haplotypes for E1b1a8 individuals (Cont'd)

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA H4	DYS437	DYS438	DYS448
NWP 2	16	13	24	29	16	14	11	14	13	11	13	23	13	12	15	11	19
NWP 13	16	14	24	30	17	14	10	14	13	11	12	24	13	13	14	12	19
NWP 15	15	13	25	29	17	14	11	11	13	10	12	23	13	11	14	11	18
NWP 20	18	14	23	30	18	15	11	13	13	11	11	23	13	11	15	12	19
NWP 37	16	13	25	29	17	14	11	13	13	11	13	23	14	12	15	12	18
NWP 40	16	13	24	30	16	14	11	14	13	11	13	23	13	12	15	11	19
NWP 43	16	13	24	29	16	14	11	14	13	11	12	23	13	12	15	12	19
NWP 44	15	13	24	30	17	13	11	14	14	10	12	23	13	14	15	12	18
NWP 46	15	13	23	29	17	14	12	14	13	10	12	24	13	11	15	12	20
NWP 54	15	12	24	29	17, 18	14	11	15	13	11	12	23	13	12	14	12	19
NWP 56	15	13	24	29	16	14	11	14	13	11	13	23	13	11	14	12	18
NWP 60	16	13	24	30	16	14	11	14	12	11	12	23	13	11	15	12	19
NWP 63	16	13	24	29	17	15	11	14	13	11	12	23	13	12	15	12	19
NWP 98	15	13	25	29	17	14	12	12	13	11	12	23	13	13	15	12	19
NWP 102	16	13	25	29	17	14	11	14	13	10	11	23	13	12	15	12	18
NWP 106	17	13	23	29	17	14	11	14	13	11	12	23	13	12	15	12	19
NWP 125	15	13	25	29	17	14	11	14	13	11	12	23	13	12	15	12	19
NWP 148	15	13	25	29	15	14	15	15	13	10	11	24	13	12	15	12	18
NWP 176	16	13	24	30	17	12	11	15	13	10	13	24	13	12	15	12	19
NWP 179	16	13	24	29	21	14	11	14	13	11	12	23	13	12	15	12	19
NWP 205	15	13	25	29	16	14	11	14	13	11	12	23	13	12	15	12	19
NWP 209	16	13	24	29	18	14	11	14	13	10	12	23	13	12	15	12	19
NWP 220	14	13	24	29	20	14	11	14	13	11	12	23	14	12	15	12	19
NWP 221	16	13	24	29	17	14	11	14	13	11	12	23	13	12	15	11	19
NWP 223	16	13	24	29	17	14	11	11	13	11	12	23	13	11	14	12	18
NWP 784	16	13	23	29	17	14	11	15	13	11	11	23	15	12	15	12	19
GRB 232	16	13	23	28	17	14	11	11	13	11	11	23	13	12	15	12	18
GRB 233	16	13	24	29	16	14	11	13	13	11	11	23	13	12	15	12	19
GRB 246	16	14	23	30	17	14	11	14	13	10	12	23	13	12	15	12	19
GRB 315	16	13	24	29	17	14	11	14	13	11	12	23	13	12	15	12	19

Supplementary Table 3: Y-STR haplotypes for R1b1b1 individuals

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA_H4	DYS437	DYS438	DYS448
GRB 321	15	13	24	29	17	14	11	14	13	10	12	23	13	12	15	12	19
GRB 329	16	13	25	29	16	14	11	14	13	11	11	23	13	12	15	12	19
GRB 339	15	13	24	29	17	14	11	14	13	11	13	23	13	12	15	12	19
GRB 354	15	13	24	29	18	14	11	13	13	12	12	23	13	12	15	12	19
ELU 364	16	13	24	29	17	14	11	14	14	10	12	23	13	12	15	12	19
ELU 403	15	14	23	30	17	14	11	14	13	11	12	23	13	11	15	12	19
ELU 404	16	13	25	29	17	14	12	14	13	11	13	23	13	12	15	12	19
ELU 430	15	13	24	29	17	14	11	15	13	10	11	24	13	12	15	12	19
ELU 455	15	12	24	29	16, 18	14	11	15	13	11	12	23	13	12	14	12	19
ELU 467	16	13	25	30	17	14	11	15	13	11	12	23	12	12	15	12	18
LIS 469	15	13	23	28	16	14	11	14	13	10	11	23	13	12	15	12	19
LIS 473	15	13	24	30	17	13	11	14	14	10	12	23	13	13	15	12	18
LIS 474	15	13	24	30	17	13	11	14	14	10	12	23	13	13	15	12	18
LIS 475	16	13	25	29	17	14	11	14	13	10	11	23	13	12	15	12	18
LIS 476	15	14	23	30	16	14	11	14	13	10	14	23	13	12	15	12	19
LIS 478	16	12	24	28	18	15	11	15	13	11	12	23	13	13	15	12	19
LIS 483	17	13	23	29	17	14	11	14	13	11	12	23	13	12	15	12	19
LIS 487	17	13	24	30	16	14	11	13	13	11	12	23	13	12	15	12	19
LIS 489	15	13	23	28	16	14	11	14	13	10	11	23	13	12	15	12	19
LIS 499	16	12	24	28	18	15	11	15	13	11	12	23	13	13	15	12	19
LIS 500	16	13	24	28	17	15	11	15	13	11	13	23	13	12	15	12	19
LIS 506	15	13	24	29	18	14	11	14	13	10	11	23	15	12	15	12	19
LIS 517	15	13	24	29	18	14	11	14	13	10	11	23	15	12	15	12	19
LIS 518	16	13	25	29	18	14	11	14	13	10	11	23	13	12	15	12	18
LIS 519	15	13	24	29	15	14	11	14	12	10	12	24	13	12	15	12	19
LIS 520	15	13	24	29	18	14	11	14	13	10	11	23	15	12	15	12	19
LIS 522	16	13	24	28	17	15	11	15	13	11	13	23	13	12	15	12	19
LIS 531	17	12	25	28	17	14	11	13	13	11	12	23	14	12	15	12	18
LIS 532	15	13	24	29	18	14	11	14	13	11	12	24	13	12	15	12	19
LIS 541	15	13	24	29	15	14	11	14	12	10	12	24	13	12	15	12	19

Supplementary Table 3: Y-STR haplotypes for R1b1b1 individuals (Cont'd)

Sample	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a	DYS385b	DYS393	DYS391	DYS439	DYS635	DYS392	GATA H4	DYS437	DYS438	DYS448
LIS 542	15	13	24	29	16	14	11	14	13	11	13	23	13	11	14	12	18
LIS 545	16	13	24	29	17	14	10	14	13	11	12	24	13	13	14	12	19
LIS 551	15	13	24	29	16	14	11	14	13	11	13	23	13	11	14	12	18
LIS 553	16	13	24	29	16	14	11	14	13	11	13	23	13	11	14	12	18
EXU 610	16	12	24	27	16	14	11	15	13	11	11	23	13	12	15	12	19
EXU 622	16	13	23	29	16	14	11	15	13	11	12	25	13	12	14	12	19
EXU 626	17	13	23	29	17	14	11	14	13	11	12	23	13	12	15	12	19
EXU 647	16	13	23	28	16	14	12	14	13	10	11	23	13	12	15	12	19
EXU 662	17	13	23	29	17	14	11	14	13	11	12	23	13	12	15	12	19
ABA 669	15	12	23	28	18	14	11	14	13	11	12	23	13	12	15	12	19
ABA 679	16	14	23	30	17	14	11	14	13	11	12	25	13	12	15	12	18
ABA 681	15	12	24	28	17	14	12	14	13	11	13	23	13	12	16	12	19
ABA 699	15	13	21	29	18	14	11	15	13	11	11	24	13	12	15	12	19
ABA 700	16	12	23	28	18	14	11	14	13	11	12	23	13	12	15	12	19
ABA 731	16	13	25	30	17	14	11	15	13	11	12	23	12	12	15	12	18
ABA 732	17	14	23	30	20	14	11	14	13	10	11	24	13	11	15	12	19
ABA 744	16	13	25	30	17	14	11	15	13	12	12	23	12	12	15	12	18
ABA 763	15	13	24	29	16	14	11	14	13	11	13	23	13	11	14	12	18
ABA 766	16	13	23	30	16	14	11	12	13	11	14	23	13	12	15	12	19
ABA 767	16	13	24	29	16	14	11	14	13	11	13	23	13	12	15	11	19

Supplementary Table 3: Y-STR haplotypes for R1b1b1 individuals (Cont'd)

Haplogroup and Population	Abbreviation	N	References
E1b1a7a			
Abaco	ABA	13	<i>present study</i>
Angola	ANG	46	Coelho et al., 2009; de Filippo et al., 2011
Benin (Beninese)	BEN	20	Brucato et al., 2010
Botswana	BOT	10	de Filippo et al., 2011
Burkina Faso (Gur & Mande)	BRF	13	de Filippo et al., 2011
Cameroon (Bantu)	CAB	13	Berniell-Lee et al., 2009; de Filippo et al., 2011
Cameroon (Pygmy)	CPY	10	Berniell-Lee et al., 2009; de Filippo et al., 2011
Central African Republic (Pygmy)	CRP	10	de Filippo et al., 2011
Democratic Republic of the Congo (Bantu)	DRC	16	de Filippo et al., 2011
Democratic Republic of the Congo (Pygmy)	DRP	3	de Filippo et al., 2011
Eleuthera	ELU	13	<i>present study</i>
Exuma	EXU	14	<i>present study</i>
Gabon (Bantu)	GAB	302	Berniell-Lee et al., 2009; de Filippo et al., 2011
Gabon (Pygmy)	GAP	3	Berniell-Lee et al., 2009; de Filippo et al., 2011
Grand Bahama	GRB	14	<i>present study</i>
Ivory Coast (Ahizi & Yacouba)	IVC	13	Brucato et al., 2010
Kenya (Bantu)	KEB	4	de Filippo et al., 2011
Kenya (Nilotic)	KEN	10	de Filippo et al., 2011
Long Island	LIS	1	<i>present study</i>
New Providence	NWP	25	<i>present study</i>
Nigeria	NIG	8	de Filippo et al., 2011
Tanzania (Bantu)	TAB	15	Tishkoff et al., 2007; de Filippo et al., 2011
Tanzania (Khoisan)	TAK	19	Tishkoff et al., 2007; de Filippo et al., 2011
Uganda (Nilotes)	UGA	6	Gomes et al., 2010; de Filippo et al., 2011
Zambia (East & West Bantu)	ZAM	125	de Filippo et al., 2011

Supplementary Table 4: Populations examined in E1b1a7a-U174 Y-STR based analyses

Haplogroup and Population	Abbreviation	N	References
E1b1a8			
Abaco	ABA	17	<i>present study</i>
Angola	ANG	143	Coelho et al., 2009; de Filippo et al., 2011
Benin (Beninese)	BEN	7	Brucato et al., 2010
Botswana	BOT	13	Filippo et al., 2010
Burkina Faso (Gur & Mande)	BRF	86	Filippo et al., 2010
Cameroon (Bantu)	CAB	6	Berniell-Lee et al., 2009; de Filippo et al., 2011
Cameroon (Pygmy)	CAP	3	Berniell-Lee et al., 2009; de Filippo et al., 2011
Central African Republic (Pygmy)	CRP	6	de Filippo et al., 2011
Democratic Republic of the Congo (Bantu)	DRC	22	de Filippo et al., 2011
Democratic Republic of the Congo (Pygmy)	DRP	1	de Filippo et al., 2011
Eleuthera	ELU	11	<i>present study</i>
Exuma	EXU	11	<i>present study</i>
Gabon (Bantu)	GAB	289	Berniell-Lee et al., 2009; de Filippo et al., 2011
Gabon (Pygmy)	GAP	1	Berniell-Lee et al., 2009; de Filippo et al., 2011
Grand Bahama	GRB	11	<i>present study</i>
Ivory Coast (Ahizi & Yacouba)	IVC	31	Brucato et al., 2010
Kenya (Bantu)	KEB	2	de Filippo et al., 2011
Kenya (Nilotic)	KEN	6	de Filippo et al., 2011
Nigeria	NIG	1	de Filippo et al., 2011
Long Island	LIS	6	<i>present study</i>
New Providence	NWP	28	<i>present study</i>
Senegal	SEN	1	de Filippo et al., 2011
Tanzania (Bantu)	TAB	13	Tishkoff et al., 2007; de Filippo et al., 2011
Tanzania (Khoisan)	TAK	22	Tishkoff et al., 2007; de Filippo et al., 2011
Uganda (Nilotes)	UGA	7	Gomes et al., 2010; de Filippo et al., 2011
Zambia (East & West Bantu)	ZAM	309	de Filippo et al., 2011

Supplementary Table 5: Populations examined in E1b1a8-U175 Y-STR based analyses

Haplogroup and Population	Abbreviation	N	References
R1b1b1			
Abaco	ABA	11	<i>present study</i>
Eleuthera	ELU	6	<i>present study</i>
Exuma	EXU	5	<i>present study</i>
Greece (North)	GRE	19	Kovatsi, Saunier and Irwin, 2009
Grand Bahama	GRB	8	<i>present study</i>
Ireland	IRE	124	Ballard et al., 2006
Italy	ITA	57	Onofri et al., 2007
Long Island	LIS	24	<i>present study</i>
Macedonia	MAC	20	Spiroski et al., 2005
Montenegro	MON	38	Mirabal et al., 2010
New Providence	NWP	26	<i>present study</i>
Poland	POL	18	Rębała and Szczerkowska, 2005
Portugal	POR	136	Alves et al., 2007
Romania	ROM	15	Stanciu et al., 2010
Serbia	SER	8	Mirabal et al., 2010
Spain	SPN	88	Martin et al., 2004
United Kindgom (Caucasian)	UKC	165	Ballard et al., 2005

Supplementary Table 6: Populations examined in R1b1b1-M269 Y-STR based analyses

	Population	Abbreviation	N	Number of different haplotypes	Number of unique haplotypes	Haplotype diversity (HD)	Mean number of pairwise differences
BAHAMAS	Abaco	ABA	66	13	11	0.9615 ± 0.0496	2.615385 ± 1.493860
	Eleuthera	ELU	60	13	11	0.9744 ± 0.0389	3.089744 ± 1.715243
	Exuma	EXU	59	14	11	0.9341 ± 0.0611	3.406593 ± 1.853374
	Grand Bahama	GRB	58	14	14	1.0000 ± 0.0270	3.472527 ± 1.883809
	Long Island	LIS	43	1	1	1.0000 ± 0.0000	N/A
	New Providence	NWP	142	25	23	0.9933 ± 0.0134	4.073333 ± 2.101375
AFRICA	WEST						
	Angola	ANG	230	46	26	0.9498 ± 0.0181	2.679227 ± 1.452790
	Benin	BEN	78	20	16	0.9632 ± 0.0328	3.115789 ± 1.686867
	Burkina Faso	BRF	335	13	12	0.9872 ± 0.0354	2.564103 ± 1.469842
	Cameroon (Bantu)	CAB	28	13	9	0.9487 ± 0.0423	2.756410 ± 1.559815
	Cameroon (Pygmy)	CPY	27	10	6	0.8889 ± 0.0754	1.888889 ± 1.174734
	Gabon	GAB	828	302	130	0.9788 ± 0.0037	3.255484 ± 1.682299
	Ivory Coast	IVC	90	13	9	0.9359 ± 0.0507	3.423077 ± 1.870144
	Nigeria	NIG	12	8	7	0.9643 ± 0.0772	3.571429 ± 2.026089
	CENTRAL						
	Botswana	BOT	40	10	6	0.9111 ± 0.0620	1.977778 ± 1.217904
	Central African Republic (Pygmies)	CRP	23	10	7	0.9111 ± 0.0773	3.133333 ± 1.771944
	Democratic Republic of the Congo (Bantu)	DRC	69	16	11	0.9500 ± 0.0364	2.308333 ± 1.332841
	Uganda (Nilotes)	UGA	118	6	5	0.9333 ± 0.1217	2.800000 ± 1.714643
	Zambia (Bantu)	ZAM	549	125	75	0.9818 ± 0.0048	3.095613 ± 1.618909
	EAST						
	Kenya (Nilotic)	KEN	79	10	6	0.8444 ± 0.1029	3.111111 ± 1.761373
	Tanzania (Bantu)	TAB	131	15	12	0.9429 ± 0.0542	2.771429 ± 1.552708
	Tanzania (Khoisan)	TAK	135	19	10	0.9181 ± 0.0364	2.660819 ± 1.483220

Supplementary Table 7: Haplotype Diversity indices for E1b1a7a-U174 individuals

	Population	Abbreviation	N	Number of different haplotypes	Number of unique haplotypes	Haplotype diversity (HD)	Mean number of pairwise differences
BAHAMAS	Abaco	ABA	66	17	13	0.9632 ± 0.0328	4.198529 ± 2.193222
	Eleuthera	ELU	60	11	8	0.9455 ± 0.0535	2.272727 ± 1.349494
	Exuma	EXU	59	11	9	0.9455 ± 0.0659	3.181818 ± 1.780287
	Grand Bahama	GRB	58	11	11	1.0000 ± 0.0388	3.909091 ± 2.122044
	Long Island	LIS	43	6	6	1.0000 ± 0.0962	2.800000 ± 1.714643
	New Providence	NWP	142	28	21	0.9815 ± 0.0133	2.862434 ± 1.552509
AFRICA	WEST						
	Angola	ANG	230	143	65	0.9467 ± 0.0099	2.470009 ± 1.342948
	Benin	BEN	78	7	6	0.9524 ± 0.0955	4.142857 ± 2.342311
	Burkina Faso	BRF	335	86	51	0.9688 ± 0.0089	2.945554 ± 1.557865
	Cameroon (Bantu)	CAB	28	6	5	0.9333 ± 0.1217	1.800000 ± 1.200000
	Gabon	GAB	828	289	126	0.9764 ± 0.0037	3.088932 ± 1.609946
	Ivory Coast	IVC	90	31	22	0.9656 ± 0.0188	3.053763 ± 1.633555
	CENTRAL						
	Botswana	BOT	40	13	11	0.9744 ± 0.0389	3.115385 ± 1.727175
	Central African Republic (Pygmies)	CRP	23	6	3	0.7333 ± 0.1552	3.466667 ± 2.053723
	Democratic Republic of the Congo (Bantu)	DRC	69	22	17	0.9740 ± 0.0217	3.571429 ± 1.885750
	Uganda (Nilotes)	UGA	118	7	5	0.9048 ± 0.1033	3.000000 ± 1.776867
	Zambia (Bantu)	ZAM	549	309	113	0.9633 ± 0.0058	2.803282 ± 1.484925
	EAST						
	Kenya (Nilotic)	KEN	79	6	4	0.8000 ± 0.1721	2.133333 ± 1.372751
	Tanzania (Bantu)	TAB	131	13	11	0.9744 ± 0.0389	2.794872 ± 1.577781
	Tanzania (Khoisan)	TAK	135	22	15	0.9524 ± 0.0291	3.060606 ± 1.655276

Supplementary Table 8: Haplotype Diversity indices for E1b1a8-U175 individuals

	Population	Abbreviation	N	Number of different haplotypes	Number of unique haplotypes	Haplotype diversity (HD)	Mean number of pairwise differences
BAHAMAS	Abaco	ABA	66	11	10	0.9818 ± 0.0463	3.781818 ± 2.062357
	Eleuthera	ELU	60	6	6	1.0000 ± 0.0962	4.000000 ± 2.323790
	Exuma	EXU	59	5	4	0.9000 ± 0.1610	2.800000 ± 1.768560
	Grand Bahama	GRB	58	8	8	1.0000 ± 0.0625	2.392857 ± 1.450362
	Long Island	LIS	43	24	14	0.9565 ± 0.0204	3.775362 ± 1.971008
	New Providence	NWP	142	26	22	0.9846 ± 0.0160	3.326154 ± 1.764516
EUROPE	Greece (North) †	GRE	191	19	19	1.0000 ± 0.0171	3.637427 ± 1.927505
	Italy	ITA	155	57	40	0.9843 ± 0.0070	3.547619 ± 1.830824
	Ireland †	IRE	178	124	86	0.9891 ± 0.0035	3.301338 ± 1.708942
	Macedonia †	MAC	150	20	17	0.9789 ± 0.0245	3.389474 ± 1.810919
	Montenegro	MON	404	38	14	0.8094 ± 0.0596	1.990043 ± 1.148524
	Poland †	POL	208	18	16	0.9804 ± 0.0284	3.549020 ± 1.892296
	Portugal †	POR	250	136	98	0.9818 ± 0.0063	3.488780 ± 1.789699
	Romania †	ROM	122	15	14	0.9905 ± 0.0281	4.685714 ± 2.431234
	Serbia	SER	179	8	6	0.8929 ± 0.1113	1.607143 ± 1.059816
	Spain †	SPN	144	88	74	0.9919 ± 0.0046	3.730930 ± 1.901473
	United Kindgom (Caucasian) †	UKC	250	165	118	0.9916 ± 0.0025	3.529120 ± 1.805350

† Y-haplogroups were inferred from Y-STR haplotypes provided by the authors using Athey's Haplogroup Predictor 23-Haplogroup Beta program (Athey, 2006)

Supplementary Table 9: Haplotype Diversity indices for R1b1b1-M269 individuals

VI. CONCLUSION

The results of this investigation demonstrate that Afro-Caribbeans (*i.e.*, Bahamians, Haitians and Jamaicans) are a heterogeneous group, sharing different proportions of their autosomal component with African, European, East Asian and, in the case of the Bahamian collections, Native American sources. This genetic variation, in combination with the presence of unique alleles in each island sampled, advocates the establishment of insular-specific databases for the assessment of profile frequencies and probability of inclusion as well as exclusion determinations. Interestingly, the substantial proportion of African DNA present in the gene pool of each Bahamian island was also observed when utilizing high-resolution Y-chromosome binary markers, with the collections from Abaco, Exuma, Eleuthera, Grand Bahama and New Providence receiving the strongest African genetic signals while the Long Island populace, in contrast, derives the majority of its paternal component from Europeans. Therefore, it is not surprising that African influences remain an important source of cultural traditions throughout the archipelago. Altogether, this data should provide a better understanding about the formation of the present-day Bahamian population, its current genetic makeup, and how different migratory events have shaped the genetic composition of each of the six islands sampled.

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AWARDS AND CERTIFICATIONS

- FIU Dissertation Year Fellowship (2010-2011)
- Graduate Teaching Assistants Excellence-In-Teaching Award (2008)
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