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Culture and Genetics: Ghanaian Genetic Imprints in Contemporary Bahamians?

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Abstract

This study presents preliminary genetic findings from 160 individuals sampled on the island of New Providence, The Bahamas, to explore the ancestral origins and diasporic connections of contemporary Bahamians with the Akan ethnolinguistic group from Ghana. Using mitochondrial and Y-chromosomal DNA analysis, our findings reveal that over 94% of maternal lineages and approximately 73% of paternal lineages are of African origin. These results align with historical records of slave ship arrivals and suggest deep ancestral ties with West and Central Africa, particularly from the Gold Coast (roughly modern-day Ghana). Notably, the presence of Y-haplogroups E-U175 and E-L485 (upstream branch of U174) as well as mitochondrial DNA haplogroups L2a and L3e, prevalent in the Akan ethnolinguistic group from Ghana, corresponds with the earliest documented slave voyages to The Bahamas during the 18th century. Cultural correlations, including oral traditions, further support the hypothesis of a strong Ghanaian influence in the contemporary Bahamian gene pool. While European lineages are present, they are notably less frequent (5.9% mtDNA and 26.6% Y-chromosomal lineages) and align with known patterns of colonial settlement. These findings underscore the enduring legacy of African genetic and cultural heritage in The Bahamas. This highlights the need for further comparative research with populations in West Africa, such as Ghana, especially from Princess Town (which may be the origin of the Junkanoo festival).

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Introduction

The genetic landscape of contemporary Bahamians reveals deep historical connections forged by the Transatlantic Slave Trade, reflecting West and Central African origins. Previous genetic studies examining autosomal and Y-chromosomal markers have established a strong West and Central African genetic presence among contemporary Bahamians (Simms et al., 2008, 2011, 2012, 2013), which is not surprising given the various cultural practices originating from these regions. These include, but are not limited to, the use of traditional bush medicine to treat certain ailments (e.g., the usage of sage to treat chicken pox symptoms as well as cerasee for colds and the flu), community saving schemes (asue), expressive dances such as ring play, musical traditions including Goombay and Junkanoo, spiritual practices like obeah, and rich storytelling traditions (McCormack et al., 2011; Saunders, 1985; Gibson, 2015).

Despite the previously reported genetic diversity from different African ethnic groups (e.g., the Yoruba, Congo, Igbo, Mandingo, Fulani, Hausa, Kru, Ndongo, and Mbundu [Wilkie, 1993; Lawlor, 2022]) associated with the movement of enslaved people during the period of the Transatlantic Slave Trade, the current study aims to examine the genetic and cultural contributions that enslaved Africans from the area then known as the Gold Coast (roughly present-day Ghana) have had on the contemporary Bahamian population. This particular West African region is the focus of this investigation because, according to historical records (Table 1), the first documented slave ship to land in The Bahamas, the *Bahama Galley*, arrived from the Gold Coast in 1721 carrying 295 enslaved Africans, an event that more than doubled the archipelago's existing Black population at the time (Craton & Saunders, 1999; Saunders, 1985). Craton and Saunders (1999) also report that after the arrival of the captives on this vessel, various Akan names (e.g., Kwamino) began to appear in Bahamian historic records (Craton & Saunders, 1999; Davis, 2022). Furthermore, following the arrival of the *Bahama Galley*, an additional 133 and 92 enslaved Africans from the Gold Coast were brought to the island chain in 1730 (via *Nassau*) and 1755 (via *Little Billy*), respectively (Table 1). Given the initial influx of enslaved Africans from this region (1721-1755), we anticipate a Ghanaian genetic legacy in The Bahamas.

Ghana, located on the west coast of Africa, is bordered by Côte d'Ivoire, Burkina Faso, and Togo on its western, northern, and eastern sides, respectively. In 2010, the Ghanaian population was approximately 24,658,823 persons and is comprised of five major ethnolinguistic groups (the Akan [47.5%], Ewe [13.9%], Ga-Dangme [7.4%], Mole Dagbon [16.6%], and Guang [3.7%]) (Kofi et al., 2020). Mitochondrial DNA analysis of Akan individuals in the rural Asante Akim North District, Ashanti Region, revealed the prevalence of haplogroup (a group of individuals that share a common set of DNA mutations) L lineages (99%), with sub haplogroup L2a (29.8%) and L3e (18.3%) predominating and L1b (14.1%), L1c (12%), and L3b (11%) displaying similar proportions (Fendt et al., 2012). Y-chromosomal short tandem repeat (Y-STR) analysis of the aforementioned groups from Ghana also revealed a tight clustering of three contemporaneous Ghanian ethnolinguistic groups (Akan, Ga-Dangme, and Mole-Dagbon) in the principal component analysis (PCA), indicating a shared genetic ancestry (Kofi et al., 2020). A later report of Y-chromosomal lineages in Bimoba village of Northeast Ghana also reveals the presence of haplogroup E-M2 and two of its derivatives, specifically E-U-174 and its sibling clade, E-U-175, at frequencies of 10.7% and 59.6%, respectively (Sanchez-Faddeev et al., 2013).

Given the influx of captives from different ports in West Africa during the Transatlantic Slave Trade (Table 1), it is not surprising that The Bahamas exhibits such an eclectic mixture of West and Central African traditions (McCormack et al., 2011; Saunders, 1985; Gibson, 2015). There are, however, a few traditions that link The Bahamas specifically to Ghana. The most prominent of these is Junkanoo, The Bahamas' premier cultural festival, whose origins have been hypothesized to be linked to Princess Town, in the western region of

Ghana. According to Davis (2022), the enslaved Africans from the Gold Coast that came to the Bahamian archipelago on the first three slave ships (*Bahama Galley*, *Nassau*, and *Little Billy*, Table 1) included warriors that were loyal to Jan Kwaw (also known as John Canoe), a prominent Akan military leader renowned for resisting European colonisation and the transport of enslaved Africans via the Transatlantic Slave Trade. In The Bahamas (as elsewhere in the Caribbean), John Canoe is the namesake of the Junkanoo festival, during which, in recent times, elaborate costumes adorned with crepe paper, feathers, and jewels are featured as participants rush (dance) down the street to the sounds of cowbells and the goat-skin drum (Ferguson, 2000). In addition to bearing the name of an Akan leader, Junkanoo is a form of fancy dress masquerading, a popular cultural tradition in present-day Ghana (Denis, 2021). Moreover, Ghanaian influences are also evident in Bahamian folklore, particularly in those of Anancy the spider, which has its basis in West African oral traditions (Storr, 2009).

Historical Context

This section presents a data-driven overview of African arrivals into The Bahamas based on Table 1, which compiles voyage-level records from the Trans-Atlantic Slave Trade Database (SlaveVoyages, 2025). Using these data, the narrative that follows organises arrivals into analytically distinct phases that track major shifts in Atlantic trafficking and Bahamian settlement. The Loyalist migration of 1783–1785 is treated separately and not included in this analysis because those enslaved persons largely entered outside of Transatlantic disembarkations into Bahamian ports. However, given gaps in early Colonial records, the figures should be read as conservative.

The history of African arrivals into The Bahamas through the Transatlantic Slave Trade consists of distinct phases, each shaped by broader Atlantic world developments and regional colonial dynamics (Table 1). Through examination of slave ship arrivals and disembarkation data, it is possible to trace the demographic evolution of the enslaved African populations throughout the island chain. The earliest phase of African arrivals via the Transatlantic Slave Trade into The Bahamas occurred during the colonial period prior to the American Revolutionary War (1775-1783) and the Loyalist migration (1783-1785). Between 1721 and 1763, four ships of British origin transported at least 589 African captives, which accounted for 4.2% of all recorded arrivals (Table 1). These voyages mainly trafficked from what was then known as the Gold Coast (three of the four voyages). This era was characterised by relatively limited, albeit continuous, importation of African labourers to support the modest plantation and maritime economies developing in the Bahamian islands.

A significant demographic transformation began after 1783, when thousands of American Loyalists who were displaced by the American Revolution resettled in The Bahamas, bringing with them a large enslaved African population. Craton (1986) reports that an estimated 7,000 enslaved individuals accompanied the Loyalists during this migration. This marked the most active period of enslaved people entering the archipelago. From 1788 to 1806, at least 32 slave ships landed in The Bahamas, disembarking 7,243 Africans, which represents 54.2% of all ships and 52.2% of all Africans recorded in this dataset (Table 1). When combined with the enslaved Africans brought by Loyalists, this period introduced over 14,000 African or Africandescended individuals into Bahamian society, radically reshaping the colony's demographic and cultural composition.

During this Loyalist period, African captives were transported from a diverse range of African regions, including Sierra Leone, the Windward Coast, the Bight of Biafra, Senegambia, and West Central Africa (Table 1). British vessels dominated this trade, reflecting their supremacy in the Transatlantic economy just before the legal abolition of the trade in 1807 (Saunders, 1985; Thomas, 1998). The volume and variety of African origins introduced during this period significantly shaped the emerging Afro-Bahamian cultural and genetic heritage.

Although the Transatlantic Slave Trade was abolished by Britain in 1807, The Bahamas continued to receive enslaved Africans, primarily through illegal slaving vessels or ships captured by anti-slavery patrols. Between 1811 and 1860, 23 vessels transported 6,031 Africans to Bahamian shores, accounting for 39.0% of the vessels and 43.5% of the total captives recorded (Table 1). This post-Abolition period marks a shift in slaving nations from Britain to Portugal, Brazil, Spain, and Uruguay, with the regions of origin still concentrated in West Central Africa, but also included the Bight of Biafra, the Bight of Benin, and Sierra Leone. A defining feature of this era, especially in its final years, was the sharp increase in the number of children among the enslaved. The 1860 arrival of the *Peter Mowell*, the last known slave ship to disembark Africans into The Bahamas, brought 364 individuals, many of them children, from West Central Africa (Malcolm, 2007). This tragic final shipment closed a centuries-long chapter of forced African migration into the island chain.

Table 1
Slave ships that brought captives to The Bahamas between 1721 and 1860.

Year	Name of Ship	Region of Africa	Number of Africans disembarked	Ship Nationality
1721	Bahama Galley	Gold Coast	295	
1730	Nassau	Gold Coast	133	Great Britain
1755	Little Billy	Gold Coast	92	Great Britain
1763	Prince George		69	American Colonies
1788	Shirburn Castle	West Central Africa & St. Helena	211	Great Britain
1789	Peggy	Other Africa	122	Great Britain
1791	Cleveland	Other Africa	64	Great Britain
1792	Charles	Sierra Leone	208	Great Britain
1794	Colonel	Windward Coast	216	Great Britain
1796	Speedwell	Windward Coast	247	Great Britain
1797	Saint Joseph		52	France
1798	New Adventure	Senegambia & offshore Atlantic	91	United States
1799	George	Gold Coast	259	Great Britain
1799	Charlotte	Senegambia & offshore Atlantic	195	Great Britain
1800	George	Windward Coast	260	Great Britain
1800	Governor Wentworth		203	Great Britain
1800	Fanny		54	United States
1801	Harriott	Sierra Leone	279	Great Britain

1801	Tamer	West Central Africa & St. Helena	279	Great Britain
1802	Prudence	West Central Africa & St. Helena	161	Great Britain
1802	Governor Dowdeswell	West Central Africa & St. Helena	335	Great Britain
1802	Active		277	Great Britain
1802	Mary	Sierra Leone	201	Great Britain
1802	Agnes	Bight of Biafra & Gulf of Guinea islands	279	Great Britain
1802	Baron Montlambert	West Central Africa & St. Helena	79	Great Britain
1802	Martha		249	Great Britain
1802	Surprize	West Central Africa & St. Helena	340	Great Britain
1802	Urania		189	Great Britain
1803	Mary Ellen		396	Great Britain
1803	Minerva	Bight of Biafra & Gulf of Guinea islands	212	Great Britain
1803	Kingsmill	Bight of Biafra & Gulf of Guinea islands	395	Great Britain
1803	Nile		276	Great Britain
1803	Perseverance	Bight of Biafra & Gulf of Guinea islands	320	Great Britain
1803	Lord Nelson		250	Great Britain
1805	Fortune	West Central Africa & St. Helena	343	Great Britain
1806	Eleanor	Senegambia & offshore Atlantic	201	United States
1811	Joana	Gold Coast	129	Portugal / Brazil
1811	Atrevido (a) Carolina	West Central Africa & St. Helena	204	United States
1816	Rosa	Bight of Biafra & Gulf of Guinea islands	314	Spain / Uruguay
1818	Experiençia		94	Spain / Uruguay
1822	Ulysse		192	France
1831	Rosa	Senegambia & offshore Atlantic	157	Portugal / Brazil
1832	Hebe	West Central Africa & St. Helena	385	Portugal / Brazil
1834	Felicidade	Senegambia & offshore Atlantic	162	Portugal / Brazil
1834	Despique	West Central Africa & St. Helena	215	Portugal / Brazil
1836	Empresa	West Central Africa & St. Helena	434	Spain / Uruguay
1836	Crioulo	Windward Coast	307	Portugal / Brazil
1836	Vigilante	Bight of Biafra & Gulf of Guinea islands	231	Portugal / Brazil
1837	Esperança	West Central Africa & St. Helena	220	Portugal / Brazil
1837	Antonica	West Central Africa & St. Helena	185	Portugal / Brazil
1837	Flor do Tejo	Sierra Leone	417	Portugal / Brazil
1837	Invincible		50	
1837	Ingemane (a) Lince	Sierra Leone	82	Portugal / Brazil
1838	Camões	Bight of Benin	569	Portugal / Brazil
1838	Escorpião	West Central Africa & St. Helena	212	Portugal / Brazil
1838	Washington		440	Portugal / Brazil
1838	Diligente (a) Vingador	Bight of Benin	475	Portugal / Brazil
1841	Trovadore		193	Spain / Uruguay
1860	Peter Mowell (a) Heroina	West Central Africa & St. Helena	364	United States

Note: Data obtained from SlaveVoyages (2025)

Methods

Seven buccal swabs were collected from 160 individuals on the island of New Providence. This island was strategically selected as the primary sampling site due to its role as the urban hub of The Bahamas, enabling the enrolment of participants representative of all Bahamian (Family) islands. Two buccal swabs from each participant were sent to FamilyTreeDNA (Gene by Gene, 2022) for extraction and haplogroup analysis. The remaining five swabs were stored at -80℃ in the Genetics and Molecular Laboratory at the University of The Bahamas for future analysis.

Samples were collected with informed consent following the ethical guidelines granted by the Institutional Review Board (IRB) of the University of The Bahamas (IRB number: 202305). A research permit (BS-2023-229131) was also obtained from the Department of Environmental Planning and Protection (DEPP), Government of The Bahamas, ensuring full compliance with national regulations governing genetic research. At the time of consent, the participants were asked to provide their name, age, and the island they were born on as well as genealogical information for their parents and their grandparents if known (Bethel et al., 2012). This information helped to rule out siblings that unknowingly share a parent.

At FamilyTreeDNA (Gene by Gene, 2022), the DNA was isolated and amplified by Polymerase Chain Reaction (PCR) before proprietary microarray analysis. Mitochondrial DNA and Y-chromosomal DNA haplogroups were assigned by FamilyTreeDNA (Gene by Gene, 2022) based on the single-nucleotide polymorphisms (SNPs) present in each sample. Upon receipt of the above information, the authors compared these haplogroups present to those available in the literature for African, European, and Caribbean populations, with an emphasis on published data from Ghana, Sierra Leone, Angola, Nigeria, and the Central African Republic to interpret the haplogroup distributions present in the Bahamian samples collected. All frequency data used for comparison were obtained from the FamilyTreeDNA (Gene by Gene, 2022) database via haplogroup designation.

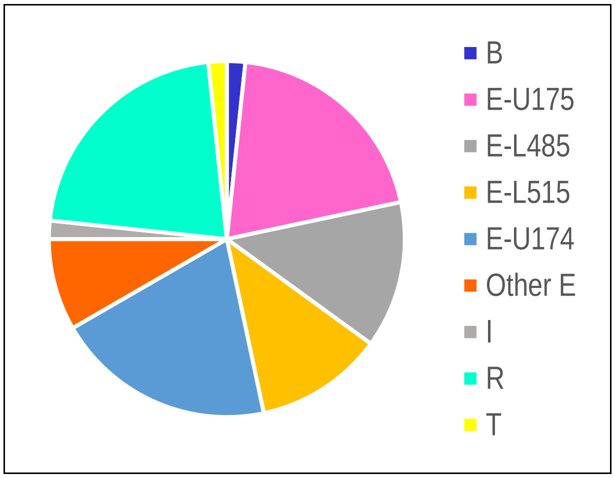
Results

Of the 160 participants, the vast majority (95%) were from The Bahamas, with a smaller number from Puerto Rico, Jamaica, Haiti, and the United Kingdom. Thus, in the current investigation, the paternal and maternal lineage results presented are only for those with Bahamian origin (n = 152, 60 males and 92 females). As illustrated in Figure 1, a strong predominance of African paternal ancestry was observed among the Bahamian male population (Table 2), with sub-Saharan African haplogroup E-M2 accounting for 70% of all male lineages (n = 42). In contrast, haplogroup R-M269 (n = 13), of European origin, was the second most common, representing 21.7% of the samples. The remaining haplogroups included B (Central African), T (Mediterranean), and I (Northern European), collectively comprising only 5% of all paternal lineages in the group.

Within haplogroup E-M2, several distinct subclades were identified. As seen in Figure 2, there are two major branches of E-M4895; these are E-CTS229 and E-M4706. Underneath the E-CTS299 branch is E-U175 and its derivatives, which are present in 20% of Bahamian males (n = 12). The other branch of E-M4895, E-M4706, has two sub branches, namely E-M58 (n = 1) and E-L485 (n = 27), with the latter Y-lineage and its derivatives being observed in Bahamian men at a frequency of 45%. Interestingly, the E-L485 branch was identified in participants with ancestral connections to Crooked Island and the Turks and Caicos Islands. Moreover, one of this branch's subsequent subclades also appeared in individuals with roots in Cat Island, Exuma, and Turks and Caicos.

Figure 1

Y-chromosomal haplogroups present in Bahamian men



Y-chromosomal lineage, E-U174, which is derived from E-M4706, was also found in 20% of Bahamian males (n = 12). These men report paternal links to Exuma, Eleuthera, and Long Island, suggesting a historical migration and settlement pattern trajectory within the Central Bahamas. When moving further down the E-M4706 branch of the tree, E-CTS7336, present in ~3% of individuals, was traced to participants with heritage in Cat Island and Eleuthera. In addition to the E lineages mentioned above, several less common younger, paternal subclades were also detected (Figure 3).

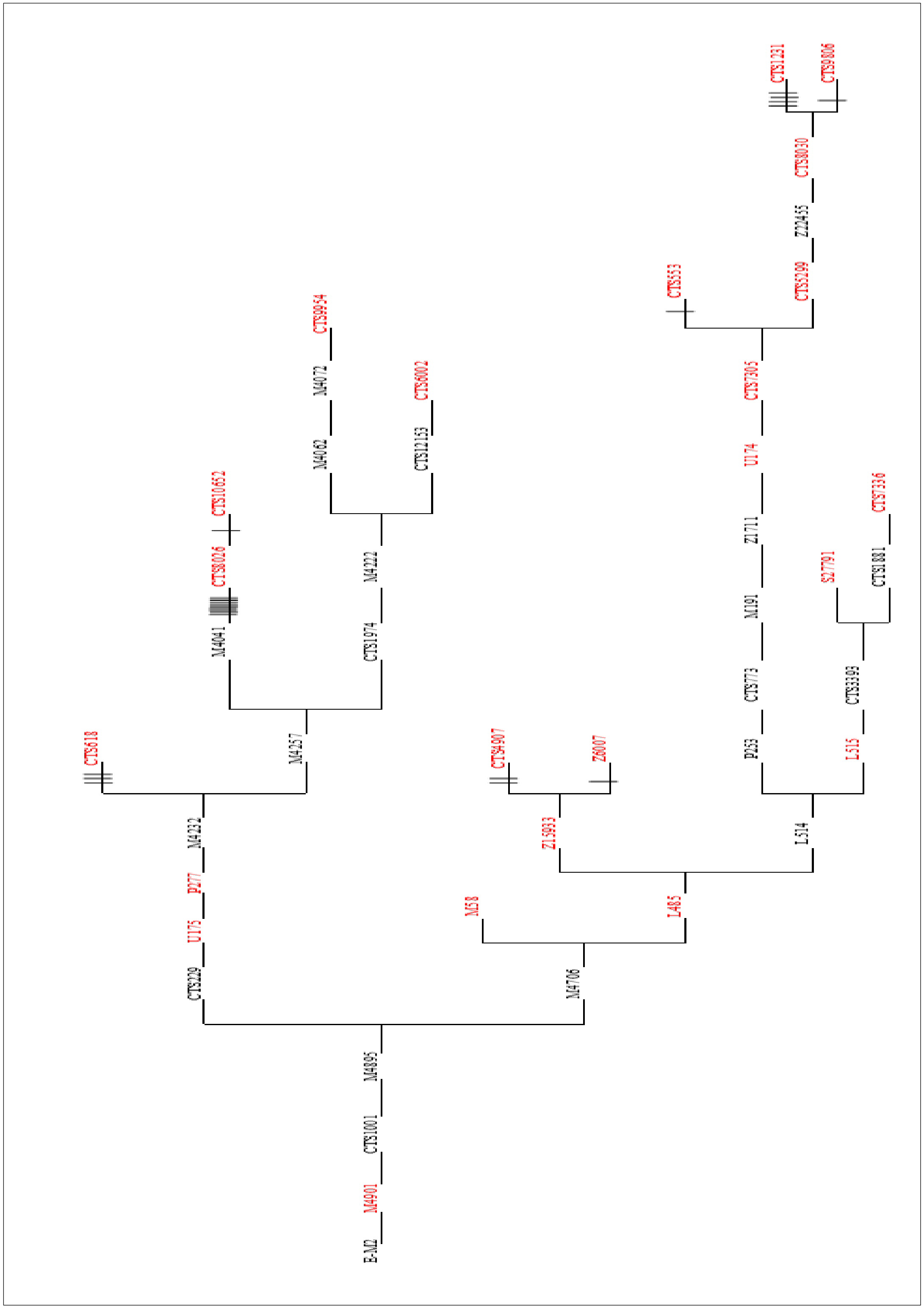
Table 2

Y-chromosomal haplogroup distribution in Bahamian males

Y-haplogroup	Defining mutation	*n* =
B	V83	1
E	CTS10652	2
	CTS1231	1
	CTS4907	1
	CTS5299	1
	CTS553	1
	CTS6002	2
	CTS618	1
	CTS7305	2
	CTS7336	2
	CTS8026	1
	CTS8030	2
	CTS9806	1
	CTS9954	3
	FGC11457	1
	L485	3
	L515	5
	M4901	2
	M58	1
	P277	1
	S27791	1
	U174	4
	U175	2
	Z15933	2
	Z6007	1
	Z878	1
I	L338	1
R	CTS3087	1
	DF13	2
	DF41	1
	L1066	1
	L257	1
	S1051	1
	S3251	1
	S691	2
	Z207	1
	Z2534	1
	Z49	1
T	PF7457	1
		60

Figure 2

Phylogeny of haplogroup E-M2 lineages.



Note: Mutations in red are those present in Bahamian males. The small vertical lines ( ) indicate the number of mutational steps to the next lineage.

Figure 3

mtDNA diversity in the Bahamian gene pool

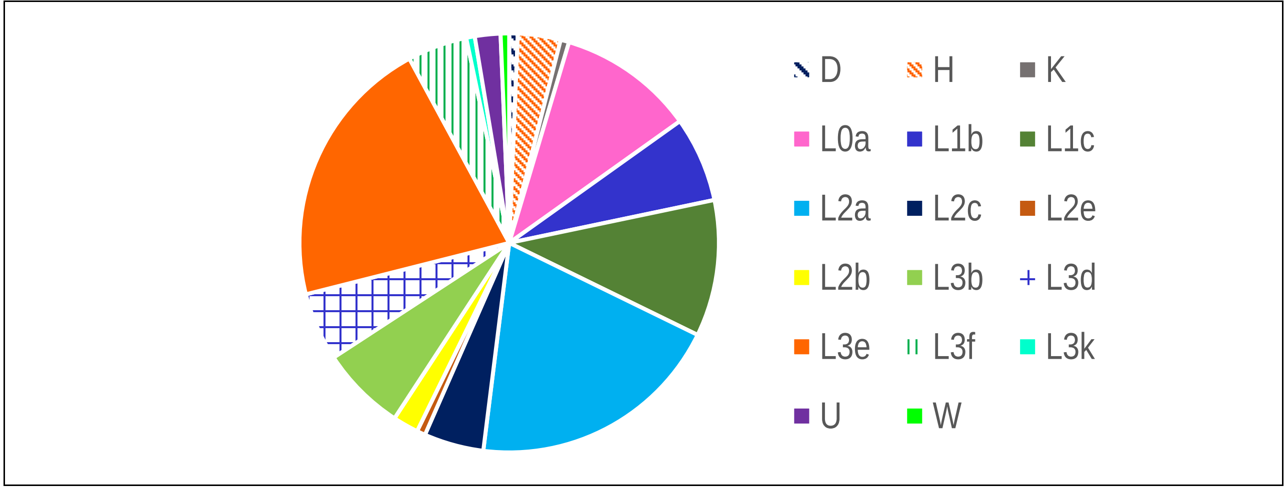


Table 3

Maternal haplogroups present in the Bahamian gene pool

mtDNA haplogroup	*n*
D1	1
H1	1
H3	1
H5	1
H6	2
K1	1
L0a	16
L1b	10
L1c	16
L2a	30
L2b	3
L2c	7
L2e	1
L3b	10
L3d	8
L3e	32
L3f	7
L3k	1
U2	1
U4	1
U5	1
W3	1
	152

Within the E- U175 branch, E-CTS8026 and its derivatives as well as E-CTS10652 were present at frequencies of approximately 1.7% and 3.3%, respectively. Moreover, one individual carrying E-CTS8030, a E-U174 derived lineage, reported Haitian heritage.

Of the 152 mtDNA samples analysed in the Bahamian population, 94.1% (n = 143) showed African maternal ancestry (Figure 3, Table 3), with sub-Saharan African haplogroups L2a and L3e predominating (19.7% and 21%, respectively). The remaining nine individuals (5.3%) had European maternal lineages, namely haplogroups H, K, U, and W. Of these, H1 and U5 were observed in participants native to Cat Island (Figure 3, Table 3). The single Native American haplogroup (D1) came from a participant with maternal roots elsewhere in the Caribbean.

Discussion

The DNA results from the 152 Bahamian participants underscore a genetic landscape shaped predominantly by African ancestry, with regional variations that echo the Transatlantic Slave Trade's complex trajectories. Among male participants, 73% carried sub-Saharan African Y-chromosome lineages, particularly haplogroup E-M2, with sub-groups E-U174 and E-U175 being the most common (Figures 1 and 3). This finding is not surprising, given that E-U174 and its downstream branches were found at nearly equal percentages (~20%) in New Providence and four of the other five Bahamian islands examined in the report by Simms et al. (2011). Likewise, E-U175 was found in similar proportions (~19%) to E-U174, its sibling clade in the same study. It is important to note, however, that the Y-chromosomes examined in the aforementioned were performed at a lower resolution than in the current investigation. In other studies, similar haplogroup findings were also noted in a population from Northeast Ghana, although E-U175 (59.6%) was found at higher frequencies than E-U174 (10.7%) (Sanchez-Faddeev et al., 2013).

In the current study, Bahamian men characterised by haplogroup E-M2 exhibited several distinct subclades, each with specific geographic and ancestral associations. As illustrated in Figure 1, E-U175 and its derivatives, which are common in Angola, Botswana, Mozambique, Liberia, Nigeria and Ghana, is one of the most common haplogroups in Bahamian males. Along the other branch of E-M4895 (Figure 2), two sub branches, E-M58 (*n* = 1) and E-L485 (*n* = 27), were also observed. The latter Y-lineage and its derivatives (including E-U174), which are very common in Bahamian men (45%), is present in approximately 45% of men from Equatorial Guinea, 38% of Nigerians, 38% of Ghanaians, and 35% of Congolese men, among other regions of the African continent (Gene by Gene, 2022). One of this branch's subsequent subclades, E-L515, found in Burkina Faso and Sierra Leone, also appeared in individuals with roots in Cat Island, Exuma, and Turks and Caicos.

The E-U174 branch is found among 20% of Ghanaian males, 31% of Nigerians, and 32% of individuals from the Central African Republic (Gene by Gene, 2022). In the current study, males carrying this lineage reported paternal links to Exuma, Eleuthera, and Long Island, suggesting a historical migration and settlement pattern trajectory within the Central Bahamas. Further down this branch of the tree (Figure 2), E-CTS7336, which shares genetic affinity with populations from Burkina Faso, Niger, Chad, and Sierra Leone (Gene by Gene, 2022), was traced to participants with heritage in Cat Island and Eleuthera. These findings suggest that despite the shared broad classification of haplogroup E, the internal variation in fact reflects diverse West and Central African origins and distinct migratory pathways across the Bahamian archipelago.

Furthermore, several less common but younger haplogroup E subbranches were detected (Figure 3), offering further insight into the diversity of male ancestry within the Bahamian gene pool. The E-U175 branch, which includes E-CTS8026 and its downstream mutation, E-CTS10652, is more genetically associated with Central (Angola) rather than West African males. One individual carrying E-CTS8030, a E-U174 derived lineage, reported Haitian heritage, underscoring regional Caribbean connections. Moreover, several other low frequency derived lineages, including E-CTS9954 (Congo and Uganda), E-CTS7305 (Nigeria), E-Z15933 (Guinea), and E-CTS6002 (South Africa and Botswana) (Gene by Gene, 2022), illustrate the widespread geographic origins of

Bahamian Y-chromosomes, a product of prehistoric dispersal across the African continent. The presence of additional rare Y-haplogroups such as E-M58, which has associations with Central and East Africa as well as the Caribbean (particularly Haiti), E-CTS618 (Gabon), and E-CTS4907 (Senegal) in Bahamian males support this broader range of African male ancestry in The Bahamas than was previously documented (Simms et al., 2011). This is likely the result of having a greater repository of sub–Saharan African genotypic data at higher resolution quality than previously recorded (Gene by Gene, 2022) for phylogenetic comparisons.

Mitochondrial DNA results further reinforce the African heritage of Bahamians, with 94.1% of participants carrying African maternal lineages (Figure 3, Table 3). Of these, haplogroups L3e was the most frequent and was followed by L2a, both of which are prevalent in Ghana and Côte d'Ivoire. In addition to L3e's presence in the western regions of the African continent, it is also found at high percentages in Angola and Mozambique (Gene by Gene, 2022). The presence of L3e in the Bahamian archipelago is anticipated, given that in the twilight years of the Transatlantic Slave Trade, enslaved Africans from more inland regions are known to have been trafficked (Thomas, 1998; Pereira et al., 2003). It may also represent some degree of East-West admixture in the African continent prior to the departure of the enslaved individuals. Interestingly, both of these lineages, i.e., L2a (29.8%) and L3e (18.3%), also predominate the Akan group from Ghana. Additionally, L3d (3.7%) and L3f (5.8%) lineages are present in the Akan (Fendt et al., 2012) at similar frequencies to those found in The Bahamas (5.3% and 4.6%, respectively, Figure 3), suggesting possible gene flow to The Bahamas from this ethnolinguistic group of Ghana.

Mitochondrial DNA haplogroup L3e, which appeared in 21% of the Bahamian participants, is most common in Côte d'Ivoire, Ghana, Nigeria, Chad, Angola, and Mozambique. It is also found in Haiti and exhibits a lesser frequency in Jamaica. In contrast, L2a, which is found in 19.7% of participants, is widespread in West Africa, with strong connections to Ghana, Côte d'Ivoire, Mali, Nigeria, Sierra Leone, Equatorial Guinea, and the Congo. It is also prevalent in Haiti and Jamaica in equal proportions. Other widely distributed haplogroups included L0a (11.2%), which is primarily associated with Benin, Zimbabwe, and the Congo, as well as L1c (10.5%), found at highest frequencies in the Congo, Gabon, the Central African Republic, and Haiti. In addition, there were three lineages (L3b, L3d, and L1c) that were each found in ~6.6 % of the participants, linking them to various West and Central African populations. Interestingly, all three of the latter lineages are found in Haiti and Jamaica but are at a higher frequency in Haiti than in Jamaica (8%, 14%, and 21% for Haiti vs. 5%, 4%, and 7% for Jamaica, respectively). Finally, haplogroups L3f (4.6%) and L2c (4.6%) were also present in the Bahamian population, thus linking their maternal lineages to those in Sudan, Chad, Nigeria, Mali, Guinea, and Senegal (Gene by Gene, 2022).

European lineages, by contrast, comprise 26.7% of Y-chromosomes and 5.9% of mtDNAs in The Bahamas (Figures 1 and 3, Tables 2 and 3). Regarding the non-African male lineages, they are primarily represented by haplogroup R-M269 and its downstream branches at a frequency of 21.7%. This percentage is slightly elevated in the current investigation when compared to those presented by Simms et al. (2011). In that study, an average frequency of 13.3% of all Y-chromosomes for four of the five Bahamian populations examined were positive for R-M269. The fifth group, Long Island, identified by Simms et al. exhibited a much higher distribution, with 55.8% of male samples characterised by this lineage. These Y-haplogroups, in addition to the presence of mtDNA haplogroups H, K, U, and W, likely reflect the legacy of colonial settlement, European migration, and admixture during and after the Transatlantic Slave Trade.

It is interesting to note that with regard to mtDNA diversity in the current investigation, regional differences were observed within the Bahamian archipelago. For instance, individuals with origins on Cat Island exhibited high diversity, with contributions from multiple sub-Saharan African haplogroups alongside minor European lineages. Y-chromosomal haplogroups, on the other hand, tend to be more homogeneous (i.e., primarily E-M2 and its derivatives), regardless of island, suggesting possible sex-biased gene flow into the archipelago.

The preliminary genetic results presented in this report strongly support the dominant African ancestry of contemporary Bahamians, as evident in both the paternal (Y-chromosome) and maternal (mtDNA) lineages. With 93% of mtDNA haplogroups and 73% of Y-chromosomal lineages of sub-Saharan African origin, these findings are consistent with historical accounts of mass movements from West and Central Africa to The Bahamas as a result of the Transatlantic Slave Trade. It is not clear from this preliminary data, however, which specific African population(s) had the greatest impact on the Bahamian maternal and paternal gene pools. Additionally, this initial study does not enable us to determine which lineages in The Bahamas were contributed directly from African captives early in the slave trade (1720-1755) versus those that came later from the United States with the Loyalists (1783-1785). Thus, the genetic patterns observed in this investigation, combined with the oral history and historical records that suggest connections to the Akan provide a compelling case for more targeted sampling in Accra, their current homeland in Ghana.

Conclusions

Altogether, these findings reflect the enduring legacy of African diasporic heritage in The Bahamas, although no exclusive direct genetic ties to Ghanaians have been established. As a next step, we aim to conduct two complementary expansions of this research. First, we propose a focused sampling of residents on Cat Island, which has shown high mitochondrial DNA diversity and African lineages with specific ties to Ghana in this preliminary dataset. This will help determine the degree of ancestral retention and genetic drift on this relatively isolated island. Second, a collaborative sampling initiative in Princes Town, Accra, Ghana, the ancestral homeland of the Akan and Jan Kwaw (John Canoe), will allow for direct comparison of Bahamian and indigenous (and relatively isolated) Ghanaian lineages. Together, these efforts will enhance our ability to reconstruct specific ancestral linkages, explore patterns of gene-culture coevolution, and deepen our understanding of the African roots of Bahamian identity. This research has the potential to reconnect descendant communities separated by the violence of the Middle Passage and contribute to global conversations on memory, justice, and diasporic belonging.

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References

Bethel, N., Minnis, J., & Fielding, W. (2012). Knowing your ancestors: A survey of Bahamians’ knowledge of their progenitor’s names. *International Journal of Bahamian Studies, 18*(1), 1-5. https://doi.org/10.15362/ijbs.v18i0.171

Craton, M. & Saunders, G. (1999). *Islanders in the stream: A history of the Bahamian people, Vol. 1*. University of Georgia Press.

Craton, M. (1986). *A history of the Bahamas.* San Salvador Press.

Davis, C. (2022). *Black rinse: A new perspective on the history of the African Diaspora in The Bahamas*. Sankofa Flamingo.

Denis, A. (2021). *A study of fancy dress masquerade costumes in Winneba, Ghana (1958-2020)* [Master's thesis, University of Cape Coast]. https://ir.ucc.edu.gh/xmlui/

Fendt, L., Röck, A., Zimmermann, B., Bodner, M., Thye, T., Tschentscher, F., Owuso-Dabo, E., Göbel, T. M. K., Schneider, P. M., & Parson, W. (2012). MtDNA diversity of Ghana: A forensic and phylogeographic view. *Forensic Science International: Genetics, 6*(2), 244–249. https://doi.org/10.1016/j.fsigen.2011.05.011

Ferguson, A. (2000). *I come to get me! An inside look at the Junkanoo festival*. Doongalik Studios.

Gene by Gene, Ltd. (2022-2025). *FamilyTreeDNA Discoverv*[website]. https://discover.familytreedna.com/

Gibson, E. (2015). Bahamian bush medicine: Fact or folklore? *International Journal of Bahamian Studies, 21*(1), 108-115. https://doi.org/10.15362/ijbs.v21i1.259

Kofi, A. E., Hakim, H. M., Khan, H. O., Ismail, S. A., Ghansah, A., David, A. A., Che Mat, N. F., Chambers, G. K., & Edinur, H. A. (2020). Population data of 23 Y chromosome STR loci for the five major human subpopulations of Ghana. *International Journal of Legal Medicine, 134*, 1313–1315. https://doi.org/10.1007/s00414-019-02099-w

Lawlor, J. (2022). *From Africa to The Bahamas*. Media Enterprises.

Malcolm, C. (2007). A summary history of the American slaving schooner *Peter Mowell* wrecked at Lynyard Cay, Abaco Islands, Bahamas, July 25, 1860. *Mel Fisher Maritime Heritage Societ*y, 1–8. https://www.academia.edu/12819967/A_Summary_History_of_the_American_Slaving_Schooner_Peter_Mowell

McCormack, J. H., Maier, K., & Wallens, P. B. (2011). *Bush medicine in the Bahamas: A cross-cultural perspective from San Salvador Island, Bahamas including pharmacology and oral histories*. JHM Designs Publications.

Pereira, L., Macaulay, V., Torroni, A., Scozzari, R., Prata, M. J., & Amorim, A. (2003). Prehistoric and historic traces in the mtDNA of Mozambique: Insights into the Bantu expansions and the slave trade. *American Journal of Human Genetics, 65*(5) 439–458. https://doi.org/10.1046/j.1469-1809.2001.6550439.x

Sanchez-Faddeev, H., Pijpe, J., Van Der Hulle, T., Meij, H. J., van der Gaag, K. J., Slagboom, P. E., Westendorp, R. G. J., & de Knijff, P. (2013). The influence of clan structure on the genetic variation in a single Ghanaian village. *European Journal of Human Genetics, 21* (10), 1134–1139. https://doi.org/10.1038/ejhg.2013.12

Saunders, G. (1985). *Slavery in the Bahamas, 1648-1838*. The Nassau Guardian.

Simms, T. M., Barrett, D. A., McCartney, Q., & Herrera, R. J. (2012). Divergent genetic strata in five Bahamian islands. *Forensic Science International: Genetics, 6*(1), 81–90. https://doi.org/10.1016/j.fsigen.2011.02.005

Simms, T. M., Garcia, C., Mirabal, S., McCartney, Q., & Herrera, R.J. (2008). The genetic legacy of the Transatlantic Slave Trade in the island of New Providence. *Forensic Science International: Genetics, 2,* 310–7. https://doi.org/10.1016/j.fsigen.2008.04.003

Simms, T. M., Martinez, E., Herrera, K. J., Wright, M. R., Perez, O. A., Hernandez, M., Ramirez, E. C., McCartney, Q., & Herrera, R. J. (2011). Paternal lineages signal distinct genetic contributions from British Loyalists and continental Africans among different Bahamian islands. *American Journal of Physical Anthropology, 149*(4), 441–450. https://doi.org/10.1002/ajpa.21616

Simms, T. M., Wright, M. R., Martinez, M., Reguiero, M., McCartney, Q., & Herrera, R. J. (2013). Y-STR diversity and sex-biased gene flow among Caribbean populations. *Gene, 516*(1), 82–92. https://doi.org/10.1016/j.gene.2012.11.006

SlaveVoyages. (2025). The Trans-Atlantic Slave Trade database. Emory University. https://www.slavevoyages.org

Storr, V. H. (2009). B'Rabby as a "true-true Bahamian": Rabbyism as Bahamian ethos and worldview in the Bahamas' folk tradition and the works of Strachan and Glinton-Meicholas. *Journal of Caribbean Literatures, 6*(1), 125–146. https://www.jstor.org/stable/40986304

Thomas, H. (1998). *The Slave Trade: The history of the Atlantic Slave Trade, 1440–1870*. Macmillan.

Wilkie, L. A. (1993). Continuities in African naming practices among slaves of Wade's Green Plantation, North Caicos. *Journal of the Bahamas Historical Society, 15*(1), 32–37.