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Introduction

Hello, and welcome to the March 2014 issue of DNA Tribes® Digest. This month’s article explores the Horn of Africa’s links with Africa and Eurasia, in search of genetic traces of the first human migrations out of Africa.

According to the tree model of human expansions described in a recent paper,¹ these early migrations involved a **Basal Eurasian** population that later became ancestral to **EEF** (“First Farmers”) in both Europe and the Middle East.² This Digest article features iterative analyses of non-local genetic components in the Horn of Africa, where the Basal Eurasians might have first split off from ancestral African and Eurasian populations, only later to re-join with Eurasian hunter-gatherer populations in the founding of the first agricultural societies.

Best regards,
Lucas Martin
DNA Tribes

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¹ “Ancient Human Genomes Suggest Three Ancestral Populations for Present-Day Europeans” by Lazaridis *et. al.* (preprinted December 2013); available at <http://biorxiv.org/content/early/2013/12/23/001552>.
² For more detailed discussion, see <http://dnatribes.com/dnatribes-digest-2014-02-01.pdf>.

The First Human Diaspora: Basal Eurasians and the Horn of Africa

Background: Out of Africa Migrations and Early Population Structure

The current understanding of human origins is that our species first emerged in Eastern Africa around 200 thousand years ago. Based on fossil and tool remains, these First Humans then migrated out of Africa along two main routes: (1) **via the Nile Valley** between 120 and 100 thousand years ago (attested by the Qafzeh fossil discovered in Israel); and (2) **via the Red Sea** and Arabian Peninsula between 125 and 106 thousand years ago (attested by discoveries in Oman and the United Arab Emirates).

Early fossils from around this time have been discovered in the East Mediterranean (the Skhul and Qafzeh fossils) are characterized by a **mixture of archaic hominid and modern human traits**. This has been interpreted as evidence that during the African exodus, some early modern humans mixed with older Neanderthal related (archaic) hominids in the Middle East. Similarly, fossils discovered in Tabun Cave and elsewhere suggest coexistence and possibly cultural interchange and mixture between African “moderns” and Eurasian “archaics” during these expansions.

In later periods, Northeast Africa and the East Mediterranean continued as a contact point between Africa and Eurasia that generated periodic waves of technological and cultural evolution. For instance, the **Natufian culture** (12,500 - 9,800 BCE) established semi-sedentary patterns of life that laid foundations for agricultural civilization.

This development continued with the **Pre-Pottery Neolithic A** cultures (PPNA; 8,000 - 7,000 BCE) that built the first communal structures (such as granaries) and walled town (Jericho), creating a new type of organized social space that could persist over time (unlike fortuitous non-settled patterns of occupation or resource use). The subsequent **Pre-Pottery Neolithic B** (PPNB; 7,000 - 6,000 BCE) period continued Natufian-PPNA traditions, but also incorporated a new influx of culture from Anatolia (not unlike similar mixing of Hittite and Canaanite societies in the Bronze Age Levant).

However, these stable patterns of life were interrupted by the 8.2 kiloyear event, a climate change that brought cool temperatures (and drought) to the Middle Eastern cradle of the First Farmers. Local PPNB communities continued in places (such as Amuq), possibly becoming ancestors of the Ghassulian culture of the Copper Age.³ Other PPNB populations mixed with hunter-gatherer (Harifian) cultures and created a new way of life based on mobile pastoralism (animal herding), establishing a new peripatetic **Circum-Arabian Nomadic Pastoral Complex** in the region.

Within Africa, these innovations were integrated into the Pre-Dynastic cultures of Egypt (such as Naqada) and Nubia (further south along the Nile River). This included the emergence of a distinctive African cattle culture attested in the Laas Gaal rock carvings (dated to between 9,000 – 3,000 BCE). As the climate changed and Africa’s “Green Sahara” became a desert, the fertile Nile Valley emerged as an important population and civilization center linking the East Mediterranean with the interior of East Africa, continuing the cycle of contacts that generated the first Out of Africa migrations.

Although the model of human population history described in Lazaridis⁴ does not identify a geographical location where **Basal Eurasian** populations developed, the paper’s tree model suggests an origin after an initial split from African moderns and prior to the divergence of Eastern Non-African

³ For more information, see <http://dnatribes.com/dnatribes-digest-2012-09-01.pdf>.

⁴ See <http://biorxiv.org/content/early/2013/12/23/001552.full.pdf>, p. 17 (Figure 2A).

(ENA), Western European Hunter-Gatherers (WHG), and Ancestral North Eurasians (ANE). This would be consistent with **Basal Eurasian origins near the Nile Valley and East Mediterranean, where the early agricultural settlements formed the basis of the world's first civilizations (highlighted in red in Figure 1).**

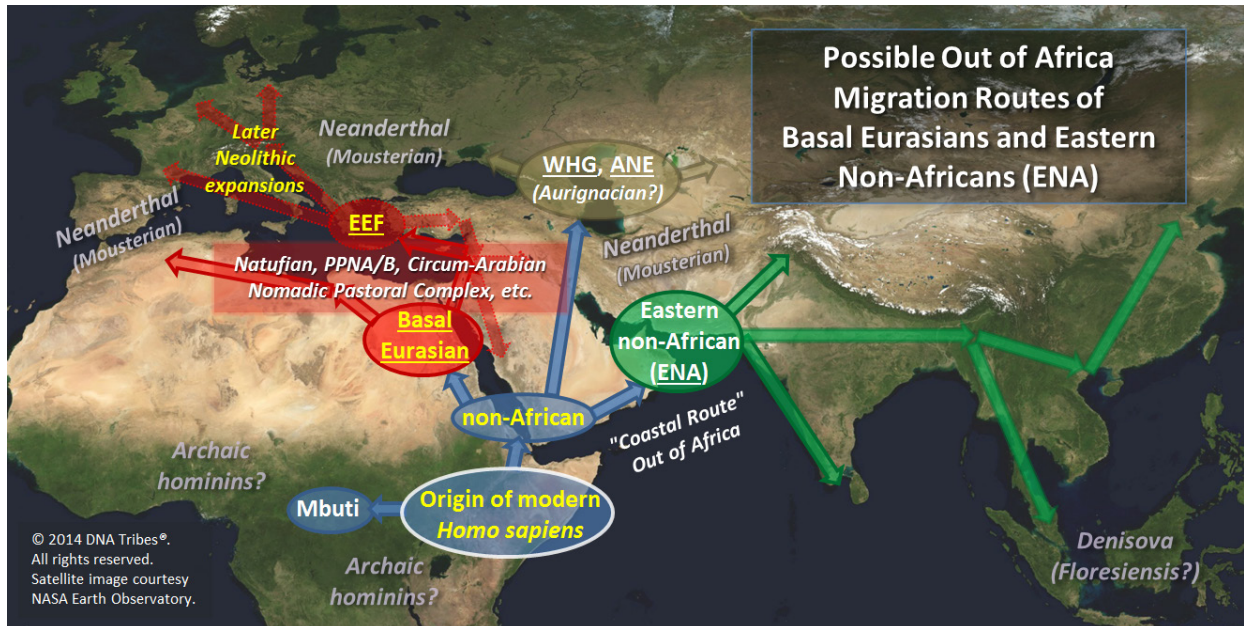


Figure 1: Map of possible migration routes Out of Africa (**Basal Eurasian** and descendant **EEF** populations shaded in red), based on the fitted tree model of West Eurasian population history described in Lazaridis *et al.*⁵

To explore the role of the Horn of Africa in early population history and the emergence of Basal Eurasians, this month's Digest article examines the Horn of Africa's links with world population structure using autosomal SNP and STR data. This analysis surveys not only local links with neighboring populations of Sub-Saharan Africa and the Middle East, but also more distant relationships that might reflect genetic traces of the earliest human expansions from Africa.

Iterative Mixture Analysis of the Horn of Africa (SNP)

To explore the genetic traces of Basal Eurasian populations near the migration routes linking Africa with Eurasia, non-local genetic components of the Horn of Africa were identified based on autosomal SNP data.⁶

For each non-local component expressed in the Horn of Africa, a **sequential analysis** was performed by excluding that component (for instance, Nilotic in **Table 1**) and the next largest related component (for instance, West African in **Table 2**). This was repeated until no new components were identified that were related to that group (for instance, Sub-Saharan African regions in **Table 2**). Results are listed in **Tables 1-5** and illustrated in **Figure 2**.

⁵ See <http://biorxiv.org/content/early/2013/12/23/001552.full.pdf>, p. 17 (Figure 2A).

⁶For information about DNA Tribes® SNP analysis (raw genome data from a SNP microarray test required), see <http://dnatribes.com/snp.html>.

Discussion: Results in **Tables 1-3** express a variety of African and West Eurasian genetic components at each stage of the sequential analysis (*possibly reflecting links with Out of Africa migrations and Basal Eurasians*). At later stages, Asian-Pacific percentages are also expressed (*possibly reflecting deeper relationships between African and Eurasian archaic and/or modern populations*).

Step 1 (Remove Horn of Africa): The initial admixture analysis of the Horn of Africa excludes the local Horn of Africa component, expressing instead Nilotic (52.3%), Arabian (31.4%), North African (14.9%), and Khoisan-Aka (1.4%) percentages (see **Table 1**):

Iteration	Removed this Step	New Components Expressed >1.0%	Most Increased	Nilotic	Arabian	North African	Khoisan-Aka
1	Horn of Africa	First Iteration	First Iteration	52.3%	31.4%	14.9%	1.4%

Table 1: Non-local SNP components of the Horn of Africa (Step 1): excluding Horn of Africa percentages.

A majority of these percentages are expressed for **geographically African regions** (total 68.6%), possibly in part related to early African populations of modern *Homo sapiens* (represented by present day Mbuti in the Lazaridis tree model; see **Figure 1**). A smaller percentage is expressed for **only one geographically Eurasian region: Arabian** (31.4%). This might reflect early Non-African populations in the Lazaridis tree model (see discussion earlier in article).

However, in terms of genetic structure (rather than geographical location), the modern Arabian and North African components are primarily related to West Eurasian (European and Middle Eastern) populations. Nilotic populations are genetically related primarily to other Sub-Saharan African populations, but are to some degree genetically intermediate between Sub-Saharan African and West Eurasian populations.⁷ In terms of Lazaridis' tree model (discussed in the Background section of this article), these components might in part reflect traces of both African and Non-African populations during the earliest human migrations out of Africa.

Step 2 (Remove Sub-Saharan African components): The next part in the series additionally excludes the Nilotic component (Step 2A in **Table 2**) and sequentially removes the largest Sub-Saharan African component expressed in each subsequent step (Steps 2B-2C in **Table 2**; shaded **green** in **Figure 2**). For instance, Step 2B removes Horn of Africa (Step 1), Nilotic (Step 2A), and West African (Step 2B) components. The Nilotic related component expressed is then Khoisan-Aka (31.2%), with new Southeast Asian (1.3%) and Tibetan (1.0%) percentages expressed.

This sequential analysis indicates that the Sub-Saharan African genetic component in the Horn of Africa that is best expressed as **Nilotic** (see Step 1) can instead be expressed as **West African** (36.1%) and **Khoisan-Aka** (7.9%) percentages (Step 2A), or as a larger percentage of the Khoisan-Aka component (31.2%; Step 2B).

However, when all Sub-Saharan African percentages are excluded (causing these components to be expressed as percentages of the most genetically similar non-Sub-Saharan regions; Step 2C), a combination of North African (89.9%) Oceanian (3.8%), Tibetan (3.0%), and Southeast Asian (2.6%)

⁷ For more detailed discussion, see <http://dnatribes.com/dnatribes-snp-admixture-2013-05-14.pdf> (p. 21) and <http://dnatribes.com/dnatribes-digest-2013-04-02.pdf> (p. 4).

percentages appears (Step 2C). This suggests that Sub-Saharan linked components in the Horn of Africa include components that are better represented by Asian-Pacific (including Oceanian) populations than by North African or Middle Eastern percentages.

Iteration	Removed this Step	New Components Expressed >1.0%	Most Increased	Khoisan-Aka	West African	Nilotic	North African	Arabian	South India	Oceanian	Southeast Asian	Tibetan
2A	Nilotic	West African	West African	7.9%	36.1%	XXX	22.9%	32.5%	0.0%	0.1%	0.4%	0.0%
2B	West African	Southeast Asian, Tibetan	North African	31.2%	XXX	XXX	47.1%	18.5%	0.0%	0.8%	1.3%	1.0%
2C	Khoisan-Aka	Oceanian	North African	XXX	XXX	XXX	89.9%	0.0%	0.7%	3.8%	2.6%	3.0%

Table 2: Sequential analysis of non-local SNP components in the Horn of Africa (Step 2): iteratively excluding Sub-Saharan African percentages.

This unexpected result might reflect ancestry from Non-African populations that were separate from the Basal Eurasians in Lazaridis' tree model (see Background), such as Eastern Non-Africans (ENA). However, another possibility is that these shared African and Asian-Pacific genetic components might reflect contacts with Denisovan related archaic hominens in Africa.⁸ However, additional research would be needed to explore this further.

Step 3 (Remove West Eurasian components): The sequential analysis now restarts from Step 1 by re-including all components excluded in Step 2, and removes instead the Arabian component to explore West Eurasian related ancestry in the Horn of Africa (shaded red in Figure 2). These steps (Step 1 in Table 1 and 3A-3J in Table 3) express a series of Middle Eastern and European related components across iterations in the following sequence:

- 1 (**Begin Iteration**): Arabian (31.4%), North African (14.9%); *Total: 46.3%*
- 3A (**Remove Arabian**): North African (28.7%), Mesopotamian (18.1%); *Total 46.8%*
- 3B (**Remove North African**): Iberian (10.6%), Mesopotamian (29.0%); *Total 39.6%*
- 3C (**Remove Mesopotamian**): Iberian (28.0%), Caucasus Mountains (8.7%), Indus Valley (1.7%); *Total 38.3%*
- 3D (**Remove Iberian**): Northwest European (11.8%), Caucasus Mountains (23.4%), Indus Valley (2.6%); *Total 37.8%*
- 3E (**Remove Caucasus Mountains**): Northwest European (19.5%), Slavic-Baltic (4.0%), Indus Valley (14.2%); *Total 37.7%*
- 3F (**Remove Northwest European**): Slavic-Baltic (21.7%), Indus Valley (16.1%); *Total 37.8%*
- 3G (**Remove Slavic-Baltic**): Uralic (12.7%), Indus Valley (25.3%); *Total 38.0%*
- 3H (**Remove Indus Valley**): Uralic (25.2%), South India (10.8%); *Total 36.0%*
- 3I (**Remove Uralic**): South India (30.2%), Siberian-Arctic (3.6%); *Total 33.8%*

⁸ See "Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania" by Reich *et. al.* at <http://www.cell.com/AJHG/abstract/S0002-9297%2811%2900395-8> and "Genetic evidence for archaic admixture in Africa" by Hammer *et. al.* at <http://www.pnas.org/content/early/2011/08/29/1109300108>.

→ **3J (Remove South India):** Siberian-Arctic (23.6%), Oceanian (2.6%); Mesoamerican (1.2%); Total 27.3%

Unlike the sequence of Sub-Saharan African components expressed in **Step 2** (including components from non-adjacent Asian-Pacific regions, possibly related to traces of Denisovan related populations in Africa and Oceania), the West Eurasian components in **Step 3** express a **geographically ordered progression** beginning near the Horn of Africa and continuing into adjacent regions of North Africa, West Asia, and the Mediterranean (shaded **red** in **Figure 2**).

Notably, Northern European and South Asian regions expressed only when genetic components from all regions near the East Mediterranean are excluded (**Steps 3C-3D**). The step-by-step geographical progression in **Steps 3A-3I** beginning near the Nile River and Red Sea and expanding outwards into West Eurasia is similar to the geographical distribution of **Basal Eurasian** and descendant **EEF (Early European Farmer)** ancestry described in Lazaridis (see **Figure 1**), as well as the modern *Homo sapiens* migration routes out of Africa and the East Mediterranean centered contact zone in which the first agricultural civilizations first emerged (see Background for more discussion).

For this reason, the Middle Eastern and Mediterranean related genetic components in the Horn of Africa might reflect traces of Basal Eurasian populations, which have been absorbed by neighboring African, European, and Asian populations since the beginning of the Neolithic period.

Iteration	Removed this Step	New Components Expressed >1.0%	Most Increased	Khoisan-Aka	Nilotic	Arabian	North African	Iberian	Northwest European	Slavic-Baltic	Uralic	Mesopotamian	Caucasus Mountains	Indus Valley	South India	Oceanian	Siberian Arctic	Mesoamerican
3A	Arabian	Mesopotamian	Mesopotamian	1.2%	52.0%	XXX	28.7%	0.0%	0.0%	0.0%	0.0%	18.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
3B	North African	Iberian		1.1%	59.3%	XXX	XXX	10.6%	0.0%	0.0%	0.0%	29.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
3C	Mesopotamian	Caucasus Mts., Indus Valley	Iberian	0.8%	60.7%	XXX	XXX	28.0%	0.0%	0.0%	0.0%	XXX	8.7%	1.7%	0.0%	0.2%	0.0%	0.0%
3D	Iberian	N.W. European	Caucasus Mts.	0.6%	61.7%	XXX	XXX	XXX	11.8%	0.0%	0.0%	XXX	23.4%	2.6%	0.0%	0.0%	0.0%	0.0%
3E	Caucasus Mts.	Slavic-Baltic	Indus Valley	0.4%	61.8%	XXX	XXX	XXX	19.5%	4.0%	0.0%	XXX	XXX	14.2%	0.0%	0.0%	0.0%	0.0%
3F	Northwest European	None this step.	Slavic-Baltic	0.3%	61.9%	XXX	XXX	XXX	XXX	21.7%	0.0%	XXX	XXX	16.1%	0.0%	0.0%	0.0%	0.0%
3G	Slavic-Baltic	Uralic	Uralic	0.1%	61.9%	XXX	XXX	XXX	XXX	XXX	12.7%	XXX	XXX	25.3%	0.0%	0.0%	0.0%	0.0%
3H	Indus Valley	South India	Uralic	0.0%	64.0%	XXX	XXX	XXX	XXX	XXX	25.2%	XXX	XXX	XXX	10.8%	0.0%	0.0%	0.0%
3I	Uralic	Siberian-Arctic	South India	0.0%	66.0%	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	30.2%	0.0%	3.6%	0.2%
3J	South India	Mesoamerican, Siberian-Arctic, Oceanian	Siberian-Arctic	0.0%	72.7%	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	2.5%	23.6%	1.2%

Table 3: Sequential analysis of non-local SNP components in the Horn of Africa (Step 3): iteratively excluding West Eurasian related percentages.

However, when all West Eurasian components are excluded (**Step 3J**), Siberian-Arctic (23.6%), Oceanian (2.5%), and Mesoamerican (1.2%) percentages are expressed in their place. This suggests that ancestry components shared between the Horn of Africa and West Eurasians might also

reflect older processes not related to the Neolithic, such as Eastern Non-African (ENA) expansions and/or archaic (Neanderthal and/or Denisovan related) introgression in Eurasia.⁹

Steps 4-5 (Remove North African and Khoisan-Aka components): Unlike the earlier iterations, no new components are expressed when each of these components is separately removed. This suggests that North African and Khoisan-Aka related ancestry in the Horn of Africa is either local to each of these regions or better represented by other components (such as West Eurasian and/or Sub-Saharan African percentages).

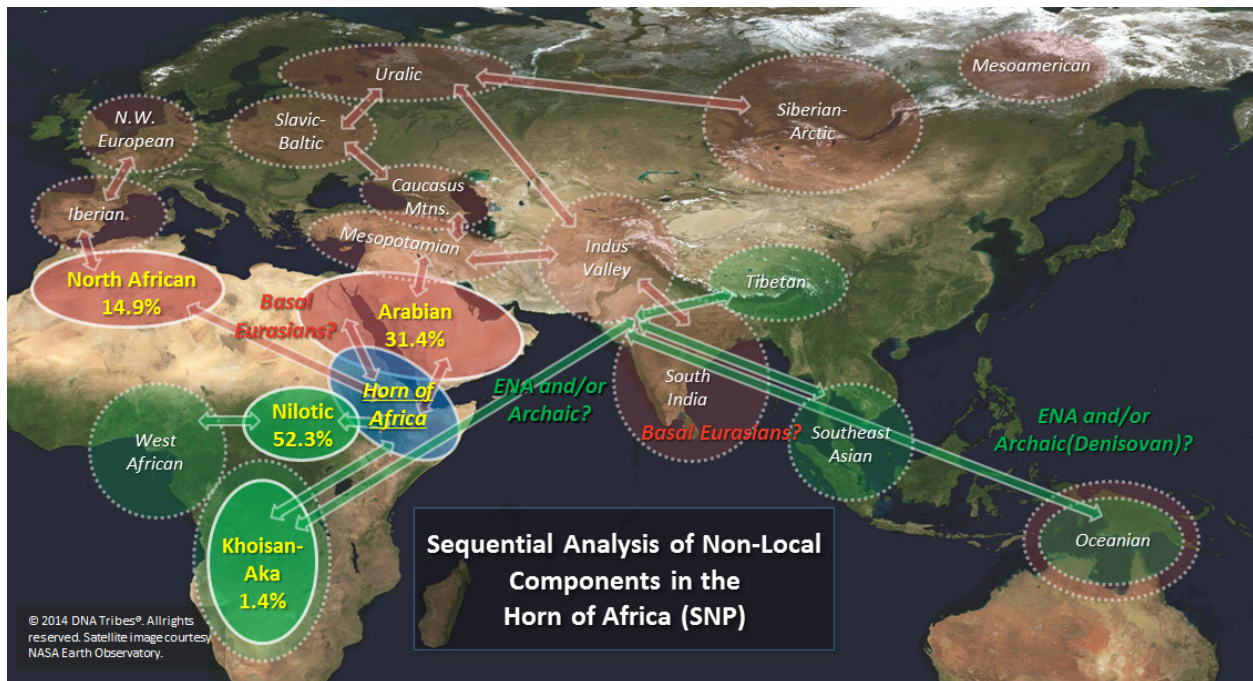


Figure 2: Non-local SNP components of the Horn of Africa are shown in **solid circles**. These percentages exclude local Horn of Africa components. Regions expressed in later steps of the sequential analysis performed for each component are shown in **dotted circles**.

Conclusion (SNP): Sequential analysis of non-local genetic components in the Horn of Africa expresses substantial Sub-Saharan African and West Eurasian (Middle Eastern and European) related percentages, possibly expressing genetic traces of **modern *Homo sapiens*** expansions in Africa (**Sub-Saharan African**; possibly also reflecting Eastern Non-African and/or archaic Denisovan related introgression in Africa and Oceania) and **Basal Eurasian** expansions near the Nile River and East Mediterranean (**West Eurasian**; possibly also reflecting Eastern Non-African and/or archaic Neanderthal and/or Denisovan introgression in Eurasia).

⁹ For more discussion, see "Neanderthal Admixture in Eurasia Confirmed by Maximum Likelihood Analysis of Three Genomes" at <http://www.genetics.org/content/early/2014/02/10/genetics.114.162396.abstract>.

Iterative Mixture Analysis of the Horn of Africa (STR)

To further explore the genetic traces of Basal Eurasian populations near the migration routes linking Africa with Eurasia, non-local genetic components of the Horn of Africa were identified based on autosomal STR data.¹⁰

For each component, a **sequential analysis** was performed by excluding that component and the next largest related component. This was repeated until no new components from that part of the world were expressed. Results are listed in **Tables 4-6** and illustrated in **Figure 3**.

Discussion: Results in **Tables 4-6** express Sub-Saharan African, West Eurasian (Middle Eastern and European), and Asian-Pacific STR components in the Horn of Africa.

Step 1 (Table 4; Remove Horn of Africa): The initial admixture analysis excludes the local Horn of Africa component, expressing instead Arabian (41.4%), African Great Lakes (28.6%), Sahelian (14.0%), Arctic (7.1%), Australian (7.0%), Paleo-Indian (*non-Arctic Native American*) (1.0%), and North African (0.8%) components. As with SNP results, STR percentages include Sub-Saharan African (African Great Lakes and Sahelian), West Eurasian (Arabian and North African), and Asian-Pacific related components (Australian, Arctic, and Paleo-Indian). The following steps (**Steps 2-8**) will explore each of these genetic relationships in more detail.

Iteration	Removed this Step	New Regions >1.0%	Largest Increase	African Great Lakes	Sahelian	North African	Arabian	Australian	Arctic	Paleo-Indian
1	Horn of Africa	Initial Step	Initial Step	28.6%	14.0%	0.8%	41.4%	7.0%	7.1%	1.0%

Table 4: Non-local STR components of the Horn of Africa (Step 1): excluding Horn of Africa percentages.

Step 2 (Remove Sub-Saharan African components): The next part in the series additionally excludes the African Great Lakes component (Step 2A in **Table 5**) and sequentially removes the largest Sub-Saharan African component expressed in each subsequent step (listed in **Table 5** and shaded **green** in **Figure 3**). For instance, Step 2C removes Horn of Africa (Step 1), African Great Lakes (Step 2A), Sahelian (Step 2B), and West African (Step 2C) components. The Sub-Saharan African related component expressed is then Southern African (26.5%).

This sequential analysis indicates that the Sub-Saharan African genetic component in the Horn of Africa that is best expressed as **African Great Lakes** (see Step 1) can instead be expressed as **Sahelian** (33.8%) and **Tropical West African** (2.5%) percentages (Step 2A), or as a larger percentage of the Tropical West African component (34.9%; Step 2B).

However, Asian-Pacific related percentages (such as Arctic) increase when Sub-Saharan African components are iteratively removed in later steps (2B-2D), which might reflect distant genetic relationships (Eastern Non-African and/or Denisovan or other archaic) similar to the Sub-Saharan and Asian-Pacific links discussed in the previous SNP analysis included of this article.

¹⁰ For information about the 32 world genetic regions distinguished in **DNA Tribes® 22 and 26 Marker Kit autosomal STR tests**, see <http://dnatribes.com/populations.html>.

Iteration	Removed this Step	New Regions >1.0%	Largest Increase	Southern African	Tropical West African	Sahelian	North African	Arabian	Australian	Arctic	Paleo-Indian
2A	African Great Lakes	Tropical West African	Sahelian	0.0%	2.5%	33.8%	1.4%	46.5%	10.8%	4.6%	0.4%
2B	Sahelian	None this step.	Tropical West African	0.0%	34.9%	XXX	3.5%	44.1%	9.2%	8.3%	0.0%
2C	Tropical West African	Southern African	Southern African	26.5%	XXX	XXX	10.4%	45.4%	7.7%	10.1%	0.0%
2D	Southern African	None this step.	North African	XXX	XXX	XXX	35.3%	40.8%	11.9%	12.0%	0.0%

Table 5: Sequential analysis of non-local STR components in the Horn of Africa (Step 2): iteratively excluding Sub-Saharan African percentages.

Step 3 (Remove West Eurasian): The sequential analysis now restarts from Step 1 by re-including all components excluded in Step 2, and removes instead the Arabian component to explore West Eurasian related ancestry in the Horn of Africa (shaded red in Figure 2). These steps (Step 1 in Table 1 and 3A-3J in Table 6) express a series of Middle Eastern and European related components across iterations in the following sequence:

- 1 (**Begin Iteration**): North African (0.8%) and Arabian (41.4%); *Total 42.3%*.
- 3A (**Remove Arabian**): North African (12.4%) and Levantine (24.3%); *Total 36.7%*.
- 3B (**Remove Levantine**): North African (36.7%); *Total 36.7%*.
- 3C (**Remove North African**): Iberian (17.2%) and Mesopotamian (9.0%); *Total 26.3%*.
- 3D (**Remove Iberian**): Aegean (20.7%) and Mesopotamian (4.1%); *Total 24.8%*.
- 3E (**Remove Aegean**): Northwest European (6.0%), Mesopotamian (20.6%); *Total 26.6%*.
- 3F (**Remove Mesopotamian**): N.W. European (18.8%), Eastern India (2.9%); *Total 21.7%*.
- 3G (**Remove Northwest European**): Slavic-Baltic (13.6%), Eastern India (5.4%); *Total 19.1%*.
- 3H (**Remove Slavic-Baltic**): Indus Valley (12.9%), Eastern India (4.8%); *Total 17.8%*.
- 3I (**Remove Indus Valley**): South India (4.6%), Eastern India (9.3%); *Total 13.9%*.
- 3J (**Remove Eastern India**): South India (12.9%).

As with SNP results (see previous section of this article), the sequence of West Eurasian genetic components in the Horn of Africa expresses a **geographically ordered progression** of regions that begins near the Nile River and Red Sea (North Africa and Arabian in Step 1) then in later steps includes West Asian and Mediterranean (Levantine, Iberian, and Mesopotamian in Steps 3A and 3C) and finally Northern European and South Asian regions (such as Northwest European and Eastern India percentages in Steps 3E-3F).

However, total percentages of West Eurasian components become progressively smaller in later iterations (starting at 42.3% in Step 1 and ending with only 12.9% in Step 3J). This suggests that the Horn of Africa's West Eurasian related genetic components are substantially better represented by regions in early steps (such as North African and Arabian) than by regions in later steps (such as Slavic-Baltic or Eastern India).

Notably, the geographic progression of these components might reflect the expansions of **Basal Eurasians** (possibly including the earliest Nile River and/or Red Sea migration routes of behaviorally modern *Homo sapiens* out of Africa, as well as the early Neolithic centers of the East Mediterranean).

However, additional small Asian-Pacific percentages, such as Japanese, Arctic, and Paleo-Indian (*non-Arctic Native American*) might reflect older processes not related to the Neolithic, such as Eastern Non-African (ENA) migrations in Lazaridis' tree model (see Background of this article) and/or archaic (Neanderthal and/or Denisovan related) introgression in Eurasia.¹¹

Iteration	Removed this Step	New Regions >1.0%	Biggest Increase	African Great Lakes	Sahelian	North African	Levantine	Iberian	Northwest European	Slavic-Baltic	Aegean	Mesopotamian	Indus Valley	South India	Eastern India	Australian	Japanese	Arctic	Paleo-Indian
3A	Arabian	Levantine	Levantine	36.6%	10.3%	12.4%	24.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	9.6%	0.0%	4.4%	2.3%
3B	Levantine	None this step.	North African	36.2%	7.2%	36.7%	XXX	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	11.7%	0.0%	3.7%	4.4%
3C	North African	Iberian, Mesopotamian	Iberian	42.6%	11.1%	XXX	XXX	17.2%	0.0%	0.0%	0.0%	9.0%	0.0%	0.0%	0.0%	12.9%	0.7%	2.4%	4.1%
3D	Iberian	Aegean	Aegean	42.7%	11.8%	XXX	XXX	XXX	0.0%	0.0%	20.7%	4.1%	0.0%	0.0%	0.0%	13.0%	1.0%	2.5%	4.2%
3E	Aegean	Northwest European	Mesopotamian	44.2%	9.7%	XXX	XXX	XXX	6.0%	0.0%	XXX	20.6%	0.0%	0.0%	0.0%	12.7%	0.0%	3.3%	3.6%
3F	Mesopotamian	Eastern India	Northwest European	44.5%	11.7%	XXX	XXX	XXX	18.8%	0.0%	XXX	XXX	0.0%	0.0%	2.9%	13.4%	2.4%	1.0%	5.3%
3G	Northwest European	Slavic-Baltic	Slavic-Baltic	45.4%	12.5%	XXX	XXX	XXX	XXX	13.6%	XXX	XXX	0.0%	0.0%	5.4%	13.5%	1.8%	0.8%	6.9%
3H	Slavic-Baltic	Indus Valley	Indus Valley	50.8%	8.9%	XXX	XXX	XXX	XXX	XXX	XXX	XXX	12.9%	0.0%	4.8%	12.1%	2.1%	2.2%	6.3%
3I	Indus Valley	South India	South India	52.8%	9.3%	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	4.6%	9.3%	12.1%	1.9%	1.3%	8.8%
3J	Eastern India	None this step.	South India	52.6%	8.8%	XXX	XXX	XXX	XXX	XXX	XXX	XXX	XXX	12.9%	XXX	12.6%	3.5%	2.4%	7.2%

Table 6: Sequential analysis of non-local SNP components in the Horn of Africa (Step 3): iteratively excluding West Eurasian related percentages.

¹¹ For more discussion, see "Neanderthal Admixture in Eurasia Confirmed by Maximum Likelihood Analysis of Three Genomes" by Lohse *et al.* at <http://www.genetics.org/content/early/2014/02/10/genetics.114.162396.abstract>.

Steps 4-8 (Remove Sahelian; North African; Australian; Arctic; Paleo-Indian): Separately removing each of these components expressed in **Step 1** does not result in new components expressed. This suggests that these genetic relationships are either local to each of these regions or else better represented by other components (such as Sub-Saharan African and/or West Eurasian percentages). In particular, components expressed as Asian-Pacific percentages in Step 1 might reflect genetic traces of Eastern Non-African (ENA) expansions in Lazaridis' tree model and/or introgression from archaic hominins in both Eurasia and Africa.

Conclusion (STR): STR components of the Horn of Africa include both Sub-Saharan African (**green** in **Figure 3**), West Eurasian (Middle Eastern and European; shown in **red** in **Figure 3**) and Asian-Pacific (**purple** in **Figure 3**) percentages.

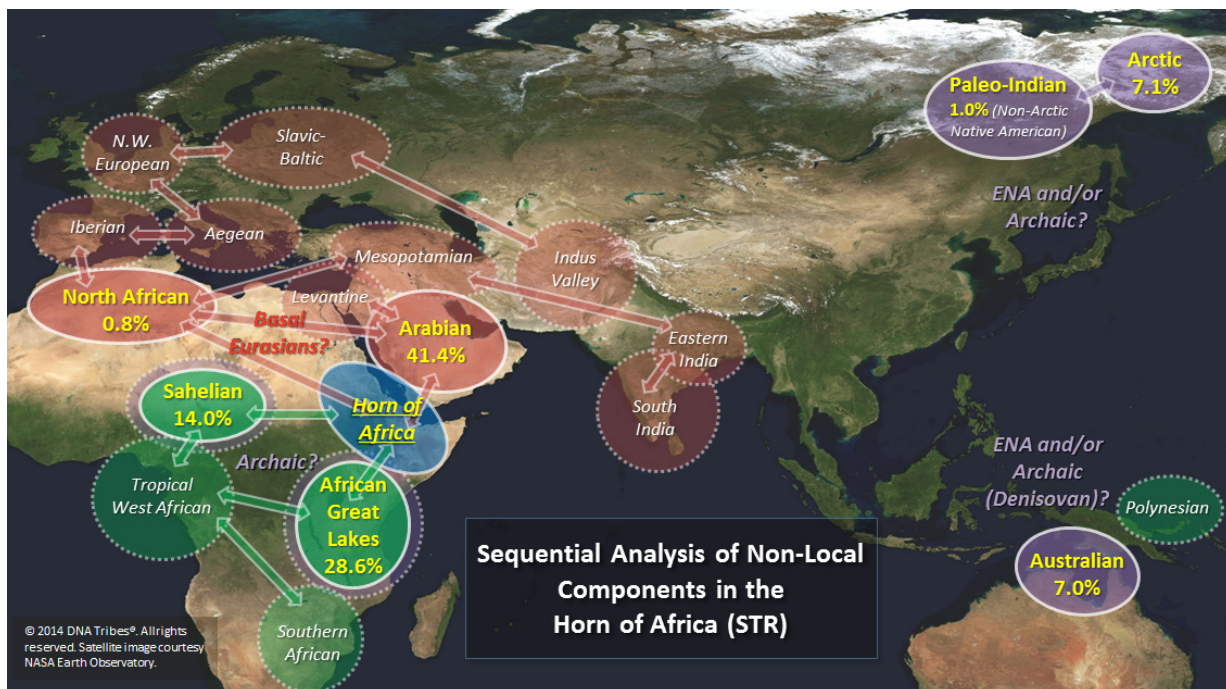


Figure 3: Non-local STR components of the Horn of Africa are shown in **solid circles**. These percentages exclude local Horn of Africa components. Regions expressed in later steps of the sequential analysis performed for each component are shown in **dotted circles**.

Conclusion

Sequential analyses of non-local genetic components in the Horn of Africa using both autosomal SNP and STR data express substantial Sub-Saharan African and West Eurasian (Middle Eastern and European) related percentages, perhaps expressing genetic traces of **modern *Homo sapiens*** expansions in Africa (**Sub-Saharan African**; possibly also reflecting *Eastern Non-African and/or archaic Denisovan related introgression in Africa and Oceania*) and **Basal Eurasian** expansions near the Nile River and East Mediterranean (**West Eurasian**; possibly also reflecting *Eastern Non-African and/or Neanderthal introgression in Eurasia*).



DNA Tribes® Announcements for March 2014

End of Winter Sale for 22 Marker and 26 Marker Kit STR Tests

DNA Tribes® is pleased to offer 22 Marker Kit and 26 Marker Kit tests at great prices. Each 22 and 26 Marker Kit tests includes your Autosomal STR Profile for industry standard markers used in DNA fingerprinting around the world.

Both kits options feature the most detailed and comprehensive comparison of your autosomal DNA to world populations available anywhere. Your genetic ancestry report will include DNA Tribes® Native Population Match, Global Population Match, and World Region Match analysis.

DNA Tribes® 22 Marker Kits (Sale Price: \$119.99) test the following autosomal STR markers:

Amelogenin, CSF1PO, D13S317, D16S539, D18S51, D21S11, D3S1358, D5S818, D7S820, D8S1179, FGA, Penta D, Penta E, TH01, TPOX, vWA, D19S433, D2S1338, D10S1248, D12S391, D1S1656, D22S1045, and D2S441.

DNA Tribes® 26 Marker Kits (Sale Price: \$139.99) test the following autosomal STR markers:

Amelogenin, CSF1PO, D13S317, D16S539, D18S51, D21S11, D3S1358, D5S818, D7S820, D8S1179, FGA, Penta D, Penta E, TH01, TPOX, vWA, D19S433, D2S1338, D10S1248, D12S391, D1S1656, D22S1045, D2S441, F13A1, F13B, FES/FPS, and LPL.

More information and new 22 and 26 Marker Kit test orders are available through our secure online checkout system at <http://www.dnatribes.com/order.html>.

Upgrade testing for customers who have previously tested using DNA Tribes® 15 or 21 Marker Kit tests are available at http://dnatribes.com/order_upgrades.html.

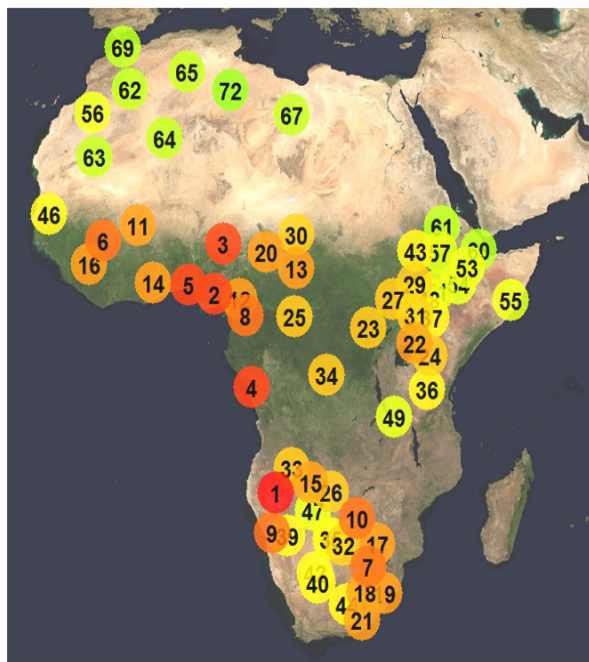
Updates incorporating new populations and world region definitions for previous 15, 21, or 27 Marker Kit tests (including all previously ordered add-on reports) are available using the \$24.99 “Update Your STR Analysis” option at http://dnatribes.com/order_addons.html.

About DNA Tribes® SNP (genome data required)

Do you have genome data from a SNP test? DNA Tribes® SNP is a detailed "deep ancestry" analysis that can be performed based on your genotype raw data from any of several SNP microarray tests. (*Genome Data from Previous Testing Required*)

DNA Tribes® SNP reports (<http://dnatribes.com/snp.html>) include:

- **Admixture Percentages**
 - Continent, Region, Native Population, and Global Population Percentages.
- **Multi-Dimensional Scaling (MDS) Graphs**
 - Continent, Region, Native population, and Global Population.
- **Total Similarity**
 - Compare your Genotype to over 280 Populations in our SNP Database.



Population	Percentage
Yoruba Nigeria	26.9%
Bambara West Africa	9.6%
Igbo Nigeria	6.7%
Kaba Chad	5.2%
Fang Cameroon	5.1%
Bantu South Africa	5.0%
Kongo	4.2%
Tunisia	3.8%
Herero Namibia	3.6%
Hausa Nigeria	3.4%
Dogon West Africa	3.2%
England	2.5%
France	2.5%
Pima Mexico	2.4%
Mandenka Senegal	2.4%

More information (including sample reports) and orders are available at: <http://dnatribes.com/snp.html>.