

# North African Populations Carry the Signature of Admixture with Neandertals

Federico Sánchez-Quinto<sup>1,9</sup>, Laura R. Botigué<sup>1,9</sup>, Sergi Civit<sup>3</sup>, Conxita Arenas<sup>3</sup>, María C. Ávila-Arcos<sup>4</sup>, Carlos D. Bustamante<sup>2</sup>, David Comas<sup>1¶</sup>, Carles Lalueza-Fox<sup>1¶\*</sup>

**1** Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Barcelona, Spain, **2** Department of Genetics, Stanford University, Stanford, California, United States of America, **3** Departament d'Estadística, Universitat de Barcelona, Barcelona, Spain, **4** Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark

## Abstract

One of the main findings derived from the analysis of the Neandertal genome was the evidence for admixture between Neandertals and non-African modern humans. An alternative scenario is that the ancestral population of non-Africans was closer to Neandertals than to Africans because of ancient population substructure. Thus, the study of North African populations is crucial for testing both hypotheses. We analyzed a total of 780,000 SNPs in 125 individuals representing seven different North African locations and searched for their ancestral/derived state in comparison to different human populations and Neandertals. We found that North African populations have a significant excess of derived alleles shared with Neandertals, when compared to sub-Saharan Africans. This excess is similar to that found in non-African humans, a fact that can be interpreted as a sign of Neandertal admixture. Furthermore, the Neandertal's genetic signal is higher in populations with a local, pre-Neolithic North African ancestry. Therefore, the detected ancient admixture is not due to recent Near Eastern or European migrations. Sub-Saharan populations are the only ones not affected by the admixture event with Neandertals.

**Citation:** Sánchez-Quinto F, Botigué LR, Civit S, Arenas C, Ávila-Arcos MC, et al. (2012) North African Populations Carry the Signature of Admixture with Neandertals. PLoS ONE 7(10): e47765. doi:10.1371/journal.pone.0047765

**Editor:** David Caramelli, University of Florence, Italy

**Received:** July 17, 2012; **Accepted:** September 20, 2012; **Published:** October 17, 2012

**Copyright:** © 2012 Sánchez-Quinto et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Funding:** FS-Q, SC, CA and CL-F are supported by a grant from the Ministerio de Ciencia e Innovación of Spain (BFU2009-06974) and CGL2010-14944/BOS. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Competing Interests:** The authors have declared that no competing interests exist.

\* E-mail: carles.lalueza@upf.edu

<sup>9</sup> These authors contributed equally to this work.

<sup>¶</sup> These authors also contributed equally to this work.

## Introduction

Probably the most striking finding derived from the Neandertal genome project [1] was the evidence for admixture between Neandertals and a population of modern humans that left Africa between 80 Kya and 50 Kya subsequently expanding into the rest of the world. The study involved the sequencing and comparison of the Neandertal genome to five modern human genomes: two African (Yoruba and San) and three non-Africans (French, Chinese and Melanesian); all the non-African human genomes shared with Neandertals between 1–4% of their genome, in regions of low recombination placed along ten chromosomes [1]. Additional genomic region introgressions from Neandertals, Denisovans and also putative archaic African hominins have been recently described in Eurasian, Oceanic and even African populations, respectively [2–7].

However, an alternative scenario in which the ancestral population of today non-Africans was more closely related to Neandertals than the ancestral population of current Africans due to ancient substructure within the African continent, cannot be totally excluded with the present data [8], although it seems unlikely [9]. In light of this, it is unfortunate that North African individuals have not been included in these admixture analyses, since both the putative African substructure and the admixture are

likely to differentially affect North African and sub-Saharan African populations.

The importance of North Africa in the emergence of modern Homo sapiens has been traditionally neglected. However, recent archaeological and paleontological evidence increasingly points to this area as a potential source of out-of-Africa migrations [10],[11]. Recent dating of the characteristic North African lithic industry, called Aterian, has provided much older dates than previously assumed, now ranging from 145 Kya to 40 Kya [12],[13]. These Aterian people made personal ornaments with shells, a sign of modern human symbolic behavior [14]. Morphometric analyses of the 80 Kya Dar es-Soltan skull (Morocco) and of Aterian hominin teeth show similarities with early modern humans from Qafzeh and Skhul (Israel) and with the later skull of Pestera cu Oase (Romania) [15],[16].

Recent genetic analysis of North African populations [17] have found that, despite the complex admixture genetic background, there is an autochthonous genomic component which is likely derived from “back-to-Africa” gene flow older than 12,000 years ago (ya) (i.e., prior to the Neolithic migrations). This local population substratum seems to represent a genetic discontinuity with the earliest modern human settlers of North Africa (those with the Aterian industry) given the estimated ancestry is younger than 40,000 years ago [17]. The estimated time of Neandertal

**Table 1.** Average ancestry proportions in North African populations estimated by ADMIXTURE for  $k=4$  different ancestries (the best  $k$  value determined by cross-validation error).

Population	N	Maghreb*	Europe*	Near East*	Sub-Saharan Africa*
Morocco North	18	0.44	0.31	0.14	0.11
Morocco South	16	0.44	0.13	0.10	0.33
Saharawi	18	0.55	0.17	0.10	0.18
Algeria	19	0.39	0.27	0.16	0.18
Tunisia	18	0.93	0.04	0.02	0.01
Libya	17	0.31	0.28	0.25	0.16
Egypt	19	0.19	0.37	0.30	0.14

\*Ancestries are labeled according to the region where the component is the commonest.

doi:10.1371/journal.pone.0047765.t001

admixture with modern human populations is between 37,000–86,000 years ago [18].

The aim of this work was to investigate if this autochthonous North African ancestry bears any traces of the introgression with Neandertals, by applying the  $f_4$  ancestry ratio statistic test, previously used to detect Denisovan admixture in Asia [3]. We show that North African populations, like all non-African humans [1], also carry the signature of admixture with Neandertals, and that the real geographical limit for Neandertal admixture is between sub-Saharan groups and the rest.

## Materials and Methods

To ascertain whether or not current North African populations show any signs of Neandertal admixture, we analyzed recently published data of 125 North African individuals genotyped with the Affymetrix 6.0 chip and accounting for 780,000 SNPs were analyzed [17]. Individuals are representative of seven different North African locations (Table 1) spanning from west to east. To have a broader coverage of Eurasia and to allow comparison with Sub-Saharan populations, African and Eurasian populations were included in the analysis [17],[19],[20].

In order to compare the human SNP data to the Neandertal, bam read files from all Neandertal samples from the UCSC ftp site (ftp://hgdownload.cse.ucsc.edu/gbdb/hg18/neandertal/seqAlis) were downloaded and merged. Base and mapping quality filters reported in previous studies were implemented in the analysis

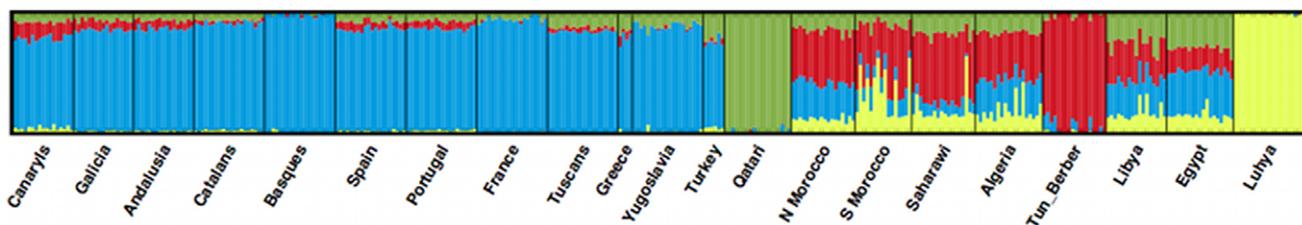
[2],[21]. To avoid any confusion with ancient DNA postmortem modifications, C-T and G-A human – ancient hominin nucleotide sites, were discarded. For all sequencing data, a single read was randomly sampled for each individual at positions overlapping the array SNPs coordinates. Furthermore all human and Neandertal data were merged with sequence data from chimpanzee (CGSC 2.1/Pantro), and data were further processed to control for strand misidentification [3], to conform a final data set of 142,720 SNPs.

North African populations have a complex genetic background. In addition to an autochthonous genetic component, they exhibit signals of European, sub-Saharan and Near Eastern admixture as previously described [17]. Moreover, the use of genotype data can suffer from potential biases that arise from discovering SNPs in a limited number of individuals, thus resulting in enrichment of common alleles, particularly in the populations from which the discovery panel was constructed [22],[23] (in the present case would be a bias towards European populations). Two challenges arise from these effects: first, patterns of gene flow detected between Neandertal and North Africans could be the consequence of subsequent admixture between North Africans and other modern human populations and second, the ascertainment bias towards European and East Asian populations could magnify differences in signals of Neandertal gene flow in individuals with high Sub-Saharan ancestry compared to individuals with high European ancestry.

In order to overcome these problems we initially assessed the different genetic components in North African populations using an unsupervised clustering algorithm, ADMIXTURE [24], on a sample set of around 50,000 SNPs that included all North African individuals, together with populations of European, Near Eastern and Sub-Saharan origin [17],[25],[26].

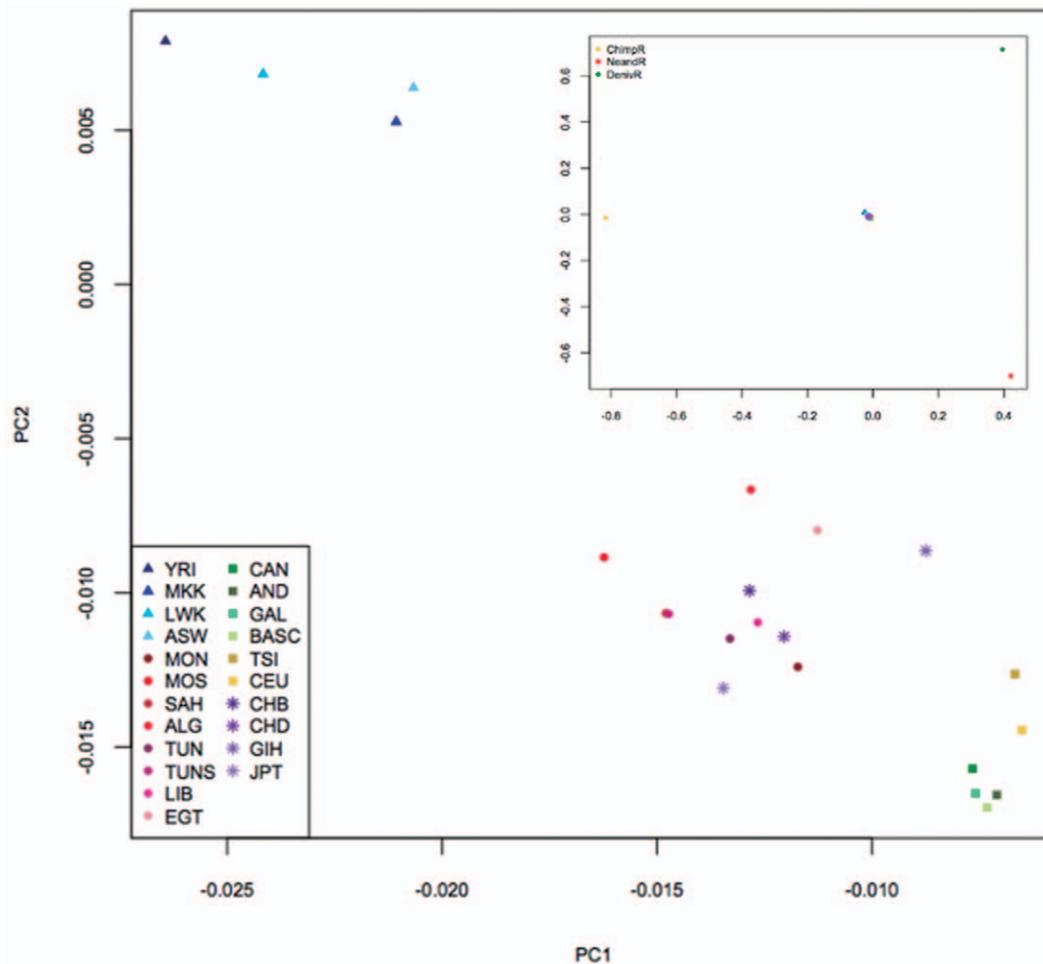
As a first approach to establish the relationship between North African populations and Neandertal, a projected Principal Component Analysis (PCA) was performed. In addition to the chimpanzee and the Neandertal genomes, data from the Denisova genome were downloaded and merged in this case resulting in 111,991 SNPs (after filtering for strand bias SNPs and ancient DNA miscoding lesions). Given that the ancient hominin and chimpanzee genomes have been originally sequenced at low coverage no SNP polymorphism data are available, and therefore individuals were considered at the haplotype level only. First, a PCA was generated using Neandertal, chimpanzee, and Denisova. Then, SNP loadings for the first two components were used to project the sample set of modern humans.

Next, we aimed at estimating the amount of Neandertal admixture in North African populations using the  $f_4$  ancestry ratio test [27]. Although a previous simulation study [28] suggested that the analysis of SNP data from arrays can provide biased results in admixture estimates, there is more recent evidence supporting that



**Figure 1. Results of the ADMIXTURE analysis ( $k=4$ ) with North African populations.** ADMIXTURE was performed on a set of European, North African, Near Eastern and Sub-Saharan populations in order to account for the different admixture proportions in North Africa. Tunisians and Saharawi are the North African populations with highest proportion of autochthonous component, whereas the rest of the populations have greater amounts of admixture with neighboring populations.

doi:10.1371/journal.pone.0047765.g001



**Figure 2. PCA analysis of North African, Sub-Saharan, European and Asian populations.** Upper right box: PCA analysis with the African populations (dark blue, Sub-Saharan, light blue, North African), along with three outgroups: chimpanzee, Neandertal and Denisovan. It can be seen that North African populations are placed in the direction of the Neandertal. In the population analysis, the North African groups tend to be placed in an intermediate position between Sub-Saharan and non-African human populations. Population abbreviations are the same as in Table 2. doi:10.1371/journal.pone.0047765.g002

$f_4$  ancestry ratio statistic is unaffected by those biases [3]. The  $f_4$  ancestry ratio test measures the proportion of archaic hominin genetic fraction in a modern human population as a fraction of the known amount of archaic introgression in another modern human population. Consequently, the  $f_4$  ancestry ratio test basically measures the correlation in allele frequency differences between two populations used as outgroups (e.g., chimpanzee and Neandertal), a Sub-Saharan African population (Yorubans) and the X-tested population, normalized by the correlation in allele frequency differences between chimpanzee, Neandertal, a Sub-Saharan African group (Yorubans) and a human population previously known to have experienced Neandertal admixture (in this case, CEU) [1]. If Yorubans and X descend from a single ancestral population without any subsequent admixture with Neandertals, then the allele frequency differences between Yorubans and X must have arisen solely after their separation from their common ancestor; the two frequency differences should be uncorrelated and thus the  $f_4$  ancestry ratio statistic should have an expected value of zero.

Finally, a block jackknife [29],[30] approach was used to estimate standard errors; blocks were separated by dropping each non-overlapping five cM stretch of the genome in turn, and

studying the variance of each statistic of interest to obtain a approximately normal distributed standard error [25]. Further combinations (e.g. San instead of Yoruban and Chinese instead of CEU) were also calculated to test the consistency of the results (Table S1).

## Results and Discussion

We ran ADMIXTURE for  $k$  equal 2 to 7 and obtained CV errors, and determined that the best  $k$  (the one with lowest cross-validation error) is  $k=4$ . Results (Figure 1) are coincident with those previously published [17] and show that North Morocco, Libya and Egypt carry high proportions of European and Near Eastern ancestral components, whereas Tunisian Berbers and Saharawi are those populations with highest autochthonous North African component. Particularly, ten Tunisian individuals have more than 99% of their genome assigned to North African ancestry and therefore have been analyzed separately (subsequently referred to as N-TUN) from the overall Tunisian population.

In the PCA analysis (Figure 2) Eurasian populations are the closest to Neandertals among modern humans, which is in agreement with previous studies [1]. Sub-Saharan Africans are, as

**Table 2.** Estimates of Neandertal ancestry in North African populations, along with European, Asian and Sub-Saharan African groups.

Population	Code	N	Estimated ancestry	Standard error	Z score
Algeria	ALG	19	44.57%	6.24%	7.15
Tunisia	TUN	17	100.16%	7.18%	13.95
Tunisia 100%	N-TUN	9	138.13%	10.32%	13.39
Egypt	EGT	19	58.45%	5.73%	10.2
Libya	LIB	17	56.36%	5.91%	9.53
Morocco North	MON	18	69.17%	5.37%	12.87
Morocco South	MOS	16	17.90%	6.76%	2.65
Saharawi	SAH	18	50.90%	6.30%	8.08
Canary Island*	CAN	17	101.44%	4.62%	21.95
China Beijing	CHB	84	193.43%	16.41%	11.79
China	CHD	85	195.41%	16.62%	11.76
Japan	JPT	86	201.18%	17.22%	11.69
Texas Indu Gupti	GIH	88	84.37%	5.77%	14.62
Andalusia*	AND	15	118.66%	5.34%	22.22
CEU	CEU	112	100.00%	0.00%	inf
Tuscan	TSI	88	94.90%	3.12%	30.4
Basque	BASC	20	129.48%	6.34%	20.44
Galicia*	GAL	16	115.86%	4.82%	24.06
Yoruba	YRI	113	0.00%	0.00%	nan
Luyha	LWK	90	-14.89%	4.50%	-3.31

European HapMap CEU was selected as the known to have experience Neandertal admixture, Chimpanzee as the out-group and Sub-Saharan YRI as the non Neandertal admixed population. \* unpublished data. doi:10.1371/journal.pone.0047765.t002

expected, more distant to Neandertal, whereas North African individuals are placed between these two groups. North African individuals with the highest Sub-Saharan African component (as detected by ADMIXTURE) are distant from Neandertal and closer to Sub-Saharan populations. It is interesting to notice that the North African populations closer to Neandertals are populations with a large known European or Near Eastern admixture, but also the Tunisians that have an almost complete autochthonous North African genetic component.

The results of the  $f_4$  ancestry ratio test (Table 2 and Table S1) show that North African populations vary in the percentage of Neandertal inferred admixture, primarily depending on the amount of European or Near Eastern ancestry they present (Table 1). Populations like North Morocco and Egypt, with the highest European and Near Eastern component (~40%), have also the highest amount of Neandertal ancestry (~60–70%) (Figure 3). On the contrary, South Morocco that exhibits the highest Sub-Saharan component (~60%), shows the lowest Neandertal signal (20%). Interestingly, the analysis of the Tunisian and N-TUN populations shows a higher Neandertal ancestry component than any other North African population and at least the same (or even higher) as other Eurasian populations (100–138%) (Figure 3).

Some results of the estimated ancestry in Table 2 are higher than 100%. Because the amount of Neandertal admixture provided by this statistic is in relation to the fraction found in another population, populations with more than 100% values, have more than the observed Neandertal admixture levels found in the “source population” used for comparison (i.e CEU). On the other hand, a negative  $f_4$  ancestry ratio value such as that one observed for the Luyha in Table 2 could have several explanations. One possibility is that it reflects an artifact of ascertainment bias on SNP arrays. Ascertainment bias is likely to affect the joint information from Europeans and East Asians, since SNP arrays are most commonly designed based on information from these populations. On the other hand it could also reflect a more complex demographic history (i.e population structure between the populations being compared) than previously assumed.

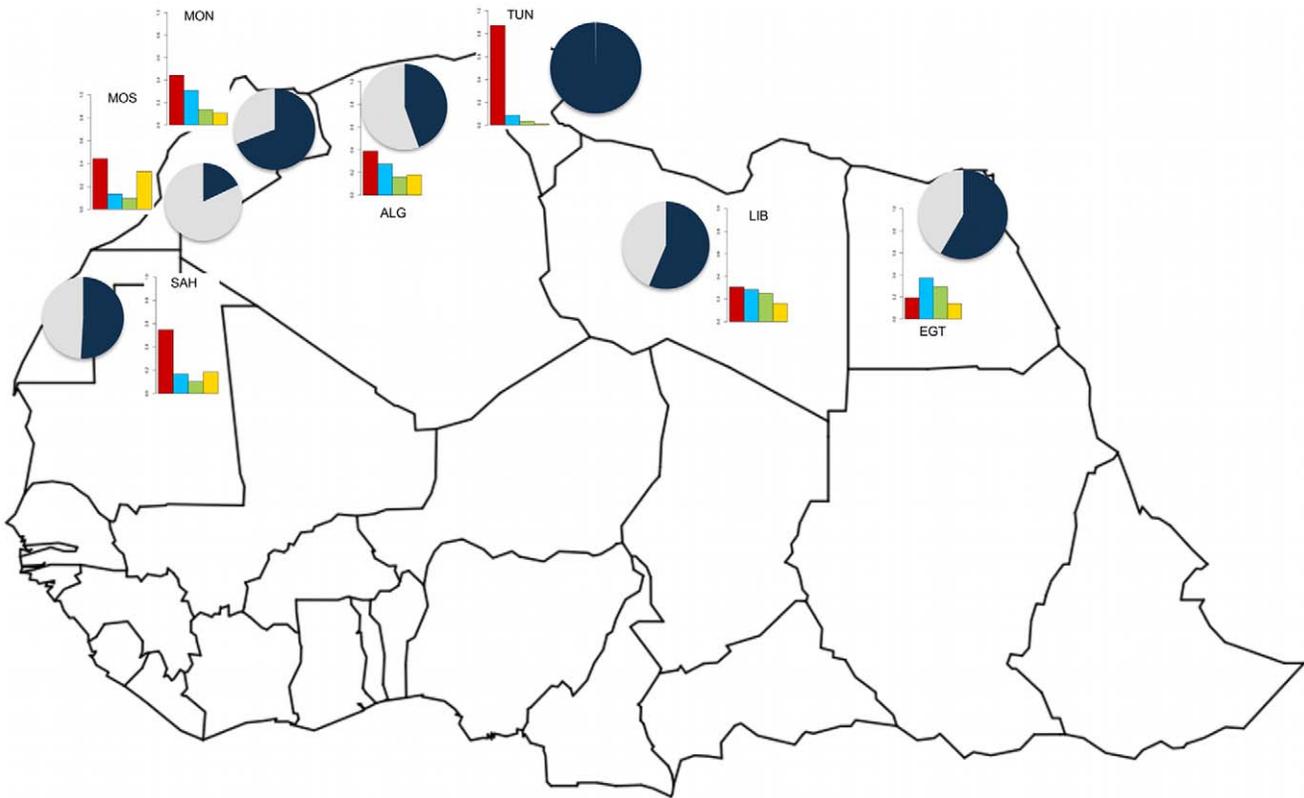
Subsequently, we aimed to compare the results revealed by ADMIXTURE and by the  $f_4$  ancestry ratio statistic in an attempt to corroborate that the signal of Neandertal admixture revealed in North African populations is not caused by Eurasian admixture. For this purpose, we performed a Pearson correlation test between the ancestry proportions estimated with ADMIXTURE and the proportions of Neandertal admixture estimated by the  $f_4$  ancestry ratio test. Specifically, we tested the correlation between a) both European and Near Eastern components and Neandertal admixture and b) European, Near Eastern and North African admixture components and Neandertal admixture. If signals of gene flow from Neandertals were due exclusively to the European and the Near Eastern components, we would expect that the correlation should significantly decrease in test b), when the North African component is included. On the contrary, the Pearson correlation test reaches significance only when the North African component is included, which is maintained even when Tunisians are removed from the analysis (Table 3).

Overall, the correlation analysis and the  $f_4$  ancestry ratio statistic show that the North African component actually contributes to the signal of gene flow from Neandertals. Given that the North African autochthonous ancestry seems to be 12,000–40,000 years old [17],

**Table 3.** Pearson's product – moment correlation between modern human ancestry in North African groups and Neandertal admixture.

Comparison		Correlation (p-value)
European, Near Eastern vs. Neandertal	With Tunisia	-0.44 (0.8384)
	Without Tunisia	0.49 (0.1572)
European, Near Eastern, North Africa vs. Neandertal	With Tunisia	0.91 (0.0020*)
	Without Tunisia	0.90 (0.0068*)

doi:10.1371/journal.pone.0047765.t003



**Figure 3. Neandertal genetic introgression in North African populations as a fraction of that found in Europeans.** Relative proportion of Neandertal ancestry for each population is presented as the dark blue section of the pies on a map of North Africa. Additionally, each population is also represented as a barplot of the different geographic genetic components; in red: North African, in blue: Sub-Saharan, in green: European, in yellow: Near East. Populations are shown as having Neandertal ancestry if the estimates are more than two standard errors from zero. Full name descriptions of these population labels are found in Table 2.  
doi:10.1371/journal.pone.0047765.g003

our hypothesis is that this ancestral population was descendant from the populations that first interbred with Neandertals about ~37,000–86,000 years ago [18] somewhere in the Middle East. Nonetheless further analyses in populations around the contact areas are needed to confirm this hypothesis.

A previous study [26] observed that the similarity to Neandertals increases with distance from Africa and suggested this could be explained by SNP ascertainment bias plus a strong genetic drift in East Asian populations. Nonetheless more complex, population-biased, ascertainment schemes might have additional effects (i.e. bottlenecks), but these are not expected to significantly increase the rate of false positives in admixture tests [31]. The Tunisian population has been reported to be a genetic isolate [17] so it is plausible that part of the signal detected is actually due to genetic drift. However, this should not affect the other North African groups in our study. Finally, given that SNP arrays are based on common alleles and probably the relevant admixture information is encoded within the rare and very rare alleles, the potential bias, if anything, will underestimate ancient hominid admixture signals, as shown in previous studies [2],[3].

With the current data, however, it is not possible to discard the ancient African substructure hypothesis [8]. Although ours and some previous results [9] tend to favor the admixture hypothesis as the most plausible one, we think that a complete clarification of this issue can only be achieved with a Neandertal high coverage genome, such as this recently achieved for Denisova [32]. This, and sequencing data of North African populations, especially those with a high autochthonous component, may help elucidate more

precisely the interbreeding process with Neandertals. In any case, our results show that Neandertal genomic traces do not mark a division between African and non-Africans but rather a division between Sub-Saharan Africans and the rest of modern human groups, including those from North Africa.

## Supporting Information

**Table S1 Stability of the Neandertal admixture estimates.** We present each population's estimate ancestry, the standard error in the estimate, and the Z score for different combinations of Sub-Saharan and non-African populations. O (Out-group), BP (Benchmark population, i.e. population which didn't experience any introgression from Neandertals) and SP (Source population i.e. populations in which the amount of introgression from Neandertal is known). (DOC)

## Acknowledgments

We are grateful to Brenna M. Henn and Pontus Skoglund for helpful comments on some aspects of the manuscript and the ancestry ratio test, respectively.

## Author Contributions

Conceived and designed the experiments: DC CDB CL-F. Performed the experiments: FS-Q LR-B SC CA MCA-A. Analyzed the data: FS-Q LR-B SC CA MCA-A. Contributed reagents/materials/analysis tools: DC CDB CL-F. Wrote the paper: DC CL-F.

## References

- Green RE, Krause J, Briggs AW, Maricic T, Stenzel U, et al. (2010) A draft sequence of the Neandertal genome. *Science* 328: 710–722.
- Reich D, Green RE, Kircher M, Krause J, Patterson N, et al. (2010) Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* 468: 1053–1060.
- Reich D, Patterson N, Kircher M, Delfin F, Nandineni MR, et al. (2011) Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. *Am J Hum Genet* 89: 516–528.
- Abi-Rached L, Jobin MJ, Kulkarni S, McWhinnie A, Dalva K, et al. (2011) The Shaping of Modern Human Immune Systems by Multiregional Admixture with Archaic Humans. *Science* 334: 89–94.
- Hammer MF, Woerner AE, Mendez FL, Watkins JC, Wall JD (2011) Genetic evidence for archaic admixture in Africa. *Proc Natl Acad Sci USA* 108: 15123–15128.
- Rasmussen M, Guo X, Wang Y, Lohmueller KE, Rasmussen S, et al. (2011) An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. *Science* 334: 94–98.
- Yotova V, Lefebvre JF, Moreau C, Gbeha E, Hovhannesian K, et al. (2011) An X-linked haplotype of Neandertal origin is present among all non-African populations. *Mol Biol Evol* 28: 1957–1962.
- Eriksson A, Manica A (2012) Effect of ancient population structure on the degree of polymorphism shared between modern human populations and ancient hominins. *Proc Natl Acad Sci USA* 109: 13956–13960.
- Yang MA, Malaspina AS, Durand EY, Slatkin M (2012) Ancient structure in Africa unlikely to explain Neanderthal and non-African genetic similarity. *Mol Biol Evol* Apr 18. [Epub ahead of print].
- Osborne AH, Vance D, Rohling E, Barton N, Rogerson M, et al. (2008) A humid corridor across the Sahara for the migration “Out of Africa” of early modern humans 120,000 years ago. *Proc Natl Acad Sci USA* 105: 16444–16447.
- Balter M (2011) Was North African the launch pad for Modern Human migrations? *Science* 331: 20–23.
- Barton RNE, Bouzouggar A, Collcutt SN, Schwenninger J-L, Clark-Balzan L (2009) OSL dating of the Aterian levels at Grotte de Dar es-Soltan I (Rabat, Morocco) and possible implications for the dispersal of modern *Homo sapiens*. *Quaternary Sci Rev* 28: 1914–1931.
- Garcea EAA (2010) The spread of Aterian peoples in North Africa. In: Garcea, E.A.A., editor. *South-Eastern Mediterranean Peoples Between 130,000 and 10,000 years ago*. Oxford: Oxbow Books.
- Bouzouggar A, Barton RNE, Vanhaeren M, D’Errico F, Collcutt S, et al. (2007) 82,000-year-old shell beads from North Africa and implications for the origins of modern human behavior. *Proc Natl Acad Sci USA* 104: 9964–9969.
- Harvati K, Hublin J-J (2012) Morphological continuity of the face in the late Middle and Upper Pleistocene hominins from northwestern Africa – A 3D geometric morphometric analysis. In: Hublin J-J, McPherron S, editors. *Modern Origins: A North African Perspective*. Dordrecht: Springer.
- Hublin J-J, Verna C, Bailey S, Smith T, Olejniczak A, et al. (2012) Dental evidence from the Aterian human populations of Morocco. In: Hublin J-J, McPherron S, editors. *Modern Origins: A North African Perspective*. Dordrecht: Springer.
- Henn BM, Botigué LR, Gravel S, Wang W, Brisbin A, et al. (2012) Genomic ancestry of North Africans supports back-to-Africa migrations. *Plos Genetics* 8: e1002397.
- Sankararaman S, Patterson N, Li H, Pääbo S, Reich D (2012) The date of interbreeding between Neandertals and modern humans. arXiv: 1208.2238v1.
- International HapMap 3 Consortium, Altshuler DM, Gibbs RA, Peltonen L, Altshuler DM, et al. (2010) Integrating common and rare genetic variation in diverse human populations. *Nature* 467: 52–57.
- Novembre J, Johnson T, Bryc K, Kutalik Z, Boyko AR, et al. (2008) Genes mirror geography within Europe. *Nature* 456: 98–101.
- Skoglund P, Malmström H, Raghavan M, Stora J, Hall P, et al. (2012) Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. *Science* 336: 466–469.
- Kuhner MK, Beerli P, Yamato J, Felsenstein J (2000) Usefulness of single nucleotide polymorphism data for estimating population parameters. *Genetics* 156: 439–447.
- Albrechtsen A, Nielsen FC, Nielsen R (2010) Ascertainment biases in SNP chips affect measures of population divergence. *Mol Biol Evol* 27: 2534–2547.
- Alexander DH, Novembre J, Lange K (2009) Fast model-based estimation of ancestry in unrelated individuals. *Genome Res* 19: 1655–1664.
- Hunter-Zinck H, Musharoff S, Salit J, Al-Ali KA, Chouchane L, et al. (2010) Population genetic structure of the people of Qatar. *Am J Hum Genet* 87: 17–25.
- Lao O, Lu TT, Nothnagel M, Junge O, Freitag-Wolf S, et al. (2008) Correlation between genetic and geographic structure in Europe. *Curr Biol* 18: 1241–1248.
- Reich D, Thangaraj K, Patterson N, Price AL, Singh L (2009) Reconstructing Indian population history. *Nature* 461: 489–494.
- Skoglund P, Jakobsson M (2011) Archaic human ancestry in East Asia. *Proc Natl Acad Sci USA* 108: 18301–18306.
- Kunsch HK (1989) The jackknife and the bootstrap for general stationary observations. *Ann Stat* 17: 1217–1241.
- Busing F, Meijer E, Van Der Leeden R (1999) Delete-m jackknife for unequal m. *Stat Comput* 9: 3–8.
- Durand EY, Patterson N, Reich D, Slatkin M (2011) Testing for ancient admixture between closely related populations. *Mol Biol Evol* 28: 2239–2252.
- Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, et al. (2012) A High-Coverage Genome Sequence from an Archaic Denisovan Individual. *Science*. Aug 31. [Epub ahead of print].