Size does matter: Variation in tooth size apportionment among major regional North and sub-Saharan African populations

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ABSTRACT In the 1980s Edward Harris proposed an approach using principal components analysis to compare mesiodistal and buccolingual crown diameters in humans. A major goal was to remove overall "size" from the measurements – which is ineffective for biological affinity. Relative size, however, is important, i.e., to assess how it is apportioned along the tooth rows. To get at such data, Harris utilized three size predictors in multiple linear regression to calculate PC 1 residuals, which were then used with other uncorrected components in analysis.

Here we demonstrate that it is still an effective method, by comparing 32 MD and BL measurements in 12 (n=712) and 18 (n=1251) samples from sub-Saharan and North Africa. Plotting of the first three components (50% of variance) shows clear separation between regions. North Africans are characterized by: 1) small LI1s, and BL dimensions of the UM1, LI2, and LM1, and 2) large MD diameters of the UM2 and LM1, and BL diameters of the LM2 and LM3. Comparisons of North Africans only show the ability to distinguish among samples from the Maghreb, Egypt, and Nubia. In other words, basic crown diameters can be successfully used for affinity estimation, if relative size, a.k.a., "shape" is accounted for.

Over 20 years ago, Edward Harris proposed an approach to compare mesiodistal (MD) and buccolingual (BL) crown diameters that employed principal components analysis (PCA) (Harris, 1997; Harris and Bailit, 1988; Harris and Rathbun, 1991). One major goal, like that of other workers (e.g., Penrose, 1954), was to remove overall "size" -- which is ineffective for biological affinity estimates and phylogenetic analyses. However, relative size is important, i.e., how it is apportioned among crowns along the tooth rows. To get at such data, Harris used three size predictors in multiple linear regression to calculate PC 1 residuals; these and the other uncorrected components were then used in analysis. This approach is called tooth size apportionment (TSA) analysis. It was used by several other researchers (e.g., Hemphill, 1991; Hemphill et al., 1992; Irish and Hemphill, 2001, 2004) to quantify sample differences ranging from global to local in scale -- before its appeal diminished.

Like clothing, analytical methods go in and out of style. When "sexy" approaches involving lasers, aDNA, and stable isotopes emerge, the "old ways" are often forgotten. The purpose here is to show that "old" is not the same as "out-dated;" through TSA, useful results can be achieved with easy-to-obtain odontometric data – all without destructive sampling and at a fraction of the cost.

MATERIALS

Up to 32 MD and BL measurements in the left maxillary and mandibular dentitions of 12 (n=712 inds) sub-Saharan and 18 (n=1251) North African samples for the present study were recorded. Nonmetric findings in these same samples support a known biocultural dichotomy between populations living north and south of the Sahara (Irish, 1997, 1998a,b, 2005, 2006). The names (incl. abbreviations in Figs. 3 and 6), composition, and origins of these 30 samples are presented in the aforementioned publications. Their approximate geographic locations are plotted in Figure 1.

METHODS

Following Harris' [and Hemphill's (1991)] approach, sexes-pooled mean measurements were obtained for each sample (sex dimorphism relates to crown size not shape). Ordinarily, either these data or their z-scores would be submitted to PCA to obtain a rotated (Harris) or unrotated

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(Hemphill) solution. The PC1 size factor would be addressed through use of residuals as noted above. However, this approach was questioned by Jungers et al. (1995), among others, who prefer size correction via Darroch and Mosimann's (1985) geometric mean (GM). Following their lead, the product of all 32 measurements in this study by sample was calculated, the 32nd root obtained, and the resulting GM used as divisor of each measurement to effect correction. These DM values were then submitted to PCA, to yield unrotated PC loadings and factor scores.

RESULTS AND DISCUSSION

To illustrate the effectiveness of DM size correction, the eight sexes-pooled mean MD maxillary measurements for combined samples of North and sub-Saharan Africans are plotted in Figure 2. North Africans exhibit smaller dimensions in all cases. Compare this line graph to that at the top of Figure 5 after size correction. It can be seen that relative between-sample size (a.k.a. shape) varies; that is, it is apportioned differentially along the tooth row: in this example, North Africans have relatively larger UI1, UP4, UM1, and UM3 MD dimensions.

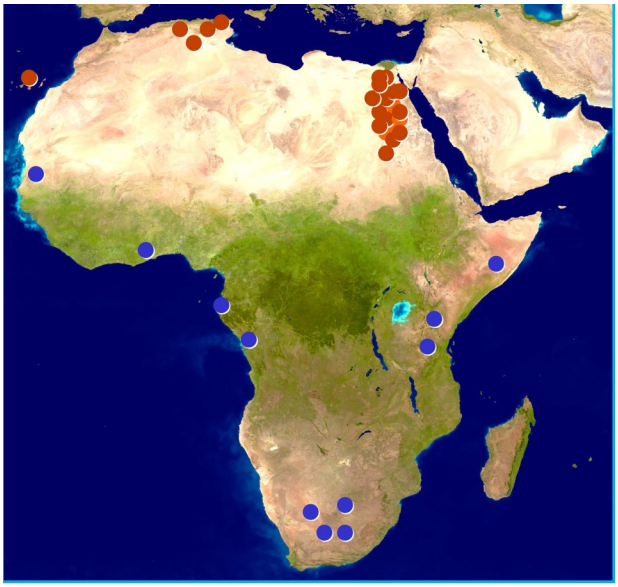

Fig.1. Origins of the 30 North (red dots) and sub-Saharan (blue) samples.

Five components with eigenvalues of >2.0 were retained (see Table 1); they account for >63% of the total variance. Plotting of first three factor scores (<50% of variance) yielded the distribution in Figure 3. The North and sub-Saharan samples show

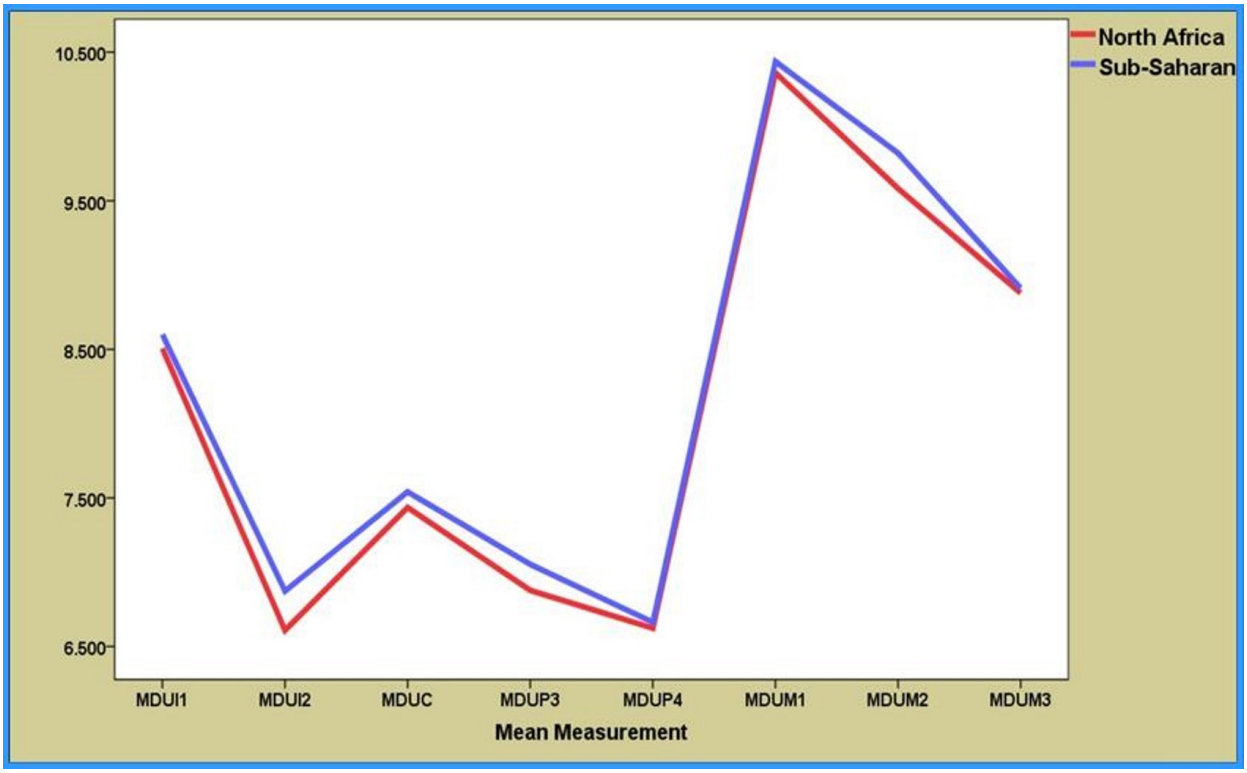

Fig. 2. MD maxillary measurements in pooled North and sub-Saharan samples.

TABLE 1. PCA loadings (high-magnitude values in boldface)

Measure	PC1	PC2	PC3	PC4	PC5
DM_MUI1	-.098	-.246	.123	**.596**	.356
DM_MUI2	**.546**	.466	-.026	-.082	.401
DM_MUC	.151	**-.575**	.234	-.224	.209
DM_MUP3	.429	.343	-.083	.111	**.527**
DM_MUP4	-.294	.138	-.130	.219	.242
DM_MUM1	-.419	.252	.028	-.238	.175
DM_MUM2	.099	**.543**	.467	-.113	-.317
DM_MUM3	-.377	.371	.246	.393	-.407
DM_BUI1	.085	**-.698**	.057	.053	.110
DM_BUI2	.400	-.310	.196	**-.512**	.471
DM_BUC	.429	**-.654**	.115	-.175	.035
DM_BUP3	**.777**	.121	.158	.319	.117
DM_BUP4	.456	-.179	.344	.437	-.073
DM_BUM1	**-.588**	-.170	**.501**	.095	.262
DM_BUM2	.287	-.153	**.784**	-.099	-.328
DM_BUM3	**.600**	.067	.255	.243	-.080
DM_MLI1	**-.512**	-.234	-.023	**.635**	.064
DM_MLI2	-.342	-.265	-.329	**.539**	-.220
DM_MLC	.498	-.078	-.225	-.329	**-.511**
DM_MLP3	**.653**	.323	-.352	.144	-.138
DM_MLP4	-.044	.366	**-.649**	.022	.053
DM_MLM1	-.079	**.523**	-.329	-.013	.346
DM_MLM2	-.479	.432	.079	-.368	.333
DM_MLM3	-.379	.382	.092	-.162	.319
DM_BLI1	**-.684**	-.489	-.162	-.025	-.212
DM_BLI2	**-.645**	-.499	-.257	-.179	-.219
DM_BLC	-.030	**-.659**	-.222	**-.603**	.025
DM_BLP3	**.674**	.068	-.170	-.003	-.292
DM_BLP4	.299	.132	**-.644**	-.081	-.353
DM_BLM1	**-.705**	.402	.088	-.150	-.125
DM_BLM2	-.279	**.517**	.388	-.282	**-.521**
DM_BLM3	-.094	**.628**	.203	-.145	-.019

obvious separation, as previously as identified by dental nonmetric (Irish, 1997, 1998a,b, 2005, 2006) and other biocultural findings. The PC loadings in the table provide specifics on TSA. High magnitude negative PC1 loadings characterize North Africans on the right of the x-axis in Figure 3, i.e., relatively large LI1, and BL-only values for UM1, LI2, and LM1. High positive PC1 loadings for the sub-Saharan samples show a relatively large LP3, MD-only for UI2, and BL-only for UP3 and UM3. The TSA differences on PC2 and PC3 similarly account for sample locations on the y- and z-axes (Figure 3). To utilize information in all five PCs, Ward's cluster analysis was used to classify samples (Figure 4) based on the factor scores derived from DM_values (Figure 5).

Three main clusters are evident in Figure 4: (1) sub-Saharan only, (2) North African only, and (3) North African with four sub-Saharan samples. Interestingly, the latter samples are from regions

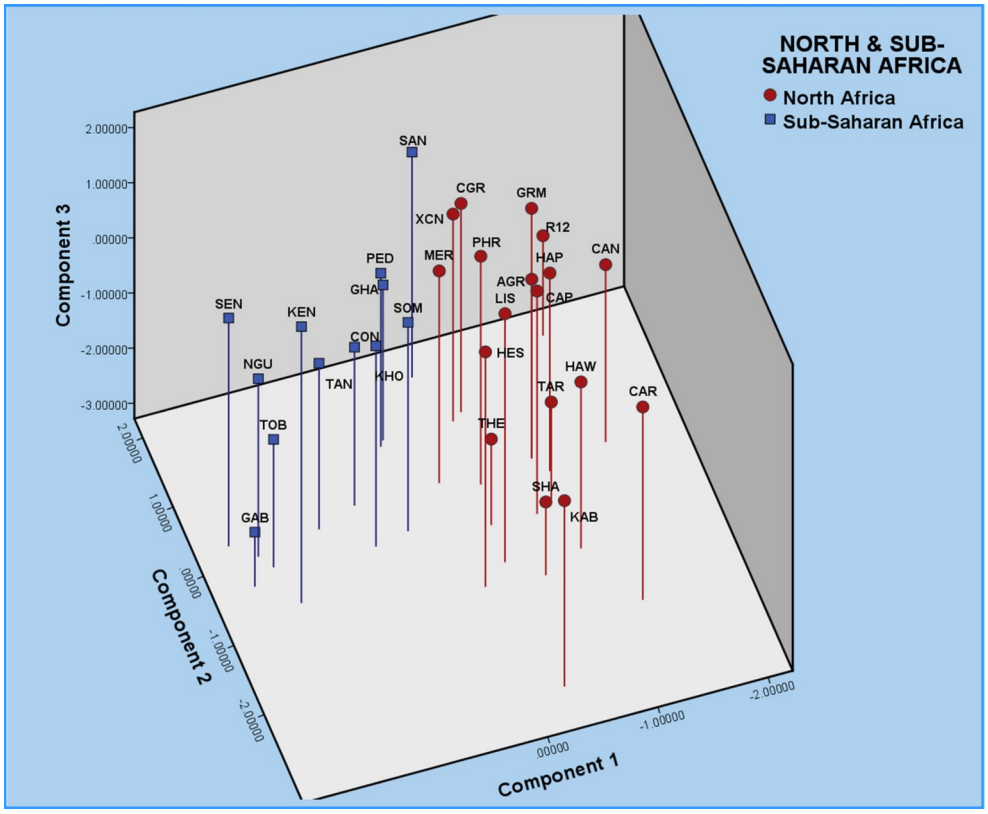

Fig. 3. Samples plot of first three factor scores.

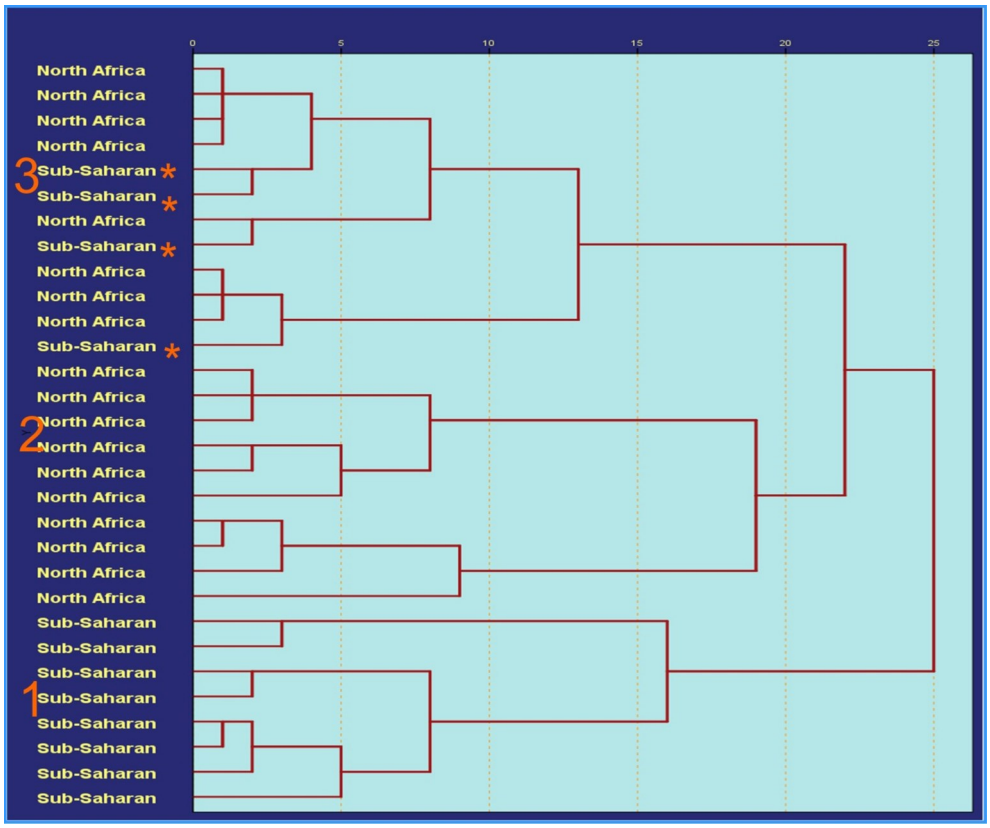

Fig. 4. Ward's cluster analysis of all five factor scores (showing three main clusters as identified in the text).

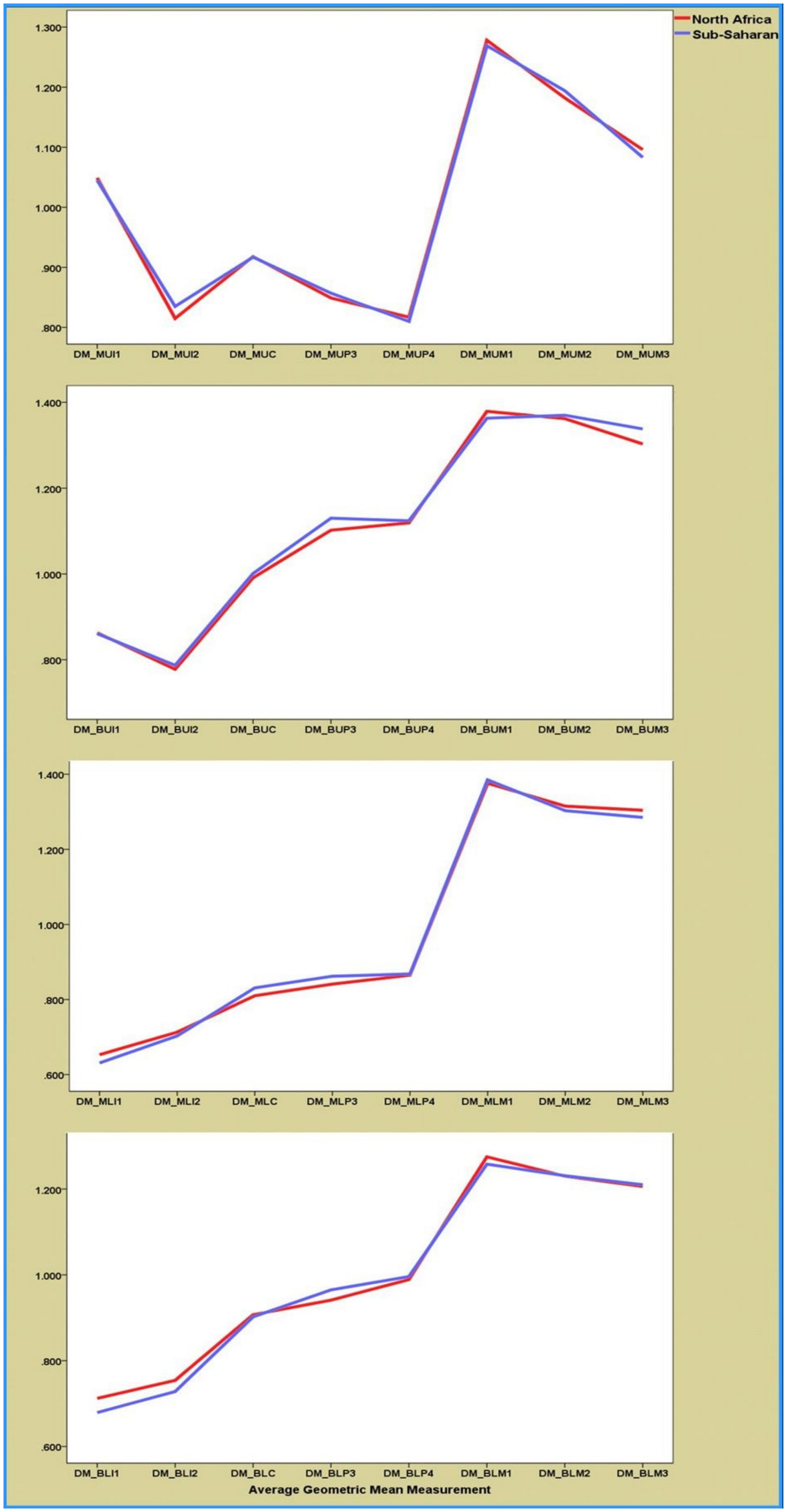

Fig. 5. Average MD and BL DM-values in upper and lower jaws.

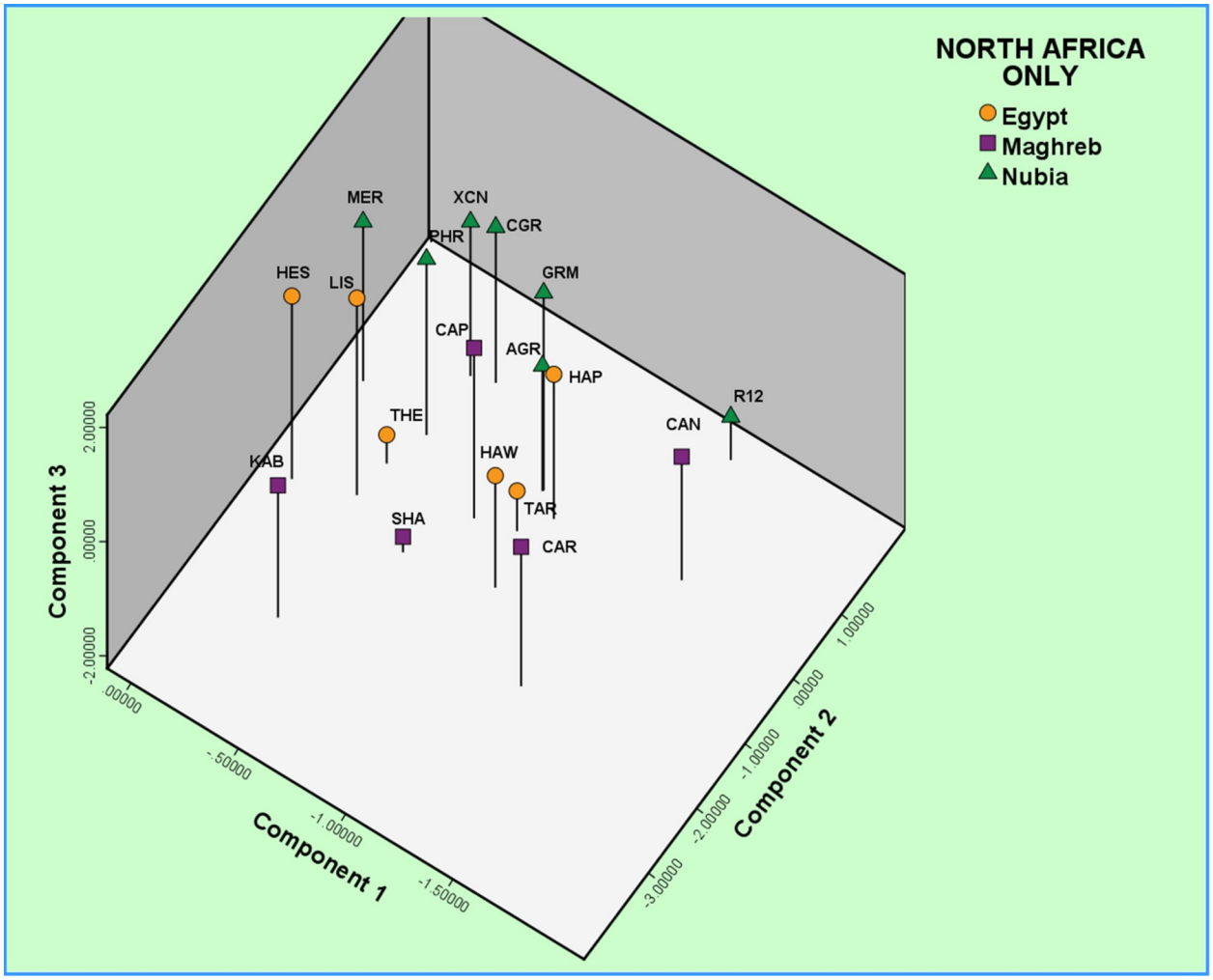

Fig. 6. Samples plot of first three factor scores for North Africans only.

in the proximity of "northern" peoples (e.g., Somalia) -- which may reflect evidence of admixture.

Finally, to demonstrate that TSA analysis can be applied on a regional scale as well, just the 18 North African samples were compared. Figure 6 illustrates that, even at this finer-grained level of study, some differentiation among the Nubian, Egyptian, and Maghreb samples is possible. In other words, the results presented here indicate that an "old" method and basic crown diameter data can be successfully used for affinity estimation, if overall size is accounted for and "shape" is considered. Thus, (relative) size does matter.

ACKNOWLEDGMENTS

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