

## Critical Short Report

# Human population genetics and “ancestrality” business

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Following the foundation of theoretical population genetics by Wright, Fischer, Haldane and Malécot, in the first half of the 20<sup>th</sup> century, applied human population genetics developed with great success with the improvement and accumulation of new technologies to measure genetic polymorphism, first through protein polymorphisms since the 1960's, then through DNA typing and sequencing since the 1980's.

The field of population genetics and biological anthropology was developed by a handful of devoted labs headed by Newton Morton, Derek Roberts, Luca Cavalli Sforza and James Neel, followed by Harris, Workman, Niswander, Friedlander, Yasuda, Piazza, Takahata and some others. The objectives of the new science were twofold: 1) medical : looking for disease genes, their frequencies and circulation among and within populations 2) anthropological : comparing gene frequencies worldwide and reconstructing long term populations history and its mechanisms from these data.

From the beginning, two main results appeared which have continuously been confirmed and reinforced by accumulating new molecular data:

1<sup>st</sup>) all present day people, almost 7 billion, are descended from a single very small Paleolithic population. Investigators agree about the effective size (between 5 000 and 15 000 breeders) of this last common ancestral population, but disagree about how old it is (from 60 000 to 400 000 years) and where to localize it (definitely sub-Saharan Africa for some scholars, East Asia for some others, likely Africa in the present state of the art, but not proved for others)

2<sup>nd</sup>) in all presently analyzed genetic systems, polymorphism within populations is considerable, polymorphism between populations is limited, mostly made of important frequency differences of the same genes rather than differences by presence-absence of population-specific genes. So, we don't know at now any population specific gene, except neo- mutations, rare where they are found. The exception to this pattern is that small and/or isolated peripheral populations commonly lost, by genetic drift and/or founder effect, a part of the alleles regularly present in large continental populations. In large continental populations, Newton Morton, following Malécot's theory of genetic isolation by distance, has demonstrated for long that most of human genetic variation was explained by migration according to geographic or communication distances. Lots of following studies validated this view with all possible human genetic data sets.

Disagreement occurred for a long while between others and Cavalli-Sforza and his heirs who, despite recognizing the validity of the isolation by distance model, went on using cladograms and phylogenetic models to assess history of populations within the present human species. Many investigators oppose to these practices because 1) phylogenetic models apply to separate entities such as molecule sequences or isolated species, but not to inter migrating sets of populations 2) cladograms can be statistically correct, but without featuring correctly population history. Moreover, they have no reason to be alike between different genetic systems, so that such methods can lead to discordant and meaningless population classifications.

Nevertheless, "classical" laboratories went on, very carefully, in the interdisciplinary approach of local population history, facing molecular and DNA data to anthropological, archeological, paleontological and linguistic evidences and theories.

The late E.O. Wilson and co – workers introduced a lot of confusion when launching in the medias the “African Eve” theory about mtDNA phylogenies in mankind. Not only the results were over interpreted if not simply false, but they induced the very stupid idea that one could reconstruct the complexity of the world population history from a ridiculous set of one or two hundred DNA samples. From there, lots of divergent “studies” alike appeared in the best journals, ridiculizing those people working hard on the bench or in genetic data banks concerning thousands of samples from hundreds of populations throughout the world.

From there it appears to some people who had been working in the best labs, that there was a lot of money to make in expertise for police and justice, or even for private use if one could decide of the ethnic origin of someone from DNA testing. Unfortunately (or fortunately), this type of Ethnic Affiliation Estimation proved not to work, or with error rates unacceptable for legal purposes.

But the development, out of any scientific and legal control, of the e-business induced the proliferation of private societies in California, Florida, England and Switzerland that pretend, against any truth, to be able to determine the geographic and historic origins of the ancestors of anyone from an easy to collect DNA sample. The costs billed for such analyses may go from 300 to 3000 dollars, according to the “precision” requested. The worst is that all this “ancestrality” business address in priority populations having trouble or heavy concern about their origins, such as Afro – Americans, Jews, admixed orphans or others motivated to know where they do come from.

These private companies are sometimes backed and exploited by former or present scholars of famous universities. Of course, the sailed results giving localization, religion, sometimes names and activities of invented ancestors centuries or millenniums ago or sharing parts of German, Jew, Oriental, African or other ancestries of anyone are, most of the time, pure invention that can only be compared to astrology.

Astrologists are inventing their customers’ future from stupid considerations on space and stars. Ancestrality business invents the past of its victims from as stupid considerations about DNA. In both cases, the western society has no way to protect science and peoples from such robberies.