Meta Gene 2 (2014) 427–438

Contents lists available at ScienceDirect

Meta Gene

Genetic ancestry of a Moroccan population as inferred from autosomal STRs

K. Bentayebi [a,*], F. Abada [a], H. Ihzmad [b], S. Amzazi [a]

[a] Laboratoire de Biochimie Immunologie, Faculté des Sciences, Université Mohammed V, Morocco
[b] Laboratoire d'épidémiologie, Institut National d'Hygienne, Rabat, Morocco

ARTICLE INFO

Article history:
Received 3 March 2014
Accepted 19 April 2014
Available online 21 June 2014

Keywords:
North Africa
Morocco
Population genetics
Iberia
STR
Ancestry
Gene flow

ABSTRACT

Detecting population substructure and ancestry is a critical issue for both association studies of health behaviors and forensic genetics. Determining aspects of a population's genetic history as potential sources of substructure can aid in design of future genetic studies. Within this context, fifteen autosomal short tandem repeat (STR), were used to examine population genetic structure and hypotheses of the origin of the modern Moroccan population from individuals belonging to three different ethnical groups from Morocco (Arab, Berber and Sahrawi), by comparing their autosomal STR variation with that of neighboring and non-neighboring populations in North Africa, Europe and Middle East as well as proposed ancestral populations in Morocco (Berber). We report on the results that the gradient of North African ancestry accounts for previous observations of low levels of sharing with Near East and a substantially increased gene flow especially from Morocco and Spain.

Introduction

The question of Moroccan ancestry has been addressed for ages to answer questions of human evolutionary, historical and medical significance. Human evolutionary or anthropological studies have focused on vast array of DNA-based genetic markers, each of which has different attributes but complementary roles (Garrigan and Hammer, 2006). The nuclear genome contains the higher rate of polymorphisms. These include microsatellites that consist of tandemly repeated DNA sequences with a

* Corresponding author at: 4 Avenu Ibn Battouta, B.P 1014 RP, Rabat, Morocco. Tel.: +212 624689630; fax: +212 537774261.
E-mail address: kaoutar.bentayebi@gmail.com (K. Bentayebi).

http://dx.doi.org/10.1016/j.mgene.2014.04.011

variable number of repeats from one individual to another. Thousands of microsatellite polymorphisms have now been identified in human. Their mutation rate is much higher than that of single nucleotides, approaching 10^{-3} per generation (White et al., 2007; Zhang and Hewitt, 2003). Because of this high mutation rate, microsatellites have the potential to provide information about recent evolutionary events which made them the markers of choice in population genetics and forensic applications (El Amri et al., 2011, Chbel et al., 2003). By comparing the autosomal and X chromosome, it has been clear that the lower mutation rate, smaller population size and higher linkage disequilibrium make the X chromosome less informative than autosomes but record substantially older histories than the Y chromosome (Bentayebi et al., 2012a, 2012b). In the other hand, the mitochondrial genome as well as the Y chromosome offer a very different perspective on human evolution. The absence of recombination in these regions of the genome and their uniparental characteristics (maternal for the mtDNA and paternal for the Y-chromosomal DNA) allows researchers to infer past human behaviors and evolutionary events such as migrations, founder events, population bottlenecks or expansions, relative male and female contributions to an admixed population, marriage practices, and mode of transmission of languages (Underhill and Kivisild, 2007; Xue et al., 2008). Interestingly, a joint analysis has the potential of providing more robust information (Jorde et al., 1998), as these markers give an independent (for autosomal and X chromosome) and dependent (for mitochondrial DNA and Y chromosome) picture of sex-specific demography (Ségurel et al., 2008; Ouborg et al., 2008, White et al., 1998, Schaffner, 2004; Bentayebi et al., 2012a, 2012b). Mitochondrial DNA studies of Moroccan population, at times, provided interesting results that together with autosomal and other genetic markers will help to understand the genetic landscape of the Moroccan population. In molecular evolution, a haplogroup is a group of similar haplotypes that share a common ancestor having the same polymorphism in all haplotypes. Some haplogroups exhibit specific geographic homelands (Aboukhalid et al., 2013). Haplogroup U6 in the mtDNA phylogenetic tree descends from the haplogroup U, who lived around 55,000 years ago. Recent studies based on the distribution of mtDNA of haplogroup U6 raised two theories about the origins of modern human populations in North Africa. The first put forward that groups of the proto-U6 lineage spread from the Near East to North Africa around 40–45 ka (thousands of years ago) (Olivieri et al., 2006), followed by some degree of regional continuity, while the second proposes a westward human migration from the Near East, followed by further demographic expansion at 22 ka centered on the Maghreb and associated with a microlithic bladelet culture known as the Iberomaurusian (Maca-Meyer et al., 2003; Pereira et al., 2003). In the other hand, a recent leading evolutionary theory envisages that the first modern humans in Europe, called the Cro-Magnon (Iberomaurusian), arrived from North-west Africa and are believed to have completely replaced the previous inhabitants "the Neanderthals" (Caramelli et al., 2008). Present day genetic diversity of North African populations has been revised through a wide variety of uniparental and autosomal genetic markers.

Morocco is an appropriate region for population genetic studies and a good example for answering and completing the previous questions and theories. Located in northwest Africa with a total of 13 living languages listed by Ethnologue (Gordon, 2005), Morocco is important for studies concerning human migration, because it is bounded by the Mediterranean Sea to the North with just 14 km away from Spain across the Gibraltar strait and the Atlantic Ocean to the west, which is part of the traditionally favored model of the migratory route out of Africa for anatomically modern humans (Bilgili and Weyel, 2009). Berber-speaking populations, as representative of the autochthonous inhabitants of North Africa, inhabit a wide ranging area extended from the Saharan desert to the Atlas Mountains and nowadays combining six different countries from Egypt to Mauritania, speaking 26 sorts of Berber dialects coming all from a unique and standard Berber language (Gordon, 2005; Hayward, 2000; Louali and Philippson, 2003). In spite of their self-identification by their common language, Berbers have a complex history of invasions, conquests and migrations, especially the Arabic conquest in the seventh century AD. The Arab-Muslim conquerors adopted a language policy that enabled them to spread Arabic and Islamic cultural values (Brunschvig R, 1975). However, today in Morocco, beside Standard Arabic, Berber language remains one of the two national languages of Morocco (Gordon, 2005).

The considerable ethnic and cultural diversity within Morocco reflects differential historic population influences and make the study of existing genetic diversity of the kingdom an attractive effort. Morocco has the most complex linguistic situation compared to the three other North African countries with a remarkably unequaled repartition of population: 90% of residents settle in the north part of Morocco. Although around half of the total population speaks one of the different Berber dialects, it is quite difficult