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UNRAVELING GENETIC TRACES OF ANCIENT MIGRATORY MIDDLE EASTERN ROUTES: A SURVEY OF Y-CHROMOSOME VARIATION IN IRAN

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Iran is one of the main southwestern Asian countries and had a central role in human evolution. Its geographic location between the Caspian Sea in the north and the Persian Gulf in the south made it an important passageway for the early spread of modern humans from Africa to Asia. It was also one of the regions in which agriculture had origin about 10,000 years ago, home of the first urban civilizations, subject to the arrival of Indo-Iranians in the 2nd millennium and, in historical time, home of big empires and invaded by several populations such as Arabs, Mongols and Ottoman Turks. At present, the Iranian population is an interesting mix of more than 100 different ethnic groups speaking a variety of Indo-Iranian, Semitic and Turkic languages. Arabs, Armenians, Assyrians, Azeris, Baluchs, Bandaris, Gheshmi people, Gilaks, Kurds, Lurs, Mazandarani, Persians, Turkmens, Zoroastrians and a group of so called Afro-Iranians, who might be the result of the slave trade with Zanzibar, are the most represented ones.

Despite this scenario is of great interest to reconstruct traces of ancient migrations, only few studies (based on small sample sizes and a low resolution genotyping) have investigated the gene pool of modern Iranians.

To shed some light on the genetic structure of this Levantine population and on the ancient migrations that affected this area, 930 Iranian male DNAs belonging to 15 ethnic groups from 14 Iranian provinces were analysed for Y-chromosome variation.

Due to its uniparental transmission, absence of recombination and wide dataset availability, the Y-chromosome is (together with mtDNA) among the best genetic systems for detecting signs of ancient migrations and for evaluating socio-cultural behaviours.

All the 930 chromosomes belonged to 15 main haplogroups (B, C, D, E, G, H, I, J, L, N, O, P, Q, R and T) the most frequent of which are J (31%), R (29%), G (12%) and E (9%) with great differences in frequencies and sub-haplogroup distribution among provinces and ethnic groups. The comparison of the Iranian haplogroup frequencies with those of neighboring Asian, European and African populations allowed to identify some external contributions (for example: the sub-Sahara African Hg E-M2 in Southern Iran and the Central Asian Hgs H and Q in Eastern Iran) and to evaluate the extent of the *in situ* differentiation of the autochthonous haplogroup J.

Overall, the results of this study provide an accurate and reliable portrait of the Y-chromosomal variation in the Iranian region, useful for generating a more comprehensive history of the peoples of this area as well as for reconstructing ancient migration routes.