

## Analysis of 15 STRs in the Italian population of Alia

M. Pizzamiglio <sup>a,\*</sup>, C.M. Calò <sup>b</sup>, G. Vona <sup>b</sup>, A. Mameli <sup>a</sup>, L. Garofano <sup>a</sup>

<sup>a</sup>Raggruppamento Carabinieri Investigazioni Scientifiche, Reparto di Parma, Parma, Italy <sup>b</sup>Dipartimento di Biologia Sperimentale, Sezione Scienze Antropologiche, Università degli studi di Cagliari, Italy

A preliminary typing on the Italian population of Alia (Sicily) was carried out.

Situated at 800 m above sea level and about 80 km from Palermo, Alia today has a population of about 4000 inhabitants. In 1837, Alia was hit by an epidemic of cholera and the population was reduced dramatically. In 1995, an excavation brought to light the remains of about 300 individuals who had died of cholera. This event attracted the attention of anthropologists and geneticists to the Alia population.

Blood specimens were obtained from 50 healthy and unrelated individuals of both sexes, born and living in Alia as well as their parents and grandparents.

The analysed markers in the current study were: TH01, D2S11, D18S51, VWA, FIBRA, D8S1179, TPOX, CSF1PO, D16S539, D7S820, D13S317, D5S818, D3S1358, D19S433, and D2S1338. DNA has been extracted through the phenol–chloroform method and amplified by PCR. Separation and detection of the amplified STR fragment was carried out by use of 377 automated system (Applied Biosystem Division/Perkin Elmer).

All loci, except TH01, met Hardy-Weinberg expectations. The linkage disequilibrium test, applied to the loci which lie on the same chromosome (D2S1338 and TPOX, D5S818 and CSF1PO), did not show significant values.

Polymorphism information content (PIC) and power of discrimination (PD) results were generally high, underlining the usefulness of these markers both in the linkage and forensic analysis.

Obtained data were compared with ones of other Mediterranean populations obtained from the literature, so that it was possible to analyse the genetic structure of the Alia population in relation to the other comparison populations. Some genetic characteristics of the Alia population seem to be modelled by the effects of genetic drift and preserved by isolation, as demographic and historical events demonstrate.

<sup>\*</sup> Corresponding author.

The results stressed the importance of studying subpopulations, which proved to be useful in the study of microgeographic variation and in forensic analysis. Moreover, it will be interesting to compare data on the present population of Alia with the ones of subfossil population who died of cholera, which the University of Göettingen (Germany) is carrying out. This will clarify if this dramatic event changed the genetic structure of the population who survived to the cholera.