

## **ABSTRACT**

The population genetic study was carried out on 188 unrelated individuals from 5 populations of the Sahel. Relationships of nomadic Fulani to sedentary populations of different linguistic backgrounds and geographic origins were inferred from 16 polymorphic Alu insertions. Bayesian clustering approaches could be applied due to biallelic multilocus nature of the data. Fulani were shown to be divergent from neighbouring sedentary populations (Kassena and Mossi) and similar to Somali of East Africa. In context of already published genetic data, these results could be interpreted as Saharan origin of Fulani diaspora that was caused by Sahara drying out around 6 000 BP. After this initial migration of nomads to West Africa, a primarily female gene flow (integration of females) must have influenced the Fulani population. In contrast to Fulani, Songhai have shown a signal of recent admixture in concordance with historical and linguistic assumptions.

## **KEY WORDS**

Alu insertions, Fulani, population genetics, Sahel