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Genetic characterization of Algerian honey bees reveals a geographic pattern

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Background

The original geographical distribution of the honey bees *Apis mellifera* is Africa, Europe, and Western Asia, from where their export throughout the world was mediated by human beekeeping activities [1].

In recent years, many studies have been carried out in order to better understand *Apis mellifera* genetic diversity.

However, the genetic composition of some subspecies located in the African continent is still poorly described.

The Algerian honey bee populations are currently regarded as being members of two African honey bee subspecies: *Apis mellifera intermissa* and *Apis mellifera sahariensis*. Introduction of foreign queens and migratory beekeeping practices are factors that can affect the genetic diversity of Algerian honey bees [2].

Materials and methods

To analyze the genetic relationships with Algerian honey bee subspecies we used reference specimens from different parts of the world, representing *A. m. carnica*, *A. m. ligustica*, *A. m. mellifera*, *A. m. iberiensis* and *A. m. caucasica* for a total of 270 samples.

Concerning Algerian population, a total of 42 drones were sampled in 12 cities of Algeria and DNA was extracted from the thorax of adult bees or from pupae as described in Wragg et al. (2016) [3] and sequencing reads were mapped to the reference genome Amel_HAv3.1 [4]. In order to test whether genetic structure correlates to geography or not, we have first computed correlations between spatial coordinates (latitude and longitude) and the top genetic PCs (data not shown). Then, we have computed the correlation between the pairwise geographic distances between sampling locations (in km) and between genetic PCs 1 and 2. Significance of that correlation was then obtained through a Mantel test [5], achieved on all possible permutations (N = 713).

Results

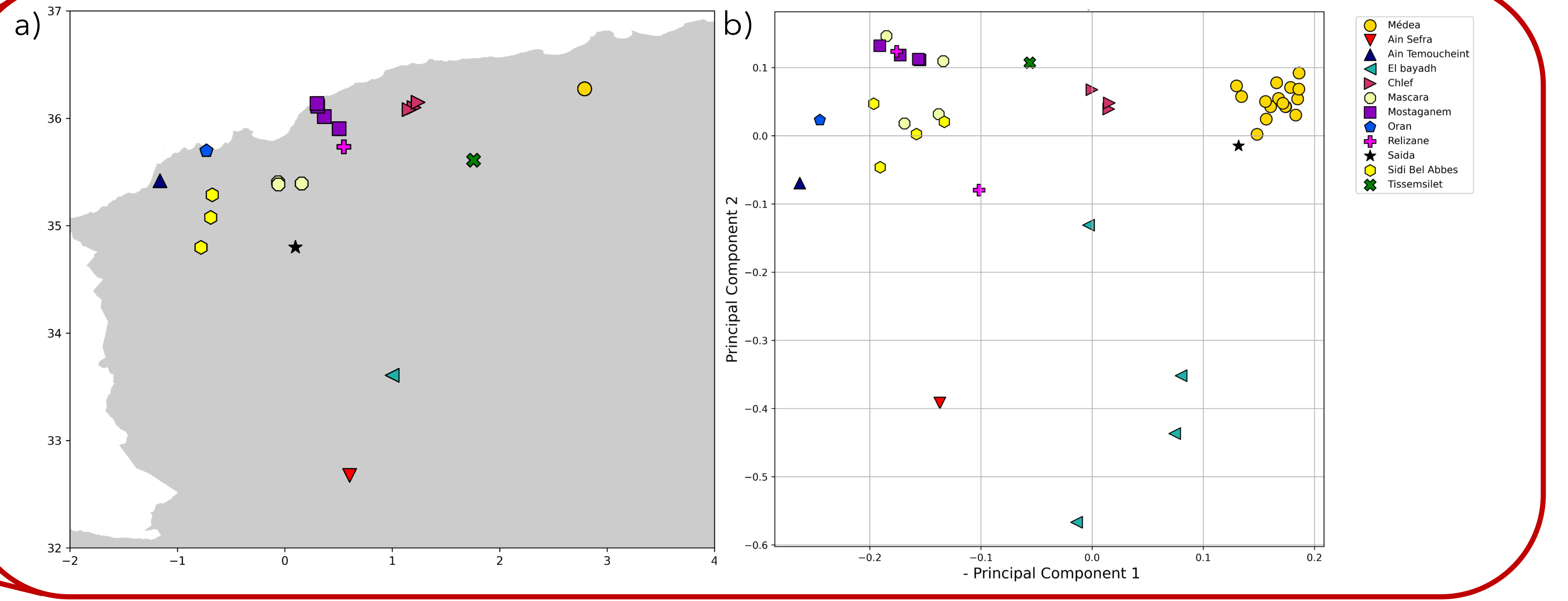
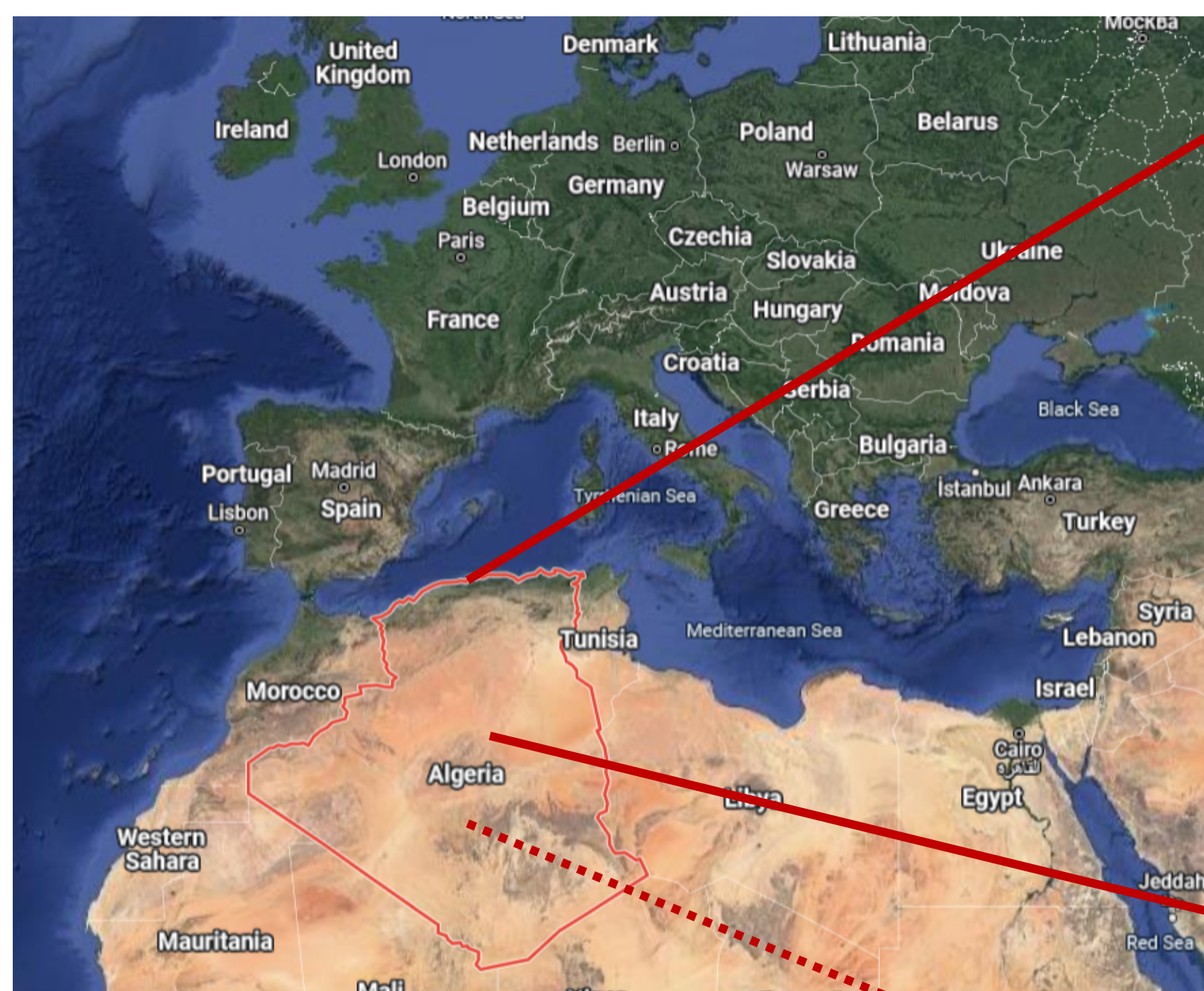


Figure 1: (a) Map showing the geographic origin of the considered Algerian samples. (b) Scatterplot of the Principal Component Analysis, considering the entire Algerian population

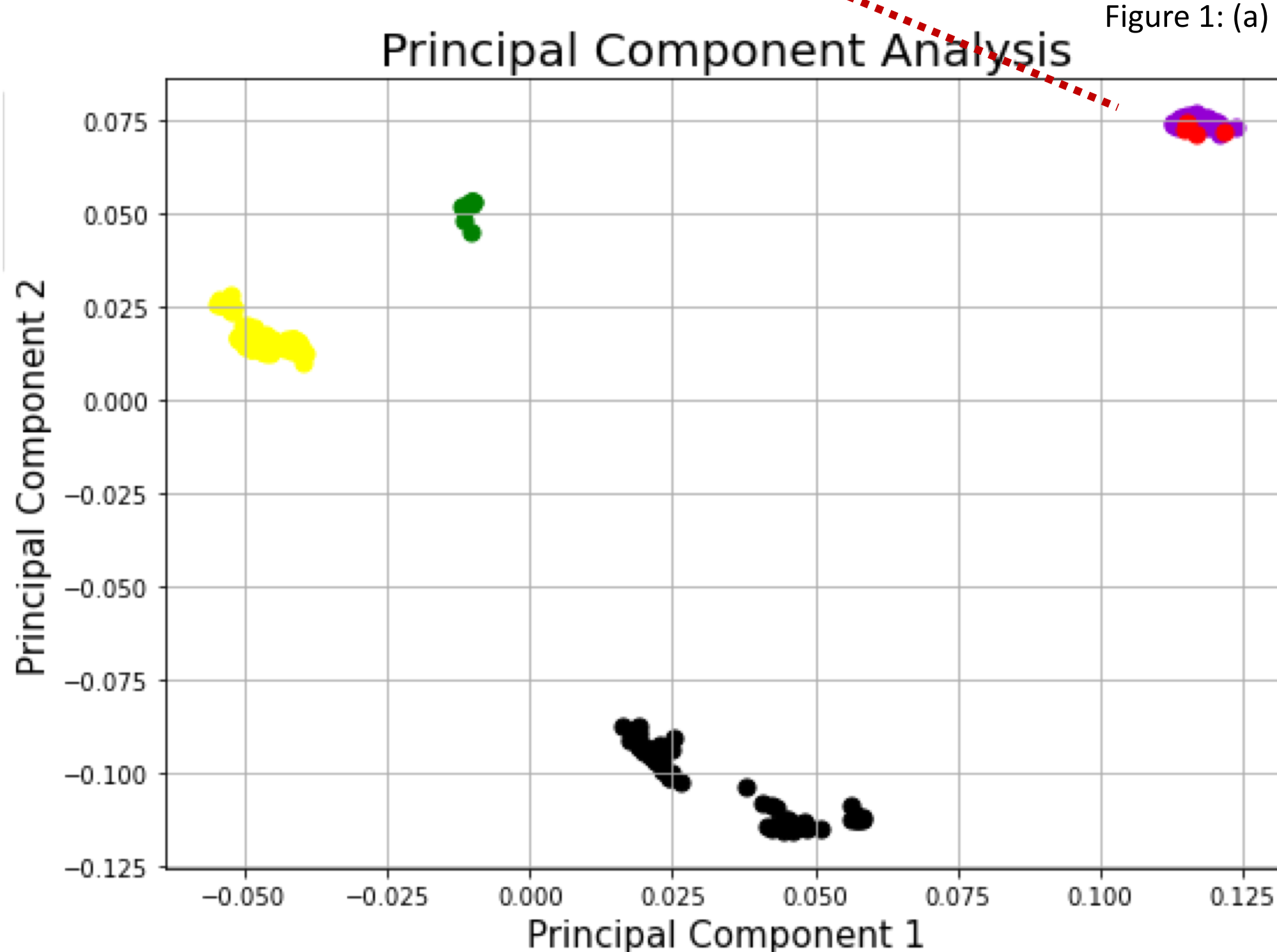


Figure 2: Figure 6: Scatterplot of the Principal Component Analysis showing clustering of the considered subspecies. Algerian subspecies, *A. m. intermissa* and *A. m. sahariensis*, respectively in purple and in red, showed a cluster separated from all the other subspecies.

Our results suggest the presence of a genetic pattern characterized by continuous east-to-west and north-south gradients.

The subspecies *A. m. intermissa* and *A. m. sahariensis* from Algeria showed unique characteristics and are genetically isolated than all other studied honey bee subspecies.

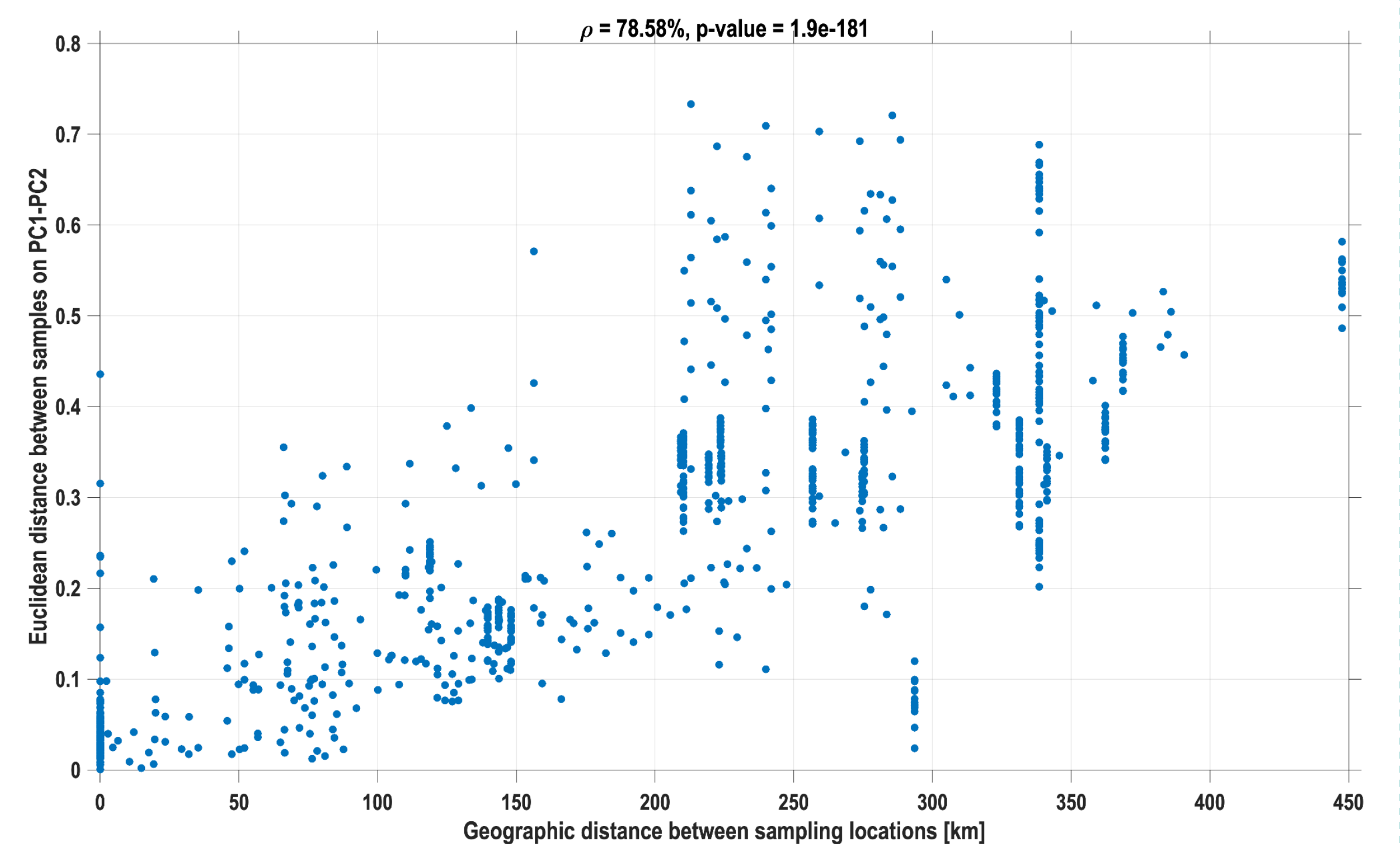


Figure 3: Mantel tests between the genetic distance and the geographical parameters.

Our genetic analysis demonstrates a clear clustering of Algeria samples, which are geographically isolated from the other subspecies in our dataset.

Within the Algerian population, the east-west gradient along the north coast and mountains demonstrates the persistence of a genetic structure within the *Apis mellifera intermissa* population, despite potentially high levels of gene flow that could happen following the exchange of queens for breeding purposes and transhumance. Honey bees samples collected in more southern parts of the country showed higher genetic divergence from the other and likely correspond to *Apis mellifera sahariensis* subspecies colonies. The outcomes of our study should be considered in local honey bee biodiversity improvement and conservation initiatives.

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2- Marghitas et al., 2008. Sci. Pap. Ani. Sci. Biotechnol., 41 (2008), pp. 309-315

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4- Wallberg et al. 2019. BMC Genomics, 20(1), 275.

5- Mantel N. Cancer Res. 1967;27:209-220.