



IUFRO Landscape Ecology Conference

**SUSTAINING
ECOSYSTEM SERVICES
IN FOREST LANDSCAPES**

concepts, research, and applications

23 - 30 August 2015 Tartu ESTONIA

PROGRAMME



MONDAY, 24 August

17:30 - 19:00 Poster Session

The campus of the Estonian University of Life Sciences

S PIROGOV HALL

A1

Ülle Napa, Naima Kabral, Kaie Kriiska, Ivika Ostonen, Jane Frey
Cd, Cu, Pb, and Zn concentrations and accumulation in soil organics and retention in fine roots of coniferous stands

A2

Edina Schimanski, Sandra Scheffer, Augusta Pelinski Hahier
The connection between rural and urban spaces: Changes in the landscape and the consequences of pesticides for people from community in Brazil

B1

Diana Laarmann, Henn Korjus, Teele Vaarend
Effects of restoration treatments of natural forest structures in Karula National Park, Estonia

B2

María Lencinas, Francisco Sola, Juan Cellini, Guillermo Martínez Pastur
Monitoring variable retention harvesting in southern Patagonia *Nothofagus* forests using ground beetles as potential indicators

B3

María Lencinas, Guillermo Martínez Pastur, Cristian Grismado
Spider assemblages in Tierra del Fuego landscape and their impact on variable retention harvested forests

B4

Emilia Cojoc, Carmen Postolache, Roxana Ion, Bogdan Olariu
Boundary connectivity effects on species biomass in grassland vegetation sustained by grazing

B5

Maria Alice Pinto, Julio Chávez-Galarza, Dora Henriques, José Rufino, João Azevedo
Spatial patterns of single nucleotide polymorphisms (SNPs) support a scenario of secondary contact in Iberian honey bees (*Apis mellifera iberiensis*)

B6

Kristi Nigul, Ahto Kangur, Henn Korjus, Andres Kiviste, Diana Laarmann, Allan Sims, Marek Metslaid
Assessment of tree diameter distributions for describing structural legacies in hemiboreal forest in Estonia

B7

Teele Paluots, Henn Korjus
Assessing conservation value of forest ecosystems in Lahemaa National Park, Estonia

B8

Līga Liepa, Inga Straupe
The persistence of edge effect on Fennoscandian deciduous swamp woods in Southern Latvia

B9

Pille Tomson, Robert G.H. Bunce, Kalev Sepp
The contribution of former slash and burn fields to forest biodiversity

B10

Dainis Jakovels, Janis Donis, Juris Taskovs, Jevgenijs Filipovs, Gatis Erins
Wooded dune habitat mapping and evaluation using airborne remote sensing data: Case Study of Lake Engure Nature park

B11

Antoine Brin, Anne Jacquin, François Calatayud, Michel Goulard, Laurent Larrieu, Claire Crassous, Marie-France Leccia, Daniel Demontoux, Sylvie Duthoit, Alexandre Ravelet, Lionel Valladares, Hervé Brustel, Marc Deconchat
Using connectivity analysis to optimize a network of set-aside forests in a managed landscape: A case study in a French mountain national park

C1

Pablo Cuenca, Cristian Echeverría, Rodrigo Arraigada, Anibal Pauchard, Mauricio Aguayo
Measuring the avoided deforestation of protected area in Tropical Andean Forest

C2

Andres Kiviste, Kobra Maleki
The effect of thinning on survival of silver birch trees in Estonia

C3

Sandra Metslaid, Henn Korjus, Andres Kiviste
Forest productivity and growth variation on degraded post-mining landscapes: Assessment based on long-term observations

C4

Sorina Mihaela Bogdan, Ileana Pătru-Stupariu, Liliana Zaharia, Andreea Andra-Topârceanu
Assessing ecosystem services across landscape scenarios: The sediment retention service in a mountain landscape in the Romanian Carpathians

C5

Ilze Jankovska, Guntis Brūmelis, Edgars Baranovs, Pēteris Cepurnieks
Edge effect and trampling in urban forest fragments - impact on the understory vegetation



Transfer buses depart from the campus parking lot to city centre at 19:20.

Spatial patterns of single nucleotide polymorphisms (SNPs) support a scenario of secondary contact in Iberian honey bees (*Apis mellifera iberiensis*)

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Introduction

- Dissecting diversity patterns of organisms endemic to Iberia has been truly challenging for a variety of plant and animal taxa, and the Iberian honey bee (*A. m. iberiensis*) is no exception.
- Here we used a genome-wide data set of 309 neutrally-tested SNPs, scattered across the 16 honey bee chromosomes, which were genotyped in 711 honey bee individuals. These SNPs were analyzed along with an intergenic locus of the mtDNA. The two markers revealed the existence of a strong and concordant structure supporting a process of secondary contact.

Sampling

- A total of 711 individuals (each representing a single colony) was collected across 3 North-South transects in Iberia (Fig. 1).



Fig. 1 – Map of the Iberian Peninsula showing the centroids of the sampling sites at each transect (AT, Atlantic; CT, central; MT, Mediterranean), sample size per site (n), site codes (CT1 to MT6). Sampling drones from hives.



Genotyping

- A panel of 383 SNPs was genotyped for the 711 individuals using the GoldenGate Assay and the Genome Studio software of Illumina. Of the 383 SNPs, 309 were selectively neutral (Chávez-Galarza et al. 2013).



- The tRNA^{leu-cox2} mtDNA intergenic region was sequenced in both directions and the sequences were aligned using MEGA 5.06.

Analysis

- Mitotypes were assigned to the western European (M) or African (A) lineage.
- Relationships among the mtDNA sequences were inferred using the median-joining network algorithm (Bandelt et al. 1999) in NETWORK 4.6.1.1.
- Populational structure was inferred from 309 neutrally-tested SNPs using STRUCTURE 3.4.
- Spatial structure was inferred from the 309 SNPs using the model-free multivariate spatial principal component analysis (sPCA) in ADEGENET.

Results

Median-joining network

- A median-joining network of the tRNA^{leu-cox2} mtDNA region reveals the presence of 2 highly divergent (A and M) lineages in Iberia. The 2 lineages show a highly structured geographical pattern. Mitotypes of M ancestry were predominant in the northeastern half of Iberia whereas mitotypes of A ancestry were virtually fixed in the southwestern half (Fig. 2).

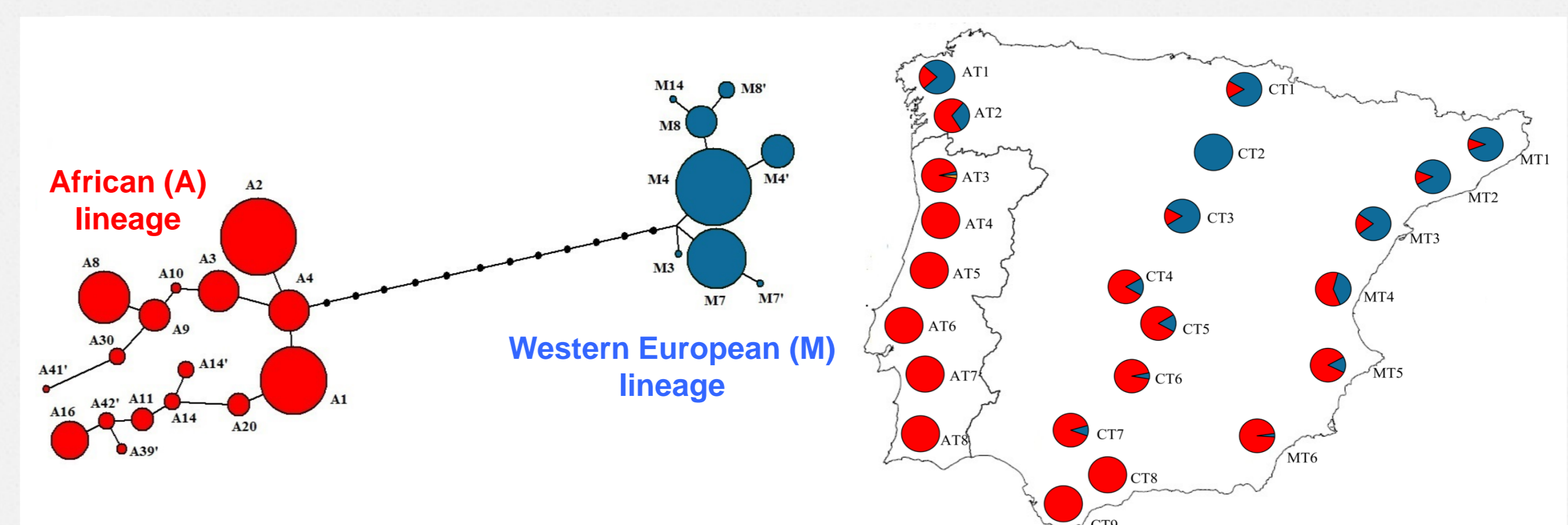


Fig. 2 - Median-joining network of the tRNA^{leu-cox2} mtDNA region. The African (A) and western European (M) mitotypes form two divergent lineages. The sizes of the circles are proportional to the mitotype frequencies. The pie charts displayed in the Iberian map show the frequencies of the A and M mitotypes at each sampling site.

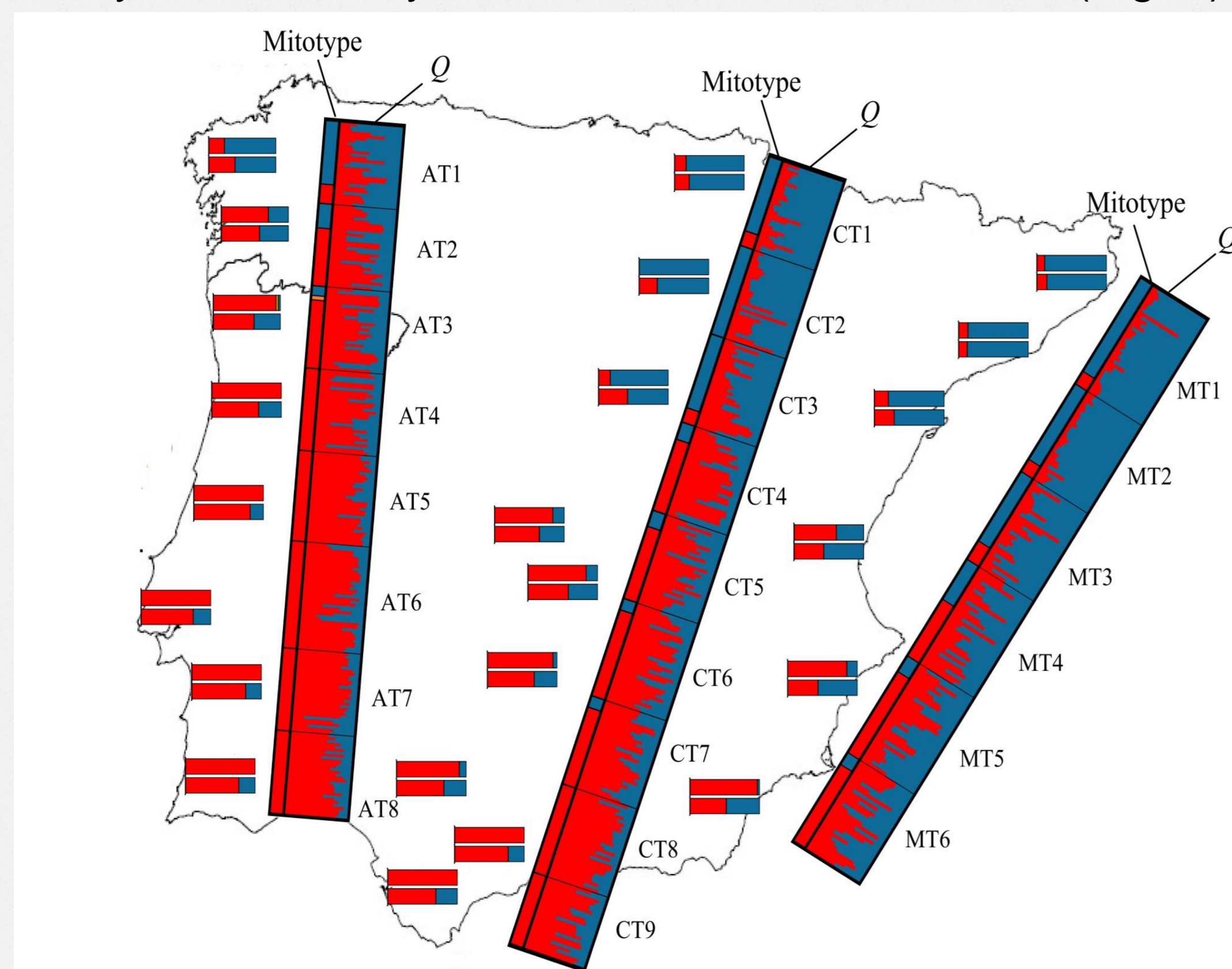


Fig. 3 - Maternal pattern and estimated structure inferred from the 309 SNPs with STRUCTURE (K=2). Vertical plots display the mitotype (A in red; M in blue) and the membership proportions (Q) for each of the 711 individuals. Horizontal bar plots show mitotype frequencies (top) and the mean Q in blue and red clusters (bottom) at each sampling site.

Populational structure analysis

- Membership proportions (Q) inferred by STRUCTURE from the 309 SNPs were contrasted with mtDNA data, at both sampling site and individual levels (Fig. 3). At the sampling site level, the partitioning of neutral SNP variation into 2 clusters corresponded remarkably to M and A mtDNA lineages ($r = 0.81$, P -value < 0.0000). At the individual level, the correlations were weaker ($r = 0.60$), yet significant (P -value < 0.0000), suggesting differential gene flow among genomic compartments.

Spatial PCA

- The interpolation of the first global score, which was associated with a strong autocorrelation (Moran's $I = 0.639$), detected 2 clusters forming a cline (Fig. 4a).
- The second global score (Moran's $I = 0.560$) clearly differentiated the 4 northernmost sampling sites of the Atlantic transect and the southern half of central and Mediterranean transects (Fig. 4b).
- The third global score (Moran's $I = 0.443$) further partitioned the Atlantic populations into 2 groups (north and south) and the southern half of central transect (Fig. 4c).
- The northern half of the central transect was differentiated by the fourth global score producing a Moran's $I = 0.392$ (Fig. 4d).
- While the global test corroborated the presence of global spatial structure (max(t) = 0.0017; P -value = 0.0001), there was also structure at the local level (max(t) = 0.0019; P -value = 0.0001). The first local score (Moran's $I = -0.075$) highlighted the differences among individuals of northern Atlantic and central transects (Fig. 4e) while the second local score (Moran's $I = -0.071$) differentiated the individuals from sampling sites in the middle part of the central transect (Fig. 4f).

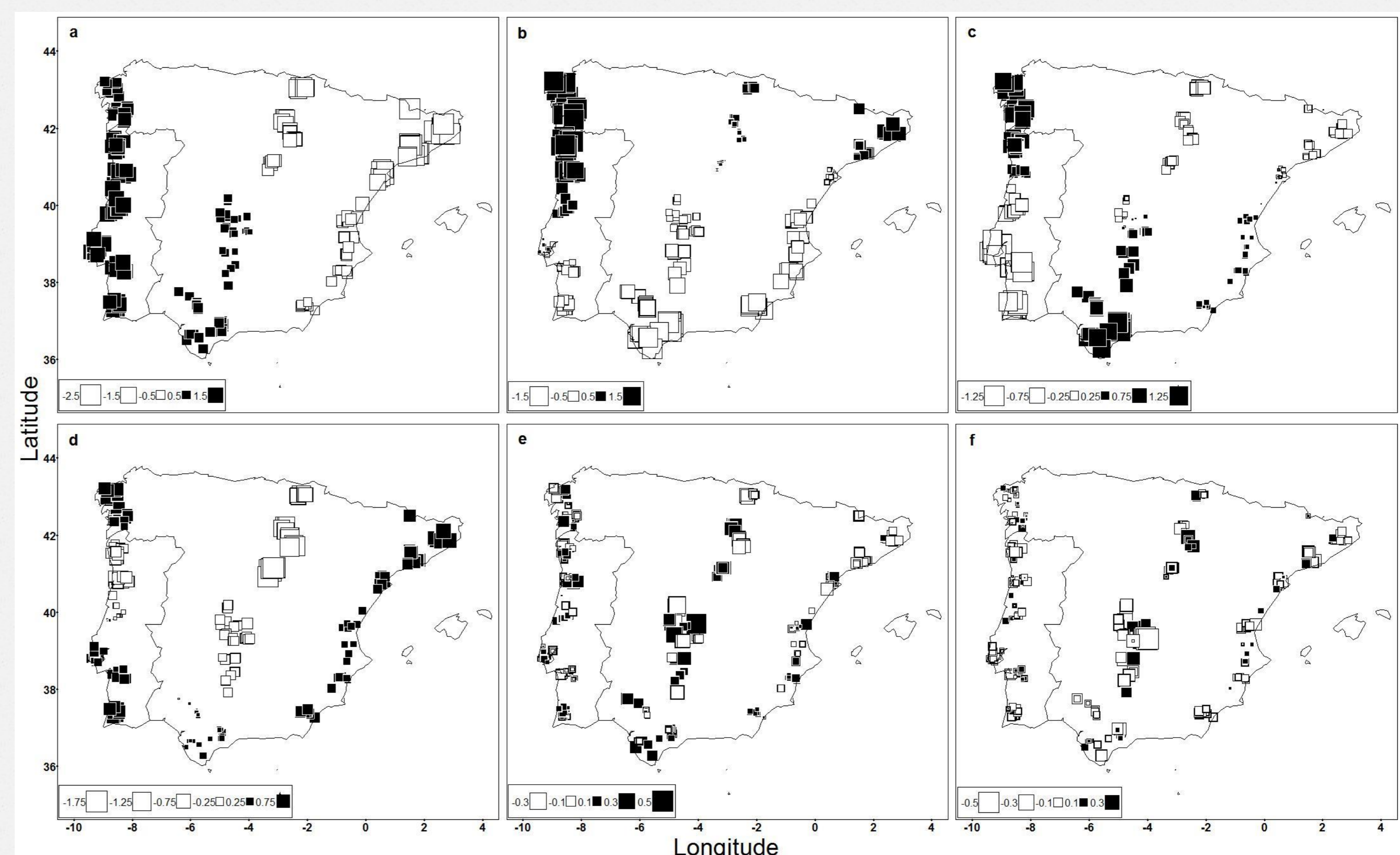


Fig. 4 - Analysis of global and local structures sPCA using 309 neutral SNPs. Each square represents the score of an individual, which is positioned by its spatial coordinates. (a-d) The first four global scores of sPCA. (e-f) The first two local scores of sPCA.