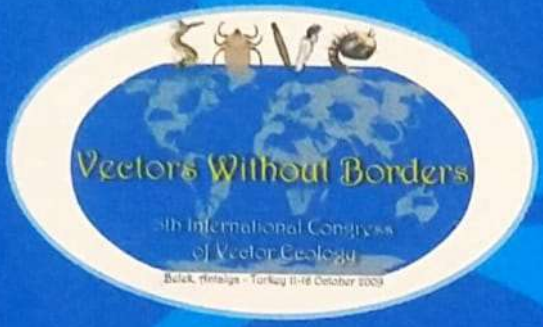


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SP-17

Effects of environmental changes on the genetic diversity and distribution of *Phlebotomus ariasi*, a vector of visceral leishmaniasis in southwest Europe

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Abstract

Leishmania infantum is the causative agent of zoonotic visceral and cutaneous leishmaniasis in the Mediterranean region and western Asia, with the domestic dog as the main reservoir host. Most of the phlebotomine sandfly vectors are classified in the subgenus *Phlebotomus* (*Larroussius*), of which six species have been incriminated as vectors in southern Europe. One of these, *Phlebotomus* (*Larroussius*) *ariasi*, is the principal vector in cooler, forested ecotopes in southwest Europe, where it is subject to environmental and geographical isolation. Fragments of one mitochondrial gene (cytochrome b) and four nuclear genes (elongation factor-1 alpha, apyrase and two microsatellite loci) were isolated by (allele-specific) PCR from 793 individuals of *P. ariasi* sampled from 32 geographical populations, and the sequences were used to investigate: the post-glacial spread of this sandfly in France and northern Spain, when compared with populations from Portugal and Morocco: the effects of habitat fragmentation on this spread and the species' current distribution; and, the selection pressures on apyrase, a salivary peptide that has been implicated in modulating parasite transmission. The presentation will review the main findings, based on results obtained by using a range of tests: to distinguish positive / balancing selection from neutral evolution; and, based on neutral variation, to estimate the dates of divergence of different lineages now showing both discontinuous and continuous genetic differentiation by geographical distance. These findings will help to inform predictions of the risk of spread of visceral leishmaniasis in response to climate change, and this will be discussed briefly.

SP-18

Sand flies from Middle East to Europe: Do borders limit their distribution?

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Abstract

Sand fly vectors are the widely studied flies, because of their medical and veterinary importance in the world. In parallel with the epidemiological research on leishmaniasis, the distribution of the Phlebotomine sand flies is better understood in Turkey. Most recent data showed that there are 21 *Phlebotomus* species belonging to

the 4 subgenera (*Phlebotomus*, *Paraphlebotomus*, *Larroussius*, *Adlerius*) in Turkey and 13 of them can transmit several *Leishmania* species to humans as well as to canine reservoirs.

Turkey is considered to be one of the geographical bridges for the dissemination of the sand flies to Europe from East/Middle East, where their ancestors were believed to be originated. In this presentation, the role of Anatolia as a geographical and biological bridge for the distribution of sand fly species will be discussed. The data gathered from the studies related to clinical types of leishmaniasis and its relationship with the Phlebotomine fauna of Turkey and the neighboring countries will be comparatively analyzed and discussed to justify possible new hypotheses.

SP-19

The bionomic and genetics of the human malaria vector *Anopheles nili sl* in Africa

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Abstract

Mosquitoes from the Anopheles nili group are spread across most of forest and humid savannah areas in tropical Africa, were they are involved in malaria transmission together with *An. gambiae*, *An. funestus* and *An. moucheti*. While *An. gambiae*, *An. funestus* and *An. moucheti* has been studied extensively, basic data on the bionomics and genetics of *An. nili* sl are currently lacking, although such data are a requisite to properly devise and implement efficient and sustainable vector control strategies on the field. Here, we present original data that contribute to fill this gap in our knowledge. *An. nili* sl specimens were collected at larval (dipping) or adult (human landing catches and pyrethrum spray collections) stages in Senegal, Burkina Faso, Ivory Coast, Nigeria, Cameroon and the Democratic Republic of Congo. Field-collected *An. nili* sl specimens were sorted from the other Anophelines based on morphological criteria. A specific PCR diagnostic was then performed for accurate identification of species within the group. The feeding preferences and infectious status of adult mosquitoes were determined by ELISA. Eleven recently developed microsatellite loci were used to compare the level of genetic diversity and differentiation between 17 populations. *An. nili* s.s. was highly anthropophilic and partially endophagic and was the only member of the group collected out of Cameroon. Specimens of *An. ovengensis* and *An. carnevalei* collected in South Cameroon were highly exophagic and exophilic. All three species were found infected by *P. falciparum* with mean infection rates ranging 4.3-13.6% in (N=3646), 0.9% in *An. carnevalei* (N=516) and 1.0% in *An. ovengensis* (N=978). *An. somalicus* was collected only at larval stage and was suspected to be zoophilic. Genetic diversity indices were high in *An. nili* s.s. and lower in *An. carnevalei*, *An. ovengensis* and *An. somalicus*. High and significant levels of genetic differentiation were estimated across species (Fst>0.19, P<0.0001). Within *An. nili* s.s. the population structure is consistent with isolation by distance, although demographic and/or selective events probably resulted in a higher level of genetic isolation in marginal populations. This study confirmed that *An. nili* s.s. is the major malaria