

## Results

1. We demonstrated that crossing is possible between *P. sergenti* laboratory-reared specimens from colonies originating from Turkey and Israel. Successful mating and insemination was observed and viable hybrid F1 and F2 offsprings were obtained from both parental combinations. No statistically significant difference was found in the egg production of the hybrids when compared to the parents.

2. RAPD analysis was able to distinguish clearly between members of Turkish and Israeli colony. When F1 progeny obtained from the cross-mating study were included in the RAPD analysis, these samples formed a distinct group with position intermediate between Turkish and Israeli subgroup, not only sharing a portion of bands with each of the parental colonies but also exhibiting several unique loci. The results of RAPD analysis were in accord with geometric morphometric analysis of wing shape of *P. sergenti* from Turkey and Israel, demonstrating that both molecular biology and morphological approaches are complementary.

3. RAPD proved to be a useful method for identification and comparison of *P. sergenti* specimens from two foci of cutaneous leishmaniasis in northern Israel which differ in the vector.

4. No microsatellite markers previously isolated for other phlebotomine species were found applicable on *P. sergenti*. A development of species-specific microsatellite markers panel was started and two suitable markers were identified so far. More markers are still under development.

5. Wild populations of *P. sergenti* from Turkey, Israel, Syria, and Uzbekistan were analysed by three different molecular methods: RAPD, sequencing of ITS2 (nuclear marker), sequencing of cytochrome b (mitochondrial marker).

RAPD analysis of samples from several localities in Turkey and Israel revealed a same grouping pattern; sand flies from each country formed their own clade, one containing all field samples originating from Turkey as well as a specimen colony of Turkish origin, second containing all field samples from Israel plus the Israeli colony specimen. Similar pattern of clades was also obtained with samples from Syria and Uzbekistan; specimens from each country formed a unique clade. There was no distinct grouping within the Turkish clade,

although the localities are separated by geographical distance and also by Amanos mountain range of a considerable height. Obtained results suggest that these mountains do not represent a sufficient barrier for sand fly dispersion and the mountain passes play a role of transitional gaps which allow a gene flow between the populations.

Results of ITS2 rDNA sequencing corroborated the previously published intraspecific division of *P. sergenti* into two branches, north-eastern and south-western. The specimens from Uzbekistan fall within the north-eastern clade, close to the samples from Pakistan, Cyprus and Lebanon. Syrian samples and Turkish samples also cluster in this clade, while Israeli samples fall within the second, south-western clade.

Sequencing analysis of cyt b mtDNA revealed that haplotypes from Turkey, Israel, Syria, and Uzbekistan formed three lineages, one containing specimens from Turkey and Israel together. This finding questions the idea of *P. sergenti* species complex.