ABSTRACT

The olive fruit fly is the major pest of the olive trees. If untreated, more than 30% of the annual oil production is lost due to the parasitism of the olive fruits. The insect is found mainly in the Mediterranean basin where 98% of the olive trees are grown. In 1998 the first detection of the insect took place in Los Angeles of California and within the next five years the fly spread in all olive-growing areas of the State.

In the present study, a few key issues of the fly's invasion in California were addressed: a) the analysis of the genetic structure of the olive fruit fly population, b) the determination of the origin of the biological invasion and c) the possibility of multiple invasion events in the area. These issues were addressed through the genetic comparison of California olive fruit fly diachronic collections (from 1999 to 2009) with Mediterranean populations of a previous analysis, based on the use of ten microsatellite markers. That analysis (Augustinos et al., 2005) on one hand had revealed the existence of three distinct Mediterranean subpopulations - that of eastern, central and western populations - and on the other hand had indicated a westward expansion of the insect on the European side of the Mediterranean basin. The present analysis showed that the Californian olive fruit fly population is fairly homogeneous and distinct from the rest of the Mediterranean subpopulations. However, the data also revealed a genetic relatedness between the Californian population and the subpopulation from the eastern Mediterranean basin, which consequently identifies as the most likely geographic area of the origin of the biological invasion. Additionally, the analysis indicates the possibility of a second incident of biological invasion, located geographically in the area of San Luis Obispo and temporally in 2004 to 2006. Furthermore, a population analysis based on three mitochondrial molecular markers (cytochrome oxidase I, cytochrome oxidase II and 12S ribosomal RNA) was also performed. In this analysis, three additional samples were incorporated, one from southern and two from northwestern Africa, which broadened the geographic base of the analysis. Results were in agreement with the findings of the microsatellite analysis. Moreover, the data showed an evolutionary relationship between olive fly populations of South Africa and the eastern Mediterranean and, in addition, that the westward expansion of the insect in the European side of the basin (previously reported by Augustinos) continued towards the north-west Africa since the Strait of Gibraltar does not seem to be an insurmountable geographic barrier.

In parallel, there was an attempt to understand the extent of genetic adaptation to artificial mass rearing conditions. Beyond the theoretical importance of such an analysis, there is also a practical interest of creating mass reared robust laboratory strains for field releases, in the context of control efforts through the application of the **S**terile **I**nsect **T**echnique (SIT). In this part of the present thesis, genetic changes that occurred in the course of 22 generations during a colonization process of an israeli population were analysed. The monitoring of fluctuating genotypic frequencies of ten microsatellite loci showed the halving of the average values of the actual and effective number of alleles and heterozygosity in 11 laboratory generations. Very little genetic change was detected in the first two laboratory generations, while substantial genetic changes occurred between generations F_2 and F_5. After generation F_8 a period of an intensive adaptive process followed, which peaked in the F_{11} generation and maintained almost constant until the F_{22} generation. To the extent that robustness of a laboratory strain is closely related to the level of polymorphism, an enrichment program of the colonized strain with wild biological material, approximately every 8 generations, would be sufficient to retain the wild character of the strain in case of re-introduction into natural ecosystems. Additionally, two different approaches based on different simulation models indicated that most of the observed adaptive evolutionary changes were due to random genetic drift, since evidence for the presence of selective forces was identified in only one microsatellite locus.