

Scientific report of the COST Short Term Scientific Mission

A. Technical data

- 1. Title of the STSM grant:** Study of the genetic variability of Mediterranean populations of *Pistacia lentiscus* L.
- 2. Dates of the visit:** 07-21 Octobre 2013
- 3. Granted person's name:** Faten Mezni / **Title:** Phd student / **Affiliation:** INRGREF / **Contact information:** faten-mez@hotmail.com
- 4. Host institution:** INRA Avignon
- 5. Responsible of the STSM:** Dr. Bruno FADY

B. Description of the work carried out during the COST grant

Introduction:

Pistacia lentiscus is a Mediterranean dioeciously evergreen shrub. The female flowers are wind pollinated, and the one-seeded drupes are actively dispersed by birds. This species have an important economic role, especially in Tunisian forest areas.

In order to understand the variability of *P. lentiscus* among Tunisian and Mediterranean regions, we planed to study this aspect by molecular markers. A STMS was proposed and accepted to implement this job in INRA Avignon under the scientific responsibility of Dr. Bruno FADY.

During this training, the genetic diversity of different Tunisian and Mediterranean populations of *Pistacia lentiscus* was studied using the microsatellite markers.

Objectives:

- Scientific capacity building
- Familiarization with statistical analysis software: GenAlex, Structure, Populaion, Microchecker, Genepop and Treeview.
- Exploitation of the obtained results by writing paper.

Methodology:

Statistical analysis software

- **GenePop / MICRO-CHECKER**

The program allows the identification of various genotyping errors, and can also detect typographic errors. It estimates the frequency of null alleles at a locus using a series of algorithms. Importantly, can also adjust allele and genotype frequencies of the amplified alleles, which allows the data to be used in further population genetic analysis, for instance with Arlequin or Fstat.

- **GenAlEx-Genetic Analysis in Excel**

This software offers analysis of codominant, haploid and binary genetic loci and DNA sequences. Both frequency-based (F-statistics, heterozygosity, HWE, population assignment, relatedness) and distance-based (AMOVA, PCoA, Mantel tests, multivariate spatial autocorrelation) analyses are provided. It also aims at providing a flexible mechanism to determine Allelic frequency, allelic richness, population structure estimates (Fis, Gst, Dst, pairwise differentiation tests) and other genetic parameters.

- **Structure**

Genetic analysis software that detects the underlying genetic population among a set of individuals genotyped at multiple markers. It computes the proportion of the genome of an individual originating from each inferred population (quantitative clustering method).

- **Population**

This genetic software allows the determination of distances between individuals and between populations. The phylogenetic trees (individuals or populations) are built using Neighbor Joining or UPGMA (PHYLIP tree format).

- **Treeview**

It is used to convert the phylip format into postscript, adobe illustrator, gif...with colors for each population.

Summary of activities and achievements

The training period was designed for the processing of genetic data on Tunisian and Mediterranean populations of *Pistacia lentiscus*. The data have already been collected before this STSM.

- The first step was the check of the presence of null alleles resulting from mutations and which induce the increase of homozygote frequency. This step was conducted using GenePop or MICRO-CHECKER software. All data containing null allele were removed to enable a better analysis.
- Data were then treated by GenAlEx software to calculate some genetic parameters such as F-statistics (Fst), heterozygosity (H)..... This software enables the determination of the relationship between genetic and geographic distances.
- Structure software was used to clarify the distribution of individuals between the studied populations and to indicate the grouping of population with reference to the genetic distance between it.
- The last step was the establishment of the phylogenetic tree that connects population with each other and still based on the genetic distance between it. Two softwares were used in this case; Population and Treeview.

All these analysis allowed the determination of the relationship between the populations of *Pistacia lentiscus*. A phylogenetic tree was established and a significant correlation between the genetic and geographic distances was determined.

This training allowed me to work in a different team and share knowledge with them. It also gave me the opportunity to realize an important part of my thesis and make progress to my studies.

Exploitation of the obtained results

In order to valorize the obtained results about the genetic variability of the Tunisian *Pistacia lentiscus*, the writing of an original scientific paper is begun. A paper will be submitted to be published.