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P3.26 - Study of genetic variation in yarrow accessions from Iran

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To study the genetic diversity of 37 *Achillea millefolium* accessions we used RAPD and ISSR markers. Nine RAPD primers and seven ISSR primers have shown good polymorphic. The Jaccard's similarity indices (J), based on RAPD and ISSR profiles, were subjected to complete linkage analysis. The dendrogram generated revealed six groups. The principle coordinate analysis (PCoA) data confirmed the results of the clustering. Application of Mantel's test for cophenetic correlation to the cluster analysis indicated the low fitness of the accessions to a group ($r = 0.6$). The results of the clustering showed that *A. millefolium* subsp. *elbursensis* is separated from other genotypes in the dendrogram, this subsp. is endemic of north of Iran. Essential oil obtained from dried plants of this subsp. was more than (0.31%) other genotypes. The results of the clustering analysis, based on RAPD and ISSR markers, corresponded closely with the geographical origins of the genotypes. The results of the present study will provide the basic information for effective conservation of these genotypes for selection and breeding programs.

P3.27 - Discrimination of Portuguese and Spanish olive cultivars using microsatellite markers

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Olive cultivation is one of the oldest agricultural activities in the Iberian Peninsula. Nowadays, Spain and Portugal contain a high diversified genetic patrimony within this species. The correct identification of the olive cultivars is very important for the conservation of genetic resources, and for the development of a competitive and sustainable olive production system. In addition it also serves research and scientific purposes.

In this work, four microsatellite markers previously described as highly recommended for olive cultivar identification, have been selected to carry out SSR screening on 22 olive accessions. Among the above mentioned accessions, 11 are originals from Spain, and 11 are originals from Portugal. A CTAB-based protocol has been employed for DNA extraction from young leaves. For the detection of alleles, microsatellites were amplified by PCR and analyzed on a capillary automatic sequencer. Genetic relationships were studied by observing the UPGMA tree obtained after calculating Dice genetic distances. Results showed that the selected microsatellites markers were able to discriminate among the studied accessions. Cultivars were separated through four important clusters while 'Arbequina' cultivar was completely separated from the remaining accessions showing a very low similarity coefficient. Furthermore, three accessions have presented an identical allelic profile and were considered as the same cultivar. The factorial analysis of correspondence has demonstrated that there is no separation between Portuguese and Spanish cultivars according to its origin, and this is probably due to the geographical continuity of the Iberian Peninsula.

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P3.28 - Study of symptoms and gene expression in four *Pinus* species after pine wood nematode infection

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Pine wilt disease, caused by the pine wood nematode (PWN) *Bursaphelenchus xylophilus* (Steiner and Buhrer) Nickle, is originating severe infections in pine trees. The disease is detected when external symptoms appear (e.g. needles chlorosis), but trees could remain asymptomatic for long periods and serve as a long-term hosts.

The primary goal of this work was to assess the effect of the inoculation with an avirulent isolate of *B. xylophilus* (C14-5) on different *Pinus* spp. seedlings (*P. sylvestris*, *P. nigra*, *P. pinea* and *P. pinaster*). At the same time, seedlings were also inoculated with a virulent strain, HF, in order to compare the phenotypic and genomic results of the two types of inoculations. The effect of inoculation was determined in terms of expression of various *Pinus* genes potentially involved in the response to the disease.

The results suggest that *P. pinea* and *P. nigra* are more resistant to infection by the nematode than *P. sylvestris* and *P. pinaster*. The phenotypic and genetic differences were more marked among *P. pinea* and *P. pinaster*.

P3.29 - Identification, characterization and utilization of unigene derived microsatellite markers from *Medicago truncatula*

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This study was conducted to identify microsatellite or simple sequence repeats (SSR) markers linked to biotic and abiotic stress genes in different plant species (Cereals and *Medicago*) and examine their cross-applicability in different genetic backgrounds and also to assess the genetic variability. In recent years, expressed sequence tag (EST) projects have generated a vast amount of publicly available sequence data from plant species and these data can be mined for microsatellites. These sequences are among the best marker technologies applied in plant genetics and breeding. These markers are valuable because of their higher level of transferability to related species, and they can often be used as anchor markers for comparative mapping and evolutionary studies. Unigene derived microsatellite markers identified from publicly available sequence database have the advantage of assaying variation in the expressed component of the genome with unique identity and position. In this direction, a total of 18,098 *Medicago truncatula* unigene sequences were selected from databases, and SSR were fished out. A total of 7,607 SSR were recovered and these SSRs will be further used for designing primers for their application in plant genetics.

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