

ASSESSMENT OF LOCAL BIODIVERSITY IN THE MIGLIARINO - SAN ROSSORE – MASSACIUCCOLI REGIONAL PARK (NORTH TUSCANY, ITALY)

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In relation to the LIFE08 NAT/IT/342 DEMETRA project, 3 test areas were defined to evaluate plant (weeds and trees), animal, and soil microorganism biodiversity. As the final aim of the DEMETRA project is to develop a quick monitoring index (QMI) to rapidly assess the potential risk generated by a selected range of transgenic crops in well determined ecosystems or biotopes, test areas were chosen also taking into account their proximity to cropped surfaces in which Genetically Modified Plants (GMPs) could be used in the near future. In particular, direct or indirect target species of the GMPs will be considered, and trophic links analysed. Monitoring of the plant biodiversity (especially herbaceous plants and weeds) in the three sites will be investigated starting from the census of the flora and proceeding to the landscape analysis. Plants with pollinators present on the cropped areas or possibly breeding with local crops will be the object of a detailed investigation. Concerning tree biodiversity, the major effect of GMPs on local tree populations can be direct as in the case of poplar or indirect in the case some pollinator target species which become reduced in numbers and abundance. A drastic reduction of insect pollinators of some trees species could cause a drastic reduction in their seeds production and therefore on future natural regeneration of the species determining a decrease of biodiversity or species loss. Therefore, some tree species with entomophily pollination will be studied. These investigations assess the outcrossing and inbreeding level of the population, and predict if the reduction of outcrossing in consequence of a decrease of pollinator species can strongly reduce tree regeneration ability. The most important species will be chosen strictly in relation with the possible pollinators present at the study site and in accordance with the plant biodiversity task. Target species, will be identified through information on their abundance and functional role in the trophic chain. Furthermore, trophic levels of the most abundant species will be identified at each site. Species with

different functional roles such as scavengers (Isopoda, Coleoptera), detritivores (Isopoda, Coleoptera), granivores (Coleoptera), herbivores (Mollusca, Hemiptera, Lepidoptera), pollinators (Hymenoptera, Lepidoptera) and predators (Chilopoda, Arachnida, Coleoptera) will be analysed. In addition, plants are known to have an effect on the abundance, diversity and activity of soil microorganisms living in close proximity with their roots (rhizosphere), resulting in a distinct microbial population that is larger and more active than that found in the surrounding zones. The rhizobacteria/michorriza biodiversity of the tree and weeds species identified as possible target for breeding or correlated to pollinator target species will be studied. The data will individuate sensitive or relevant species providing the necessary information to define a QMI in order to assess the potential risk generated by the use of GMPs in the ecosystem.