Form (ENG):	**AGR/07 − Agriculture Genetics**		**Year: 2016**
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N. Research: main topics and strategic initiatives   Notes

01 Genomic and trascriptomic approaches for the analysis of grapevine phenotypic plasticity in relation to berry quality and the study of genetic and molecular mechanisms controlling tolerance to biotic and abiotic stresses aimed at the identification of candidate genes for grapevine breeding.

02 Functional genomics of plant reproductive systems, with particular reference to the study of the genetic-molecular factors controlling apomixis in model species and the cloning and mapping of the genes responsible for reproductive barriers like male-sterility and self-incompatibility in crop and fruit species (e.g. chicory and olive).

03 Use of molecular markers for the genetic characterization of biodiversity and for the genetic selection of varieties (MAB, marker-assisted breeding) along with the development of diagnostic assays for the genetic traceability of agri-food products of plant origin by means of SSR genotyping, AFLP fingerprinting, SNP haplotyping and DNA barcoding.

04 Characterization of genetic (genomic and transcriptomic) and epigenetic (DNA methylation, histone variants and modifications, ncRNAs and sRNAs) variability induced by environmental challenges and climate changes on crop development.

Laboratory: Laboratories of Plant Genetics and Biotechnologies; LabGen, Laboratory of Genomics.

Species: grapevine, olive, chichory (radicchio), corn and cereals (eeg. wheat and barley), horticulture crops (e.g. Solanaceae), Hypericum spp., forest species (e.g. willows).

Technologies/Metodologies: Genome analysis with PCR-derived molecular markers, including SSR genotyping and DNA barcoding. Transcriptomics: gene expression studies by means of mRNA profiling, NG sequencing and Microarray, Real-Time RT-qPCR, in situ hybridization of messengers, immunolocalization of proteins using confocal microscopy. Methylation analysis of DNA by bisulfite conversion and sequencing, immunoprecipitation of chromatin and sequencing, and analysis of histone modifications. In vitro cultures. Bioinformatics for genome and transcriptome assembly, and gene prediction and annotation (GO). Analysis of genetic polymorphisms and calculations of genetic diversity/similarity statistics.

Main ERC fields and subfields: LS2_1 Genomics, comparative genomics, structural and functional genomics; LS2_2 Transcriptomics; LS2_7 Quantitative genetics; LS8_4 Biodiversity, conservation biology; LS9_4 Plant Sciences (including Plant Genetics, Genetics of Reproductive Systems, Population genetics and Plant Breeding).

Notes: