STUDY OF *OROBANCHE CUMANA* GENETIC DIVERSITY

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ABSTRACT

The study of *Orobanche cumana* genetic diversity is critical to better understand the evolution of this sunflower parasitic plant and develop new resistant sunflower hybrids. A broad collect of *Orobanche cumana* populations has been organised since 2012 in major countries affected by broomrape (Spain, Turkey, Romania, Hungary, Ukraine, Russia and France) resulting in the harvest of more than 500 orobanche seed lots. A subset of 12 populations representing different level of aggressiveness and different countries has been submitted to transcriptome sequencing in order to performed SNP discovery. This approach lead to the discovery of 368,000 SNP bi-allelic among which 1536 were selected for genotyping of the entire set of collected seed lots. This large diversity study outlined contrasted level of fixity between populations, more specifically French and Spain populations are largely homozygous compared to populations coming from Eastern Europe greatly heterozygous. The principal component analysis based on the relationship matrix (PCoA), allows the discrimination of population according to their geographical origin with 2 opposed clusters on axis 1 representing French and Spanish populations and a third cluster representing eastern Europe populations that can be split by countries on axis 3. Finally, this study allowed the definition of a diversity kit of 200 SNP that can be routinely used for *Orobanche Cumana* diversity study, this SNP toolkit is freely available upon demand to Biogemma.

Key Words : broomrape, genetic diversity, SNP

The authors acknowledge the financial support of SOFIPROTEOL under the FSRSO Project DIVO.