GENETIC AND BIOLOGICAL APPROACH TO DECIPHER OROBANCHE CUMANA RESISTANCE IN SUNFLOWER WILD RELATIVES

Xavier GRAND¹, Isabelle ANDRÉ¹, Sylvie LORAS¹, Ludovic LEGRAND², Jérôme GOUZY², Nicolas RIBIÈRE¹, Amandine LARIÈPE¹, Bruno GREZES-BESSET¹, Thierry ANDRÉ³, Sebastien CHATRE⁴, Stéphane MUÑOS², Marie COQUE^{1*}

> ¹Genetics & Genomics in Oilseeds, BIOGEMMA, Mondonville, France ²Laboratory of Plant-Microbe Interactions, INRA de Toulouse, France ³SOLTIS, Mondonville, France ⁴RAGT2N, Gaillac, France ^{*}Corresponding author: marie.coque@biogemma.com

Abstract

Sunflower broomrape (Orobanche cumana Wallr.), a parasitic plant that connects to sunflower roots, became one of the most important constraints to sunflower production since it can cause complete yield loss. Breeding for resistant sunflower hybrids is an effective way to control O. cumana. However, sources of resistance to O. cumana in sunflower have been mainly based on vertical resistance mechanisms, controlled by single dominant genes. This has led to a rapid overcoming of the resistances and subsequently to the need of finding new resistance sources. Interestingly, helianthus species constitute a substantial reservoir of genes conferring resistance to new virulence broomrape races. To elucidate the genetic control of these resistances, interspecific populations (from crosses between cultivated H. annuus and wild relatives) have been evaluated for broomrape resistance during two years in field trials in Spain where race F is located. One of these populations segregated for a high level of resistance. We selected the most resistant lines from this population for further analysis. At the physiological level, they have been phenotyped for the most important steps of the interaction (efficiency of the O. Cumana seeds germination and resistance at the earlier stage of the interaction). Resistance spectrum has also been evaluated against more aggressive O. cumana races. At the molecular level, a whole genome expression study by RNAseq and RT-qPCR permitted to describe large scale genes expression reprogramming in both sunflower and O. cumana during the interaction. At the genetic level, Genome Wide Association Study and QTL analysis highlighted new genomic regions controlling sunflower broomrape resistance. Fine-mapping of these genomic regions are now underway using a large F2 segregating population. Combining Physiology, Genetics and functional Genomics allowed to investigate the most relevant candidate genes. Finally, this work will contribute to a O. cumana and sunflower interaction and will provide new resistance better understanding of the genes for future breeding programs in sunflower.

Keywords: wild sunflower, broomrape, genetic approach, biological approach, resistance