

GENETIC DIVERSITY OF SUNFLOWER BROOMRAPE POPULATIONS IN CHINA REVEALED BY GENOME RE-SEQUENCING

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Abstract

Sunflower broomrape (*Orobanche cumana*) is an obligate parasitic plant that only infects sunflower (*Helianthus annuus*) by fixing to its root. The first massively infested fields by *O. cumana* were reported in Russia in the 19th century. It is now found in the main sunflower-producing countries in Europe. *O. cumana* has been reported in China, mainly in the Inner Mongolia and Xinjiang regions located in North China, decreasing sunflower yield in the infested fields.

Five representative populations of *O. cumana* from China (Inner Mongolia) were selected for genome re-sequencing using Illumina HiSeq3000 with an average depth of 19.6X. By mapping the sequence reads on the full genome sequence of *O. cumana* (1.4 Gb), we performed SNP calling for each population. A set of few markers will be selected to characterize more Chinese populations and to follow their evolution in the future. Molecular diversity of these populations will be compared to European populations and their virulence level (race structure) will be determined in a set of differential sunflower lines. Our results will enable a better understanding of the history of *O. cumana* in China and its genetic diversity.

Keywords: *Orobanche cumana*, China, re-sequencing, genome, diversity