

GENES EXPRESSION MEASUREMENT BY USING THE GENOME SEQUENCES OF *OROBANCHE CUMANA* AND SUNFLOWER

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Abstract

Orobanche cumana (the sunflower broomrape) is an obligate parasitic plant that needs to fix to the sunflower roots for collecting water and nutrients from sunflower. For sunflower physiology, *O. cumana* can be considered as a new sink that leads to yield losses. During the early stages of the interaction, the connection of *O. cumana* to the vascular system of sunflower reprograms genes expression in both species. A better understanding of the regulation mechanisms could help in breeding for new resistant sunflower varieties. RNA-Seq experiment is the main technology for large-scale gene expression measurement. The full sequence of the sunflower genome (Badouin et al., 2017) made possible the monitoring of genes expression from sunflower during the interaction. However, the lack of the *O. cumana* genome sequence didn't allow to measure genes expression from broomrape. In a consortium with French and Spanish research institutes and by using a similar approach than for the sunflower genome sequencing, we obtained the complete genome sequence of *O. cumana*. We used the two annotated genomes to simultaneously measure genes expression from *O. cumana* and *H. annuus* during the early stages of the interaction using several sunflower genotypes.

Keywords: genome sequence, RNA-Seq, genes expression, interaction