**Gene expression during parasitism interactions between faba bean and *Orobanche foetida***

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Faba beans cover about 72% of the area used for all food legumes in Tunisia. The main threat to this crop is the parasitic plant *O.foetida*, which may cause up to 90% yield loss in heavily infested fields. Identifying genes involved in the interaction between faba bean and *O. foetida* is crucial for breeding resistant varieties. However, there's no available transcriptome data on faba bean's response to *O. foetida* parasitism. In this study, we employed RNA sequencing technique to investigate gene expression changes in faba bean varieties at the root level during interactions with *O. foetida*. Our analysis focused on differential gene expression and Gene Ontology enrichment. We found changes in genes related to secondary metabolites like flavonoids, auxin, thiamine, and jasmonic acid. We also examined WRKY genes, important in plant-parasitic interactions. Given the crucial role of parasitic plant seed germination in this interaction, we investigated *V. faba* genes involved in the orobanchol biosynthesis pathway. This study clearly enhances our understanding of the *V. faba*/*O. foetida* interaction, highlighting the primary differences in gene expression between susceptible and resistant faba bean varieties during *O. foetida* infestation.