

# MORDOR

Project title: Seed-carried **M**icrobiota from **O**robanche during the early parasitic (**O**robanche) cycle.  
Microbiote de l'Orobanche apporté par la graine à travers le cycle parasitaire.

Acronym: MORdOR

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## Summary:

Holoparasitic weeds of the Orobanchaceae family – or broomrapes- are of great concern for a number of cultivated crop species in France including rapeseed, tobacco, melon and sunflower. Especially in western France, *Phelipanche ramosa* broomrape species is expanding every year on rapeseed crop fields. No gene of resistance has been yet found and breeders struggle to produce sustainable varieties of crops that are less susceptible to those parasites. Moreover no treatment is available beside agricultural approaches such as crop rotation. However, parasitic seeds are produced in large quantities and remain in soils for years, which can result in devastating infestations when climatic conditions allow it. In the last decade, studies on host --- parasite rhizospheric interactions have unravelled certain aspects of the parasitic cycle. It is well established that parasitic seeds of *P. ramosa* germinate in response to stimulants of germination (SGs) such as strigolactones or isothiocyanates (degradation products of glucosinolates) that are present in the rhizosphere and are contained most largely in plant root exudates. Besides, microbiota is likely to contribute largely to the parasitic plant development.

The MORdOR project aims to participate in the global comprehension of the parasitic overall diversity and host range and in an original way with a focus on microbial communities. More particularly, the research project focuses exclusively on the parasitic seed-carried microbiota and intends to characterize *P. ramosa*-carried microbial communities depending on its genotype and upon host type stimulation for germination.

Metabarcoding methods will be used for characterizing bacterial and fungal diversity and communities. In a first approach, seed-carried microbiota from different representative *P. ramosa* genotypes will be characterised and compared. In a second approach, the variation of microbial communities of the same parasitic seeds upon interaction with different host will be evaluated.