

Detecting *Orobanche* Species by Using cpDNA Diagnostic Markers

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Some species of the genus *Orobanche* are among the most devastating parasitic weeds, causing extensive damage in agricultural fields. Considering the difficult control due to seed longevity in the soil, small seed size, high fecundity and a subterranean phase that allows them to parasitize the host before they emerge and become evident, the development of diagnostic markers is highly recommended. In our study we identified potential molecular diagnostic markers from the plastid genome in order to distinguish among the most important *Orobanche* species attacking crops in Andalusia, the southern region of the Iberian Peninsula. The study has considered *O. crenata*, *O. ramosa* and *O. cumana* causing serious losses in legumes, solanaceous crops and sunflower fields, respectively, and *O. minor* that, although abundant in Andalusia, has to our knowledge not yet been found parasitizing agricultural hosts. We amplified a non-coding region from the plastid genome, studied sequence differences among the amplified fragments and digested those of the same length with selected restriction enzymes. Here, we propose a molecular protocol to distinguish the main parasitic plants in crop fields of southern Spain. Different applications such as identification of *Orobanche* seeds in soil or crop seed lots are discussed in order to offer right crop recommendations or to prevent new infestation of parasite-free fields. Recommendations for further development of these diagnostic markers are also considered.

KEY WORDS: *Orobanche*; diagnostic markers; plastid DNA; agricultural fields, Andalusia.

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