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# IMPROVING OOMYCETES RESISTANCE IN *OCIMUM BASILICUM* BY GENOME EDITING TECHNOLOGY

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Basil (*Ocimum basilicum* L.) is the most widely cultivated horticultural species in Liguria in a protected environment and it has a high commercial value. In particular"Italiko FT"is one of the elite cultivar used for the production of"Pesto Genovese DOP". Downy mildew is a fungal disease caused by the oomycete pathogen *Peronospora belbahrii* that appeared in Europe in 2001 (Belbahri et al., 2005) and quickly widespread, causing serious damages to basil cultivation and loss of production up to 80%. The short cultivation cycle and the few authorized pesticides on sweet basil made difficult the defence of the crop by chemical means. The aim of the present research is to apply genome editing technique in order to improve resistance to *P. belbahrii*. The CRISPR-Cas9 technology was used for knocking out candidate susceptibility genes that are early expressed during the infection phase between host and pathogen (Fawke et al., 2015; Shan-e-Ali Zaidi et al., 2018). The S gene *DMR6* (Downy Mildew Resistance 6) was originally identified and characterized by Van Damme et al. (2008), it belongs to the superfamily of 2-oxoglutarate Fe(II) dependent oxygenase and it is specifically up-regulated during pathogen infection. Interestingly, mutation of tomato DMR6 gene with CRISPR-Cas9 has conferred resistance against oomycetes (de Toledo Thomazella et al., 2016). In the absence of genomic and transcriptomic data on sweet basil, *O. basilicum DMR6* orthologue was cloned and characterized (83 % identity with *Sesamum indicum* DMR6-like protein) and is was used for CRISPR-Cas9 constructs preparation. An efficient regeneration protocol was set up for the cultivar "Italiko FT". Several starting explants (cotyledons, hypocotyls, leaves) were tested onto different media: first true leaves of *in vitro* and/or *in vivo* seedlings cultured onto MS basal medium with BA 1 mg/L and antioxidants (100 mg/L of ascorbic acid and 10 mg/L of citric acid) guaranteed the best regeneration percentage (35,45.%). In order to evaluate the transformation aptitude of the cultivar"Italiko FT", two different *Agrobacterium*-mediated (wild type ATCC 15834 *A. rhizogenes* and *A. tumefaciens* carrying 35S GUS marker gene) transformation protocols were evaluated.