

Identified Transcription Factors and Gene Regulation in Scent Biosynthesis in Ophrys Orchids

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Abstract : The genus *Ophrys* is remarkable for its mimicry, flower-lip closely resembling pollinator females in a species-specific manner. Therefore, floral traits associated with pollinator attraction, especially scent, are suitable models for investigating the molecular basis of adaptation, speciation, and evolution. Within the two *Ophrys* species groups: *O. sphegodes* (S) and *O. fusca* (F), pollinator shifts among the same insect species have taken place. Preliminary data suggest that they involve a comparable hydrocarbon profile in their scent, which is mainly composed of alkanes and alkenes. Genes encoding stearoyl-acyl carrier protein desaturases (SAD) involved in alkene biosynthesis have been identified in the S group. This study aims to investigate the control and parallel evolution of ecologically significant alkene production in *Ophrys*. Owing to the central role those SAD genes play in determining positioning of the alkene double-bonds, a detailed understanding of their functional mechanism and of regulatory aspects is of utmost importance. We have identified 5 transcription factors potentially related to SAD expression in *O. sphegodes* which belong to the MYB, GTE, WRKY, and MADS families. Ultimately, our results will contribute to understanding genes important in the regulatory control of floral scent synthesis.

Keywords : floral traits, transcription factors, biosynthesis, parallel evolution

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