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C0253 IDENTIFICATION OF CANDIDATE GENES FOR METHYLKETONES CONTENT IN A COLLECTION OF EUROPEAN WOODLAND STRAWBERRY.

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1 Abstract

Woodland strawberry (*Fragaria vesca*, 2x) is the diploid closest ancestor of the cultivated strawberry (*Fragaria x ananassa*, 8x) and the model species for genetic studies in the *Fragaria* genus. It is naturally distributed all across Europe and it is appreciated for their delicate aroma and flavor.

Methylketones are compounds with demonstrated insect repellent effects. Its synthesis, reported to take place in glandular trichomes of wild tomato (*Solanum habrochaites*), is mediated by a thioesterase (ShMKS2) and a decarboxylase (ShMKS1) (Ben Israel et al. 2009; Yu et al. 2010).

A natural population of 199 accessions of *F. vesca* that represents the European diversity was resequenced (>1.8M SNPs) and characterized for the accumulation of methylketones and their derived alcohols. By genome wide association analysis (GWAS), we have detected a stable series of polymorphisms associated to the accumulation of C7, C9 and C11 methylketones and their respective alcohols. Three different haplotypes in the candidate region with different patterns of methylketones were found, suggesting differences in enzymatic activity and/or substrate affinity.

The candidate region includes two genes annotated as thioesterases that are homolog to ShMKS2, FvMKS2A, FvMKS2B. Functional validation of both genes has revealed methyl ketones synthesis ability in transient expression in *Nicotiana benthamiana*. The function and specificity of these candidate genes is currently under study through several approaches, including transient expression in different hosts and enzymatic function characterization.