Ascertaining the segregation of four mutations in a recombinant inbred line of Antirrhinum majus x Antirrhinum linkianum

Benjamin Hermans

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Introduction
The wild species Antirrhinum linkianum shows striking differences with the laboratory line of A. majus 165E in four volatile organic compounds (VOCs), i.e. methyl benzoate, methyl cinnamate, ocimene and acetophenone. Although the scent profiles of both species are complex, the segregation of the four aforementioned VOCs in the F2 population of a recombinant inbred line (RIL) under construction of Antirrhinum majus x A. linkianum could be explained by mendelian genetics.

Objective
The current work aims to confirm the identified genetic segregation using the F3 population.

Methodology
A F3 population of 94 plants was analysed for VOC emission. The volatiles were trapped by headspace collection using Gerstel twisters and analysed by GC-MS via thermal desorption. The corresponding profiles were analysed. A random survey of the A. majus was also analysed to calculate the phenotypic space used for categorization.

Results
Independent plants of the RIL-F3 population did not produce acetophenone, ocimene, methyl benzoate or methyl cinnamate. Despite the complexity of the scent profiles, scent production followed a mendelian segregation.

Conclusion
Analysis of the GC-MS profiles confirmed the mendelian segregation found in the F2 population. Furthermore at least one plant with a high level of emission in the F2 had daughter plants with very low or no emission in the F3. This confirms the segregation of a wild type active allele. These results rule out an environmental effect in the F2 determination and confirmed the identified genetic segregation being correct. Some discrepancies found were presumably caused by allele instability in the gene involved in acetophenone synthesis.

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