

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

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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.

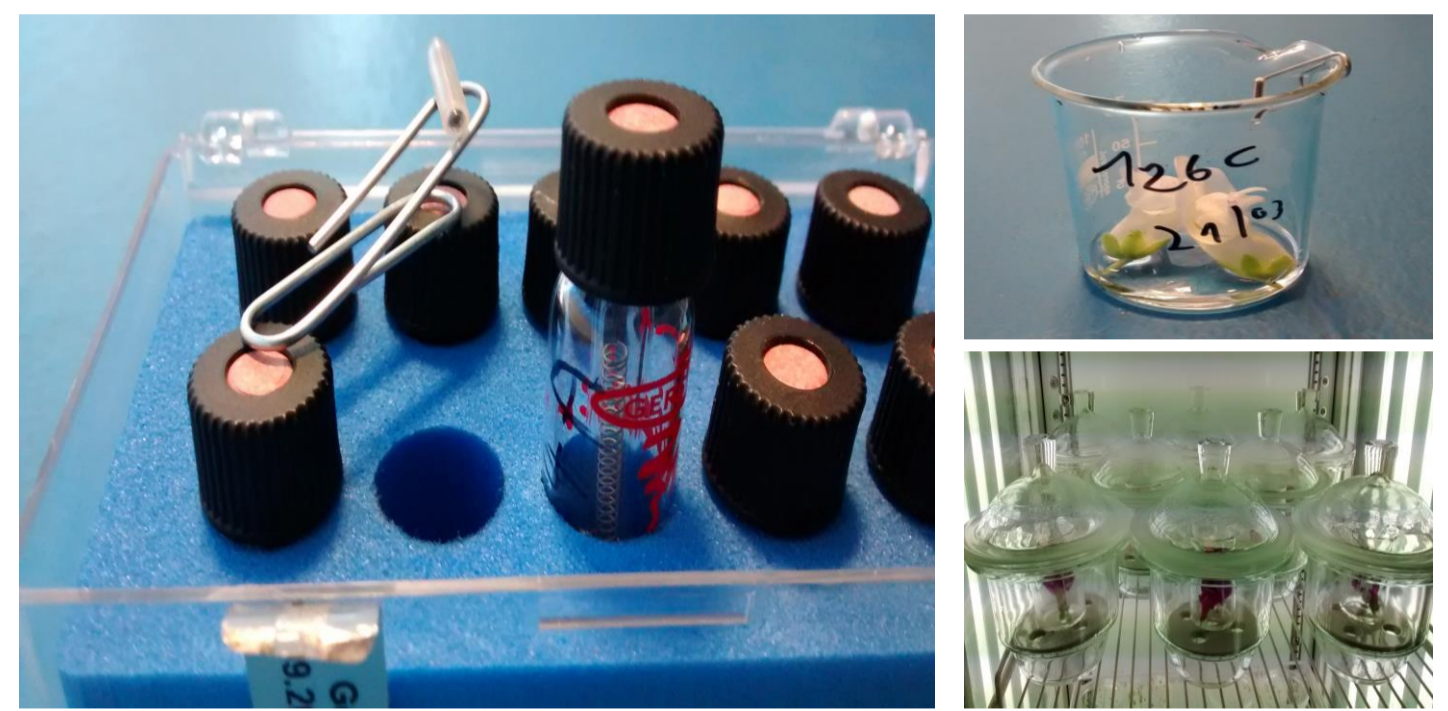
### Objective

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

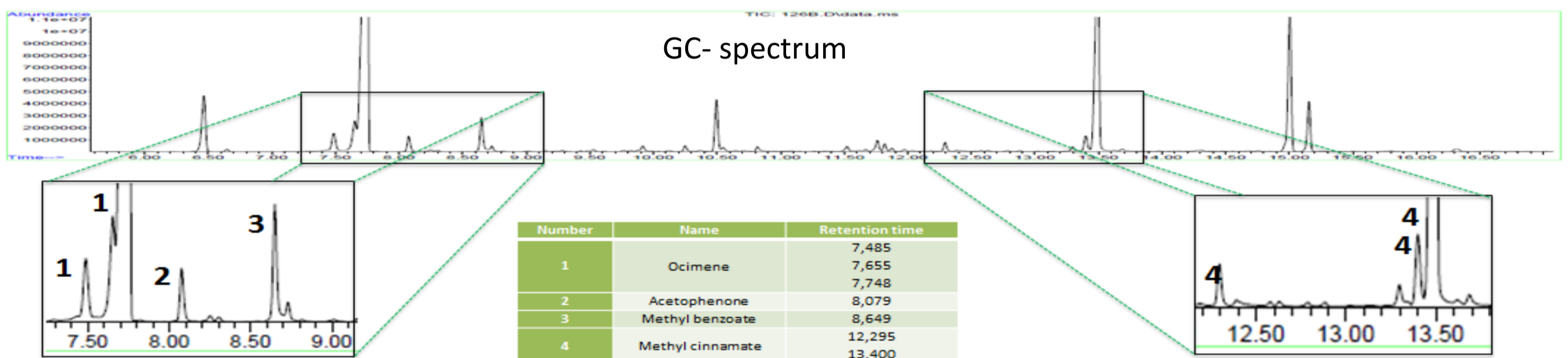


### Methodology

A F3 population of 94 plants was analysed for VOC emission. The volatiles were trapped by headspace collection using Gerstel twistors 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



F3 plants show a mixture of fixed alleles as homozygotes and a possible reversion of plants that do not produce acetophenone, back to wild type

Name	Previous phenotype (F2)	Descendants (F3) ratio low/high	Mendelian meaning
126	Ocimene high	1/3	Heterozygote segregating
	Acetophenone high	4	Homozygote fixed
	Methyl benzoate high	2/2	Heterozygote segregating
	Methyl cinnamate high	4	Homozygote fixed
9	Acetophenone low	0/7	Possible revertant
	Methyl benzoate low	7/0	Homozygote fixed
86	Methyl cinnamate low	2/2	Heterozygote segregating
13	Acetophenone high	0/4	Homozygote fixed
	Methyl cinnamate high	0/4	Homozygote fixed

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.

	N° plants producing	N° plants that do not produce	Chi square test for mendelian segregation	P value
Ocimene	59	34	3:1	0.01004
Acetophenone	88	5	15:1	0.7278
Methyl benzoate	64	29	3:1	0.1685
Methyl cinnamate	85	8	13:3	0.01217

### 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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