

UNDERSTANDING DIFFERENCES AND SIMILARITIES BETWEEN TWO MEDITERRANEAN ORCHIDS: MORPHOMETRY, GENETIC DIVERSITY AND GENE FLOW

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INTRODUCTION



Fig. 1. 1. *Ohprys fusca* subsp. *fusca* (*O. fusca*); 2. *O. omegaifera* subsp. *dyris* (*O. dyris*); 3. Intermediate phenotypes

- *Ophrys dyris* and *O. fusca*, have similar morphologies and are frequently misidentified in the field. It is possible to find populations with individuals clearly assigned to each taxon occurring in sympatry, populations with intermediate morphology; as well as populations where only one morphological type occurs

QUESTIONS

- Identify **morphological and phenological traits** that best characterise and distinguish the taxonomic entities being studied;
- Assess **gene flow** and **hybridization** between both species (indirect methods), testing the following **hypothesis** regarding genetic structure of data:
 - A. **Two** main genetic groups prevail in the dataset, species keeping their genetic identity
 - B. **Three** genetic groups, gene flow happening in both ways
 - C. **Three** genetic groups, gene flow mainly in one direction, one species acting as genetic donor

METHODS

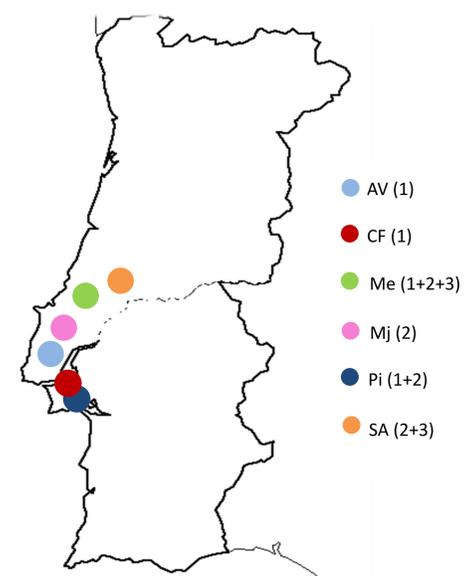
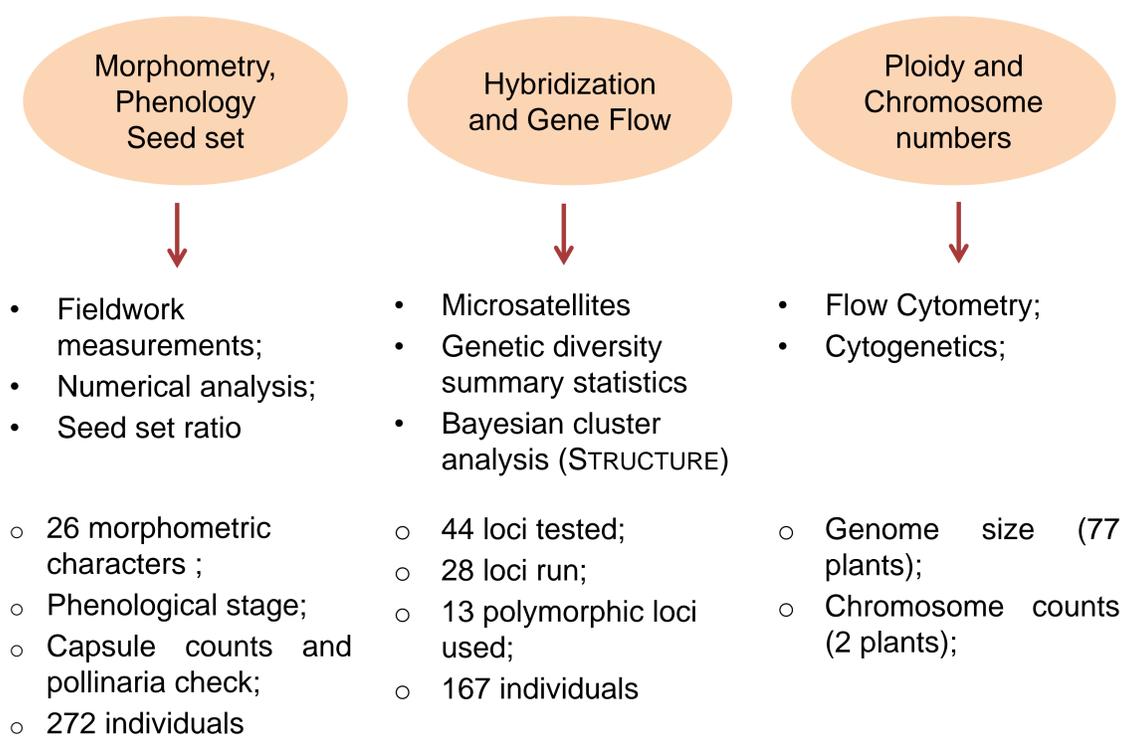


Fig. 2. Geographic location of populations studied, named by the acronym used in the project. Between () is the expected presence of the studied taxa, according to field observations

RESULTS

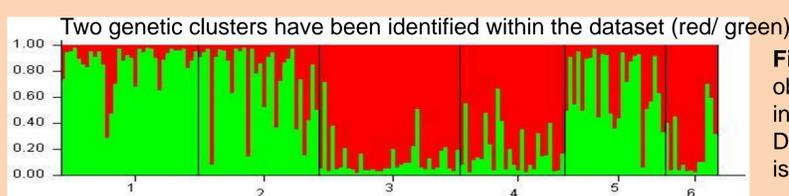


Fig. 3. Admixture proportions (Q) obtained in Structure software for each individual of the 6 populations. Different distribution of clusters 1 and 2 is visible in the populations sampled

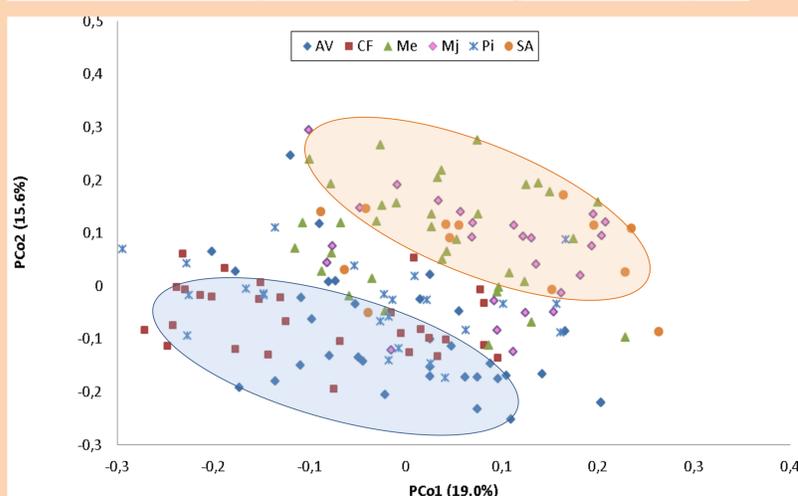


Fig. 4. Principal Coordinates Analysis performed on Bruvo distance obtained in Popsat. The first axis explains 19.0% of the total variation, the second 15.6%

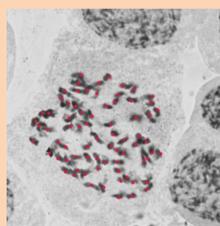


Fig. 5. Cells from root tips of *O. fusca*. Chromosomes (72, highlighted in red), counted in metaphase

PRELIMINARY CONCLUSIONS

- **Speculum dimensions**, a morphological character referred as distinguishing both species, allow us to segregate the different populations, according to the species represented in each one
- Bayesian cluster analysis confirms **hybridization** and **introgression**, which seems to be happening in only one direction
- Despite genetic exchange between the two species, each one keeps its **genetic identity**, as the number of genetic groups identified is two
- All the individuals from the six populations, phenotypically assigned to the different species, have the **same ploidy level: $2n = 4x = 72$**

ACKNOWLEDGMENTS

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