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Is there a phylogeny behind this diversity? A molecular assessment of *Romulea* in the Mediterranean

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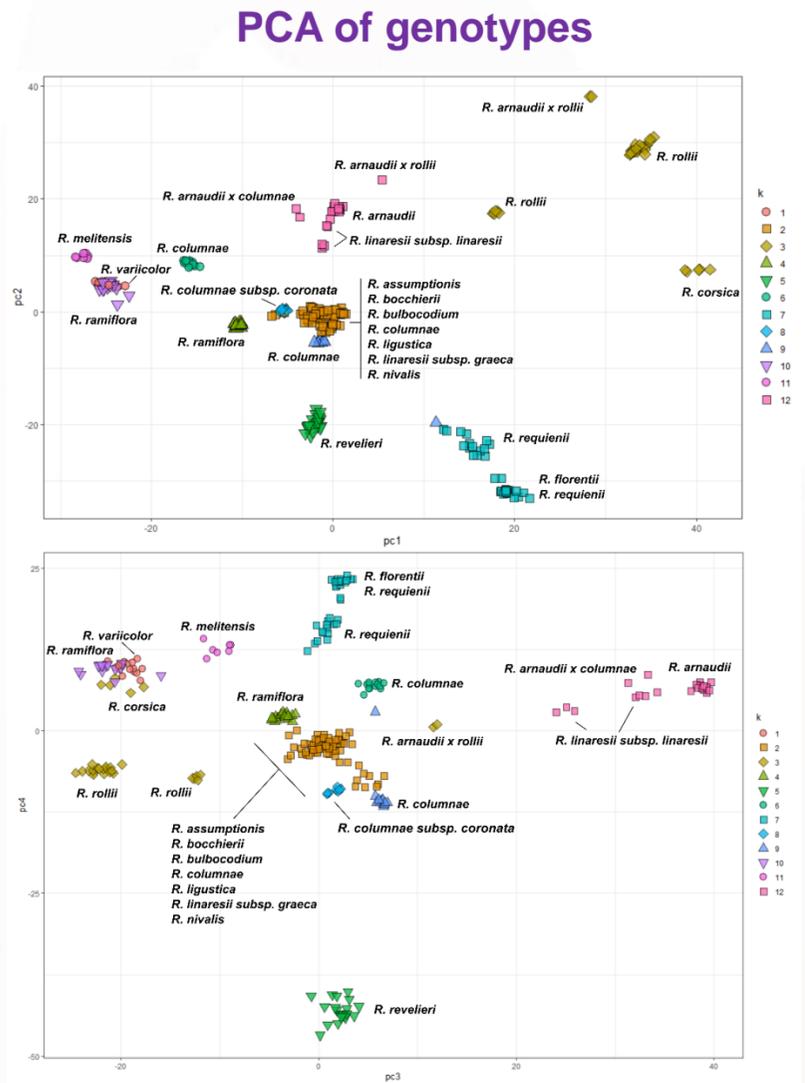
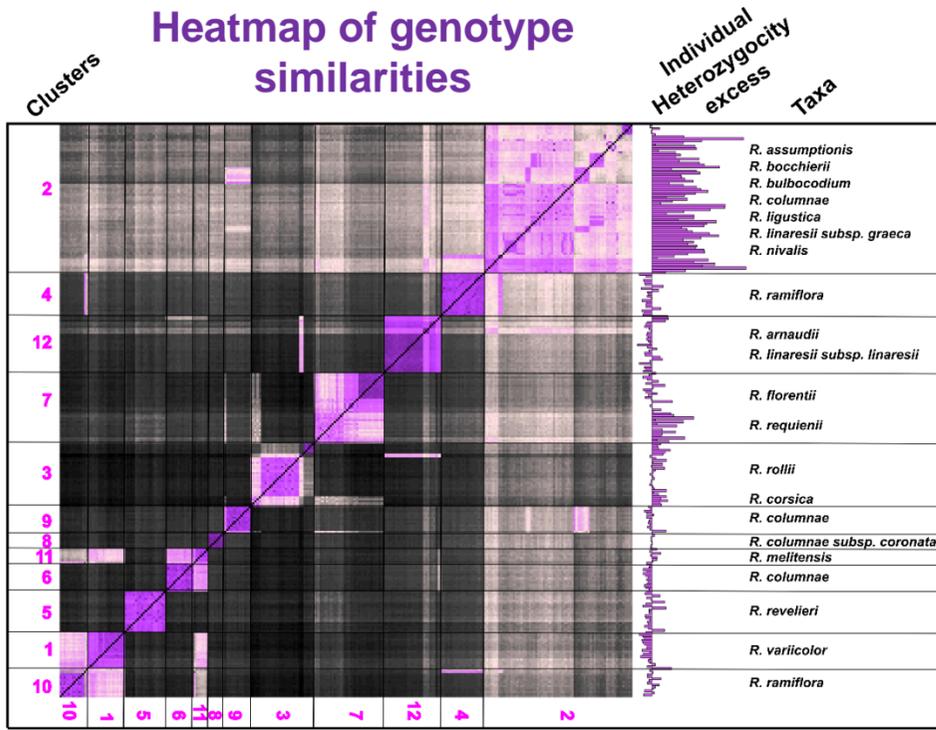
Is there a phylogeny behind this diversity? A molecular assessment of *Romulea* in the Mediterranean



Romulea arnaudii

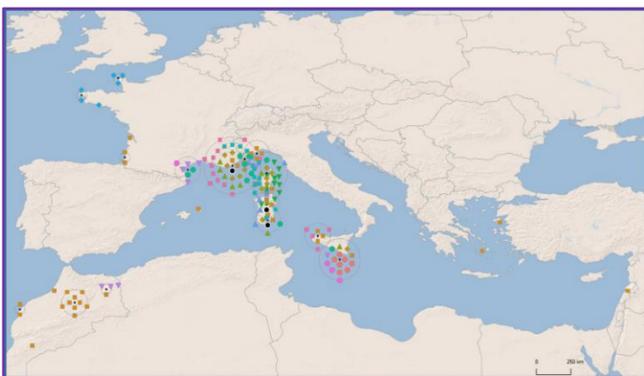
Alex Baumel¹, Frédéric Médail¹, Anouar Toumi¹, Cécile Chemin¹, Manon Candas¹, Virgile Noble², Henri Michaud², Katia Diadema², Germain Waroquier², Annie Aboucaya³, Alain Delage⁴, Lisandru Leandri⁴, Mathieu Chambouleyron⁵, Jean-François Léger^{5,6}, Stephen Mifsud⁷, Andrea Lallai⁸, Gianluca Iiriti⁸, Gianniantonio Domina⁹, Gabriele Casazza¹⁰, Baptiste Pierre¹¹, Juan Viruel¹²

The genus *Romulea* (Iridaceae) comprises ca. 90 species distributed in two hotspots of diversity: South Africa and the Mediterranean. Hybseq data using the Angiosperm353 baitset were generated to disentangle the relationships between 288 *Romulea* samples belonging to 18 taxa from Mediterranean. Our results are based on (1) 4K SNPs following a tetraploid genotyping approach using Freebayes from 331 nuclear genes and (2) 652 informative SNPs obtained from plastomes of 120 individuals.



Results

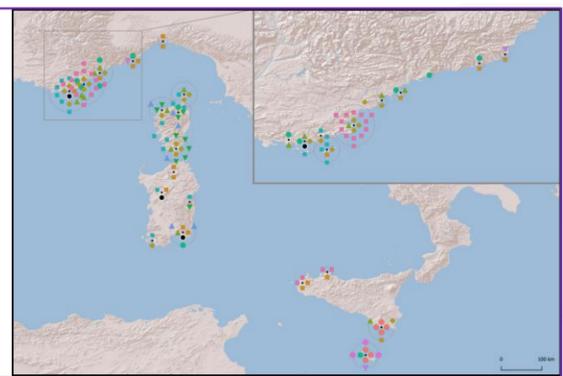
- 10 taxa are congruent with 7 unique clusters (clusters: 1, 3, 5, 7, 8, 11, 12)
- One cluster (n°2) comprises 7 taxa
- Genotypes similarities suggest or confirm hybrids (e.g. *R. melitensis*)
- Excess of heterozygosity (Hind/He), not compatible with auto-tetraploidy, is associated to hybridization



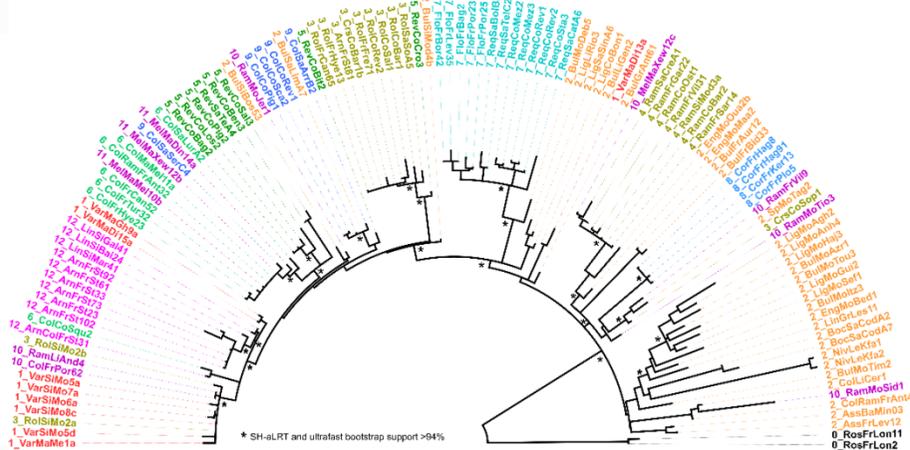
Maps of genetic clusters

Cluster 2 is widespread all over the Mediterranean region

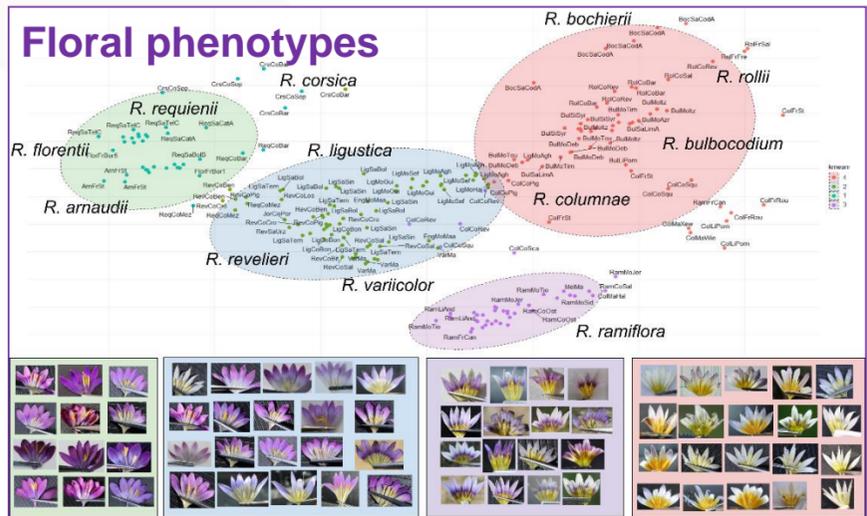
The Tyrrhenian sector has several endemic clusters with low differentiation between disjunct populations or taxa



Plastid phylogeny



Floral phenotypes



- Nuclear, plastid and floral data mismatch but some congruences were also observed and need further investigations.
- Allopolyploidy with multiple origins is suspected, and separating homeologs is required to better understand the phylogenetic relationships between the Mediterranean *Romulea* taxa.
- Incongruence between taxa and genetic clusters highlight the need for a taxonomic revision.