

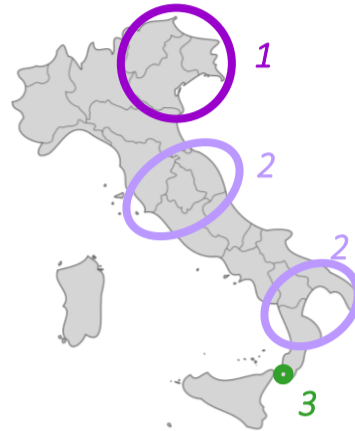
First steps towards the Conservation of Endemic Italian *Salvia* Species through Population Genomics

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BACKGROUND

25 species of *Salvia* can be found in the wild in Italy. *S. pratensis* (right) is one of the most common and is closely related to some endemic taxa with debated species rank: 1) *S. saccardiana*; 2) *S. haematodes*; 3) *S. ceratophylloides* (left: known range). To assess genetic separation between these taxa, study the phylogeny of the genus in Italy, and develop better *ex situ* collections, we sequenced the whole genome of *Salvia pratensis* and sampled wild populations across Italy, which we characterized with Genotyping-By-Sequencing.



METHODS

1. Genome assembly

We sequenced the genome with HiFi reads and annotated it with RNAseq.

2. Sampling of wild populations

We sampled 16 taxa across Italy thanks to a network of 47 collaborators.

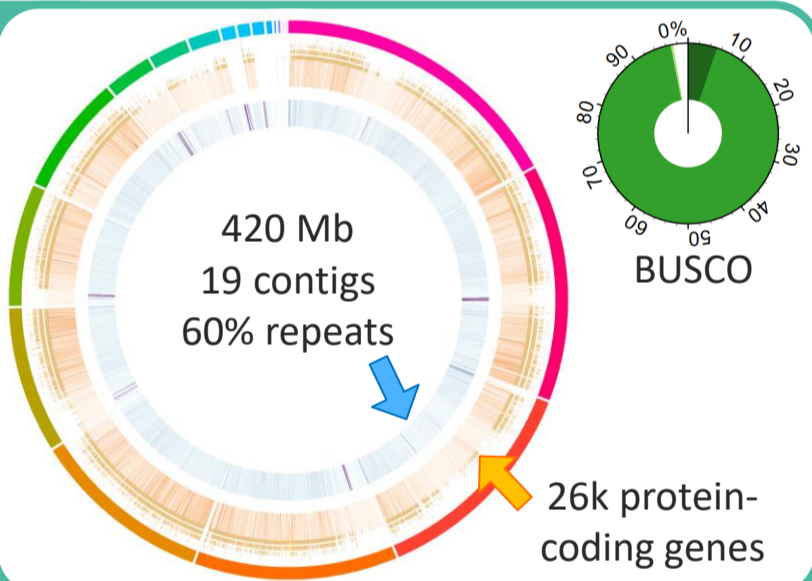
3. Genetic characterization

We obtained genome-wide variation data with Genotyping-By-Sequencing (GBS).

4. Population genomics analysis

We performed species delimitation and phylogeny of Italian *Salvia*.

GENOME ASSEMBLY



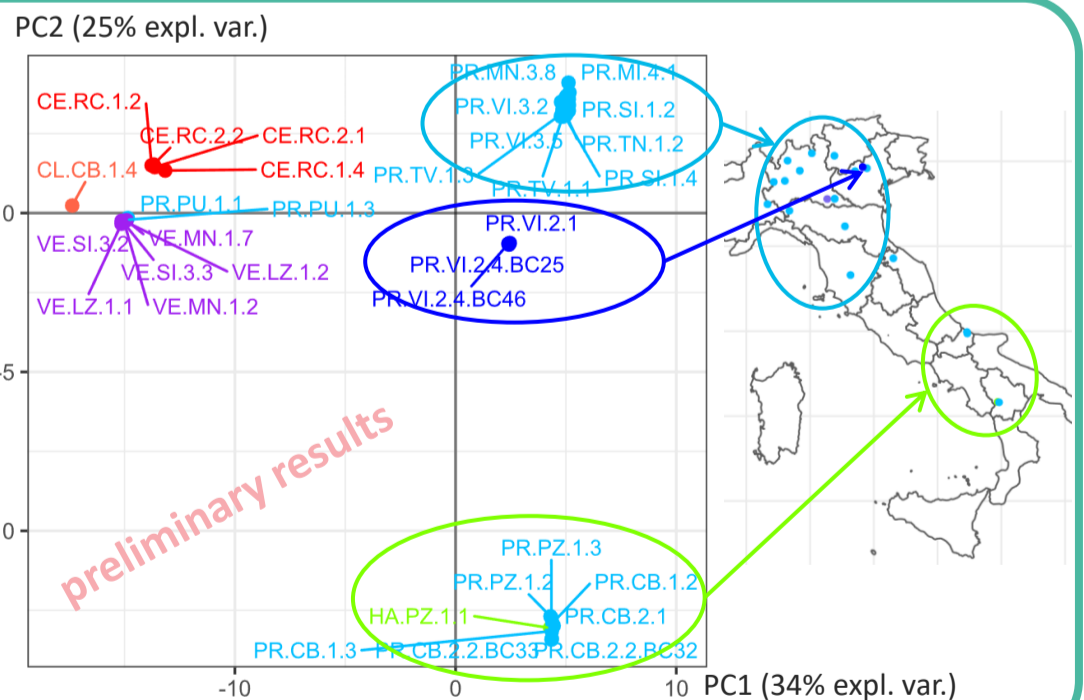
SAMPLING

total
1071 samples
199 populations
16 taxa
analysed
57 samples
~7,000 SNPs
WIP
>200 samples
40 populations
14 taxa



POPULATION GENOMICS

We sequenced 57 samples and studied the distribution of genetic diversity; here, we show the principal component analysis (PCA). Samples are colored by species. *S. ceratophylloides* (CE, in red) is separated from *S. pratensis* (PR, light blue). *S. pratensis* is split in three lineages, each linked to its location: northern and central regions (top right), *S. haematodes* (HA, green, bottom right), *S. saccardiana* (PR.VI, dark blue).



CONCLUSION

Preliminary results suggest the existence of three *S. pratensis* lineages: northern and central Italy, southern Italy + *haematodes*, and *S. saccardiana*. There is no continuous gradient of genetic variation correlated to geographical distance, rather a stark divide between the three lineages. *S. saccardiana* already has species rank according to recent classifications. This data supports separation between three separate species, *pratensis*, *saccardiana* and *haematodes*. However, more data is needed from the boundary region between *pratensis* and *haematodes* as well as comparison with morphological observations.

References

S. saccardiana: Del Carratore et al., 1999 ([10.1080/11263509909381544](https://doi.org/10.1080/11263509909381544)); *S. haematodes*: Linnaeus C. Species Plantarum: 24, 1753; *S. ceratophylloides*: Arduino P. Animadversiorum Botanicorum Specimen Alterum. Ex Typographia Sansoniana: Venetis; 1764. Distribution data from the Portal to the Flora of Italy (<http://dryades.units.it/floritaly>) and Spampinato et al., 2019 ([10.5772/intechopen.84905](https://doi.org/10.5772/intechopen.84905)). Sequencing performed by: Next Generation Sequencing Platform, University of Bern, Switzerland (PacBio HiFi); Azenta Life Sciences (GBS); IGATech, Udine, Italy (RNAseq).