

Continental scale variation of Saccharomyces yeasts

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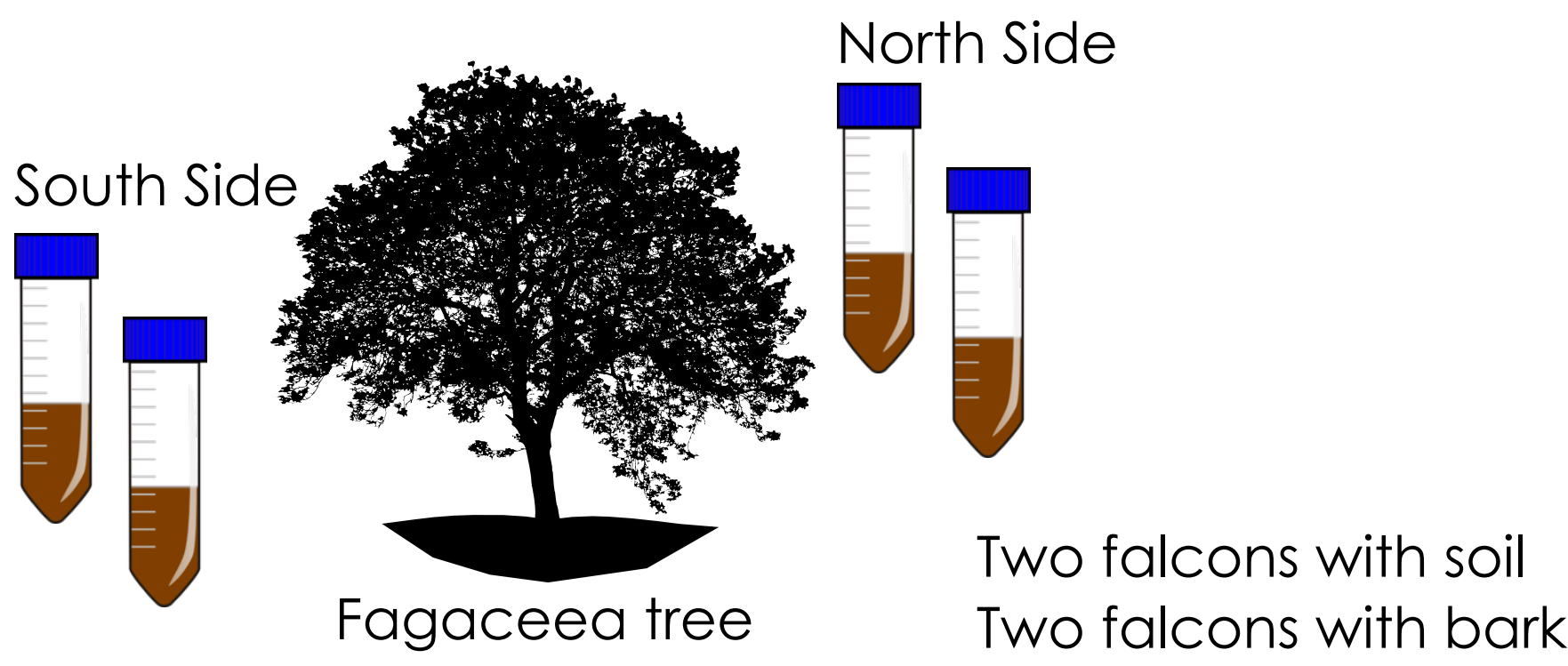
Background

The evolution of microorganisms is a challenging aspect to address because of their microbial size. While mutations arise dipersal as well as selective and neutral forces draw biogeographic patterns. With the invaluable help of the **Saccharomyces Yeast Sampling Consortium**, We gathered over 5,000 environmental samples to investigate biogeographic patterns of the free-living cosmopolitan Saccharomyces genus across temperate forests of Europe and the Mediterranean basin. We undertake a project of isolation and deep DNA sequencing, named **Saccharomyces Genome Resequencing Project number 5** (SGRP5), to investigate Saccharomyces **geographical ranges** in order to reconstruct **dispersal trajectories** and trace Saccharomyces historical evolutionary paths across continental-scale spatial distances.

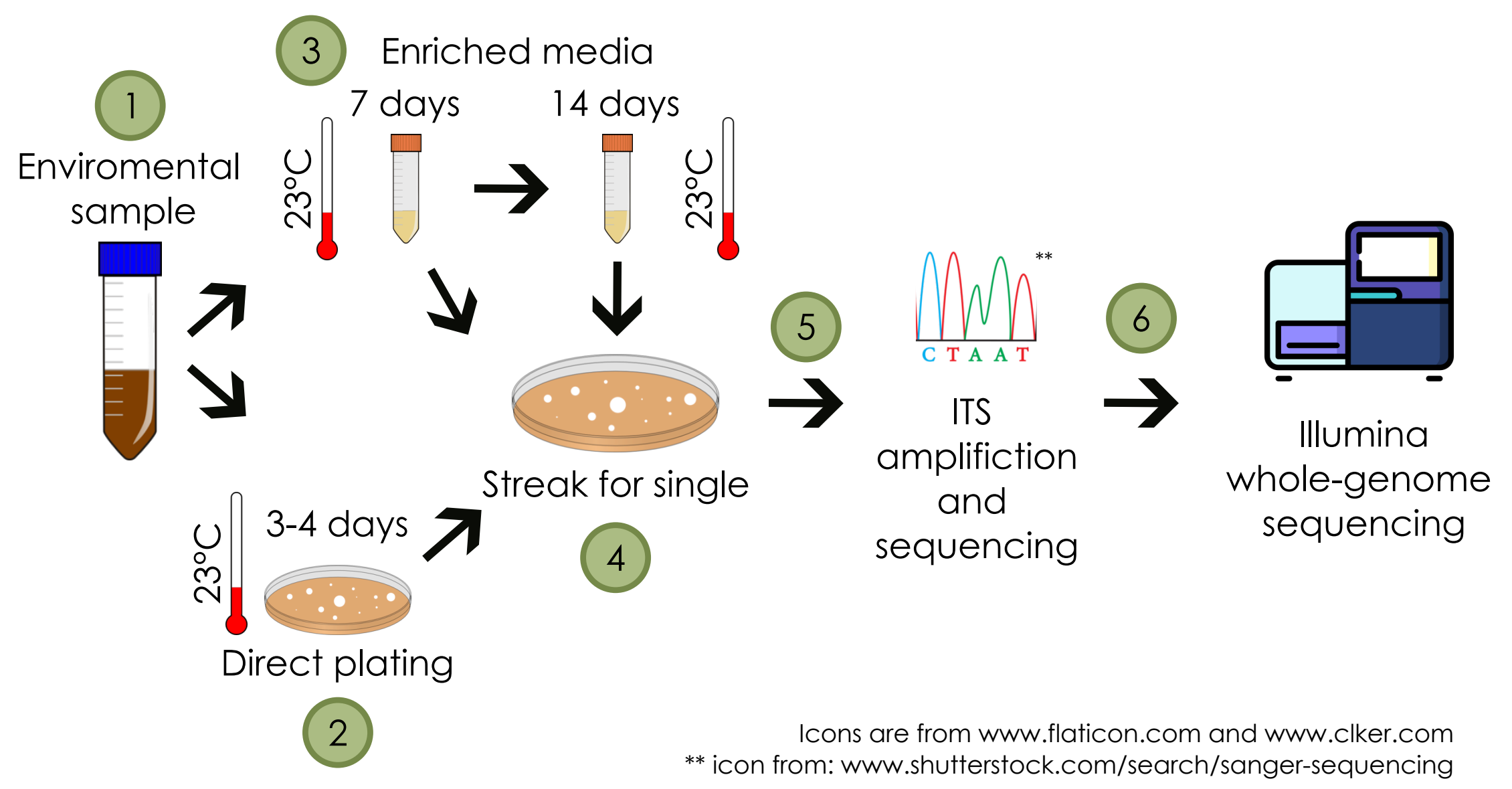
About the consortium

The Saccharomyces Yeast Sampling Consortium counts over 100 scientists with broad scietific interests in cellular biology, ecology, evolution of Saccharomyces but also botanists, representatives of forest management bodies and responsible of public Saccharomyces Collections. We collaborated in a joint effort to collect environmental samples, primarily targeting Fagaceae trees, the preferred wild niche of Saccharomyces.

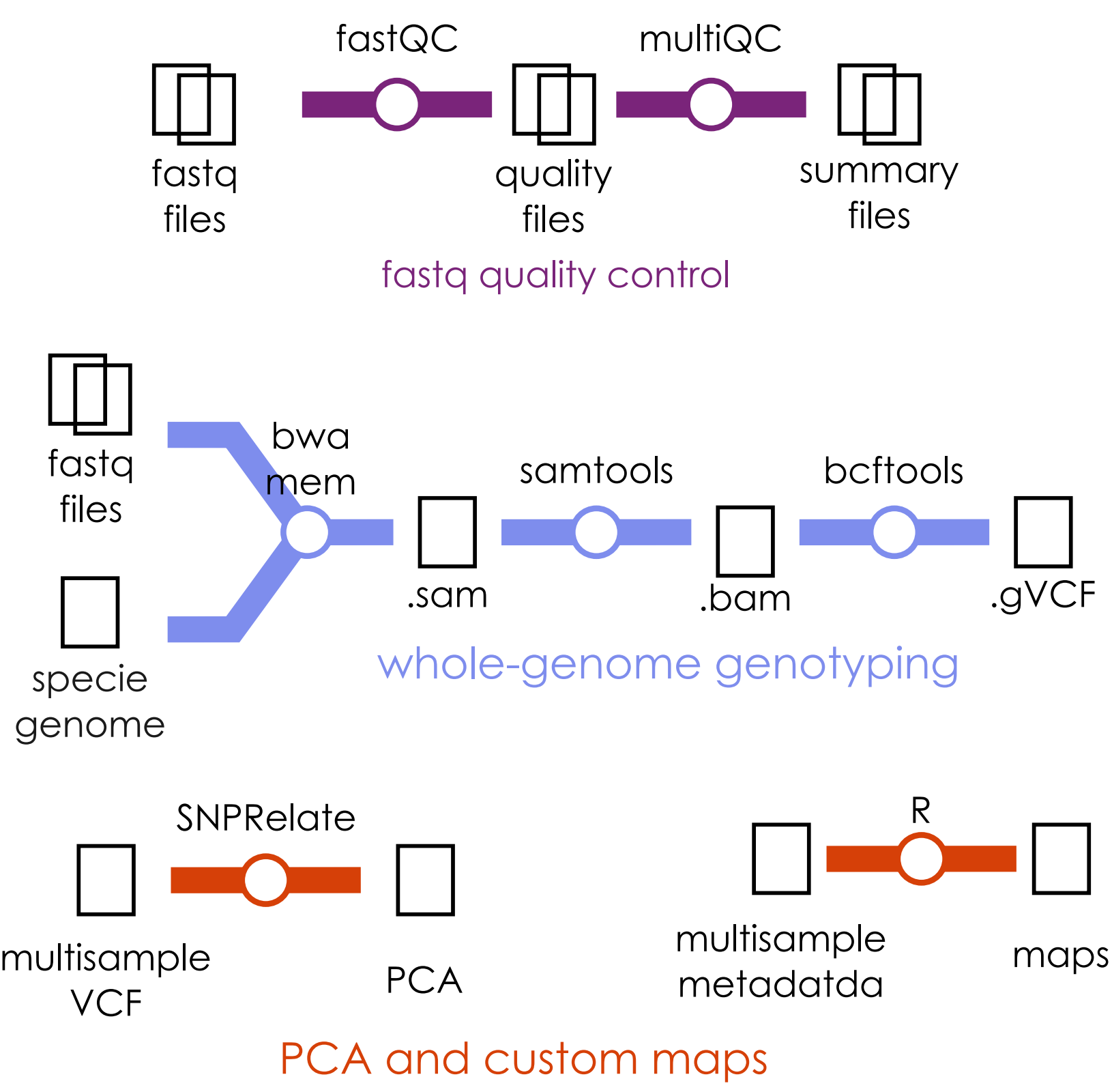
The sampling strategy



The isolation protocol

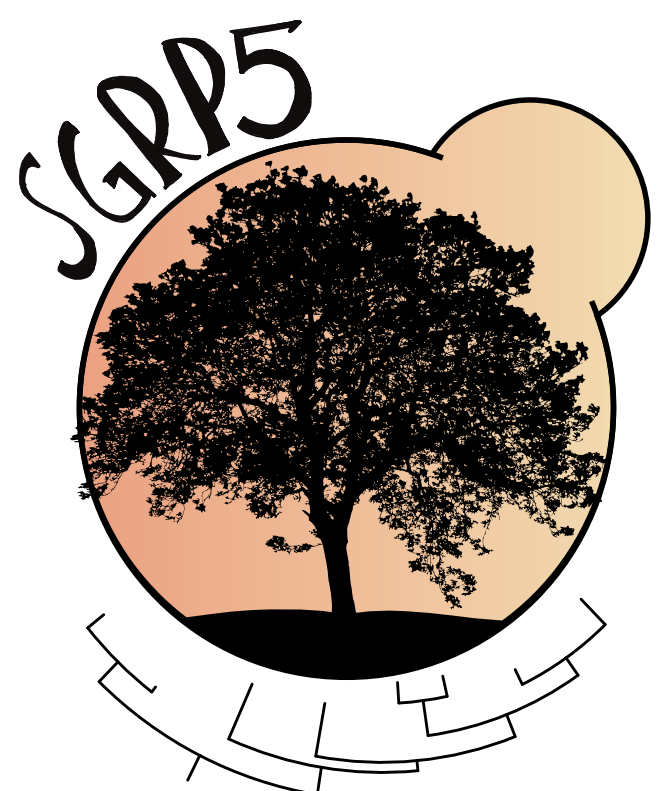


Data analysis

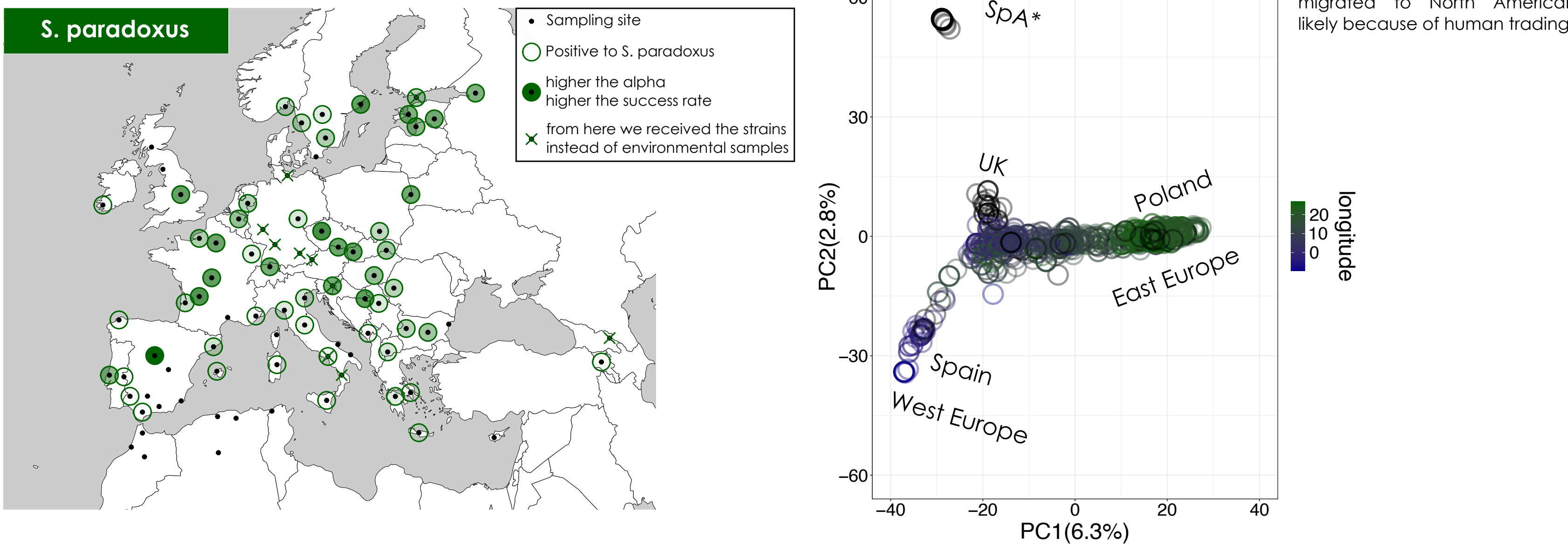


Contacts and main funding bodies

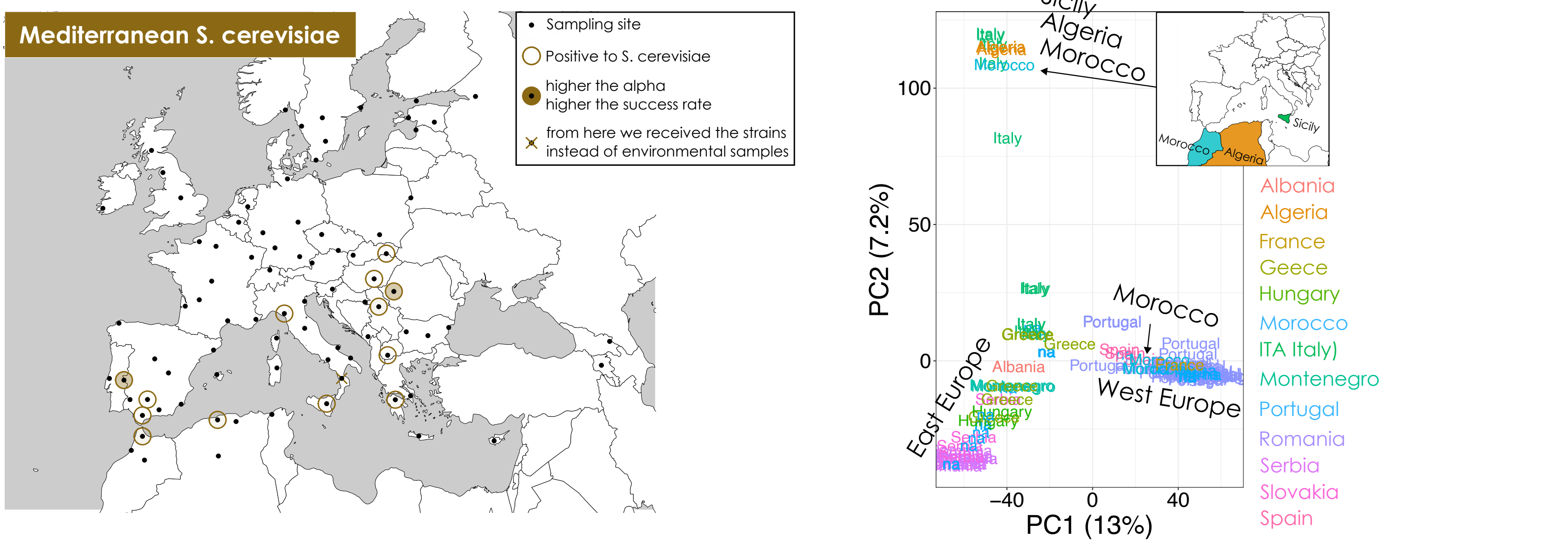
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Genomes mirror geography

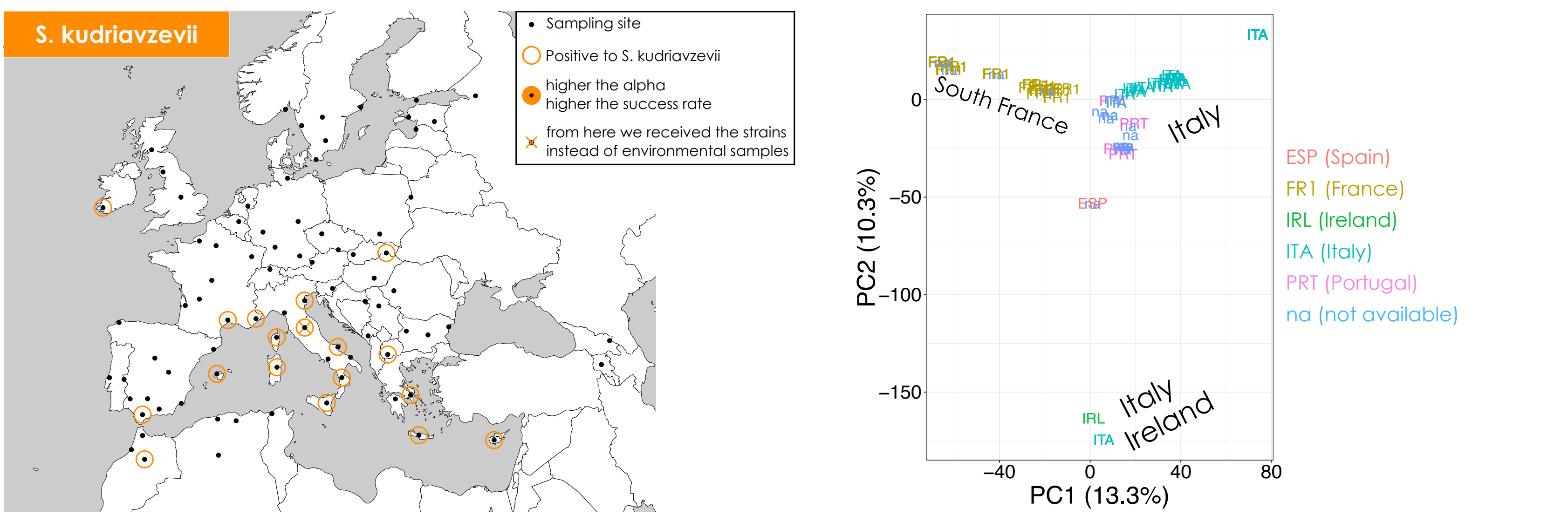


Saccharomyces paradoxus is the most frequently isolated species across Europe, with over 840 isolates collected, covering a vast geographic range from southeastern Cyprus to the cold Scandinavian fjords. Its genetic background closely resembles that of the reference strain CBS432 (known as the European *S. paradoxus*). The species genetic structure mirrors its geographical distribution, reflecting a longitudinal gradient across the European continent, from east to west.



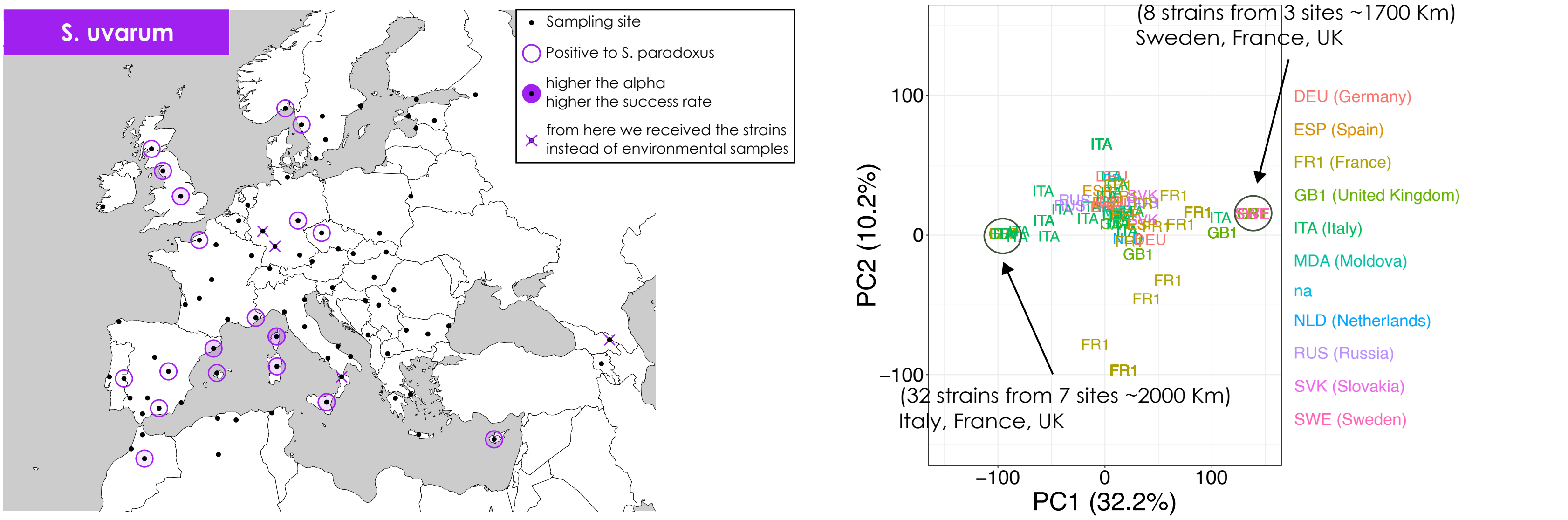
The Mediterranean population of *Saccharomyces cerevisiae* represents the wild strains inhabiting Europe. Its distribution shows a net separation between populations in Western and Eastern Europe, with an additional third group found across Sicily, Algeria, and Morocco—regions that may have served as ancestral refugia during the Last Glacial Maximum (26,500–19,000 BP).

Controversial patterns



The European population of *Saccharomyces kudriavzevii* is mainly found in the Mediterranean basin, a curious finding given that it is one of the most cold-tolerant species within the *Saccharomyces* genus, making it particularly well-suited for fermentation at low temperatures. Two genetically similar isolates (positioned at the bottom of the PCA plot) highlight this adaptability: one was discovered in Sardinia and the other in Ireland. This conciliates both the species' ability of favoring southern regions while also persisting in the cold climate of Ireland.

Fast dispersal



European *Saccharomyces uvarum* is found across both southern and northern regions of Europe. Two major populations, separated by more than 50,000 SNPs, explains up to one-third of the total genomic variation across the continent (PC1). Interestingly, these two populations do not have fixed geographic boundaries, as strains from each can be found over 1,000 Km apart (see PCA plot). In contrast, distinct French and Italian populations are recognizable at opposite extremity of the plot, though they remain more closely related to each other, with over 30,000 SNPs among them.

The Saccharomyces consortium

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