

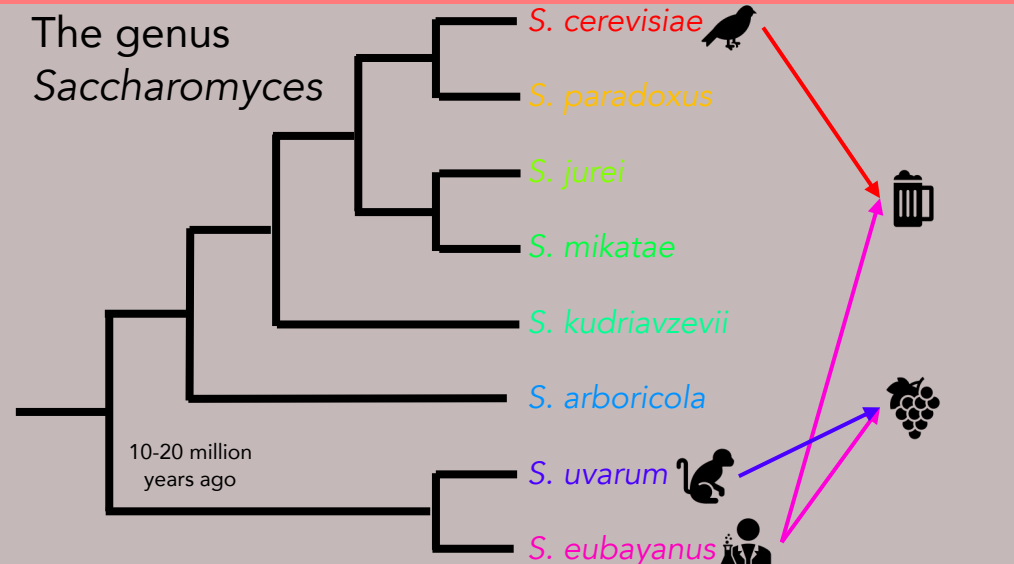
Saccharomyces eubayanus population genomics: wild diversity and contributions to domesticated hybrids

Quinn Langdon ^{1, 4}; David Peris ^{1, 2}; EmilyClare Baker ¹; Dana Opulente ¹; Juan Eizaguirre ³; Kelly Buh ¹; Kayla Sylvester ¹; Martin Jarzyna ¹; Diego Libkind ³; Chris Todd Hittinger ¹

¹ University of Wisconsin- Madison; ² Institute of Agrochemistry and Food Technology (IATA), CSIC, Valencia, Spain; ³ Universidad Nacional del Comahue; ⁴ Stanford University



Hybridization and Admixture

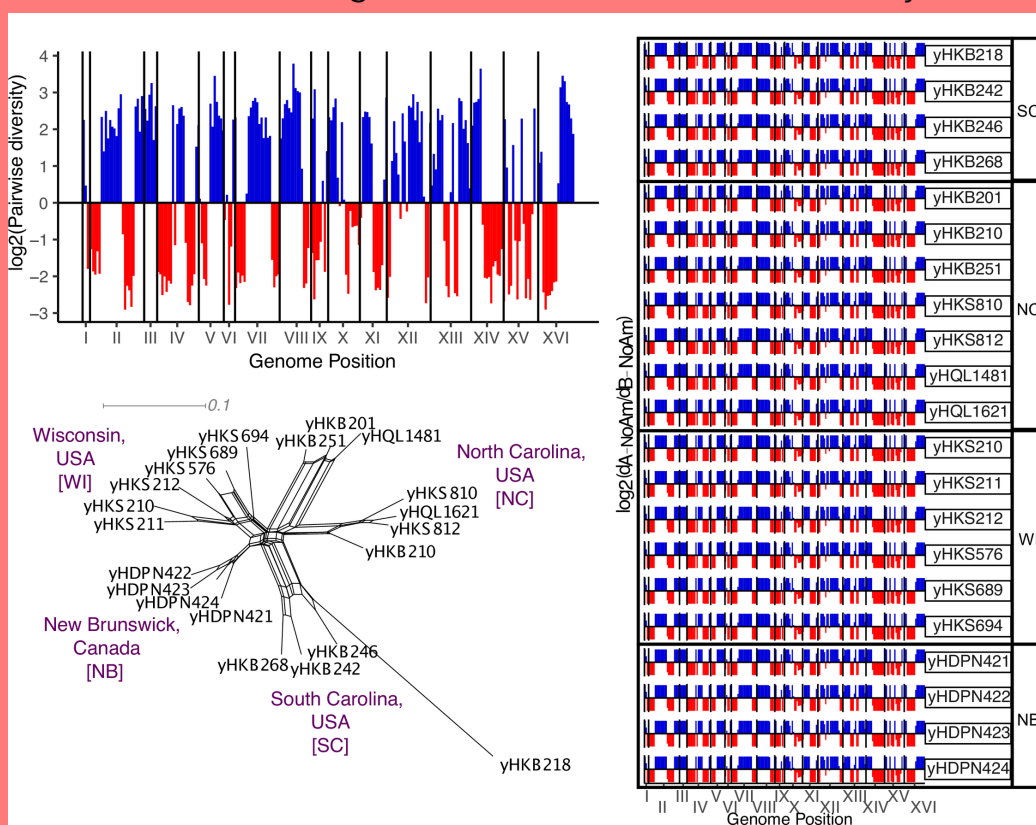


Lager-brewing yeasts are hybrids of *S. cerevisiae* and *S. eubayanus*

- ~25% nucleotide divergence (on par with humans and birds)

Hybrids of *S. eubayanus* and its sister species *S. uvarum* have been isolated from many environments

- ~7% nucleotide divergence (~humans and old-world monkeys)



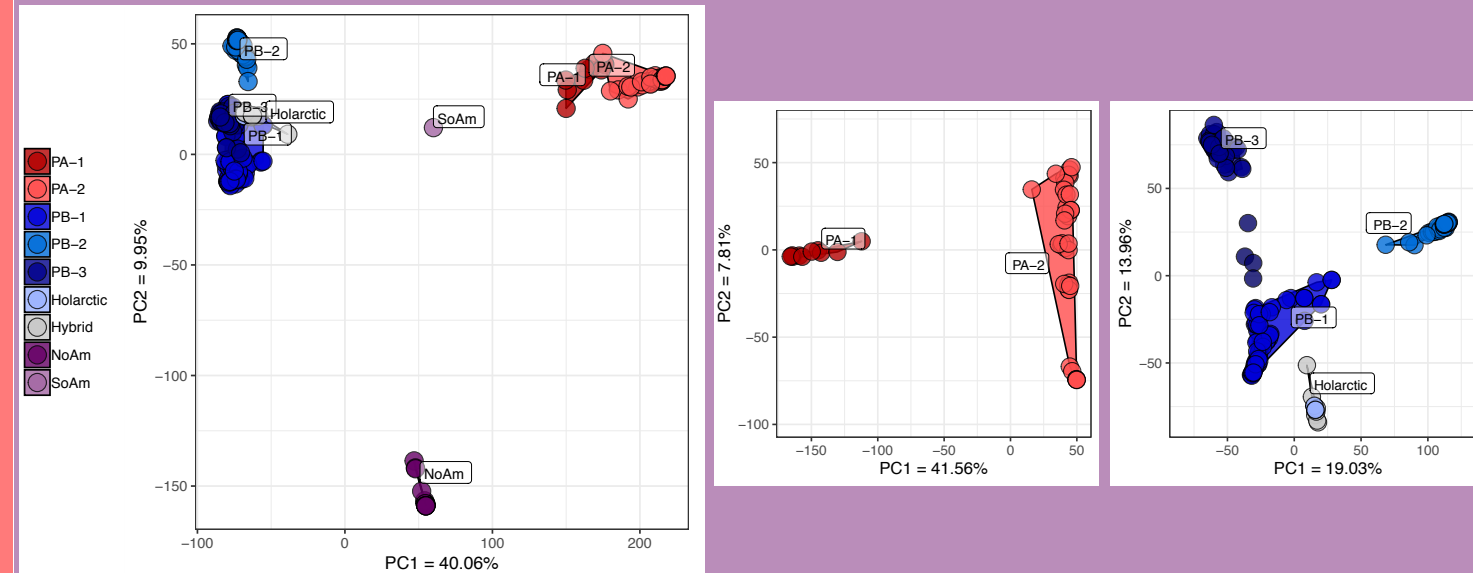
Admixed subpopulation is abundant in North America

- 21 strains share exact same genome-wide ancestry profile
- Most common lineage in North America, found in four locations

Reference: Langdon QK, Peris D, Eizaguirre JI, Opulente DA, Buh KV, Sylvester K, et al. (2020) Postglacial migration shaped the genomic diversity and global distribution of the wild ancestor of lager brewing hybrids. PLoS Genet 16(4): e1008680.

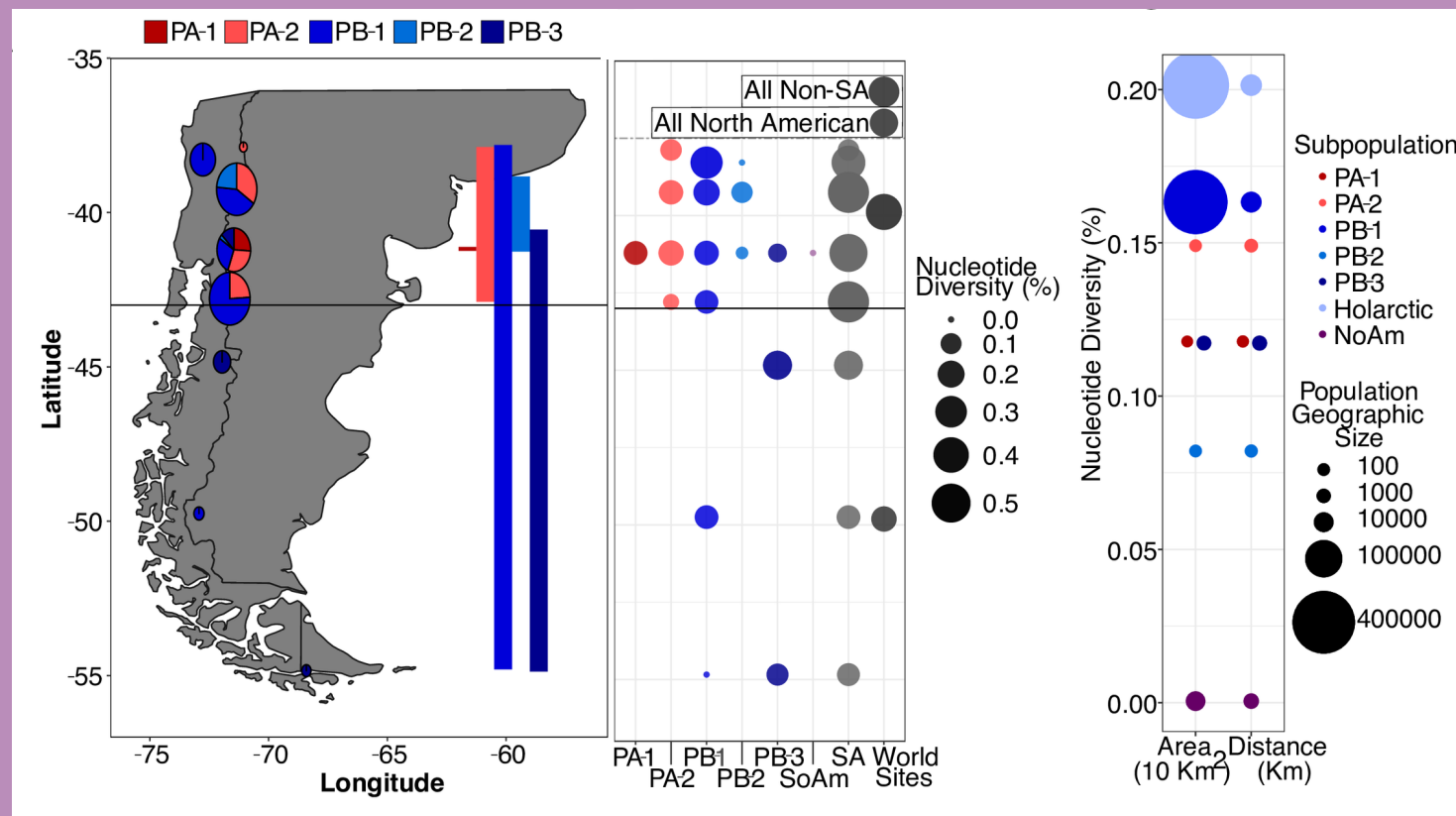
<https://doi.org/10.1371/journal.pgen.1008680>

Population Structure and Genetic Diversity



Two major populations, consisting of six subpops

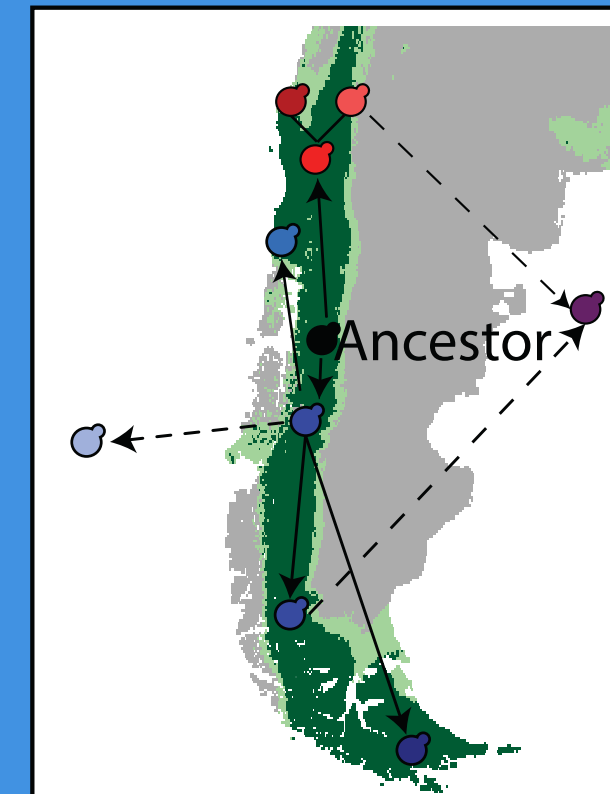
- Pop A – Only found in Northern Patagonia
 - PA-1 and PA-2
- Pop B – Globally distributed, but primarily in Patagonia
 - Holarctic, PB-1, PB-2, and PB-3



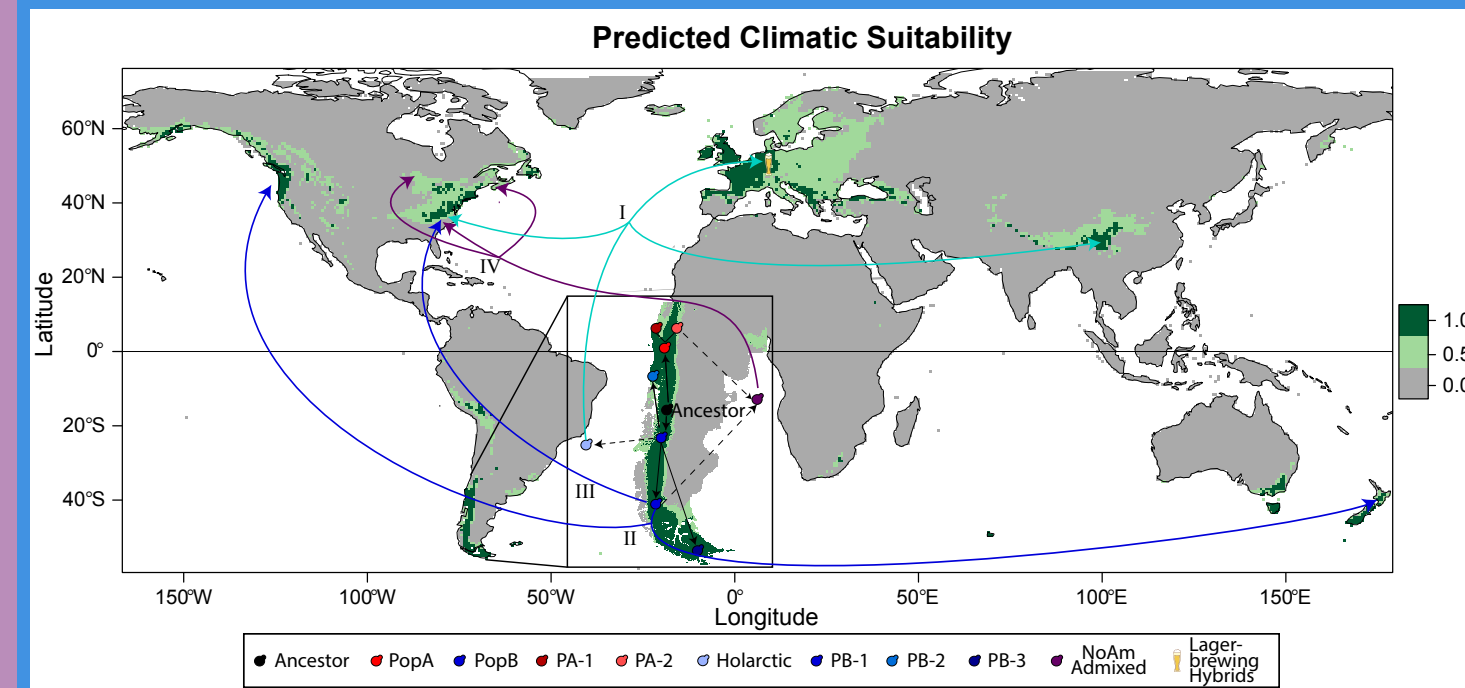
Northern Patagonia is a hotspot of diversity

- More genetic diversity in Patagonia than found globally
- Within Patagonia more diversity north of 43°S
- Genetic diversity generally, but not always, scales with geographic area encompassed

Migration and Climatic Suitability



- Environmental niche modeling suggests other regions of the globe are climatically suitable.
- *S. eubayanus* likely radiated into six subpops in Patagonia then migrated globally.
- I. The Holarctic subpopulation was drawn from the PB-Holarctic gene pool and colonized the Holarctic ecozone.
- II. PB-1 colonized the Pacific Rim, including New Zealand and Washington state, USA
- III. An independent dispersal event brought PB-1 to North Carolina, USA.
- IV. Outcrossing between PA-2 and PB-1 gave rise to a low-diversity admixed lineage that has recently invaded a large swath of North America



Acknowledgements: This material is based upon work supported by the National Science under Grant Nos. DEB-1253634 (to CTH) and DGE-1256259 (Graduate Research Fellowship to QKL), the USDA National Institute of Food and Agriculture Hatch Project Nos. 1003258 and 1020204 to CTH, and in part by the DOE Great Lakes Bioenergy Research Center (DOE BER Office of Nos. DE-SC0018409 and DE-FC02-07ER64494 to Timothy J. Donohue). QKL was also supported by the Predoctoral Training Program in Genetics, funded by the National Institutes of Health (5T32GM007133). DP is a Marie Skłodowska-Curie fellow of the European Union's Horizon 2020 research and innovation program (Grant Agreement No.747775). DL was supported by CONICET (PIP11220130100392CO), FONCYT (PICT 3677, PICT 2542,) Universidad Nacional del Comahue (B199), and NSF-CONICET grant. CTH is a Pew Scholar in the Biomedical Sciences and H. I. Romnes Faculty Fellow, supported by the Pew Charitable Trusts and Office of the Vice Chancellor for Research and Graduate Education with funding from the Wisconsin Alumni Research Foundation (WARF), respectively.

