

A collection of indigenous *Saccharomyces cerevisiae* strains from appellations of origin in Portugal and France

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Introduction

The model organism *Saccharomyces cerevisiae* stands today at the forefront of molecular biology, functional analysis and genomics.

This yeast is predominantly found in association with human activities, particularly the production of alcoholic beverages such as wine.

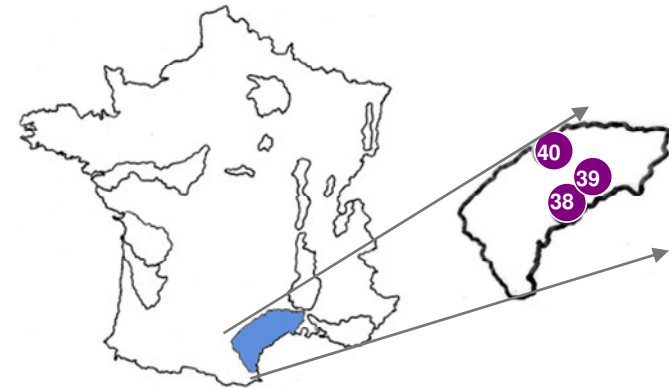
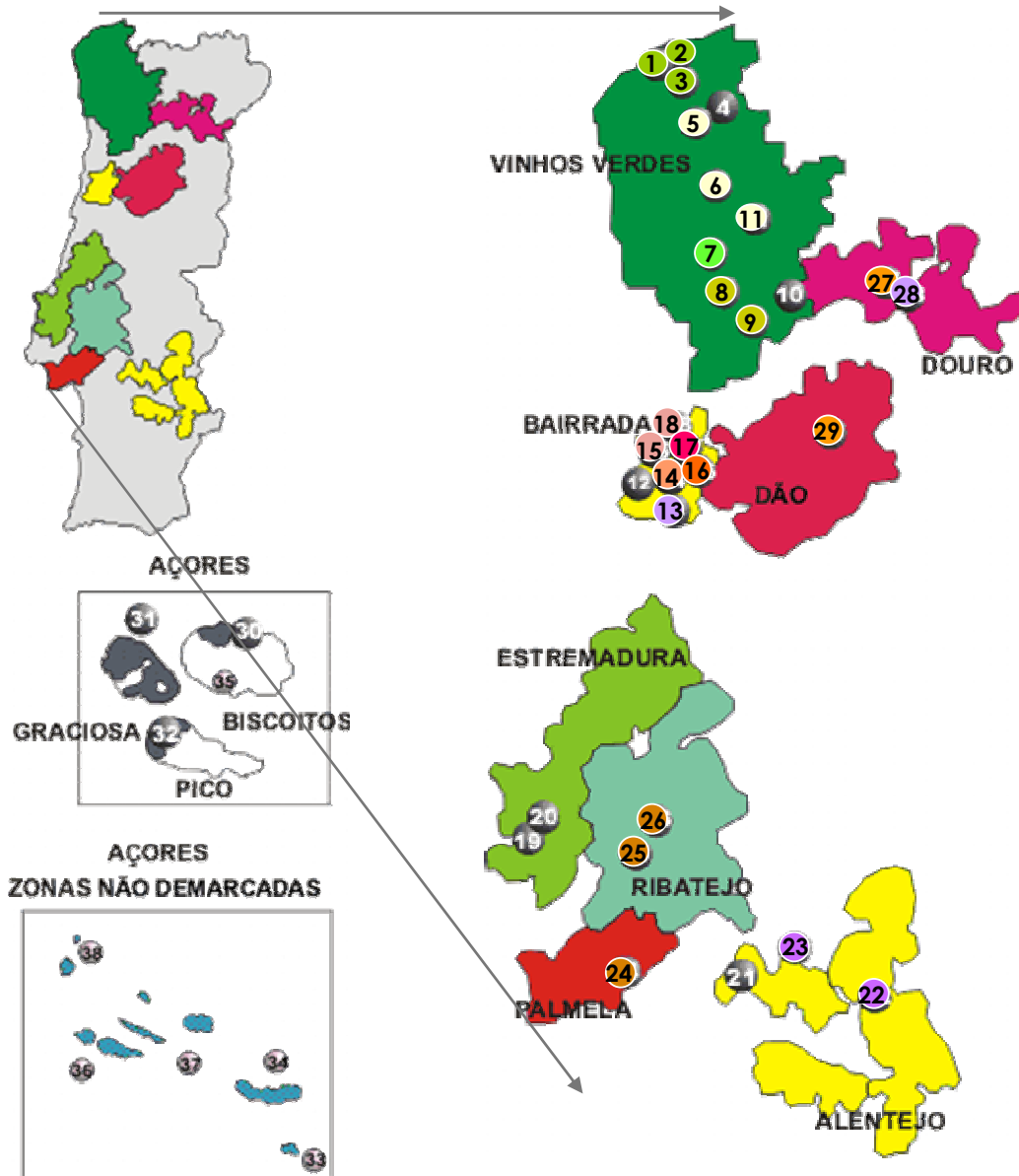
In winemaking environments, a huge phenotypic diversity of *S. cerevisiae* strains can be encountered, and this diversity has been explored for several decades to select strains with the best oenological properties.

Previous studies:

- ❖ Great biodiversity of *S.cerevisiae* strains in Vinhos Verdes and Languedoc wine region,
 - ❖ each vineyard contains differentiated *S. cerevisiae* populations, hypothesizing the occurrence of specific native strains that can be associated with a *terroir* (Schuller *et al.*, 2005; Schuller *et al.*, 2007)
 - ❖ Microsatellite analysis showed that genetic differences among *S. cerevisiae* populations derived from both “diagnostic” vineyard-, specific alleles and the accumulation of small allele-frequency differences across ten microsatellite loci (Schuller and Casal, 2007)
- ❖ Dissemination of commercial yeasts in the vineyard is restricted to short distances and limited periods of time (Valero *et al.* 2007).

From the biological materials that were collected under the mentioned research projects, in winemaking environments in Portugal and France, we constituted one of the largest bio-databanks of *S. cerevisiae* strains.

Sampling sites



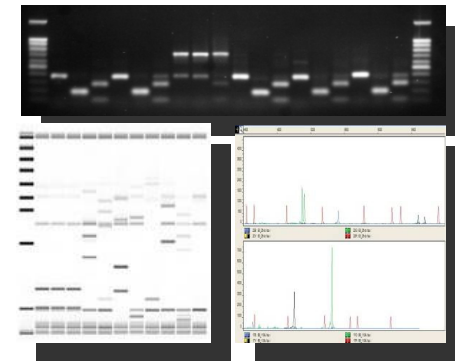
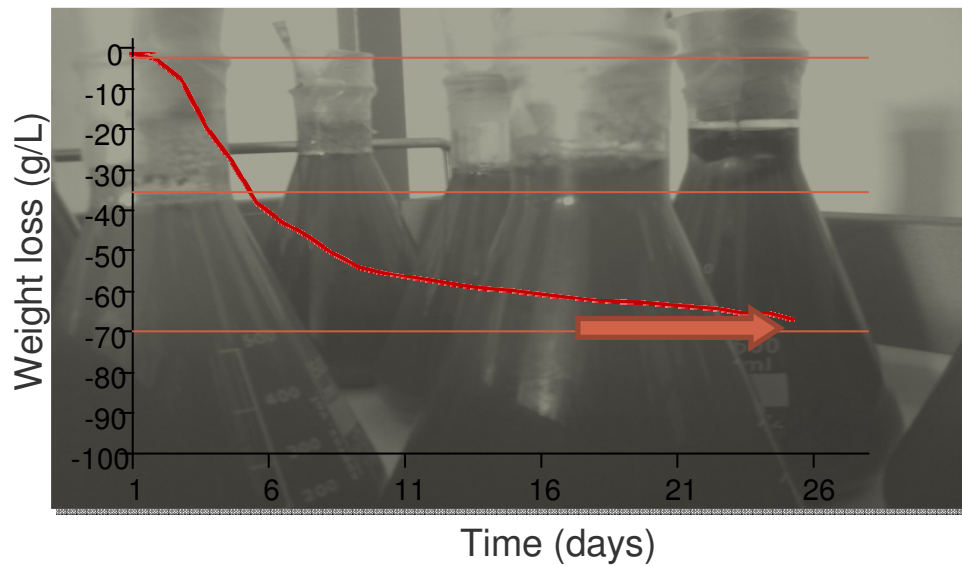
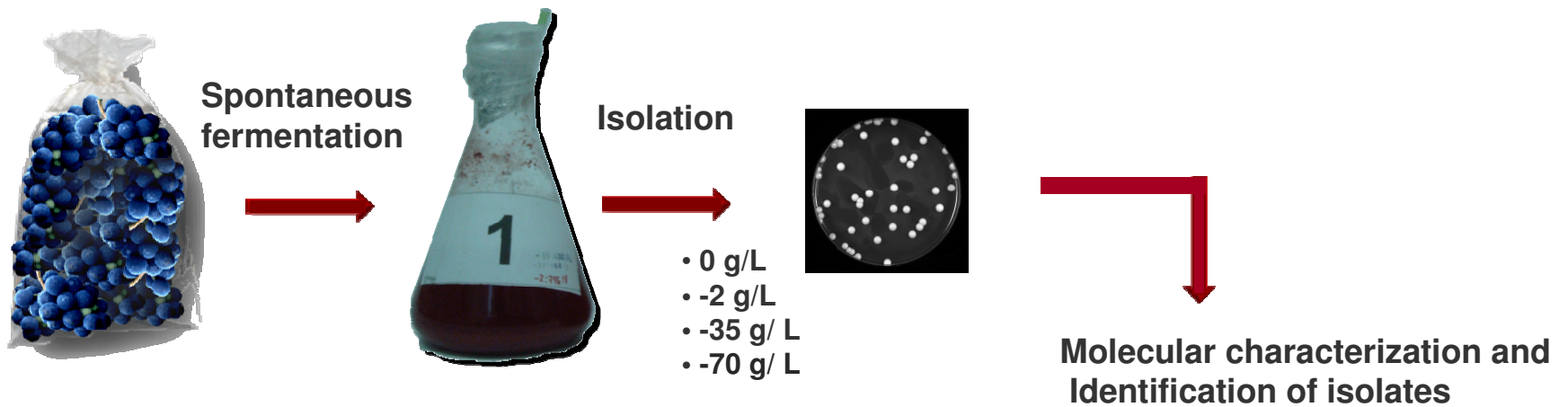
- Alvarinho ● Avesso ● Arinto
- Loureiro ● Aragonês ● Castelão
- Touriga Nacional ● Baga ● Bical
- M. Gomes ● Verdelho ● Terrantez
- Carignan

Since 2001, 604 grape samples were collected

10 Wine Regions
13 Grape varieties
40 Vineyards

Materials and Methods

Yeast isolation



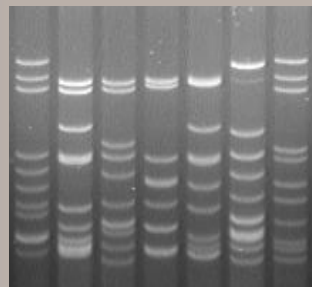
Materials and Methods

Molecular typing

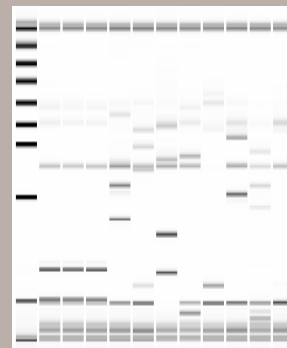
A previous survey performed with 23 commercial yeasts strains showed the same discrimination power of the methods.

(Schuller *et al*, 2004)

Mitochondrial DNA restriction analysis (mtDNA RFLP)



Interdelta sequence analysis



Preliminary screening

Microsatellite analysis



Microsatellite	Chromosome	Position/ORF	Repeat
ScAAT 1	XIII	86 901 – 87 129	ATT
ScAAT 2	II	YBL084c	ATT
ScAAT 3	IV	YDR160w	ATT
ScAAT 4	VII	431 334 – 431 637	ATT
ScAAT 5	XVI	897 028 – 897 259	TAA
ScAAT 6	IX	105 661 – 105 926	TAA
YPL009	XV	YOR156c	TAA
ScYOR267C	XV	YOR267c	TGT
C4	XV	110 701-110 935	TAA+TAG
C5	VI	210 250-210 414	GT

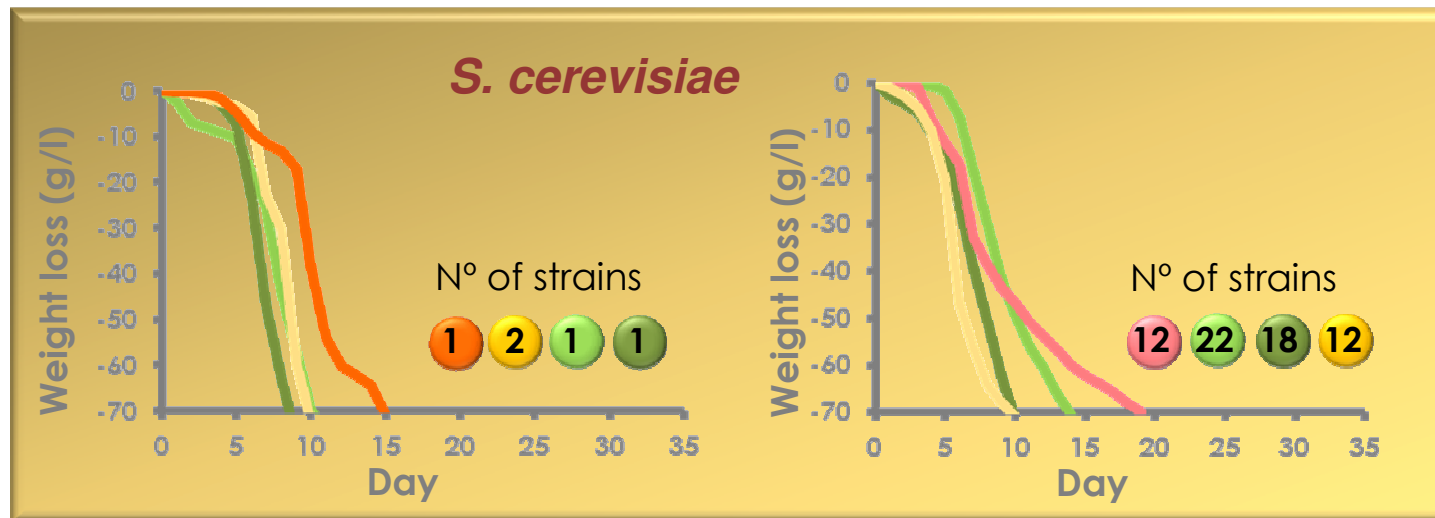
In depth characterization

Results

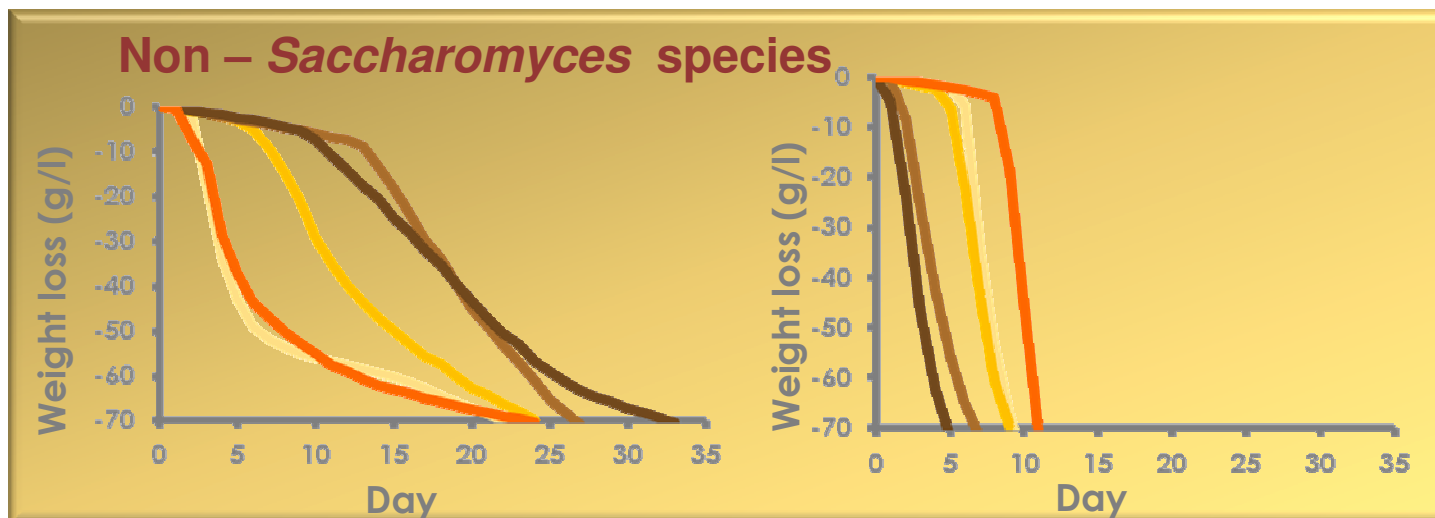
Number of *S. cerevisiae* strains obtained from the wine regions

	Nº of grape samples	Nº of spontaneous fermentations	Nº of isolates	Nº of <i>Saccharomyces cerevisiae</i> strains
Vinhos Verdes	282	115	3450	516
Bairrada	126	22	660	137
Açores	88	49	1470	169
Languedoc	108	72	2160	103
Total	604	258	7740	752

Fermentation kinetics

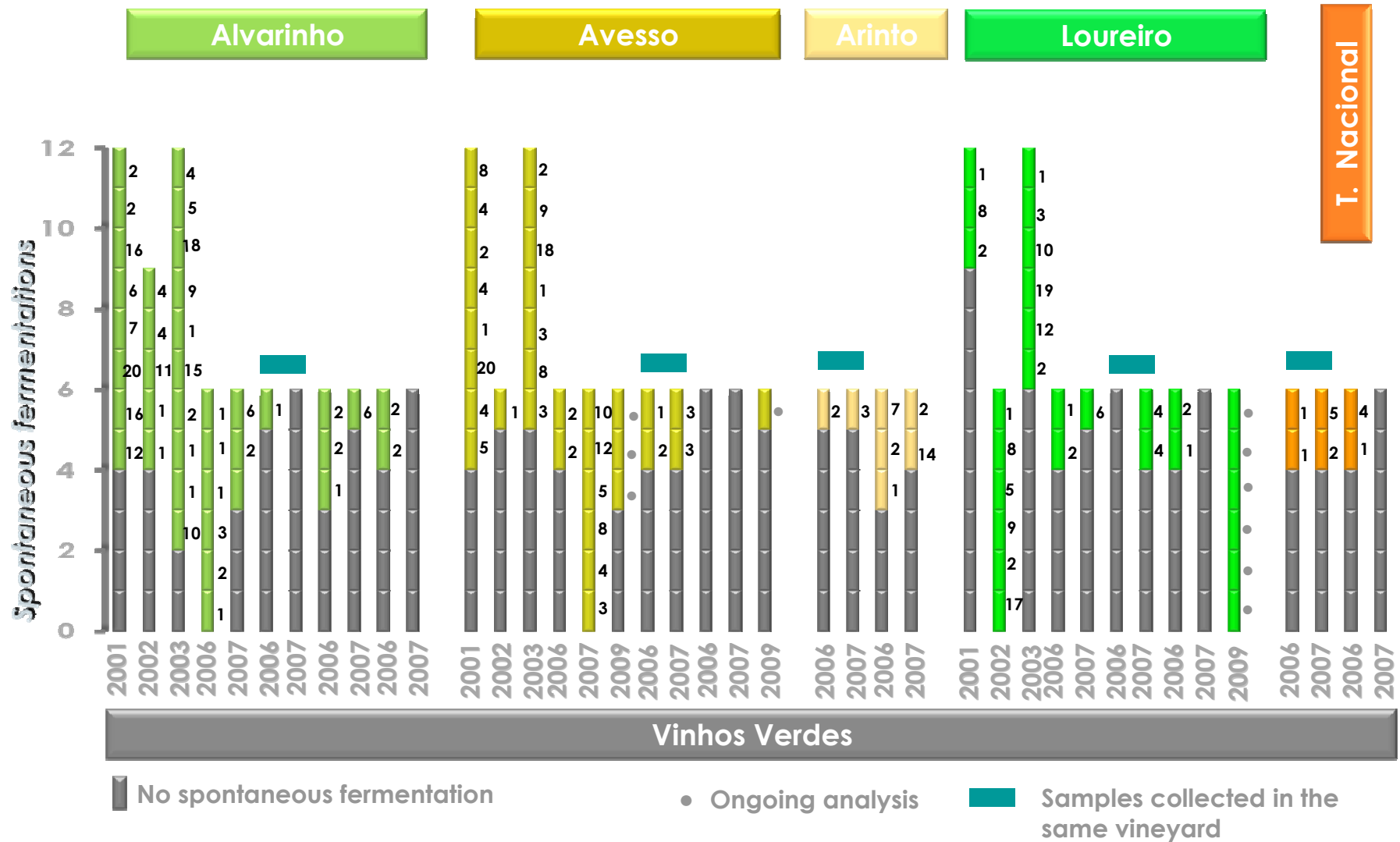


- Aragonês
- Arinto
- Touriga Nacional
- Castelão
- Trincadeira
- Baga
- Alvarinho
- Loureiro

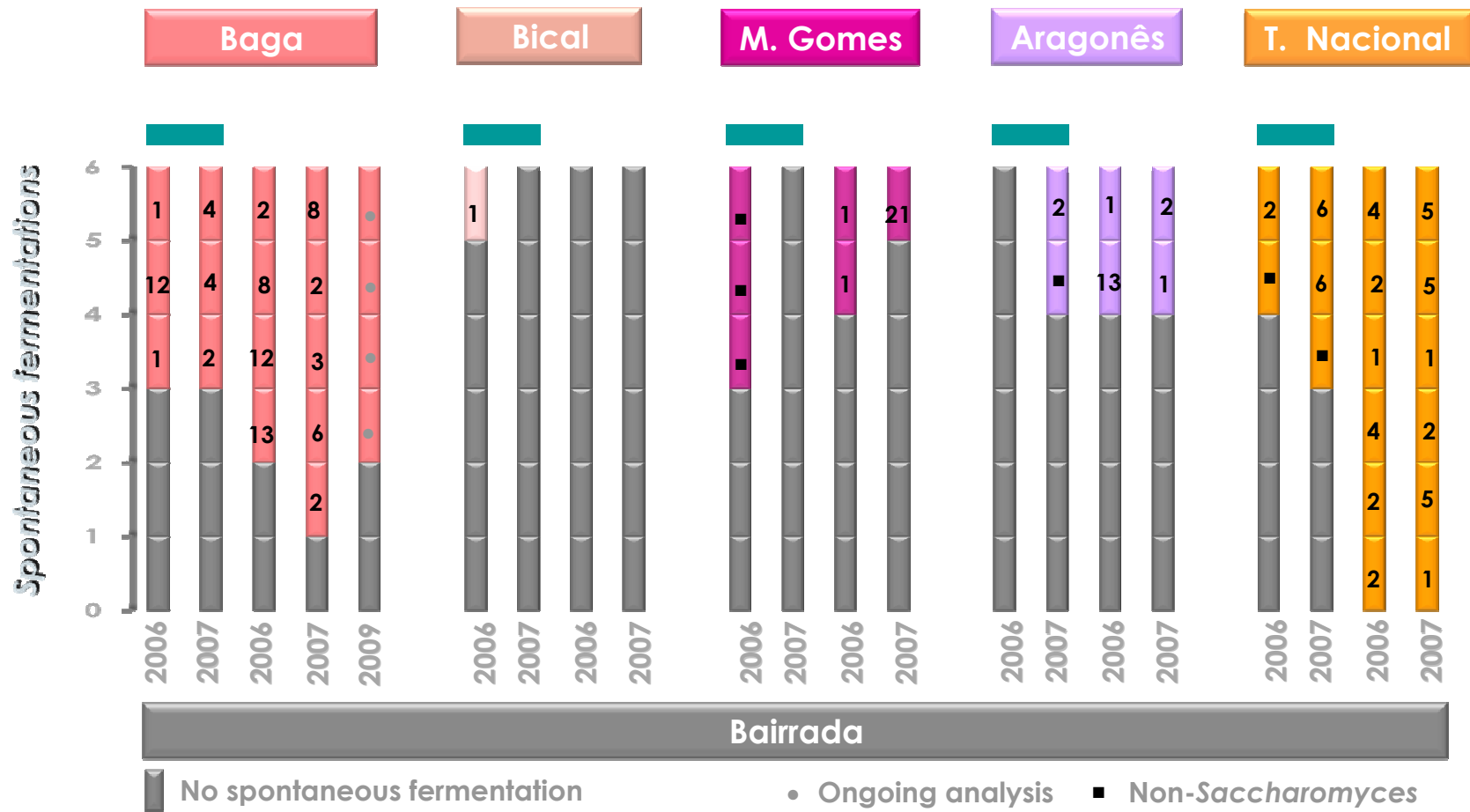


Results

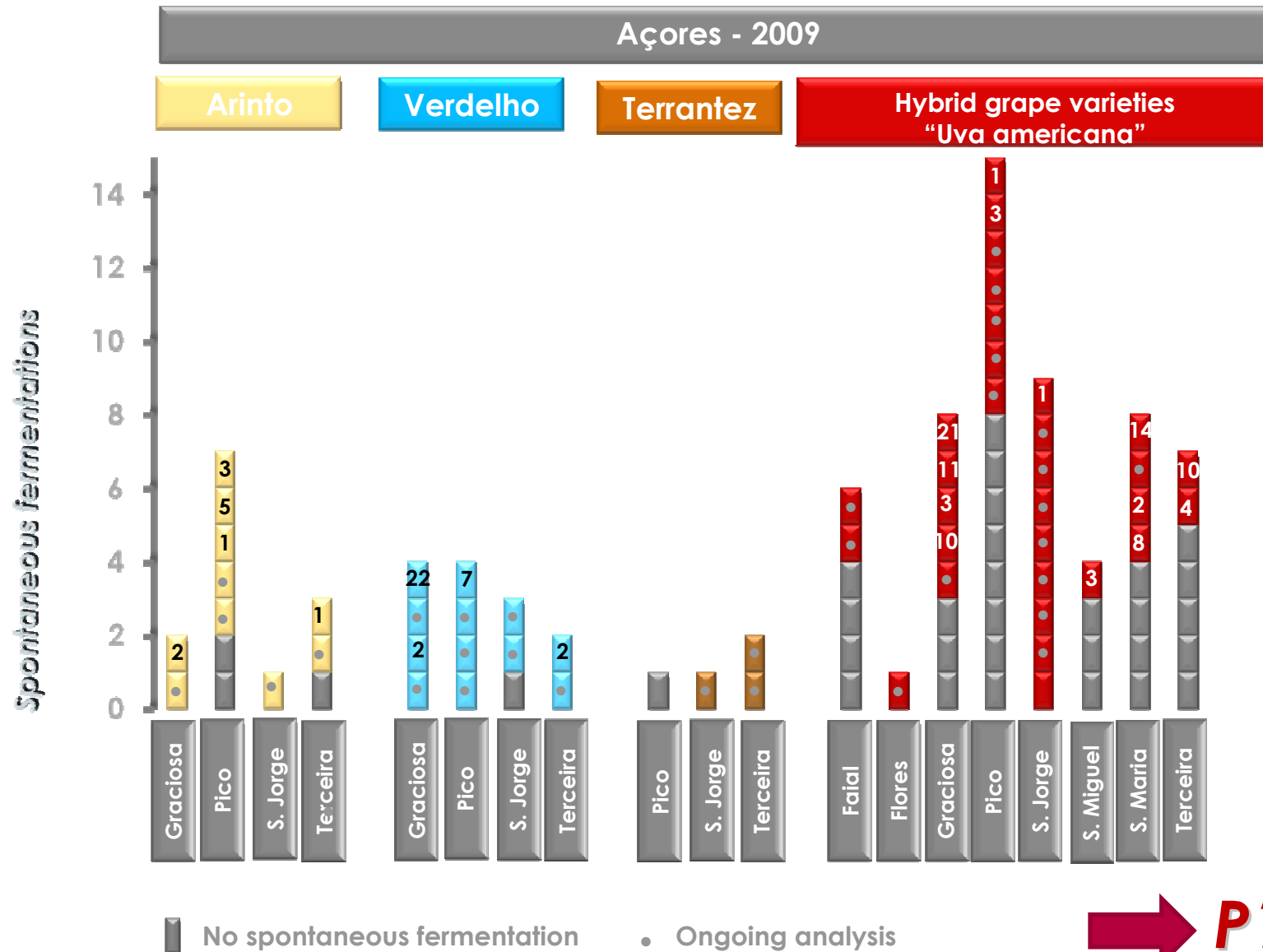
S. cerevisiae strains involved in spontaneous fermentations



S. cerevisiae strains involved in spontaneous fermentations



S. cerevisiae strains involved in spontaneous fermentations



Saccharomyces cerevisiae wine strain collection

<http://scwsc.bio.uminho.pt>

The site encloses information about:

- Grape varieties
- Wine Regions
- Molecular methods
- Genetic data
- Publications

Saccharomyces cerevisiae
wine strain collection

Home
Database
Yeast Strain Isolation >
Molecular analysis >
Methods >
Wine Regions >
Vineyards >
Grapes >
Our Publications
Acknowledgements

Saccharomyces cerevisiae is the yeast responsible for alcoholic fermentation that has been used for millenia in wine making, baking, brewing and distilling - as mankind's oldest domesticated organism. This species became the model organism par excellence, was the first eukaryotic genome to be completely sequenced, and provided a wealth of knowledge on its molecular and cellular biology, standing today at the forefront of molecular biology and functional analysis in genetics and genomics.

However, as for many other laboratory model organisms, understanding of the ecological, evolutionary and population genetic features that shaped the biology of *S. cerevisiae* is underscored by a wealth of knowledge on molecular and cellular biology, mainly obtained from a very limited number of reference laboratory strains. In the last few years yeast researchers developed a keen interest to identify genomic variability between wild-type yeast strains from different ecological niches or strains that are used for different technological applications.

Phenotypic variation among wine yeast is well-known among strains and was recognized by winemakers before being appreciated by geneticists. Significant heterogeneity is apparent among strains in the production of ethanol, acetic acid, sulfite, and other metabolic products. In this context emerged the *S. cerevisiae* wine yeast strain collection for the conservation of biodiversity, sustainable development of genetic resources and for an equitable sharing of genotypic data.

This *S. cerevisiae* strain collection was obtained from different winemaking regions in Portugal and France by collecting strains in yearly sampling campaigns from 2001 on. For each strain record, numerous characters are annotated, including metadata and allelic data for a set of highly polymorphic microsatellites.

This strain collection has been constituted at the Centro de Biologia Molecular e Ambiental (CBMA, Minho University, Braga, Portugal) in collaboration with the Unité Mixte de Recherche Sciences pour Oenologie of the Institut National de la Recherche Agronomique (Montpellier, France), BIOCANT, Centro de Inovação em Biotecnologia (Cantanhede, Portugal), CESAM and Biology Department of the Universidade de Aveiro (Aveiro, Portugal), L-INIA Dois Portos, INRB IP, (Dois Portos, Portugal) and the Centro de Investigação de Tecnologias Agrárias (Dep. Ciências Agrárias, University of the Açores).

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Saccharomyces cerevisiae
strains for winemaking
Molecular characterization
and genetic diversity

CBMA
VITH

biocant
CENTRO DE INOVAÇÃO EM BIOTECNOLOGIA

EVN

INRA

EUROPEAN UNION
EUROPEAN COMMISSION

Ciência, Inovação
2010

FCT
FUNDAÇÃO PARA A CIÊNCIA E A TECNOLOGIA
MINISTÉRIO DA CIÊNCIA, TECNOLOGIA E ENSINO SUPERIOR

Agro

GOVERNO DA REPÚBLICA PORTUGUESA

Saccharomyces cerevisiae wine strain collection

The database allows different searches among the *S. cerevisiae* strains:

- Collection number
- wine region
- vineyard
- grape variety

Saccharomyces cerevisiae
wine strain collection

SCWSC Search

Go to Collection Number

Collection Number:

Search Parameters

Country: Wine Region:

Vineyard: Grape Variety:

Collection Number contains:

Number of search results: 501

Collection Number	Country	Wine Region	Vineyard	Grape Variety	Location
GMYP002	Portugal	Vinho Verde Wine Region [Info]	Quinta de Covela	Avesso [Info]	41° 07' N 7° 58' W [Go]
GMYP005	Portugal	Vinho Verde Wine Region [Info]	Quinta de Covela	Avesso [Info]	41° 07' N 7° 58' W [Go]
GMYP008	Portugal	Vinho Verde Wine Region [Info]	Quinta de Covela	Avesso [Info]	41° 07' N 7° 58' W [Go]

Each strain contain complete information about all microsatellite data, origin and isolation.

SCWSC Strain Detail

Collection Number: [GMY002](#)

Country: [Portugal](#) [Search]

Wine Region: [Vinho Verde Wine Region](#) [Search] [Info]

Vineyard: [Quinta de Covela](#) [Search] [Website]

Grape Variety: [Avesso](#) [Search] [Info]

Location: [41° 07' N 7° 58' W](#) [Go]

Microsatellite Details:

ScAAT1-1	ScAAT1-2	ScAAT2-1	ScAAT2-2	ScAAT3-1	ScAAT3-2	ScAAT4-1	ScAAT4-2
216	0	372	378	247	265	329	0
ScAAT5-1	ScAAT5-2	ScAAT6-1	ScAAT6-2	C4-1	C4-2	C5-1	C5-2
216	219	258	258	0	0	0	0
C11-1	C11-2	YPL009c-1	YPL009c-2	YOR267c-1	YOR267c-2		

Conclusions

The collection of *S. cerevisiae* strains is an important resource for:

- ❖ ecological studies and biodiversity conservation;
- ❖ sustainable development of genetic resources;
- ❖ equitable sharing of genotypic and phenotypic data;
- ❖ selection of winemaking strains that could be used to produce wines with characteristic aromas.

Acknowledgements

To all producers that provided samples...

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