

Hi, how are you?. My name is Diego Libkind and I'm yeast scientist from Argentina. I work at the Applied Microbiology and Biotechnology Lab. in the city of Bariloche, which is located in the northwestern area of Patagonia as shown in the map at the right. I have been working on yeast biodiversity and biotechnology for more than 10 years but recently I had the luck to entered the fascinating world of Brewing science. In the lower part of the slide you can see 3 pictures, two of which you should easily recognize: a bunch of yeast cells on the top and tempting glass of Lager beer on the right. The connection between these two I believe is pretty obvious. The third picture belongs to a south hemisphere endemic fungus named «Cyttaria» (is the name of the genus). Our group has demonstrated that Cyttaria fruiting bodies (the orange gall-type structure) are a natural habitat for a wide range of yeast species. So one of my purposes today is to show you a potential connection between the Cyttaria fungi and the crispy Lager.



First let me show you how Bariloche looks like, so that you can imagine how boring is the place where I perform my investigations. The city is located near the Nahuel Huapi lake and the Andes mountain chain. It is one of the most important touristic cities in Argentina, and definitely from Patagonia. If you plan to visit this region of the planet sometime you must visit Bariloche, not only because of the nice sightseeing you will get but also due to our great beers. We have about 12 microbreweries in a city that has 100.000 thousand inhabitants. So probably one of the cities with highest density of breweries in Argentina. Only 150 km apart from Bariloche you can also find the most important hop production region of Argentina. So you can see that Brewing science and beer itself is quite important from where I come from.

Structure of the talk:



Ok, then. The presentation will be somehow structured as follows. First, a fast overview of what yeast, but from probably a different perspective to what you are used to. We will briefly discuss their diversity, habitats, role in nature and finally how humans use them. Second, I will introduce you to the details of the recent discovery of the new species Saccharomyces eubayanus, and its implications in brewing yeast taxonomy. Also, I will like to introduce you to the concept of microbe domestication and to the new hypothesis of the origin of the unique Lager yeasts. Finally, I will share with you some unpublished data on the diversity of S. eubayanus, in fact you are the first to which I will be discussing these new results. I hope you enjoyed.

What are Yeasts?



As you may already know the English word yeast and its equivalents in many other languages are based on words meaning "foam" and "to rise", which are a direct reference to the fermentation processes that produce beer and bread. For this reason, yeasts are often thought of as fermentative ascomycetous fungi similar to Saccharomyces cerevisiae. In fact, it is not uncommon in some areas of molecular biology to treat the words "yeast" and "Saccharomyces" as synonyms. The discovery that some yeast taxa are basidiomycetes has broadened our perception of the nature of yeasts. As a consequence, we have come to view yeasts as fungi that asexually reproduce by budding or fission, which results in growth that is comprised mainly of single cells.



Today, more than 1500 yeast species are known which are distributed in a wide range of taxonomic groups. In other words, yeast represents a very heterogeneous group of fungi. As can be seen from the pictures, yeasts are highly variable in cell shape, size and colony colors. Pink to orange pigmentation in the colonies are the result of the accumulation of carotenoids inside the cells (like B-carotene).



In natural environments, yeasts occur together in communities and are widely distributed throughout all biomes of the world. They have been found in the upper levels of the atmosphere (above the clouds in the stratosphere), in the deepest parts of the oceans, in ancient glacial ice, and are abundant throughout the phyllosphere. I have found them in large quantities and diversity in extreme environments of Patagonia like acidic waters of volcanic origin (pH~1,5), glacial ice, highly UV exposed tree leaves and ultra-oligotrophic waters (which is almost distilled water due to the lack of nutrients and salts).

Yeasts participate in a number of complex processes in ecosystems. Free-living yeasts are primarily decomposers and are among the earlier colonizers of nutrient rich substrates, where they are followed by a succession of organisms that degrade dead organic matter. However, yeasts are not just decomposers but can assume a diversity of forms and functions in the natural world. Along with their role in the transformation of nutrients, they can engage in intimate relationships with other organisms as mutualists, competitors, parasites, or opportunistic pathogens.

Even though S. cerevisiae is commonly perceived as a harmless microorganism, given its more than 1000-year association with food and beverages production, numerous reports of human infections caused by this yeast exist in the medical literature. However, these typically occur in patients with other underlying illnesses that have their immunological system compromised or suppressed. It should be noted also, that among brewing yeasts only ALE yeast might be considered potential opportunistic pathogens due to their ability to grow at 37°C (human body temp). Lagers have no record of pathogenicity so far, and probably will remain so due to their lower growth temperatures.

Ironically, despite the huge importance of S. cerevisiae and related species, relatively little is known about its origins and natural lifestyle.



Yeasts are currently applied in a wide range of biotechnological disciplines as shown in this slide: besides traditional yeast fermentations, yeast are employed to obtain food and feed ingredients, and used as biocatalysts for the production of for example pharmaceuticals molecules. Yeasts are also used for the production of heterologous proteins such as enzymes, hormones, vaccines, etc. In other words, genes from other organisms are inserted into yeast and these are used as bio factories. They are also used for fundamental research in multiple biological disciplines. Also applied for Biomedical research, Bio control strategies and environmental biotechnology.

Note that brewing is just one of many applications that yeasts have (as a group, not meaning *Saccharomyces* species).

Yeasts: What are they used for?

Food	Yeast Species Involved	Food	Yeast Species Involved	
Beers and ales	Saccharomyces cerevisiae		Candida valida	Saccharomycos
	Saccharomyces bayanus		Saccharomyces bayanus	Jaccharonnyces
	Saccharomyces pastorianus		Yarrowia lipolytica	
	(=S. carlsbergensis)	nented olives and	Debaryomyces spp.	browing was a
	Saccharomyces bayanus var. uvarum	oucumbers	Candida spp.	E orewing veasi
Breads and bakery products	Saccharomyces cerevisiae		Kluyveromyces marxianus	- 81011119 90401
	Torulaspora delbruecki i		Lachancea cidri	
	Candida krusei (sourdough)		Pichia spp.	
	Candida milleri (sourdough)		Rhodotorula spp.	
	Kazachstania exigua (sourdough)		Saccharomyces spp.	
	Zygosaccharomyces rouxii	Kenkey (African fermented	Candida spp.	
Cachaça	Saccharomyces cerevisiae	maize)	Debaryomyces spp.	
	Schizosaccharomyces pombe	1	Kluyveromyces spp.	
Cheeses	Debaryomyces hansenii	1	Saccharomyces spp.	
	Candida spp.		Irichosporon spp.	
	Kluyveromyces marxianus	Kimchi	Candida spp.	그는 것은 것은 것을 다 가지 않는 것을 다 가 나는 것을 가 봐.
	Kluyveromyces lactis		Cryptococcus spp.	
	Yarrowia lipolytica		Debaryomyces spp.	
	Geotrichum candidum		Saccharomycopsis spp.	
	Other Geotrichum spp.		Kluyveromyces spp.	
	khodotorula spp.		Pichia spp.	
	Tricnosporon spp.		Rhodotorula spp.	
Other data and the	Saccharomyces cerevisiae	Luc Church	Saccharomyces spp.	
Other dairy products	Kluyveromyces lactis	Lao Chao	Saccharomycopsis tibuligera	
(e.g., kerir; yognurt,	Kluvyveromyces marxianus	Coursests (Chinese Mine)	Saccharomycopsis malanga	
Termented milk)	Candida Kelyr	Soy paste (Chiang: Miso)	Zygosaccharomyces spp.	Not Wright
	Candida famata	Courses disease (change)	Candida spp.	Factor 6 states
	Candida kruser	Soy sauce (rang yu; shoyu)	Zygosaccharomyces rouxn	
	Centrichum ann didum		Candida iamata Candida ataballati	Republic
	Varrowia lipolytica		Candida elcherisii	The second se
	Farrowra iiporycica Saesbaromusos corguisiae		Canarda versaulis	
	Saccharomyces cerevisiae		Other Candida spp.	
Cocoa	Saccharomyces bayanus	Tea fungus	Zugosaccharomucas Kombuchaensis	Quality PREDUCT OF THE TO
	Saccharomyces caravisiaa	ica lungus	Condida son	The second se
	Hansoniasnom uvarum	Wines	Saccharomyces cerevisiae	
	Kloeckera apiculata		Saccharomyces bayanus	N. U. U.S. CONO
	Kluvveromvces marxianus	1	Saccharomyces bayanus var. uvarum	MWW W
	Pichia fermentans	1	Saccharomyces kudriavezii	Active Brewing
Coffee	Kluyveromyces marxianus	1	"Saccharomyces sake"	A DONNE
	Saccharomyces bayanus		Other Saccharomyces spp.	
	Schizosaccharomyces spp.		Hanseniaspora uvarum	Quality month and a
	Candida boidinii		Kloeckera apiculata	a martine a second
Fermented meats and sausages	Debaryomyces hansenii	Silage	Candida spp.	
	Candida spp.	-	Cryptococcus spp.	
	Cryptococcus spp.	1	Pichia spp.	
	Rhodotorula spp.	1	Saccharomyces spp.	
	Saccharomyces cerevisiae	1	Trichosporon spp.	
	Yarrowia lipolytica	Probiotics	"Saccharomyces boulardii"	
Fermented milks	Kluyveromyces spp.	1	Saccharomyces cerevisiae	
	Candida parapsilosis	1	Kluyveromyces marxianus	
	Candida krusei		Candida spp.	

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Section Co

If we only focus on the yeast species used in fermented foods and feeds you can see the large number of different yeast species involved. However, when focusing on beer *Saccharomyces* leads the scene. Considering that more than 300 species correspond to fermentative species, do any one know or guess why *Saccharomyces cerevisiae* and related species are the ones chosen for brewing. And please do not answer because it comes in a fancy package as a very clever argentinean homebrewer did.



The factor that unites all species of Saccharomyces is the ability to produce significant amounts of alcohol by fermenting simple sugars. However, there are many other species that can ferment simple sugars to ethyl alcohol, but the quantitative expression of this ability is extremely variable. It becomes clear from the present table that only certain species of *Saccharomyces* are able to produce (and thus also tolerate) above 8% alcohol, and this answers our open question.



As you already know, modern brewing strains are not exactly equal to those found in nature. Though they derive from once wild yeasts, they have suffered many genetic changes becoming at the end a refined fermentative machine, in other words "wort fermentation specialists". This is the result of a process called domestication. For example, domestication of crops and livestock selects for desirable characteristics through directional breeding so that domesticated lineages become genetically distinct from their wild ancestors in ways that make them more useful to Humans. Microbial domestication was different since only in the late nineteenth century yeasts were considered as responsible for the fermentation process, Even yeast were not know as important in brewing, re-utilization from batch to batch and also selection of the best batches by brewmasters definitely contributed to the shaping of the genetics and consequently to the brewing characteristics of the strains used today to produce Ales and Lagers.

Some of the mechanisms that generate such genetic modifications include genome duplication, which involves duplicating the complete set of genes and thus to have gene products produced twice as much. Hybridization between two closely related species, which, for certain traits result in the merge of both species characteristics in a single strain. Also incorporation of other species DNA through horizontal gene transfer and specific mutations that occur randomly in the genome. It should be noted that any of these events has a reduced probability of occurrence and even less if we consider those events that significantly change something that might affect the cell fitness or adaptation to the brewing environ. But, the stress situation imposed by the wort gravity and the high alcohol among others; and the huge number of cells produced in a single batch, help to increase the odds.



The taxonomy of brewing yeasts, especially that of Lagers yeasts, is quite confusing. Even for me who I'm a member of the Systematics and Nomenclature Committee of the International Commission on Yeasts. I apologize in the name of all my colleagues that we couldn't solve this earlier. So, until recently our general view was that S cerevisiae was responsible of Ale production as well as most wines. That Lagers depending on the authors and year of publication could be any of these three species, Suva, Sbay and Spas. Two of which it was not clear if they were different species or different varieties of a single species. Both Suva and Sbay are frequent in white wines, cider and Champagne production but have been also related to Lager brewing.

The habitat of Scer was believed to be the surface of grapes or equivalent sugary rich fruits, but it has recently become clear that the bark and soil of certain tree species is the primary habitat of this species (mainly oaks). Suva has also been found in such environments in different parts of the north hemisphere. This is not the case of Sbya and Spas two species that so far have been only isolated from brewing environments (or winery in case of sbay).

Nowadays Lager brewing strains are mainly referred as *S pastorianus*. This species is a known hybrid formed by the fusion of a Scer strain with another Saccharomyces psychrophilic yeast which contributed to the ability to ferment at low temp (among other things) that characterizes Lager yeasts.

It was believed that S. bayanus could be the missing parental species due to some genetic resemblance but results were contradictory.

Tree bark: Saccharomyces natural habitat?



In recent years it has become evident that Saccharomyces primary natural habitat are not the grapes or equivalent sugary rich environments. Instead, oak forests, in particular tree bark and soil became frequent sources of wild Saccharomyces. It is difficult to assimilate at first, I know, at least it was for me when I first read about this, but after a few years capturing wild yeasts from natural forest I must say that is true. As proof I can show you this electron micrograph of Oak bark showing Saccharomyces yeast cells. Also, indicated with the orange arrow, an ascus with 4 ascospores, typical sexual structure of wild *Saccharomyces*. This Shows that saccharomyces yeasts not only can thrive in tree bark but are also happy enough to have sex!.



Several Studies have shown the occurrence of Saccharomyces in Canada/USA, europe and Japan. Five years ago, in cooperation with Dr. Jose Paulo Sampaio from the University of Nova Lisboa in Portugal we started a worlwide search to describe the natural distribution of Saccharomyces yeasts. We sampled several geographic regions but focused mainly in the south, visiting Australia and New Zealand, and off course Patagonia. We studied mainly bark and soil from the so called southern beech trees of the genus Nothofagus, but also investigated a unique habitat which is the sugary rich fruiting body of the fungus Cyttaria.



This fungus is an exclusive parasite of Nothofagus trees which are endemic of Patagonia, Australia and New Zealand. Trees infected with this fungus produce tumors from which Cyttaria fruiting bodies appear in late spring and summer. These galls contain many simple sugars and therefore when mature go through a spontaneous natural fermentation process mediated by yeasts. In fact, local Indians used to elaborate a fermented beverage from this fungus. Unfortunately, this unique habit of producing and alcoholic drink by fermenting a fungus with another fungus (yeast) has been lost. Probably due to the replacement of Cyttaria with better tasting fruits like apples (brought by the Spanish).



From our worlwide survey we obtained thousands of wild Saccharomyces strains of different species. We also found that Nothofagus forests in the south are occupied mostly by the cold tolerant Saccharomyces uvarum, although we saw that in Patagonian forests it was not alone. In certain species of Nothofagus we were able to isolate a second species, also adapted to cold, which based on preliminary genetic analysis seemed similar to S. bayanus. We will name it for now Patagonian S. bayanus, given it was only recovered from such geographic region.



Given that there were no records of wild S. bayanus strains we decided to compare it with a group representative collection strains of S. bayanus.

What we first saw is that all the strains regarded as pure S. bayanus were actually hybrids, either double hybrids with contributions of S. uvarum and patagonian bayanus, or triple hybrids with genetic contributions of a third species: S. cerevisiae. We also checked that patagonian bayanus was a clean linneage, a pure strain that had no contributions from other Saccharomyces species.



We found that S. bayanus is not a valid species, but a group of hybrids. That S. uvarum is a real species distinct of the patagonian S. bayanus strains, and that these constitute a real species too which we named S. eubayanus, meaning the true or real bayanus.

NEXT.

As a summary we can say that brewing strains are constituted mainly from genetic contributions of three biological species: S. cerevisiae, S. uvarum and the recently described S. eubayanus. S. pastorianus and S. bayanus are hybrids of different combinations of these species or of all of them, as is the case of several S. bayanus strains.

NEXT.

Sorry to complicate things further but you should know that hybrids between cerevisiae and a fourth species named kudrivazevii have been detected in Belgian beers.



Then, to reinforce this, we can say that "S. uvarum" and "S. eubayanus" should be used as descriptors of biologically meaningful species, whereas "S. bayanus" and "S. pastorianus" should be restricted to the domesticated and hybrid strains.

The next question to answer was whether S. eubayanus could be the progenitor of Lager yeast as suggested by our previous findings, and how this could happen.



For the previous experiments we studied only portions of DNA that we knew were informative. For this we decided to completely sequence the genome of several strains including off course S. eubayanus and S. pastorianus representatives. We saw that the non-cerevisiae (or non-ALE) portion of S. pastorianus genome was almost identical to the one of S. eubayanus.

But, Is it 99,5% close enough? you might be asking yourself. Well For example, wild strains that belong to the same species from different populations (like S. cerevisiae or even S. uvarum) can differ in their complete genome in up to 2 %. Here, we see only 0,5% difference. Thus we conclude that S. eubayanus is the missing progenitor of Lager Yeast.



We worked on two hypotheses. The first one meant that the parental strain of S. eubayanus naturally lived in European forests that now have disappeared, or that no one, despite the large number of surveys that have been done, could yet find it. The hypothetical scenario implies that S. eubayanus strains from Patagonia arrived there from europe and that they are not native. This is because of the high genetic similarities we see between both. But, this contradicts with the high frequency and abundance of S. eubayanus in patagonian forests, higher than any other wild saccharomyces that has been found in other parts of the world. Also, if it has colonized south America, why it has not colonized other regions like north America, australia and so on.

NEXT.

Our second hypothesis implies an epic journey of a Patagonian strain of S. eubayanus to europe. Such a journey might not represent a difficulty for wild yeasts because they produce highly resistant spores. These spores can be carried around by insects and humans. When transatlantic trade started, spores or cells could have taken a ride in timber, fermented beverages or food, native plants and so on.

We detect an approximately 200 years window whe this could have happened, initiating when Patagonia was definitely colonized and reasonable time before the first Lager yeast was isolated by Hansen in late 19th century.



We speculate that when Lager production started in Europe in 15th century fermentation was carried out by S. cerevisiae which can still ferment at low temperatures, although we know it can do it better at higher temperatures; or as an alternative, by cold tolerant European species like S. uvarum or S. kudriavzevii. Or a combination, in those years mixed fermentations were common. When S. eubayanus appeared and hybridized with a S. cerevisiae already adapted to brewing, it become an early Lager yeast. This hybrid was then further domesticated and became the modern Lager yeast that we use today.



Some of the genetic changes we detected when comparing the Patagonian eubayanus genome with that of the non-Ale portion of Lager yeast gave us some idea of the modifications that occur during the domestication process.

For example we found that the S. cerevisiae genes related to a better utilization of maltose were integrated into the S. eubayanus portion of Lager yeasts, suggesting strong selection for optimal sugar utilization during brewing.

We all know that Sulfite formation is also important in lager-brewing because sulfite is an antioxidant and flavor stabilizer. There are two types of transporters that get sulfate inside Saccharomyces cells, and they are genetically encoded by SUL1 and SUL2 genes. Both S. cerevisiae and S. eubayanus DNA portions of Lager yeast have both versions, but both SUL1 genes are inactivated due to mutations which make SUL2 the only active sulfate transporter. Coincidentally this is the most efficient transporter of the two in brewing conditions. These are only a few examples of the genetic changes that occurred during the domestication of Lager yeast, and help us to understand better the genetics of fermentation and the genes important for brewing.



Just to make it clearer, or maybe not, we speculate that a wild S. eubayanus from Patagonia hybridized with a ale-type yeast (already domesticated) within the brewing environment and formed a 50:50 hybrid, which suffered a domestication process involving the genetic inactivation of less efficient sulfate transporters, the addition of extra copies of cerevisiae genes related the assimilation of maltose, and various chromosome rearrangements including the loss of several ones.





To end, I will like to share with you some new data that resulted from a new survey we did in Patagonia that in this case covered all the distribution of the Nothofagus trees, the hosts of Cyttaria fungus and S eubayanus. Below you can see a map of Patagonia with the sampled area. Nothofagus forests are only located along the Andean mountains, in the limit with Chile. We wanted to know if there were distinct eubayanus populations in Patagonia. As you can see, we obtained hundreds of new isolates. We perform again genetic analyses with the new isolates and included additional LAGER strains typically used for brewing. What you see in the figure is a phylogenetic tree, and shows the diversity of S eubayanus. The end of each branch correspond to a different strain, if the branch ends with vertical line (like a T rotated to the right), well this means there are several strains which genetically identical. The branch distance between two strains gives a measure of the genetic differences they have.

Ok, so what is important to get from this is that there are two main populations of S. eubayanus in Patagonia, at least that we know. Population I in red and Population II in green. Within each population there is plenty of variability. For a species to diverge so much needs at least thousands of years, so the idea that this species came from Europe is not well supported. While wild Patagonian S eubayanus show large heterogeneity, the eubayanus portion of the LAGER strains are very similar among each other. This suggest that the hybridization event occurred only once or if more, it occurred with a similar S. eubayanus strain. This strain is related to the population II of the patagonian S eubayanus, but you can see still have not found the exact natural population from which this strain came from. I say still because we keep looking for it I'm positive that we will find it soon. Nevertheless, I must highlight the importance of the huge set of novel cold tolerant strains of S. eubayanus that has been collected, which make an excellent resource for brewing experimentation, and who knows, maybe the rise of a new era for LAGERS.

Acknowledgements

-C.T. Hittinger, J. Dover, M. Johnston

Dpt. Biochemistry and Molecular Genetics, Univ. Colorado, Aurora, USA.

-E. Valerio, C. Gonçalves, P. Gonçalves & J.P. Sampaio

Centro de Recursos Microbiológicos, Departamento de Ciências da Vida Universidade Nova de Lisboa, Caparica, Portugal.

- Maria Rosa Giraudo de van Broock

and the second of the second second

- Institutions: INIBIOMA, CONICET, Universidad Nacional del COMAHUE, Universidade Nova de Lisboa, Colorado University, Administración Parques Nacionales.

- Funding sources: UNComahue, CONICET, ANPCyT, Fundacao da Ciencia e Tecnología (Portugal), NIH (USA).



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