Mitochondrial Recombination and Introgression during Speciation by Hybridization

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Abstract

Genome recombination is a major source of genotypic diversity and contributes to adaptation and speciation following interspecies hybridization. The contribution of recombination in these processes has been thought to be largely limited to the nuclear genome because organelles are mostly uniparentally inherited in animals and plants, which prevents recombination. Unicellular eukaryotes such as budding yeasts do, however, transmit mitochondria biparentally, suggesting that during hybridization, both parents could provide alleles that contribute to mitochondrial functions such as respiration and metabolism in hybrid populations or hybrid species. We examined the dynamics of mitochondrial genome transmission and evolution during speciation by hybridization in the natural budding yeast Saccharomyces paradoxus. Using population-scale mitochondrial genome sequencing in two endemic North American incipient species SpB and SpC and their hybrid species SpC*, we found that both parental species contributed to the hybrid mitochondrial genome through recombination. We support our findings by showing that mitochondrial recombination between parental types is frequent in experimental crosses that recreate the early step of this speciation event. In these artificial hybrids, we observed that mitochondrial genome recombination enhances phenotypic variation among diploid hybrids, suggesting that it could play a role in the phenotypic differentiation of hybrid species. Like the nuclear genome, the mitochondrial genome can, therefore, also play a role in hybrid speciation.

Key words: mitochondrial recombination, speciation by hybridization, Saccharomyces.

Introduction

Hybridization between closely related species generates new gene combinations that may lead to reproductive isolation of hybrid individuals with the parental species and the emergence of novel phenotypes (reviewed in Schumer et al. 2014). These new combinations are made possible by the recombination of the parental genomes. Unlike the nuclear genome, the genomes of organelles in Eukaryotes (mitochondria and chloroplasts) are predominantly inherited in a uniparental manner (reviewed in Barr et al. 2005), mostly from the maternal parent in the case of mitochondrial genomes (mtDNAs). Assuming that the progeny resulting from hybridization between two species (or diverged populations) inherits only one of the parental mtDNAs, one expects that the co-occurrence of both parental mtDNA types in the progeny (heteroplasmy) is rare and that recombination in the mitochondrial genome is thus very limited in most Eukaryotes. Exceptions to maternal mtDNA inheritance however exist, for instance in the case of biparental inheritance of mtDNAs (Breton and Stewart 2015), allowing for recombination to take place. The observation of spontaneous heteroplasmy or recombinant mtDNAs in experimental hybrids (Kondo et al. 1990; Gyllensten et al. 1991) and natural populations (Kvist et al. 2003; Jaramillo-Correa and Bousquet 2005; Xu et al. 2009) also indicates that paternal mtDNA may be transmitted along with maternal mtDNA occasionally even in species that normally exhibit maternal inheritance. These observations suggest that biparental (or rare biparental) inheritance during interspecific hybridization could be followed by recombination between mtDNAs (Rokas et al. 2003), which has the potential to generate new combinations of genes and haplotypes with functional consequences for mitochondrial function.

Fungi show a large diversity of mtDNA inheritance patterns (Wilson and Xu 2012; Xu and Wang 2015). For instance, in the budding yeast Saccharomyces cerevisiae, mtDNA transmission is biparental such that the two mating cells contribute to the zygote mtDNAs. This heteroplasmic state is transient, as vegetative segregation leads to the fixation of a single haplotype in the hybrid cell lineage within a few dozen cell divisions (Birky et al. 1978; Birky 2001). However, recombination between parental mtDNAs can occur at a high rate and lead to the introgression of novel combinations. In such cases, mitochondrial genome recombination may play a role in hybrid speciation. Several studies have shown that mitochondrial recombination is a common event during hybridization in Saccharomyces cerevisiae (Kondo et al. 1990; Xu et al. 2009) and other fungi, including Saccharomyces paradoxus, for which we have recently reported the occurrence of mitochondrial genome introgression during interspecific hybridization (Leducq et al. 2016). However, these previous results were based on relatively small sample sizes, and it remains to be determined whether recombination contributes significantly to the adaptive potential of hybrid populations or species.
during this short heteroplasmic transition (Fritsch et al. 2014). Unlike many other model eukaryotes, mtDNA from Saccharomyces species is highly variable both within and between species, and both intergenic and coding regions contribute to phenotypic variation (Paliwal et al. 2014; Wolters et al. 2015). This indicates that mitochondrial recombination could contribute to novel genotypes and phenotypes in the hybrid progeny.

Closely related species from the genus Saccharomyces can be crossed with each other in the laboratory, and many interspecific hybridization events occurred during the domestication of Saccharomyces by humans for brewing and winemaking (Landry et al. 2006; Hittinger 2013). The mtDNA analysis of these experimental and industrial strains revealed many contrasting features of the mitochondrial transmission dynamics after hybridization. On the one hand, some cases of strong biased transmission have been reported. For instance, the absence of the S. cerevisiae mitochondrial type in S. cerevisiae × S. uvarum hybrid breeding strains suggests the preferential transmission and/or the postmating selection of the S. uvarum parental haplotype (Piskur et al. 1998; Kodama et al. 2006; Rainieri et al. 2008). However, under laboratory conditions, the S. cerevisiae mtDNA is preferentially transmitted in S. cerevisiae × S. uvarum hybrids, potentially caused by a higher number of replication origins (ori sequences) in the S. cerevisiae mtDNA (Lee et al. 2008) or asymmetrical incompatibilities. On the other hand, some studies have shown that there might not be inherent biases in transmission. The study of hybrid wine strains has shown that mtDNA from either parent can be transmitted (reviewed in Querol and Bond 2009).

The aforementioned cases suggest that, despite the high mitochondrial recombination rate observed within species, for instance in S. cerevisiae (Fritsch et al. 2014), mitochondrial recombination in interspecific crosses is null or limited. A possible explanation is that one parental mitochondrial type is rapidly eliminated after hybridization, before mitochondrial recombination effectively occurs. However, since many of these studies focused on a single locus for genotyping, the extent of mitochondrial recombination could not be assessed. Recently, Peris et al. (2017) observed that the transfer of specific mitochondrial genes may have occurred among Saccharomyces species, revealing a potential history of recombination in the mitochondrial genome. Most of these reported cases occurred in domesticated and sometimes distantly related species. It is thus still unclear to what extent mitochondrial recombination occurs in natural populations and whether it can contribute to phenotypic variation during the process of speciation by hybridization. To examine this question, we need to examine ongoing or recent events in natural populations.

We recently showed that a new yeast species arose through hybridization in wild populations of Saccharomyces paradoxus (Leducq et al. 2016), a budding yeast that thrives on the bark of deciduous trees and the associated soil in Eurasia and America (Sniegowski et al. 2002) (fig. 1A). In the northeast of its distribution in North America, we identified two lineages, SpB and SpC, that show growth phenotypes consistent with local climatic adaptations (Leducq et al. 2014) and nucleotide divergence (2%) that support a scenario where a population split was initiated prior to or during the last glaciation event 100 Kya (Leducq et al. 2016; fig. 1B). These two lineages show strongly reduced fertility in F1 hybrids, show a large array of distinct growth phenotypes and a limited geographical overlap, suggesting that they are incipient species (Leducq et al. 2014, 2016).

Population genomic analyses recently showed that these two incipient species hybridized in their contact zone after the glacial retreat and gave rise to a third incipient species, SpC*, which is genetically and phenotypically distinct from SpB and SpC, and also partially reproductively isolated (Leducq et al. 2016). A significant fraction of the reproductive isolation of the parental lineages with each other (Charron et al. 2014) and with the hybrid lineages could be attributed to abnormal chromosomal segregation (Leducq et al. 2016) but other mechanisms such as Bateson–Dobzhansky–Muller incompatibilities (BDMIs) could also contribute. Here, we examine mitochondrial genome evolution during this recent event of speciation by hybridization. We show that the hybrid lineage displays largely the same bias in terms of parental contributions to the mitochondrial and nuclear genomes, and that it carries a recombinant mitochondrial haplotype with a specific genome content and configuration. We demonstrate that when hybridization is reproduced in the laboratory, recombination between mtDNA parental haplotypes contributes to increase phenotypic variation of hybrid strains.

**Results and Discussion**

We previously found that the nuclear genome of the hybrid lineage SpC* was ~95% inherited from its parental lineage SpC, indicating that SpC* has experienced more backcrosses with SpC than with SpB after the original hybridization event or that it has preferentially lost SpB haplotypes by selfing or mitotic loss of heterozygosity (Leducq et al. 2016; fig. 1B). This observation suggests that, even if the original hybrid was heteroplasmic for SpC and SpB mtDNAs, repeated backcrosses with SpC could have eliminated the SpB mitochondrial type from the SpC* lineage. In order to test this hypothesis, we examined mitochondrial haplotypes in the SpC* and parental lineages by analyzing polymorphism in the mitochondrial genomes of 127 S. paradoxus strains from the American lineages SpB (n = 81), SpC (n = 34), and SpC* (n = 12). The lineage assignment of 127 strains was done based on 14,974 nuclear SNPs and whole-genome phylogeny (Leducq et al. 2016) (Supplementary information 1). A phylogeny based on 254 high-quality mitochondrial SNPs revealed that the three lineages form distinct groups (see supplementary fig. S1A, Supplementary Material online), with all strains from lineage SpC and most of the SpC* strains (92%) forming a monophyletic group, as observed for the nuclear genome (Leducq et al. 2016). This observation is congruent with a scenario under which backcrosses between SpC* and its parental lineages most likely occurred with SpC, resulting in the rapid elimination of the SpB mitochondrial haplotype during the evolution of the SpC* lineage. One
SpC* strain (LL2011_005) clusters with the SpB lineage, indicating that although rare, backcrosses between SpC* and SpB may have occurred and led to the elimination of the SpC mitochondria in some SpC* strains, or that the SpB mitochondrial haplotype is still segregating in the SpC* lineage since the initial hybridization event. Splitstree (fig. 1C) and STRUCTURE analyses (see supplementary fig. S1B, Supplementary Material online) based on the same limited number of polymorphic sites reveal admixture within and among SpB and SpC* clades, indicating a more complex evolutionary history than suggested by the phylogeny (see supplementary fig. S1A, Supplementary Material online). Interestingly, the SpC strain YPS667 clusters with SpC* in a phylogeny based on these sites. The nuclear genome of this strain was shown to be divergent from other SpC strains (0.14% of nucleotide divergence) and to have admixed regions with the SpC* hybrid lineage (Leducq et al. 2016). This observation indicates that the YPS667 mitochondria could have been inherited from SpC* through gene flow between SpC and SpC* after the formation of the hybrid lineage (Leducq et al. 2016). These crosses could have been possible due to the incomplete reproductive isolation between SpC and SpC* (Leducq et al. 2016).

The limited number of SNPs used for the analyses performed above are due to the fact that many genomes have been sequenced at low coverage, which leads to a small number of sites of high quality across the entire sample, making it
difficult to dissect the potential recombination events between the parental mtDNA that led to the SpC* mitochondrial genomes. We therefore used high-coverage data to analyze 20 complete mtDNA from the S. paradoxus SpB (n = 11), SpC (n = 6), and SpC* (n = 3) lineages to examine the pattern of mitochondrial inheritance in the hybrid lineage SpC* (Supplementary information 1). We included, as outgroups, 18 complete mtDNA sequences from S. paradoxus Asian (n = 2) and European lineages (SpA; n = 6), S. cerevisiae (n = 4) and the Saccharomyces eubayanus complex species (n = 6) to identify potential horizontal transfers or ancient hybridization events that could explain the patterns of introgression described above (see Supplementary information 1; table S1, Supplementary Material online). The assignment of strains to species and to S. paradoxus lineages was previously done based on whole-genome phylogenies and complete mtDNA sequences were retrieved from previous studies (Foury et al. 1998; Wei et al. 2007; Nakao et al. 2009; Prochazka et al. 2012; Baker et al. 2015; Wolters et al. 2015; Wu and Hao 2015; Leducq et al. 2016; Okuno et al. 2016) (see Supplementary information 1; table S1, Supplementary Material online). The assignment of strains to species and to S. paradoxus lineages was previously done based on whole-genome phylogenies and complete mtDNA sequences were retrieved from previous studies (Foury et al. 1998; Wei et al. 2007; Nakao et al. 2009; Prochazka et al. 2012; Baker et al. 2015; Wolters et al. 2015; Wu and Hao 2015; Leducq et al. 2016; Okuno et al. 2016) (see Supplementary information 1; table S1, Supplementary Material online). We improved the assembly of 22 mtDNA previously assembled with ABySS (Leducq et al. 2016; mean number of scaffolds, nS = 4.5 ± 6.1), using the software IDBA_ud (Peng et al. 2012; nS = 1.1 ± 0.3; see supplementary table S2, Supplementary Material online; accession numbers KY287641–KY287662). We obtained the RFLP band patterns after EcoRV digestion expected from our assembly for each lineage of North American strains, confirming the overall accuracy of the mtDNA assemblies (see supplementary fig. S2, Supplementary Material online).

An analysis of pairwise synteny revealed that mitochondrial genomes are collinear within S. paradoxus American lineages and with S. cerevisiae, but not with S. paradoxus Eurasian lineages mtDNAs (SpA and Asia; fig. 2A). This result is surprising considering that mtDNA is syntenic within S. cerevisiae (Wolters et al. 2015) and within the S. eubayanus complex species (Okuno et al. 2016). We thus report here the first case of mtDNA rearrangement within a Saccharomyces species. The synteny between the S. cerevisiae and S. paradoxus American lineages suggests that the S. cerevisiae-like mtDNA architecture is ancestral in S. paradoxus and that rearrangements occurred in the Eurasian lineages (fig. 2B). Another possibility is that the mtDNA architecture is derived in the American lineages and was inherited from S. cerevisiae by hybridization after the split between American and Eurasian populations, which would be supported by the fact that the S. paradoxus American lineages inherited some mtDNA elements such as cob from S. cerevisiae by horizontal gene transfer (HGT) or during an ancient hybridization event (Peris et al. 2017). However, this former study only included the SpB lineage, so we cannot conclude whether the mtDNA transferred from S. cerevisiae to S. paradoxus occurred before or after the divergence between SpB and SpC.

To test if ancient hybridization or HGT have affected the population structure and the architecture of the complete American S. paradoxus mtDNA or only affected some loci, we annotated the 38 complete mtDNAs and performed a phylogeny based on an alignment of concatenated sequences of coding elements (CDS; see supplementary fig. S3, Supplementary Material online). The global phylogeny confirms that the American S. paradoxus lineages form a monophyletic group (see supplementary fig. S3A, Supplementary Material online), which is also supported by a STRUCTURE analysis (see supplementary fig. S3B and C, Supplementary Material online). Surprisingly, the Eurasian S. paradoxus lineages cluster with S. cerevisiae, confirming that the two species experienced mtDNA recombination during ancient hybridization or HTG (Peris et al. 2017). To look in greater details at the regions that were affected by these recombination events and whether these recombination events took place before or after the divergence between Eurasian and American S. paradoxus lineages, we performed separated phylogenies of aligned nucleotide sequences for each CDS and mobile elements (introns and maturase-like genes) identified in the 38 mtDNA, using S. cerevisiae and S. eubayanus as outgroups (fig. 3). For each locus, S. paradoxus American strains share more similarity with each other than with any outgroup, suggesting that the S. paradoxus American lineages did not receive any major recent contribution from external lineage or species since their divergence with Eurasian lineages. A phylogeny of the mitochondrial gene cob3 (fig. 3A) confirms that the S. paradoxus American lineages show a higher nucleotide similarity to S. cerevisiae (98.76%) than to the Eurasian lineages (97.41%), indicating that the hybridization event that lead to the transfer of cob3 from the S. cerevisiae mtDNA to that of S. paradoxus (Peris et al. 2017) may have affected the American S. paradoxus mtDNA architecture, but the higher SpB–SpC similarity (99.21%) suggests that it took place before the SpB–SpC divergence. A similar phylogenetic signal for atp6 suggests that this gene also experienced transfers between S. cerevisiae and S. paradoxus American lineages (fig. 3A). Our analysis revealed that S. paradoxus Eurasian lineages and S. cerevisiae share more similarity for cob (fig. 3B; 98.19%) and cob1 (fig. 3C; 97.61%) than with S. paradoxus American lineages (97.56 and 97.35%, respectively), suggesting that the same or an independent ancestral recombination event between S. cerevisiae and S. paradoxus also affected the mtDNA architecture of Eurasian lineages. Overall, these results show that the architecture of the mitochondrial genome, which is known to vary between species (Aguileta et al. 2014), can also rapidly evolve within species, and that mitochondrial recombination following hybridization with other species is a major contributor to this evolution.

The aforementioned mtDNA recombination events occurred before the hybridization between SpB and SpC, and thus unlikely affected the relatively recent evolution of the SpC* mtDNA. Interestingly, the phylogeny of concatenated mitochondrial CDS reveals that the hybrid lineage SpC* and S. paradoxus SpB–SpC and strain YPS667 cluster with SpB (see supplementary fig. S3, Supplementary Material online), which is in contradiction with the phylogeny based on high-quality mitochondrial SNPs (see supplementary fig. S1A, Supplementary Material online). These conflicting phylogenies suggest that SpC* and YPS667 mtDNAs result from recombination events between
parental lineages SpB and SpC, which is also supported by the reticulate evolution of the SpC* and YPS667 mtDNA types in the Splitstree analysis (fig. 1C). To identify the relative contributions of SpB and SpC mtDNA types and the regions that were affected by recombination, we identified phylogenetic discrepancies in gene-by-gene phylogenies among S. paradoxus strains (fig. 3). This analysis revealed that most of the cox1 exons and introns were systematically inherited from SpC in all SpC* and YPS667 (fig. 3C), whereas cob introns and exons and atp6 were systematically inherited from SpB (fig. 3A and B). The analysis of other regions confirmed that the SpC* strain LL2011_005 inherited most of its mitochondrial genes from SpB, whereas other SpC* strains and YPS667 inherited these genes from SpC (fig. 3D). Within S. paradoxus American mtDNA types, we observed extensive presence–absence polymorphism of mobile elements, including introns in the cox1 and cob genes (see supplementary fig. S4A, Supplementary Material online), which resulted in extensive variation in terms of size and GC content in American S. paradoxus mtDNA relative to outgroups (see supplementary fig. S4B and C; Supplementary information 2, Supplementary Material online). Most intronic elements in cob and the maturase-like gene rf3 (located 3′ of atp6) are shared between SpB and SpC* but absent from SpC, whereas some introns from genes cox1 and a maturase-like gene located in 3′ of cox3 (cox3:3p) are present in both SpB and SpC but absent from SpC*. As observed above, the SpC strain YPS667 has the same profile as SpC* for cox3:3p, rf3 and cox1 introns.

Fig. 2. Major mtDNA rearrangements occurred within Saccharomyces paradoxus after divergence between Eurasian and American lineages. (A) The comparison of 12 complete Saccharomyces mitochondrial genomes reveals the complete synteny between American S. paradoxus lineages and S. cerevisiae but rearrangements between the S. paradoxus American and Eurasian lineages (grey: S. uvarum; black: S. cerevisiae; yellow: S. paradoxus Asian lineage; green: SpA; red: SpB; purple: SpC*; blue: SpC). Each dot indicates 100% identity between two unique 20 bp sequences. Red dots indicate inversions. The alignment origin (0 and red arrows) corresponds to the first nucleotide of rnl. (B) Schematized architecture of the S. cerevisiae and American S. paradoxus mtDNA types. White boxes indicate CDSs, grey boxes indicate tRNAs labeled with the corresponding amino-acid (letters). Breaks and curves indicate rearrangements that occurred after the divergence between American and Eurasian S. paradoxus lineages (inversion in red).
Fig. 3. SpC* mtDNA results from introgression with uneven contributions from parental mitochondrial types SpB and SpC. Pattern of introgression for fixed (CDS, exons) and mobile (introns, matrerase-like genes) mitochondrial elements, revealed by phylogenies (nucleotide sequences; maximum composite likelihood model, 1,000 permutations) among 38 strains. Branches are highlighted according to species and S. paradoxus lineages (legend on top left). SpC* strains and YPS667 are labeled with specific symbols. Phylogenies were not displayed for mobile elements when absent from SpC* (white boxes) or only present in SpC* and SpB (red boxes). Branches with American S. paradoxus lineages are magnified in circles. (A) Detailed phylogenies of cox3 and atp6 suggest mitochondrial recombination after ancient hybridization between S. cerevisiae and S. paradoxus American lineages. The positions of SpC* strains and YPS667 suggest that they inherited atp6 and cox3 from SpB, independently from this ancient hybridization event. (B) SpC* and YPS667 inherited cob from lineage SpB. Most of cob introns and the rβ maturase are only present in SpB and SpC*. (C) SpC* and YPS667 mostly inherited cox1 from lineage SpC. (D) The inheritance of other mitochondrial genes varies among SpC* strains.

(see supplementary fig. S4A, Supplementary information 2, Supplementary Material online). Overall, the presence–absence polymorphism in introns in SpC* follows the pattern of polymorphism in mitochondrial CDS, suggesting that recombination that followed hybridization between SpB and SpC is tightly linked with the dynamics of mobile elements. Mitochondrial mobile elements were previously showed to promote recombination during horizontal gene transfer between fungal and plant mtDNA (Beaudet et al. 2013) and our observations suggest that these elements could also be involved in the generation of recombined mtDNA types after hybridization.

Taken together, mobile elements and CDS only represent 22.8−30.9% of the total mtDNA length so we extended the analysis to the entire mtDNA. We therefore performed the alignment of 20 complete mtDNAs from the three American lineages to examine in details how polymorphism inherited from SpB and SpC segregated in SpC* and YPS667 mtDNAs. A STRUCTURE analysis performed on 2052 polymorphic sites from this alignment revealed that SpB and SpC mtDNAs (including YPS667) belong to two distinct populations (see supplementary fig. S5A and B, Supplementary Material online). As observed from phylogenies for most of mitochondrial genes (fig. 3), SpC* strains LL2012_016 and LL2012_018 were assigned to the SpC population whereas LL2011_005 was mostly assigned to SpB, with little contribution from SpC (7%), confirming that SpC* mitochondria received
uneven contributions from the two parental types. We calculated relative frequencies of ancestral haplotypes inherited from SpB and SpC along discrete 750bp windows of the SpC* and YPS667 mtDNAs (see supplementary fig. SSC, Supplementary Material online). This analysis indicates that 87% of the LL2011_005 mtDNA was inherited from SpB, whereas this proportion represents only 13–17% of the LL2012_016, LL2012_018, and YPS667 mitochondria. This polymorphism is not evenly distributed along the mitochondrial genome (see supplementary fig. SSC, Supplementary Material online). Different mitochondrial haplotypes were thus produced by recombination early in the initial hybridization events and are still segregating today in SpC* or were produced after the hybridization event through backcrosses with the parental lineages.

Recombination in SpC* mtDNAs after hybridization required the simultaneous presence of SpB and SpC mtDNAs in a single cell, which is compatible with biparental mtDNA inheritance followed by recombination. To experimentally validate this in S. paradoxus, we created diploid hybrids between SpB and SpC and analyzed the mtDNA haplotype inherited by each of these independently derived hybrid strains. We generated 18 independent SpB × SpC diploid hybrids (see supplementary table S3, Supplementary Material online) and analyzed their mtDNA restriction fragments length polymorphisms (mtRFLPs) to determine in each case if mtDNA was inherited from the SpB or SpC parent or corresponded to a recombinant haplotype. To strengthen the identification of mtDNA haplotypes, mtRFLPs analysis were performed with two restriction enzymes whose sites are distributed all along the genome (see supplementary fig. S6A, Supplementary Material online). Eight hybrid strains (44%) exhibited mtRFLPs that were distinct from the parental profiles (because of shifted, missing or new bands; supplementary fig. S6B and C, Supplementary Material online), indicating that these hybrids have recombinant mtDNA haplotypes.

Among the hybrids with recombinant mtDNA haplotypes, three exhibited identical mtRFLPs profiles for the two enzymes (ud_01, ud_04, and ud_09), whereas the five remaining hybrids exhibited visible differences for either or both enzymes (see supplementary fig. S6B and C, Supplementary Material online). An analysis based on the restriction maps of SpB and SpC mtDNAs revealed that the three hybrids with identical mtRFLPs have mostly SpC-like haplotypes with an SpB introgression spanning from ~55–65 kb on the mtDNA alignment (see supplementary figs. S6B and C, Supplementary Material online). Five hybrids (28%) had mtRFLPs identical to SpB and five (28%) were identical to SpC, suggesting the inheritance of parental, that is, non-recombinant, haplotypes. To support this result, we performed two independent PCR assays targeting polymorphic mtDNA loci between SpB and SpC and confirmed that the 10 hybrids with non-recombinant mtRFLP profiles have PCR profiles consistent with the parental haplotypes (see supplementary fig. S6D and E, Supplementary Material online). It is possible that many recombination events were undetected because of the inability of mtRFLPs analysis to reveal changes that preserve sequence length between restriction sites. Therefore, we cannot rule out the possibility that haplotypes classified as parental contain introgressions. Nevertheless, the obvious signatures of recombination observed in almost half of the hybrids show that mtDNA recombination is frequent in experimental crosses, although inheritance of parental mtDNAs is also likely possible.

The previously described diploid SpB × SpC hybrids harbor a completely heterozygous nuclear genome and are thus isogenic, excepted for the mitochondrial genome. Although rare nuclear mitotic recombination events cannot be ruled out because of the number of cell divisions required to produce homoplasmic hybrids, the phenotypic variation associated with such events should affect all the strains with equal probability, regardless of their mitochondrial haplotype. Therefore, any phenotypic variation observed in these hybrids between parental and recombinant haplotypes can be confidently attributed to genetic variation in the mitochondrial genome. Using colony size on high-density colony arrays as a proxy for growth rate, we measured phenotypic variation among the 18 experimental hybrids strains in 15 environmental conditions that cover combinations of three incubation temperatures (30, 35 and 37 °C) and five carbon or nitrogen sources (glucose, ethanol, glycerol, maltose, and allantoin). Within each combination of mitochondrial haplotype category (SpB, SpC, or recombinant) and environmental condition, we performed a one-way ANOVA to test for a significant contribution of interstrain variation to the overall growth rate variation (Supplementary materials 3 and 4). We found that for most environmental conditions, the fraction of overall growth variation attributable to interstrain variation within the SpB, SpC or recombinant category is larger for the strains harboring recombinant mitochondrial haplotypes than either parental haplotypes (higher ANOVA F-statistic value; fig. 4A, Supplementary information 4, Supplementary Material online). The condition for which this effect is strongest (maximum F value) is at 37 °C with glycerol, a non-fermentable carbon source that requires mitochondrial respiration for growth (fig. 4A, C). These results suggest that the frequent mitochondrial recombination occurring in S. paradoxus hybrids may contribute to phenotypic variation in these strains.

There is compelling evidence that genetic interactions between mtDNA and the nuclear genome can affect various metabolic, regulatory or life-history traits and play a role in hybrid breakdown between species or populations (Burton et al. 2011; Barreto et al. 2015; Palival et al. 2014; Zhu et al. 2014; Latorre-Pellicer et al. 2016; Mossman et al. 2016). The variation observed here could thus be caused by direct genotype-to-phenotype effects or through genetic interactions with the nuclear genome or among loci within the mtDNA. We note that much of the phenotypic variation associated with recombinant mtDNAs appears to yield reduced growth rates (fig. 4B). These altered growth phenotypes could result from negative epistatic interactions among mitochondrial alleles of the two parental populations within the recombinant haplotypes. Another possibility is that in the hybrid strains each mitochondrial locus (either from SpB or SpC) can interact with a full set of related nuclear alleles in the heterozygous nuclear genome, leading to potential dominant
interactions between a mitochondrial allele from one species and the nuclear allele of the other. Finally, incompatibilities could also arise from higher-order epistatic interactions between combinations of mitochondrial and nuclear alleles of the two parental genotypes.

**Conclusion**

The distribution of polymorphisms and mobile elements in mitochondrial genomes indicate that extensive exchanges took place between American *S. paradoxus* lineages during the recent speciation event by hybridization (Leducq et al. 2016). Such complex patterns are undoubtedly shaped by the high frequency of mtDNA recombination in yeast, which is a consequence of its biparental mtDNA transmission mode and transient heteroplasmy. A recent study on the frequency and distribution of mtDNA recombination hotspots in *S. cerevisiae* showed that the rate of recombination in this species is much higher than the rate of mutation (Fritsch et al. 2014). Fungal mitochondrial genomes are highly variable in size, content and architecture both within species and across long evolutionary distances (Aguileta et al. 2014; Freel et al. 2015) and the high rate of recombination could contribute to this rapid evolution (Fritsch et al. 2014). However, recombination will have effects on phenotypic diversity if enough divergence has accumulated in the parental mitochondrial genomes prior to recombination and if the hybridizing lineages give rise to viable progeny. Our results show that recombinant mitochondria were produced after hybridization between lineages that have diverged for more than a hundred years.
thousand years and are still segregating in a successful hybrid lineage. Future investigations should determine the generality of mitochondrial recombination during other hybridization events among natural yeast populations that have recently been revealed (Barbosa et al. 2016; Peris et al. 2016).

The numerous mitochondria-related functions that rely on both nuclear and mitochondrial genes (oxidative phosphorylation, mtDNA replication, mitochondrial transcription, and translation) suggest that co-evolution between the two genomes may be an important player in the emergence of genetic incompatibilities between diverged populations (Burton and Barreto 2012). Studies on inter and intraspecific hybrids between Saccharomyces yeasts revealed many BDMIs between mitochondrial and nuclear genes that reduce the fitness of hybrids (Lee et al. 2008; Chou et al. 2010; Albertin et al. 2013; Hou et al. 2015; Jhuang et al. 2017). Here, we did not attempt to determine whether the mitochondria themselves may have contributed to the reproductive isolation of the parental lineages SpB and SpC or between the hybrid lineage and these parents. However, we did show that mitochondrial recombination is likely to result in phenotypic changes. In our experiments, most of these changes resulted in reduced growth rates, suggesting that most mitochondrial recombinants could be deleterious to fitness in nature, although in a condition-dependent manner. Like point mutations, which under nearly-neutral theory tend to be slightly deleterious, most recombination events could be deleterious, while a small minority could be adaptive. The fact that the SpC* hybrid linkage has persisted for several thousands of years with a recombinant nuclear and mitochondrial genome suggests that some might confer adaptation to unmeasured niches in the wild.

Mitochondrial recombination could also play a role in alleviating BDMIs between parental lineages SpC and SpB while allowing for adaptive introgression. BDMIs between mitochondrial and nuclear genomes have been shown to play an important role in reproductive isolation between yeast species (Lee et al. 2008; Chou et al. 2010; Albertin et al. 2013; Hou et al. 2015; Jhuang et al. 2017). A phase of heteroplasmy, recombination and mitotic selection of recombinant mtDNA upon return to growth after mating could eliminate BDMIs. For example, the SpC* hybrids could have carried SpB-derived mitochondrial genome containing adaptive alleles and other alleles incompatible with SpC nuclear genes. Recombination between the SpC and SpB mtDNAs in the hybrids could have led to the maintenance of the adaptive SpB alleles while purging those involved in mt-SpB nuclear-SpC incompatibilities. Recombination of mtDNA among incipient yeast species can therefore contribute to complex evolutionary dynamics.

Several non-adaptive mechanisms could also contribute to the complex pattern of mitochondrial genome evolution observed in SpC*. For instance, Ma and O’Farrell (2016) showed that mtDNA recombination in Drosophila could lead to the introgression of genomic regions responsible for the selfish propagation of certain mtDNAs, yielding recombinant mtDNAs in turn capable of selfish drive. In S. cerevisiae, several cellular mechanisms were shown to regulate mtDNA transmission in heteroplasmic stages, for instance by preventing the transmission of mitochondria with lower redox potential, responsible for cell aging (McFaline-Figueroa et al. 2011) or by limiting the propagation advantage of selfish mtDNA mutants (Karavaeva et al. 2017), suggesting a complex interplay between levels of mitochondrial activity and replication advantages. In the SpB × SpC diploid, some recombinant mtDNAs may have acquired a replicative advantage that led to their overrepresentation in the early heteroplasmic lineage, increasing their probability of becoming fixed as the lineages became homoplasmic. Such selfish behavior could explain the frequent reduced growth rates associated with recombinant mtDNAs, which could have been transmitted despite their net disadvantages on growth performance. Finally, the pattern of polymorphism in mitochondrial mobile elements like introns follows the pattern on mtDNA recombination in hybrids, suggesting that, as it was observed for mtDNA gene transfer among fungi and plants (Beaudet et al. 2013), these mobile elements could contribute to mtDNA evolution during hybridization in yeasts.

### Materials and Methods

#### Mitochondrial Genome Assembly

We reconstructed mitochondrial genomes for a representative subsample of 22 S. paradoxus strains from North-east America (Supplementary material 1). On the basis of nuclear genome analysis (Leducq et al. 2016), strains were assigned to the European lineage SpA recently introduced in North America (n = 3), to the native American lineages SpB (n = 10) and SpC (n = 6) and to the American hybrid lineage SpC* (n = 3). We retrieved mitochondrial scaffolds previously assembled and identified in these strains (Leducq et al. 2016). Briefly, reads from high coverage genome sequencing (~100 ×; Truseq Illumina; BioProject number PRJNA277692, BioSamples SAMN03389655–SAMN03389678) were assembled using ABYSS (Simpson et al. 2009) with k = 64 (k-mer length). Mitochondrial fragments were identified by aligning and reordering all assembled scaffolds longer than 200 bp onto the S. paradoxus strain CBS432 reference mitochondrial genome (lineage SpA; GenBank accession: JQ623351; Prochazka et al. 2012) for each strain separately, using the “Move contigs” option implemented in MAUVE (Darling et al. 2004) with default parameters (minimum LCB weight = 200 bp). Because many of these strains had multiple mitochondrial scaffolds (only 12 mtDNA consisted of a single scaffold that could be manually circularized; see supplementary table S2, Supplementary Material online), we performed new genome assemblies using the IDBA_ud software (Peng et al. 2012). We used the default options for IDBA_ud’s parameter settings: a minimum k-mer size of 20 and maximum k-mer size of 100, with 20 increments in each iteration. Our newly assembled mitochondrial scaffolds were identified as described above. Using IDBA_ud, 20 mtDNA consisted in a single scaffold that could be manually circularized, and two mitochondria only consisted in two overlapping scaffolds (see supplementary table S2, Supplementary Material online). We further used these assemblies for the following analyses. We
manually reconstructed mtDNAs in MEGA5 (Tamura et al. 2011), using CBS432 (SpA), UTM6 (SpB), and LL2011_003 (SpC) as references to merge contiguous scaffolds. Uncertain fusions were completed by sequences of "n". Genome assemblies were deposited on NCBI under accession numbers KY287641–KY287662 (see supplementary table S2, Supplementary Material online).

Read Mapping and Variant Calling
We aligned published whole-genome sequencing paired-end reads from 127 North-American S. paradoxus strains [23] on our de novo assembly of mtDNA from the SpB strain LL2012_022 using the Bowtie2 (Langmead and Salzberg 2012) software with default parameters. We chose this strain as a reference because among SpB, SpC, and SpC*, strains, its assembly is the largest and presents the most complete catalog of mobile elements (see supplementary fig. S4A, Supplementary Material online). We marked duplicated reads in the alignments with Picard (http://broadinstitute.github.io/picard/) and called variant sites in all strains at once using FreeBayes (https://arxiv.org/abs/1207.3907) with a ploidy parameter of 1. We filtered the resulting sites and genotypes with VCFtools (Danecek et al. 2011), keeping only sites with a quality score (QUAL field) above 20 and genotypes with a sequencing depth (DP field) above 3. We removed sites that were variable for the mapping of reads from strain LL2012_022 on LL2012_022 mtDNA assembly, as those could result from mapping errors or heterozygote sites. We also removed sites showing incongruent genotypes between duplicated libraries from five strains from different lineages to control for additional sequencing and mapping errors (Supplementary material 1). To visualize incomplete lineage sorting during the evolutionary history of mitochondrial CDS, we used SplitsTree with default parameters (Huson and Bryant 2006). We performed a STRUCTURE analysis (Falush et al. 2003) using variable positions to detect the most likely number of populations (K) tested in the range 1–10. Analyses were carried out under the admixture model over 10,000 iterations of the MCMC chain with a 20,000 burn-in period (10 independent runs per K value). We detected the most likely K value based on the Delta K method (Evanno et al. 2005).

Synteny among Complete Mitochondria
To identify potential mitochondrial rearrangements within and among S. paradoxus lineages, we determined the synteny between mitochondria of representative strains from each S. paradoxus lineages (Asian lineage: n = 1; SpA: n = 2; SpB: n = 2; SpC: n = 2; SpC*: n = 2), using S. cerevisiae (n = 2) and S. eubayanus (n = 1) as outgroups. For each mitochondrion, we reported all possible 20 bp sequences in both strands and their coordinates. To avoid multiple matches due to repeated motifs and short duplications, and to shorten the computation time, we removed redundant sequences, that is, sequences having 100% match within and between strands, resulting in the removing of 5.1–11.8% sequences per mitochondrion. Then, for each pair of strains, we identified sequences having one-to-one 100% match and reported their coordinates in both mitochondria. All analyses were performed in R (R-Development-Core-Team 2011).

Mitochondrion Annotation
We performed de novo annotation for our 22 assembled mitochondria plus 16 complete mitochondria from the literature from a representative subset of outgroups (S. cerevisiae: n = 4; S. eubayanus: n = 6) and S. paradoxus lineages (Asian lineage: n = 2; SpA: n = 3; SpB: n = 1; see supplementary table S1, Supplementary Material online). Annotations for the 16 aforementioned mtDNA were already available but not homogeneous due to the different published methods. Each mitochondrion was annotated independently using MFannot tool set for Yeast Mitochondrial (http://megasun.bch.umontreal.ca/cgi-bin/mfannot/mfannotInterface.pl).

CDS that were detected but not annotated by MFannot were systematically searched by blast in the NCBI database for identification and manual annotation. These CDS mostly consisted in mature-like genes located 3’ of genes atp6 (fj3), cox2 (fj2), and cox3 (cox3p3p), or within introns of genes cox1 and cob. To identify more accurately these CDS and the bounder of introns, we performed local alignments of these regions using conserved CDS as anchors (atp6, cox2 and cox3; cox1 and cob exons). We validated the absence of CDS and intron in a strain when a gap was found at its putative position. Otherwise, we determined whether the miss-annotation resulted from diverging sequence (e.g., premature stop codon, partial deletion) or imperfect assembly. We manually modified the annotation accordingly.

Evolution of Mitochondria Based on Concatenated CDS
We inferred the evolutionary history of the 38 annotated Saccharomyces mitochondria based upon the concatenated nucleotide alignment of conserved mitochondrial CDS (atp6, atp8, atp9, cox2, cox3, rps3) and exons (cox1 and cob), for a total length of 6,357 bp. We established the global phylogeny using a Neighbor-Joining method (bootstrap test, n = 1,000 permutations). Evolutionary distances were based on a maximum composite likelihood model. Analyses were performed in MEGA6 (Tamura et al. 2013). We performed a STRUCTURE analysis (Falush et al. 2003) using variable positions observed in the alignment of the 38 concatenated sequences (602 variable positions) to detect the most likely number of populations (K) tested in the range 1–10. Analyses were carried out under the admixture model over 10,000 iterations of the MCMC chain with a 20,000 burn-in period (10 independent runs per K value). We detected the most likely K value based on the Delta K method (Evanno et al. 2005).

Identification of Introgression Based on North American Complete Mitochondria Alignment
The 20 complete and annotated mitochondria from North American lineage (including YPS138; Wu and Hao 2015; SpB: n = 11; SpC: n = 6; SpC*: n = 3) were manually aligned together in MEGA5 (Tamura et al. 2011), using CDS as anchors. Highly diverging regions were aligned separately from the full
alignment using flanking conserved regions (CDS) as anchors, with default ClustalW parameters with following modifications for both Pairwise and Multiple Alignments: Gap Opening Penalty = 2; Gap Extension Penalty = 6.66, and Transition Weight = 0 to take into account the low GC content in the mitochondrion. The alignment was then curated manually. We performed a STRUCTURE analysis (Wu and Hao 2015) using variable positions observed in the alignment of the 20 aligned mitochondria (2,052 variable positions) to detect the most likely number of populations \( K \) tested in the range 1–7. Analyses were carried out as described above.

On the basis of the above alignment, we identified potential introgressions from one parental lineage SpB or SpC in the hybrid lineage SpC* (Leducq et al. 2016). First, we divided the alignment in discrete 750 bp windows, within which we identified sites that are overall polymorphic but either fixed in SpB strains (B-sites) or fixed in SpC strains (C-sites). We removed from these categories strains that showed admixture for the most likely \( K \) number of populations in the STRUCTURE analysis. From SpC, we excluded the strain YPS667 that is highly divergent from other SpC strain at the nuclear genome level (Leducq et al. 2016). We counted the total number of variable sites in each category and for each window \( (n_B \) and \( n_C \), respectively). Then, for each strain \( i \) an each window, we calculated the number of B-sites \( (n_B) \) and C-sites \( (n_C) \) that are variable and defined the window as “B-like” (i.e., likely inherited by SpB) when \( n_B/nB > n_C/nC \) (blue), or as “C-like” in the opposite case (i.e., likely inherited by SpC; red). We could not infer ancestry for following cases: \( n_B/nB = n_C/nC \) (purple); \( n_B = 0 \) or \( n_C = 0 \) (black).

**Generation of Hybrid Strains**

SpB \( \times \) SpC hybrid strains (see supplementary table S3, Supplementary Material online) were generated by allowing haploid strains (initial OD\( \text{OD}_{695} \) 0.002 ml\(^{-1} \) each) to mate in YPD (1% yeast extract, 2% tryptone, 2% glucose) at 30°C in shaking incubator for 4 h. Selection for diploid cells and loss of heteroplasmy was performed by three 24 h passages in YPD\( \text{OD}_{695} \) (200 \( \mu \)g ml\(^{-1} \) geneticin, 100 \( \mu \)g ml\(^{-1} \) nourseothricin) at 30°C in shaking incubator, diluting to OD\( \text{OD}_{695} \) ~0.005 ml\(^{-1} \) at each passage (~25–30 generations). Diploid cultures were plated on YPD\( \text{OD}_{695} \) \% agar and incubated at 30°C. A single colony for each independent hybrid lineage was sampled to generate glycerol stocks.

**mtDNA Extraction and Restriction Profiles**

The method employed for mtDNA extraction is adapted from Defontaine et al. (1991). Strains were inoculated in 50 ml of YPGd (1% yeast extract, 2% tryptone, 3% glycerol, 0.2% glucose) and incubated at 30°C in shaking incubator until OD\( \text{OD}_{695} \) ~1.0 ml\(^{-1} \). Cells were washed twice in sterile distilled water and once in 1.2 M sorbitol, 50 mM EDTA, and 2% 2-mercaptoethanol. Cells were resuspended in 5 ml of solution A (0.5 M sorbitol, 10 mM EDTA, 50 mM Tris, pH 7.5) with 2% 2-mercaptoethanol and 0.1 mg ml\(^{-1} \) zymolyase 20T and incubated at 37°C for 3–4 h in shaking incubator for cell wall digestion. Cell debris were pelleted by centrifugation at 916 g for 13 min and mitochondria were pelleted from the supernatant by centrifugation at 15,000 \( \times \) g for 15 min. Mitochondria pellets were washed four times with solution A to minimize genomic DNA contamination and lysed by resuspension in 100 mM NaCl, 10 mM EDTA, 50 mM Tris, and 1% N-lauroylsarcosine and incubation at room temperature for 1 h. Extraction of mtDNA was performed by phenol-chloroform extraction followed by ethanol precipitation. mtDNA samples were digested using EcoRV and Ndel restriction endonucleases (NEB) following the manufacturer’s indications. Digested mtDNA fragments were separated by electrophoresis on 0.8% or 1% agarose gels at 4 V cm\(^{-1} \) for 2.5 or 3 h in TAE buffer with recirculation. Gels were stained with ethidium bromide.

**PCR Assays for Validation of Parental mtDNA Haplotypes**

We designed two pairs of PCR primers targeting mitochondrial coding loci that are polymorphic between the SpB and SpC strains used to generate the experimental hybrids (see supplementary table S3, Supplementary Material online). A 285 bp segment of the gene \( \text{atp6} \) was amplified using forward primer \( \text{GGTTCAAGATGATTAATTCCAAAG} \) and reverse primer \( \text{ACCGACGTTACATTAATG} \) with cycles as follows: 3 min at 94°C; 40 times the following cycle: 30 s at 94°C, 30 s at 57°C, 25 s at 72°C; 10 min at 72°C. The SpB amplicon contains a restriction site for the enzyme \( \text{DpniI} \) generating 182 and 103 bp fragments, whereas the SpC amplicon contains no \( \text{DpniI} \) restriction site. Amplicon digestion was performed with \( \text{DpniI} \) (NEB) following the manufacturer’s indications and the non-digested and digested amplicons were separated by agarose gel electrophoresis. A segment of the gene \( \text{m1} \) was amplified using forward primer \( \text{TAGGTCGCCCGATGAATGAC} \) and the reverse primer \( \text{ACGTACTTGTTTCACTCGTTTGT} \). The PCR reaction cycle was 3 min at 94°C, 40 times the following cycle: 30 s at 94°C, 30 s at 58°C, and 50 s at 72°C, and 10 min at 72°C. The amplicons (716 bp for SpB and 762 bp for SpC) were separated by agarose gel electrophoresis.

**Growth Measurement of the Hybrid Strains**

SpB \( \times \) SpC hybrid strains were printed in randomized 1,536 colonies arrays (24 technical replicates for each strain) on Omnitray plates containing media using a BMS-BC-48 colony processing robot (S&P Robotics Inc., Canada). The arrays were printed in triplicate on the following media: SCA (0.174% YNB, 2% glucose, 0.5% allantoin, 2% agar), SCM (0.174% YNB, 2% glucose, 0.5% maltose, 2% agar), YPD, YPE (1% yeast extract, 2% tryptone, 3% ethanol, 2% agar), and YPG (1% yeast extract, 2% tryptone, 3% glycerol, 2% agar). Plates were incubated 2 days at 30°C, 35°C or 37°C. The colonies were replicated on the same media and incubated at the same temperature a second time. Pictures of the plates were taken immediately after the replication and after 8.5, 16.5, 24.5, 32.5, 41.5, 48.5, 59.5, 72.5 and 96.5 h of incubation. Colony size data were extracted from plates images using ImageJ 1.440 software (NIH) as described in Diss et al. (2013). For all technical replicates and conditions, the colony size values at each time
point were expressed in log_2 and normalized by the colony size at time 0 expressed in log_2.

Statistical Analysis of Growth Rate Estimates
One-factor ANOVAs were performed on normalized log_2 colony sizes at 24.5 h, which correspond to growth rate estimates. Technical replicates for which there were no size values at 0 and/or 24.5 h (because of errors in the image analysis process) were filtered out for each condition individually. For each condition, the remaining number of replicates per strain was minimally 15/24, with an average of 22.5/24 across all conditions. Strains were grouped by mitochondrial haplotype (SpB, SpC, or recombinant). One-factor ANOVAs were performed separately on each combination of environmental condition and mtDNA haplotype category using the *anova.lm* function in R, with the identity of the strains as the factor tested (SpB = 5, SpC = 5, recombinant = 8). For further details about the ANOVA model used, see Supplementary material 4. To generate fig. 4A, the conditions were ranked according to the maximum F value obtained, regardless of the mtDNA haplotype category. The median of the technical replicates normalized log_2 colony size values at each time point were expressed in log_2 and normalized by the colony size at time 0 expressed in log_2.

Supplementary Material
Supplementary data are available at Molecular Biology and Evolution online.

Author Contributions
J.B.L and C.R.L designed research. J.B.L, L.N-T and Y.T analyzed data. M.H. performed experiments and analyzed results under the guidance of G.C. and C.R.L. J.B.P. and H.F. contributed reagents, methods and advice on the analysis and interpretation. J.B.L., C.R.L. and M.H. wrote the manuscript with input from all authors.

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References
Jaramillo-Correa JP, Bousquet J. 2005. Mitochondrial genome recombi-
nation in the zone of contact between two hybridizing conifers. Genet-

leads to hybrid incompatibility through pentatricopeptide repeat pro-

Karavaeva IE, Golyshin VP, Smirnova EA, Sokolov SS, Severin FF, Knorre
DA. 2017. Mitochondrial depolarization in yeast zygotes inhibits

Comparative genomics. Springer. p. 145–164.

Incomplete maternal transmission of mitochondrial DNA in

Kvist L, Martens J, Nazarenko AA, Orell M. 2003. Paternal leakage of
maternal DNA in the lager brewing yeast, an interspecies hybrid.

Leducq JB, Charron L, Charrier J. 2014. Local climatic adaptation
by hybridization and chromosomal plasticity in a wild yeast. Nat
Microbiol 1:15003.

by hybridization and chromosomal plasticity in a wild yeast. Nat
Microbiol 1:15003.

Ma H, O’Farrell PH. 2016. Selfish drive can trump function when animal

Sampaio JP, Hittinger CT, Bell G, Landry CR. 2014. Local climatic adaptation

Incompatibility of nuclear and mitochondrial genomes causes hy-

Ma H. O’Farrell PH. 2016. Selfish drive can trump function when animal

Saccharomyces paradoxus
S. cerevisiae. Mol Biol Evol

Mammal Salzberg SL. 2012. Fast gapped-read alignment with Bowtie

Latorre-Pellicer A, Moreño-Loshuertos R, Lechuga-Vieco AV, Sánchez-
Cabro F, Torojo C, Acín-Pérez R, Calvo E, Aix E, González-Guerra A,

Sylvester K, Hittinger CT, Bell G, Landry CR. 2016. Speciation driven
by hybridization and chromosomal plasticity in a wild yeast. Nat
Microbiol 1:15003.

Mann I, Persis D, Ario S, Robert C, Perez-Traves L, Querol A, Barrio E.
2017. Mitochondrial introgression suggests extensive ancestral hy-
bridization events among Saccharomyces species. Mol Phylo Evol
108:49–60.

Peng Y, Leung HC, Yiu S-M, Chin FY. 2012. IDBA-UD: a de novo assem-
bler for single-cell and metagenomic sequencing data with highly