

Evolution of Gene Order in the Genomes of Two Related Yeast Species

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Changes in gene order between the genomes of two related yeast species, *Saccharomyces cerevisiae* and *Saccharomyces bayanus* var. *uvarum* were studied. From the dataset of a previous low coverage sequencing of the *S. bayanus* var. *uvarum* genome, 35 different synteny breakpoints between neighboring genes and two cases of local gene inversion were characterized in detail. The number and the type of the chromosomal rearrangements that have lead to these differences were identified. We show that evolution of gene order in the genomes of these two yeast species is driven mainly by gene duplication onto different chromosomes followed by differential loss of the repeated copies. In addition, local gene inversions also would result from a mechanism of gene duplication, but in an inverted orientation, followed by loss of the original copy. The identification of traces of anciently duplicated genes, called relics, show that the loss of duplicates is more frequently caused by the accumulation of numerous mutations in one of the two copies than by DNA deletion. Surprisingly, gross chromosomal rearrangements such as translocations have only a minor effect on gene order reshuffling as they account for <10% of the synteny breakpoints.

[The sequence data have been submitted to the EMBL Library under accession nos. AJ316068 and AJ316069.]

The comparative genomics approach has proved to be fruitful in retracing chromosome maps evolution between eukaryotic genomes. Nevertheless, most of the studies rely on the relative localization of markers along physical and/or genetic maps (Gale and Devos 1998; O'Brien et al. 1999; Ranz et al. 2001). At this level of resolution, gross chromosomal rearrangements such as translocation or large inversion are identifiable, but small interstitial rearrangements remain undetected. The fine comparison of chromosome maps will be improved greatly by sequencing entire genomes from closely related species. In eukaryotes, large sequence datasets were only available for organisms too distantly related to yield valuable insights into the evolution of chromosome maps. A recent sequencing project, designated Génolevures, has laid the foundations of a true comparative genomics within a defined eukaryotic phylum, the Hemiascomycetes (<http://cbi.labri.u-bordeaux.fr/Genolevures>; Souciet et al. 2000). In this study, a low coverage random sequencing has been performed on 13 different yeast species. Among them, *Saccharomyces bayanus* var. *uvarum* (abbreviated here as *S. uvarum*) is the closest to *S. cerevisiae*. It belongs to the *Saccharomyces* sensu stricto complex (Vaughan-Martini and Martini 1998). A previous study on the chromosomal evolution between the six species belonging to this complex has shown that their genomes, each composed of 16 chromosomes, differed by a limited number of chromosomal translocations (Fischer et al. 2000). For instance, three reciprocal and one nonreciprocal translocations have been characterized between the genomes of *S. cerevisiae* and *S. uvarum*. The average amino acid identity between their ORF products

is approximately 80% (Malpertuy et al. 2000b), which compares to the level of divergence between mouse and human (86% amino acid identity; Makalowski and Boguski 1998). However, the synteny is very well conserved between these two genomes as 98% of the genes in *S. uvarum* have retained the same neighboring relationships as in *S. cerevisiae* (Bon et al. 2000; this work). We chose to study the evolution of gene order between these two genomes presenting a highly similar genetic organization to identify the primary events leading to changes in gene order before the accumulation of numerous rearrangements erases the traces of the initial events. The sequence data generated by the 0.4× coverage of the *S. uvarum* genome allowed us to follow gene by gene the mechanisms leading to gene order reshuffling between the two genomes by combining a computational analysis of the synteny among the 1810 gene couples identified in Bon et al. (2000) and an experimental approach to validate and map the synteny breakpoints. The results presented here uncover the central role played by the duplications in the evolution of gene order. Most of the synteny breakpoints corresponded to localized changes resulting from the ancient duplication of few genes followed by differential loss of the duplicated copies in the two species. Although it is commonly believed that gene order along chromosomes is reshuffled by large chromosomal rearrangements such as translocations and inversions, we show that these rearrangements have only a minor effect on gene order evolution between the genomes of *S. cerevisiae* and *S. uvarum*.

RESULTS

We describe the identification of a set of 35 nonsyntenic gene couples between *S. uvarum* and *S. cerevisiae*. These gene couples were identified from paired sequences obtained from

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both ends of the plasmid inserts of the *S. uvarum* library and not from sequences assembled from individual shotgun reads, thus avoiding the problem of contig misassemblies. We then describe in detail the events that lead to gene order changes. We show that chromosomal translocations account only for three of the nonsyntenic gene couples. In contrast, 10 couples clearly result from gene loss within ancestral duplications. These synteny breakpoints correspond either to *S. cerevisiae* singletons localized within and outside of the previously recognized ancestral block of duplication, which still exist as duplicates in the *S. uvarum* genome, or to alternate loss between *S. cerevisiae* and *S. uvarum* of the two copies of anciently duplicated genes. The duplication-loss mechanism also is invoked to explain the two cases of local gene inversions without loss of synteny. Finally, the remaining nonsyntenic gene couples correspond to rearrangements that are also compatible with a duplication-loss mechanism.

Identification of a Set of 35 Nonsyntenic Gene Couples

In this work, we have characterized 35 different nonsyntenic gene couples between the genomes of *S. cerevisiae* and *S. uvarum*. The “nonsyntenic gene couples” were defined here as two neighboring ORFs in the *S. uvarum* genomic library inserts whose homologs lie on different *S. cerevisiae* chromosomes or, by extension, on the same chromosome but very distant from each other.

In the previous work by Bon et al. (2000), BLASTX comparisons of 5140 paired-end random sequence tags (RSTs) of *S. uvarum* against the *S. cerevisiae* proteome defined 1810 nonredundant gene couples, 1776 couples with two nonambiguous matches and 34 couples with a least one ambiguous match. Ambiguity results from the fact that *S. cerevisiae* genes may form family of paralogs. Among the 34 pairs corresponding to ambiguous matches, we considered here 16 gene couples as nonsyntenic because none of the matches of the first ORF is located next to any of the matches of the second ORF in the genome of *S. cerevisiae* (Table 1). The colinearity of each of

these 16 plasmid inserts with the *S. uvarum* genome was shown by PCR amplification of the corresponding regions in the *S. uvarum* genomic DNA (data not shown).

Thirty-eight nonsyntenic gene couples originally were identified among the 1776 couples with nonambiguous matches (Bon et al. 2000). A closer look at these sequences allowed us to correct previous annotation mistakes (see Methods) leaving 30 couples to study. Hybridization experiments on pulse-field gel electrophoresis (PFGE) separated *S. uvarum* chromosomes revealed that another 12 gene couples corresponded to cloning chimeras (see Methods). Finally, an additional couple was identified during the course of this work, *SuYML051w-SuYJR057w* (*Su* for *S. uvarum* homolog to *YML051w* and *YJR057w*, respectively; Table 2), bringing the number of true nonsyntenic gene couples to 19. The nonchimerical nature of these 19 clones was shown by PCR amplification of the corresponding regions in the *S. uvarum* genomic DNA and/or by hybridization of the two ORFs onto the same *S. uvarum* chromosome. These nonsyntenic gene couples were examined in detail to understand the type of mechanism responsible for the loss of synteny between *S. cerevisiae* and *S. uvarum*.

Loss of Synteny by Chromosomal Translocation

One nonreciprocal and three reciprocal translocations have been characterized previously between the *S. cerevisiae* and the *S. uvarum* genomes, leading to seven synteny breakpoints (Fischer et al. 2000). Three of these translocation breakpoints also were identified during the course of the Génolevures project (Bon et al. 2000). This number is in good agreement with the expected value of 2.8 given by the genome coverage of $0.4 \times (0.4 \times 7 = 2.8)$. However, among the 35 synteny breakpoints characterized in this work, only three nonsyntenic couples are explained by translocations, which represents <10% of the total number of changes in gene order.

The breakpoint of the translocation *SuIttIV_R* (translocation of a piece of the right arm of chromosome IV onto chro-

Table 1. Nonsyntenic Gene Couples Having Ambiguous Matches

Gene couples	Insert name	Localization
(<i>SuYFL062w/SuYGR295c</i>) - <i>SuYLR098c</i>	AS0AA001E07	(subtelomeric)–internal
(<i>SuYFL062w/SuYGR295c/SuYNL336w</i>) - <i>SuYPR194c</i>	AS0AA015G05	(subtelomeric)–subtelomeric
(<i>SuYFL062w/SuYGR295c/SuYNL336w</i>) - <i>SuYIR039c</i>	AS0AA003A08	(subtelomeric)–subtelomeric
(<i>SuYOR389w/SuYPL277c</i>) - <i>SuYIR039c</i>	AS0AA008E06	(subtelomeric)–subtelomeric
(<i>SuYOR389w/SuYPL277c</i>) - <i>SuYGR234w</i>	AS0AA024A10	(subtelomeric)–internal
(<i>SuYOR390w/SuYPL279c</i>) - <i>SuYDR017c</i>	AS0AA002G12	(subtelomeric)–internal
(<i>SuYLR448w/SuYML073c</i>) - <i>SuYHR029c</i>	AS0AA018C09	(internal)–internal
(<i>SuYOR394w/SuYPL282c</i>) - (<i>SuYFL050c/SuYOL130w</i>)	AS0AA018C10	(subtelomeric)–(subtelomeric/internal)
(<i>SuYOR394w/SuYPL282c</i>) - <i>SuYER014w</i>	XAS0AA001A04	(subtelomeric)–internal
(<i>SuYAL068c/SuYBR301w/SuYEL049w/SuYGL261c/SuYGR294w/SuYHL046c/SuYIL176c/SuYJL223c/SuYLL064c/SuYLR461w/SuYNR076w/SuYOL161c/SuYOR394w/SuYPL282c</i>) - <i>SuYJL056c</i>	XAS0AA001B11	(subtelomeric except for <i>SuYEL049w</i> internal)–internal
(<i>SuYAR027w/SuYCR007c</i>) - (<i>SuYMR048w/SuYMR049c</i>)	AS0AA022E09	(internal)–(internal)
(<i>SuYOR071c/SuYLR237w/SuYOR192c</i>) - (<i>SuYJL190c/SuYLR367w</i>)	AS0AA023A08	(internal)–(internal)
(<i>SuYLR237w/SuYOR192c</i>) - (<i>SuYLR367w/SuYLR368w</i>)	AS0AA028G09	(internal)–(internal)
(<i>SuYDL246c/SuYJR159w</i>) - <i>SuYOR187w</i>	AS0AA028G01	(subtelomeric)–internal
(<i>SuYDL246c/SuYJR159w</i>) - (<i>SuYHR210c/SuYNR071c</i>)	XAS0AA001E07	(subtelomeric)–(subtelomeric)
(<i>SuYBL017c/SuYNR066c/SuYIL173w/SuYJL222w</i>) - <i>SuYNL040w</i>	AS0AA005C08	(subtelomeric except for <i>SuYBL017c</i> internal)–internal

Ambiguous matches corresponding to a single *S. uvarum* ORF are grouped into brackets. Matches corresponding to each of the two RSTs of the same plasmid insert are separated by a dash. Brackets also relate to the grouping of ambiguous matches in the Localization column. To retrieve the RST sequences in <http://cbi.labri.u-bordeaux.fr/Genolevures>, add the suffix DP1 or TP1 to the name of the corresponding plasmid insert. This list comprises the two non-syntenic gene couples *SuYNL040w-SuYBL017c* and *SuYPL273w-SuYOL130w*, which were initially classified in the non-ambiguous matches category (Bon et al. 2000).

Table 2. Nonsyntenic Gene Couples Obtained from Non-Ambiguous Matches, Inversions, and Deletion

Class	Gene couples	Insert name	Remarks
Translocations	<i>SuYBR030w-SuYDR012w</i>	AS0AA001G01/AS0AA027H07	ectopic recombination between the two copies of <i>RPL2</i> (Ryu et al. 1998) translocation breakpoint XV-VIII translocation breakpoint VIIItXVR
	<i>SuYOR018w-SuYHR015w</i>	AS0AA018B03	
	<i>SuYHR013c-SuYOR019w</i>	AS0AA020A08	
Gene loss in <i>S. cerevisiae</i>	<i>SuYBR060c-SuYDR037w</i>	AS0AA014G06	within block of duplication 3 extension of block of duplication 8, <i>SuYBR164c</i> in an inverted orientation outside duplication blocks
	<i>SuYBR061c-SuYDR037w</i>	AS0AA014G06	
	<i>SuYBR164c-SuYPL108w</i>	AS0AA026G07/AS0AA025H03	
	<i>SuYBR164c-SuYPL109c</i>	AS0AA025H03	
	<i>SuYBR164c-SuYPL110c</i>	AS0AA026G07	
	<i>SuYKR097w-SuYGL006w</i>	AS0AA019G08/XAS0AA001F03	
Alternate gene loss	<i>SuYML051w-SuYJR054w</i>	AS0AA026H05	not referenced as a non-syntenic pair in (Bon et al. 2000) <i>SuYBR008c</i> in an inverted orientation
	<i>SuYML051w-SuYJR057w</i>	AS0AA025G05	
	<i>SuYBR008c-SuYOR363c</i>	AS0AA003E06/AS0AA002A06	
	<i>SuYIL089w-SuYAR019c</i>	AS0AA022G08	
Inversions	<i>SuYOR182c-SuYOR184w</i>	AS0AA001E05	<i>SuYOR182c</i> inverted
	<i>SuYJL157c-SuYJL158c</i>	AS0AA004E05	<i>SuYJL158c</i> inverted
Composite rearrangements	<i>SuYER157w-SuYMR090w</i>	AS0AA027E03	non-subtelomeric
	<i>SuYMR091c-SuYLR039c</i>	AS0AA012C05/AS0AA019G01	
	<i>SuYLL055w-SuYEL071w</i>	AS0AA007E08	subtelomeric
	<i>SuYLL057c-SuYMR053c</i>	AS0AA009G06/AS0AA012D10/ AS0AA025G10	
	<i>SuYJL217w-SuYPL273w</i>	AS0AA017E08	subtelomeric
	<i>SuYJL217w-SuYFL053w</i>	AS0AA005D11	

mosome II, according to the nomenclature of chromosomes defined in Fischer et al. (2000)), comprising the pair *SuYBR030w-SuYDR012w* was characterized previously and sequenced (Ryu et al. 1998). The authors showed that this translocation results from an ectopic recombination event between two copies of a duplicated gene, *RPL2A* and *RPL2B*.

Two other nonsyntenic couples correspond to the two breakpoints of the same reciprocal translocation, involving chromosomes VIII and XV (Table 2). Both regions were amplified from *S. uvarum* total DNA, sequenced (accession numbers AJ316068 and AJ316069) and compared with the corresponding *S. cerevisiae* sequence (Fig. 1). On chromosome VIII in *S. cerevisiae*, the translocation breakpoint is localized in a region between *YHR014w* (*SPO13*) and *YHR015w* (*MIP6*) comprising two tRNA genes (*tS*[AGA]H and *tQ*[UUG]H) and three solo long terminal repeats (LTRs) from the retrotransposon Ty1 (truncated copies of 119, 241, and 324 bp, respectively). On chromosome XV, there is no tRNA, no LTR, or any repeated sequences in the intergenic region between *YOR018w* (*ROD1*) and *YOR019w*. Comparison of the junction sequences in *S. uvarum* with the corresponding regions in *S. cerevisiae* revealed that the translocation has occurred between the *tS*(AGA)H tRNA gene and a full-length LTR related to the delta sequence of Ty1 (331 bp flanked by the characteristic 5-bp inverted repeat TGTTG) on chromosome VIII and within the intergenic region *ROD1-YOR019w* on chromosome XV (Fig. 1). This translocation breakpoint lies in a region of 377 and 524 bp on chromosome *SuVIII*tXV and *SuXV*tXIII, respectively, where no homology with any LTR or repeated sequences were recognizable. It is noteworthy that no sequence identity is found between the two recombining regions, either in *S. uvarum* or in *S. cerevisiae*. Thus, this translocation results either from an illegitimate recombination mechanism between nonhomologous sequences or from homologous recombination between sequences that have subsequently di-

verged. During the Génolevures program, homology with *YHR016c* (*S. cerevisiae* chromosome VIII) and *ROD1* (*S. cerevisiae* chromosome XV) also was found at both ends of the same plasmid insert (RSTs AT0AA013C08D1 and AT0AA013C08T1) in the library of *S. servazzii*, a species that does not belong to the sensu stricto complex (Casaregola et al. 2000). This finding supports the idea that the *S. uvarum* chromosomes repre-

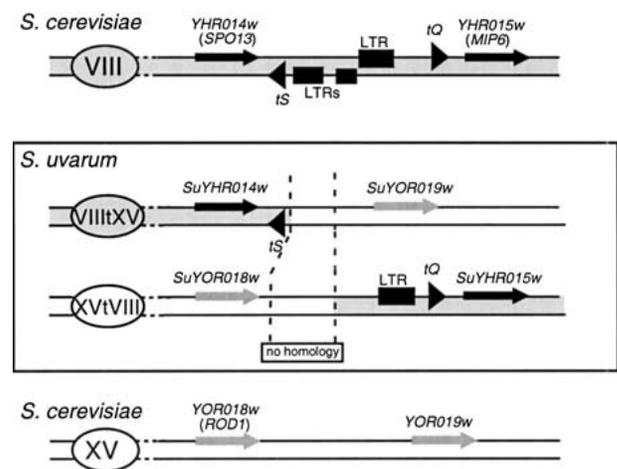


Figure 1 Junctions of the reciprocal translocation between chromosomes VIII and XV. Chromosome numbers are indicated in the ovals that represent the centromeres. Both Watson and Crick strands are represented, and the genes are symbolized by arrows. Sequences from chromosome VIII and XV of *S. cerevisiae* are drawn in gray and white, respectively. The tRNA genes are abbreviated as *tS* and *tQ* (see text) and depicted as triangles. (black boxes) LTRs from Ty1. These two corresponding regions of *S. uvarum* chromosomes were sequenced (accession numbers AJ316068 and AJ316069).

sent the ancestral form and that the translocation has occurred in the *S. cerevisiae* lineage.

Loss of Synteny by Gene Loss within Ancestral Duplications

The loss of synteny between two genes also may result from the ancient duplication onto two different chromosomes of one or both genes of the couple followed by a differential loss of the duplicated copies in the two species studied. Now, the analysis of the nonsyntenic couples between *S. cerevisiae* and *S. uvarum* offers us a possibility to examine the importance of this mechanism in genome evolution. Three distinct situations were encountered.

First, we found unique genes within the *S. cerevisiae* ancestral blocks of duplication that correspond to duplicated genes in the *S. uvarum* genome. Blocks of ancestral duplication were identified in the *S. cerevisiae* genome as arrays of

duplicated genes, called paralogs, interspersed with genes that are not duplicated (Lalo et al. 1993; Goffeau et al. 1996; Coissac et al. 1997; Mewes et al. 1997; Wolfe and Shields 1997). As it is hypothesized that random deletion of one of the two copies occurred after the initial duplication event (Achaz et al. 2000; Keogh et al. 1998), block duplication followed by individual gene loss can result in loss of synteny. This was observed in two distinct situations, the first within ancestral block of duplication 3 (according to the nomenclature of the blocks defined in Wolfe and Shields [1997]) and second on the border of duplication block 8 (Fig. 2, A and B, respectively). In *S. cerevisiae*, *YDR037w* (*KRS1*) and *YBR164c* (*ARL1*) exist as singletons. In *S. uvarum*, both genes were found as duplicates that originated from the ancestral duplication of blocks 3 and 8, respectively. This was shown by identification by dot-matrix analysis (see Methods) of traces of the second copy of these genes within the *S. cerevisiae* genome. These

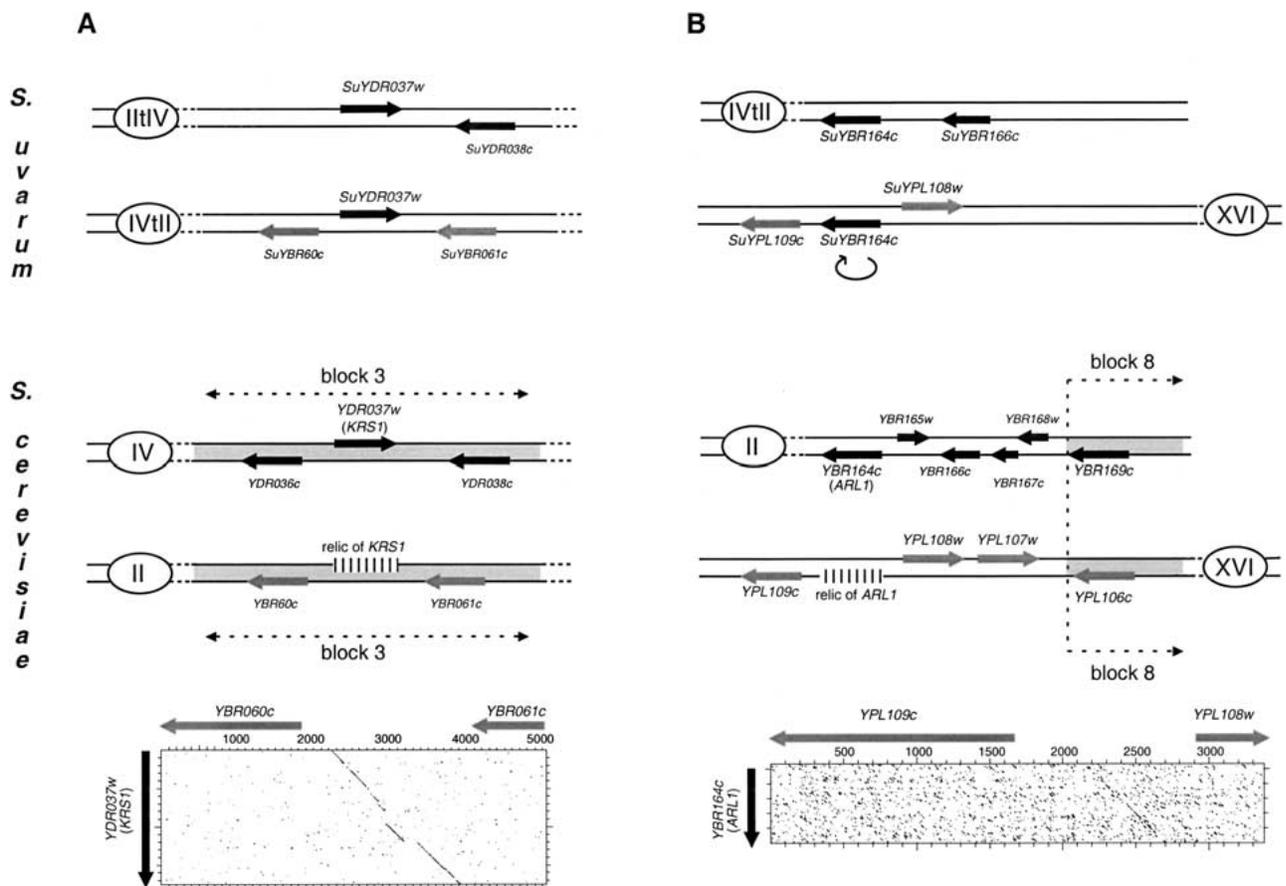


Figure 2 Loss of duplicated genes within *S. cerevisiae* ancestral duplication blocks. Symbols are the same as in Fig. 1. Shaded parts of the chromosomes correspond to duplication blocks in *S. cerevisiae* (Wolfe and Shields 1997). The relics of *YDR037w* (*KRS1*) and *YBR164c* (*ARL1*) identified in the *S. cerevisiae* genome are symbolized by the small vertical lines. (A) Loss of the second copy of *YDR037w* within the *S. cerevisiae* duplication block 3 on chromosome II: *YDR037w* is a singleton in the *S. cerevisiae* genome whereas it is duplicated in *S. uvarum*. One of the two copies was isolated next to *YDR038c*, as expected, whereas the second copy was identified between *SuYBR060c* and *SuYBR061c*. A relic of the second copy of *YDR037w* was detected by DNA dot matrix by aligning the sequence of the intergenic region between *YBR060c* and *YBR061c* with the sequence of *YDR037w*. The stringency/window parameters of the dot matrix were set at 15/23. (B) Loss of the second copy of *YBR164c* on the border of the *S. cerevisiae* duplication block 8 on chromosome XVI. *YBR164c* is a singleton in *S. cerevisiae* whereas it is duplicated in *S. uvarum*. One of the two copies was isolated associated to *SuYBR166c* whereas the other copy is located between *SuYPL108w* and *SuYPL109w*. In *S. uvarum*, the second copy of *SuYBR164c* is inverted with respect to the centromere (as symbolized by the curved arrow), as is the case for the whole of block 8 in *S. cerevisiae*. A relic of the second copy of *YBR164c* was identified in the *S. cerevisiae* genome in the intergenic region between *SuYPL108w* and *SuYPL109w*. The stringency/window parameters of the dot matrix were set at 11/19.

traces were named relics to account for the ancestral presence of a duplicated gene in the present-day corresponding intergenic region. A relic of *KRS1* was identified onto chromosome II within the duplication block 3, and a relic of *ARL1* was found onto chromosome XVI on the border of duplication block 8 (Fig. 2). The localization of the *ARL1* relic shows that the ancestral duplication between chromosomes II and XVI probably was more extended than the block 8 characterized in *S. cerevisiae*. The presence of these relics in the *S. cerevisiae* genome proves that some of the singletons within the present-day duplicated blocks existed originally as duplicates. Moreover, it shows that gene loss within the duplicated blocks occurred, at least in these cases, by accumulation of mutations rather than deletion of one copy. For instance, the relic of *KRS1*, which shows the highest sequence conservation of all relics identified in this work (see relics on Figs. 2, 5, and 6 for comparison), differs from the active copy of *KRS1*, which is 1776 nucleotides long, by 293 point mutations introducing 25 stop codons and 59 insertions/deletions from 1 to 113 nucleotides.

The second situation encountered was duplicated genes in *S. uvarum* that correspond to singletons localized outside of the recognized block of duplication in *S. cerevisiae*. Some ancestral blocks of duplication have escaped from comparison of the *S. cerevisiae* genome with itself. They were recognized only from comparisons with other species (Llorente et al. 2000). This situation is illustrated by the ORF *YKR097w* (*PCK1*), which exists as a singleton in *S. cerevisiae*, but was found duplicated in the *S. uvarum* genome (Fig. 3A). The partial sequences of the two *S. uvarum* homologs to *PCK1* (*SuYKR097w*) overlap over 213 nucleotides and share only moderate se-

quence identity (44% in nucleotides with many small insertions/deletions), which is fully compatible with the presence of two distinct loci. In addition, hybridization of the *SuYKR097w* probe (see Methods) revealed both chromosomes *SuXI* and *SuVII Δ_L* (not shown), confirming that this gene is duplicated in the *S. uvarum* genome. The localization of the two copies of the duplicated *SuYKR097w* gene in *S. uvarum* does not correspond to any identified duplicated block in *S. cerevisiae*. BLASTX comparison against the *S. cerevisiae* proteome revealed that the second copy of *SuYKR097w* is truncated in both the 5' and in the 3' regions of the gene, before residue 357 and after residue 506 (compared with the 544 residues of *PCK1* in *S. cerevisiae*, Fig. 3B). In addition, BLASTN comparison against the *S. cerevisiae* genome revealed that the region downstream of the homology with *PCK1* shares homology alternatively with chromosome VII and XI of *S. cerevisiae*. This mosaic region of two *S. cerevisiae* chromosomes probably results from an ancient duplication block whose trace is not detectable anymore in the *S. cerevisiae* genome. Despite the big size of the intergenic region between *YGL006w* (*PMC1*) and *YGL007w* in *S. cerevisiae* (2283 bp vs. an average of 500 bp [Dujon 1996]), no relic of *PCK1* could be found at this position.

Finally, the third category of rearrangement belonging to the duplication-loss mechanism corresponds to genes that seem to have transposed from one chromosome in *S. cerevisiae* to another chromosome in *S. uvarum*. In fact, a closer look at these synteny breakpoints revealed that they correspond to an unnoticed ancestral coduplication of two genes (or more) on two different chromosomes, followed by alternate gene loss in the two species. This leaves only one copy of each gene in each of the two genomes but localized on two different chromosomes. This mechanism is documented here by the following three cases.

The first example is the alternate loss of *YML051w* (*GAL80*) between *S. cerevisiae* and *S. uvarum*. Although *GAL80* belongs to chromosome XIII of *S. cerevisiae*, its *S. uvarum* homolog (*SuYML051w*) map onto chromosome *SuX* (Fig. 4A). This situation would result from the duplication of *GAL80* in the ancestry of *S. cerevisiae* and *S. uvarum* followed by the alternate loss of the two copies in the two species. This mechanism is strongly supported here by the identification in *Kluyveromyces thermotolerans* and in *K. lactis* of series of nonsyntenic couples whose homologs lie alternatively on chromosome X and XIII in *S. cerevisiae* (Bolotin-Fukuhara et al. 2000; Malpertuy et al. 2000a; Fig. 4B). These gene couples can be assembled in a single map of 12 genes corresponding to a mosaic of 2 *S. cerevisiae* chromosomes called a *trans*-chromosomal series (Llorente et al. 2000; Fig. 4C). The alternate localization of these genes along two different chromosomes in *S. cerevisiae* would be the result of an ancient duplication of the whole region onto chromosomes X and XIII, followed by a massive loss of the duplicates alternatively on each chromosome. This region was not known as an ancestral duplication block before. Indeed, it is located exactly between block 28 and block 42 on chromosome X and between block 44 and block 19 on chromosome XIII. The only remaining trace of this ancestral duplication in the present-day *S. cerevisiae* genome is the presence of the two member gene family *YML047c*/*YJRO54w* (Fig. 4C).

The second case corresponds to the alternate loss

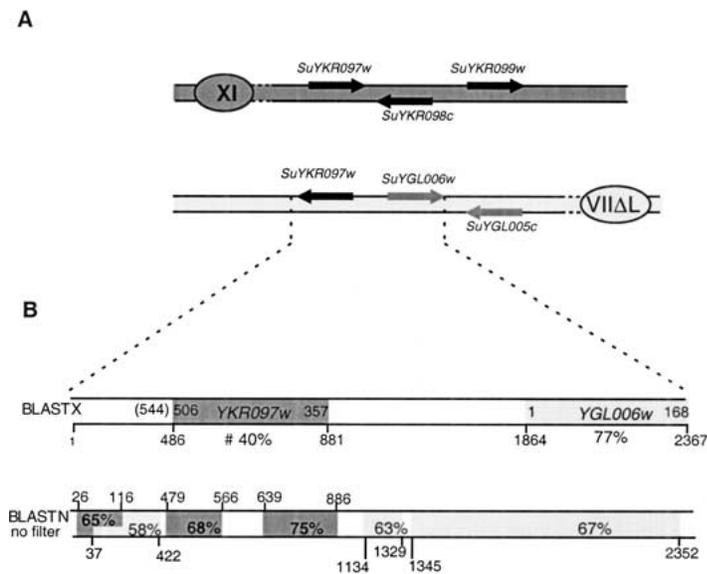


Figure 3 Loss of a duplicated gene in *S. cerevisiae* outside previously recognized duplication blocks. Symbols are the same as in Fig. 1, and the *S. uvarum* sequences homologous with *S. cerevisiae* chromosomes XI and VII are drawn in dark and light gray, respectively. (A) Chromosomal mapping of the two copies of *SuYKR097c* in *S. uvarum* genome. *SuYKR097c* was isolated twice paired with *SuYGL006w* and once associated with *SuYKR098w* and *SuYKR099w*. (B) BLASTX and BLASTN comparisons (BLOSUM62) between the *S. uvarum* *SuYKR097w*-*SuYGL006w* region and the *S. cerevisiae* genome. The sequence of the synteny breakpoint on chromosome VII Δ_L was assembled from sequences of overlapping RSTs from the Génolevures projects (XAS0AA01F03TP1, AS0AA19G08DP1, and XAS0AA01F03DP1). Percentage of identity as well as coordinates of the hits are indicated.

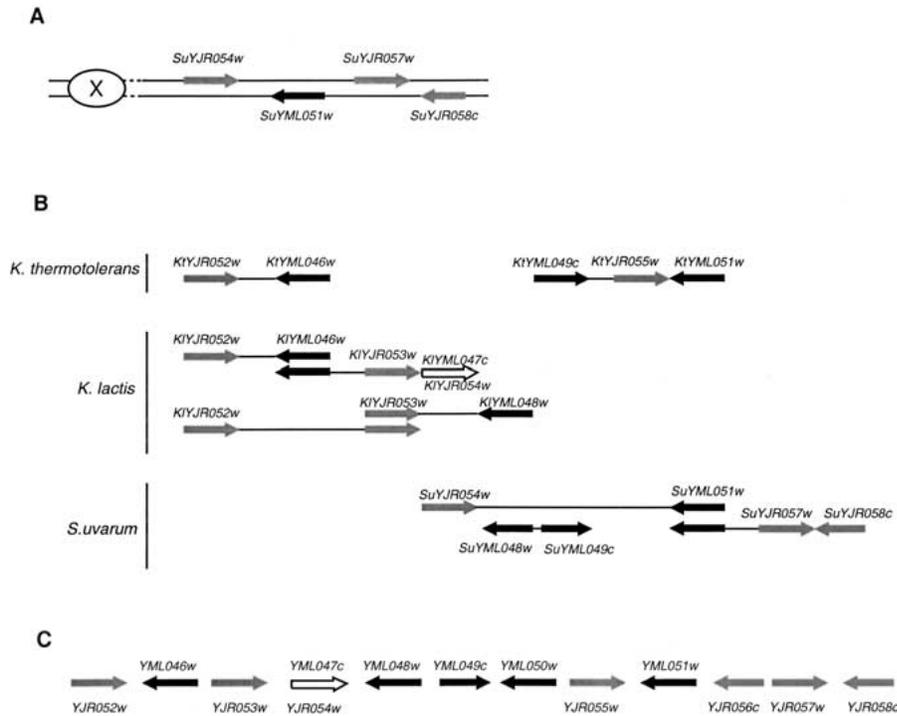


Figure 4 Alternate loss of *YML051w* between *S. cerevisiae* and *S. uvarum*. (Gray and black arrows) ORFs homologous with genes located on *S. cerevisiae* chromosome X and XIII, respectively. (White arrow) An ambiguous match with both *YML047c* and *YJR054w*. (A) Chromosomal mapping of *SuYML051w*: the ORF *SuYML051w* is associated to *SuYJR054w* and to *SuYJR057w/SuYJR058c* in two different plasmid inserts of the *S. uvarum* library (Table 2). The *SuYML051w* probe hybridized onto chromosome *SuX* (hybridization not shown). (B) *Trans*-chromosomal series: gene couples corresponding to a mosaic of *S. cerevisiae* chromosomes X and XIII identified in three different *Génolevures* species. (C) Hypothetical ancestral gene order before duplication: compilation of the gene couples identified in the three species.

of *YBR008c* (*FLR1*) between *S. cerevisiae* and *S. uvarum*. The *S. uvarum* homolog to *FLR1* (*SuYBR008c*) was isolated in the *S. uvarum* library twice associated with *SuYOR363c* (Table 2) but in an inverted orientation. Both ORFs were localized on *S. uvarum* chromosome VIIIItXV by hybridization onto PFGE karyotype (the terminal 700 kb from the right arm of chromosome XV encompassing *SuYOR363c* is translocated onto chromosome VIII [Fischer et al. 2000], data not shown). According to this localization, one can make the assumption that *SuYOR363c* has kept the same orientation relative to the centromere than *YOR363c* in *S. cerevisiae*. This would imply that *SuYBR008c* would be in an inverted orientation relative to the centromere of the *S. uvarum* chromosome VIIIItXV. This is supported by the identification by DNA dot matrix of a weak sequence similarity between *FLR1* and the intergenic region between *YOR362c* and *YOR363c* but in an inverted orientation (Fig. 5). This trace is a relic of an ancestral copy of *FLR1*. Thus, *FLR1* must have existed as duplicates and the copy on chromosome XV was lost in *S. cerevisiae* but kept in *S. uvarum* whereas the copy on chromosome II was lost in *S. uvarum* but kept in *S. cerevisiae*. Moreover, *FLR1* belongs to the block 3, which is duplicated on chromosome IV (Wolfe and Schields 1997). This means that this gene has been involved in a least two successive duplication events during the yeast genome evolution.

The last case of alternate gene loss is illustrated by the ORF *YIL089w*, belonging to *S. cerevisiae* chromosome IX and

whose *S. uvarum* homolog was isolated in the same plasmid insert that *SuYAR019c* (Table 2). Both corresponding probes hybridized onto chromosome *SuI*. No relic of *YIL089w* was found next to *YAR019c* on *S. cerevisiae* chromosome I. However, the corresponding intergenic region of 1721 bp is big enough to have accommodated a copy of this gene at one point of its evolution.

In conclusion, from the set of 19 nonambiguous synteny break-points analyzed, 10 gene couples correspond to six distinct situations of differential loss of duplicates. In addition, a similar mechanism can be invoked to explain local gene inversions as well as most, if not all, of the composite rearrangements described below.

Duplication-Loss and Local Inversion

Two cases of local gene inversion, without loss of synteny, that could result from a duplication-loss mechanism were identified (see Methods). *SuYJL158c* (*S. uvarum* homolog to *CIS3*) and *SuYOR182c* (*S. uvarum* homolog to *RPS30B*) were inverted relative to their respective centromeres (Table 2). It is noteworthy that both *CIS3* and *RPS30B* belong to ancestral blocks of duplication 45 and 40, respectively, and

have a paralog in the corresponding duplicated region. As detailed below, this is indicative of a relationship between duplication and inversion.

The detailed analysis of the *SuYJL158c* inversion was very informative about the molecular mechanism responsible for local gene inversion. In *S. cerevisiae*, *CIS3* and its two neighboring genes, *YJL159w* (*HSP150*) and *YJL160c*, are members of the same gene family (also comprising *YKL163w* [*PIR3*] and *YKL164c* [*PIR1*], see below). Sequence similarity between the three corresponding proteins is restricted to their N-terminal region, from residues 20 to 75, of 227 in total. However, the match detected between the *S. uvarum* RST (AS0AA004E05DP1) and *CIS3* corresponds to the C-terminal region of the protein, between residues 129 to 227 (Fig. 6A). As there is no sequence similarity in this region between *Cis3p*, *Hsp150p*, and *Yjl160p*, the corresponding ORF in *S. uvarum* was annotated as a nonambiguous ortholog to *CIS3* and designated *SuYJL158c*, although its orientation was inverted. However, on the *S. uvarum* RST, downstream of the homology with *CIS3*, sequence similarity was detected at the nucleotide level with the intergenic region *CIS3-HSP150* but in proper orientation relative to the rest of the insert. This pattern revealed that the match with *CIS3* in the *S. uvarum* RST corresponds to the chromosomal region of *HSP150* in *S. cerevisiae* (Fig. 6A). In *S. cerevisiae*, the gene family comprising *CIS3*, *HSP150*, *YJL160c*, *PIR3*, and *PIR1* is fully included in the duplicated block 40. The pairs *CIS3-PIR3* and *HSP150-PIR1*

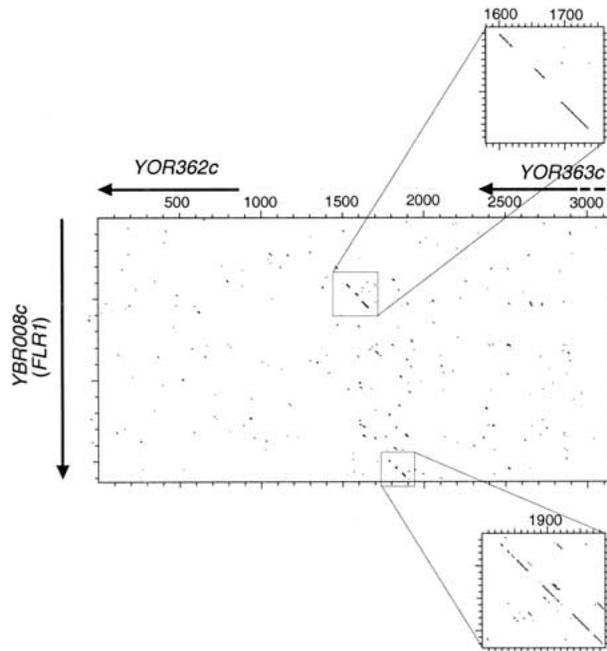


Figure 5 DNA dot matrix between *YBR008c* (FLR1) and the *YOR362c*-*YOR363c* region. The stringency/window parameters of the dot matrix were set at 15/23 for the main matrix and for the top magnification and at 13/23 for the bottom magnification.

defined in Wolfe and Schields (1997) show an inverted orientation relative to the rest of the block, and *YJL160c* has no paralog in block 40 (Fig. 6B). A closer look at these chromosomal regions allowed us to identify a relic in the intergenic region between *YKL162c* and *PIR3*, which corresponds to the true structural paralog to *CIS3*. It follows that the true structural paralogs to *HSP150* and *YJL160c* are in fact *PIR3* and *PIR1*, respectively, and that there was no physical DNA inversion between the two chromosomal regions (Fig. 6C).

Altogether, these findings strongly support a model of local gene inversion based on an initial event of duplication in the common ancestor to *S. cerevisiae* and *S. uvarum*, producing a tandem inverted repeat of one gene (Fig. 7). After the speciation process, the two copies of this gene could either be differentially lost between the two species or diverge independently from their respective paralogs in the other species. This would lead to an apparent gene inversion relative to the neighboring genes but without any physical DNA inversion between the two species.

Composite Rearrangements

Six different nonsyntenic gene couples correspond to three composite rearrangements between *S. uvarum* and *S. cerevisiae* genomes. In each case, multiple events have accumulated in a given chromosomal region. Two of these complex events involved sequences localized in the *S. cerevisiae* subtelomeric regions (Table 2).

The first composite rearrangement correspond to the triplication of *YMR090w* in the *S. uvarum* genome associated with the transposition of *YMR091c* (*NPL6*) from *S. cerevisiae* chromosome XIII to *S. uvarum* chromosome XII. *SuYMR090w* was found in three different plasmid inserts from the library associated once to *SuYER157w* and twice to *SuYLR039c* (Fig.

8A). Both *SuYER157w* and *SuYMR090w* probes hybridized onto chromosome VtVII of the *S. uvarum* karyotype, and two additional signals were obtained onto chromosomes XIII and IX with the *SuYMR090w* probe (not shown). The *SuYMR091c* hybridizes with the *S. uvarum* chromosome XII (not shown). In *S. cerevisiae*, no relic of *NPL6* could be identified next to *YLR039c*, despite a very large intergenic region of 1862 bp

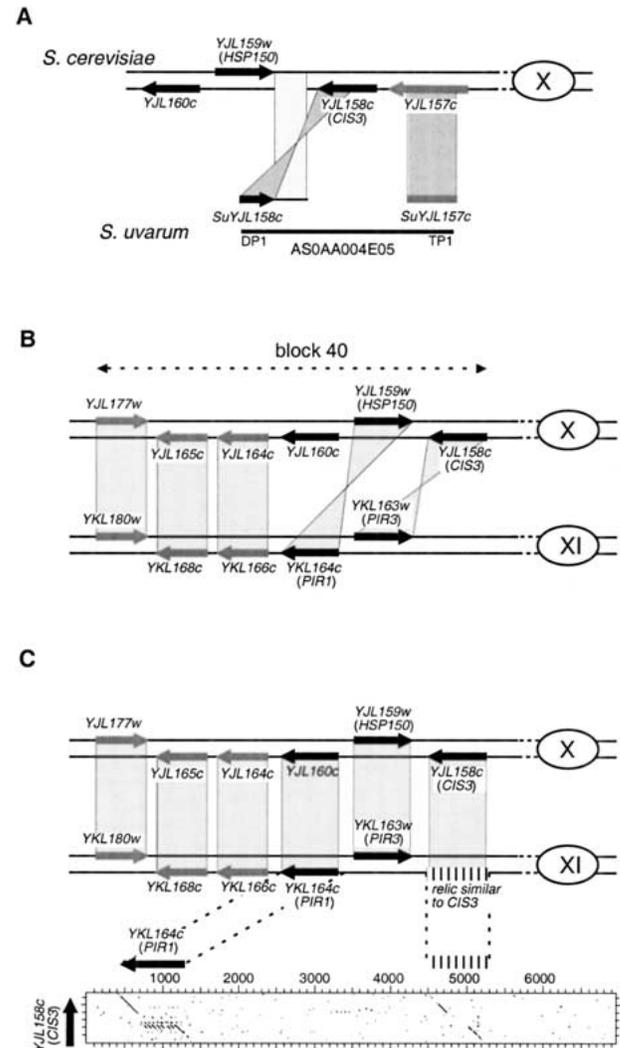


Figure 6 Local gene inversions. Symbols are the same as in Figure 1. (black arrows) Genes that are members of the same gene family. (A) Local gene inversion of *SuYJL158c*. The chromosomal neighborhood of *YJL158c* (*CIS3*) in *S. cerevisiae* chromosome X is presented at the top of the figure. At the bottom, hits are depicted that were obtained from both BLASTX (dark shading) and BLASTN (light shading) comparisons of the two *S. uvarum* paired RSTs (AS0AA004E05DP1 and AS0AA004E05TP1) with the *S. cerevisiae* genome. (B) Structure of the duplicated block 40 in *S. cerevisiae*. Only those genes being duplicated between and/or within the two blocks are represented. The shaded areas between genes represent the BLASTP-based identification of the paralogous partners (Wolfe and Schields 1997). (C) Identification of a relic of *YJL158c*. The relic on *S. cerevisiae* chromosome XI is symbolized by the small vertical lines and the corresponding DNA dot matrix is presented below (stringency/window set a 15/23). The shaded area corresponds to the new paring of duplicates in block 40.

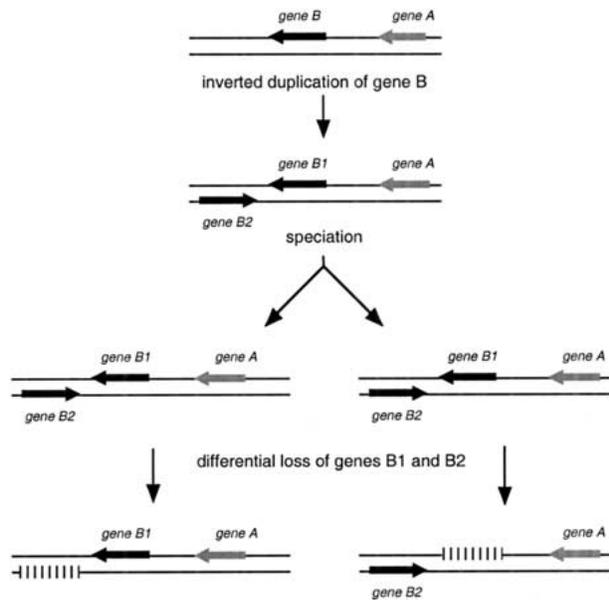


Figure 7 Model for local gene inversion. Inverted duplication of gene B in the common ancestor of two different present-day species, followed by speciation and differential loss (or divergence) of the two copies between the two species produces an apparent inversion of gene B relative to gene A.

between *YLR038c* and *YLR037c* (i.e., in the region where *SuYMR091c* was identified in *S. uvarum*, Fig. 8A). Similarly, no relic of *YMR090w* was found next to *YER157w*, the intergenic region being 1664 bp long. The differences in the chromosome map characterized at these loci imply the accumulation of at least three rearrangements, a triplication of *SuYMR090w* (most probably by two successive duplications) as well as the transposition of *NPL6* from chromosome XIII to chromosome XII, which possibly corresponds to an ancestral duplication of this gene followed by alternate gene loss in the two species.

The second composite rearrangement involves a transposition of *YLL055w* in conjunction with a duplication of the two neighboring genes *YLL056c* and *YLL057c* (Fig. 8B). Hybridization experiments onto *S. uvarum* PFGE karyotypes revealed that *SuYLL055w* is absent from chromosome XII and transposed onto chromosome VtVII. In addition, both *SuYLL056c* and *SuYLL057c* were found to be duplicated onto chromosome XIII. These chromosome map rearrangements involved genes localized in the subtelomeric regions of chromosomes V and XII in *S. cerevisiae*. At least two different rearrangements could be invoked, an ancestral duplication of *YLL055w* onto chromosome VtVII followed by the loss of the original copy on chromosome XII, and a coduplication of *YLL056c* and *YLL057c* onto chromosome XIII. However, the failure to observe any relic of these events in the corresponding intergenic regions in *S. cerevisiae* does not allow us to retrace precisely which rearrangements reshaped the ancestral gene order either in the *S. cerevisiae* or in the *S. uvarum* lineages.

The last composite rearrangement represents both a transposition and a duplication of *YJL217w* (Fig. 8C) as well as an inverted transposition of *YFL053w* (*DAK2*) in the *S. uvarum* genome. The *SuYJL217w* probe hybridizes onto both chromosomes SuXVI and SuVII (and not onto chromosome X as in *S. cerevisiae*). This ORF is associated with *SuYPL273w* and

SuYFL053w on two different plasmid inserts. Although the *SuYPL273w* probe hybridizes onto *S. uvarum* chromosome XVI as in *S. cerevisiae*, the *SuYFL053w* probe hybridizes onto chromosome IVtII (and not on chromosome VI as in *S. cerevisiae*, not shown). In addition, *SuYFL053w* shows an inverted orientation relative to the centromere compared with its *S. cerevisiae* counterpart. These three genes, *YJL217w*, *YPL273W*, and *DAK2*, are localized in the *S. cerevisiae* subtelomeric regions, and no relic of these genes could be identified. Once again, differences in the genetic organization of these loci are compatible with a duplication-loss mechanism.

These composite rearrangements correspond to a juxta-

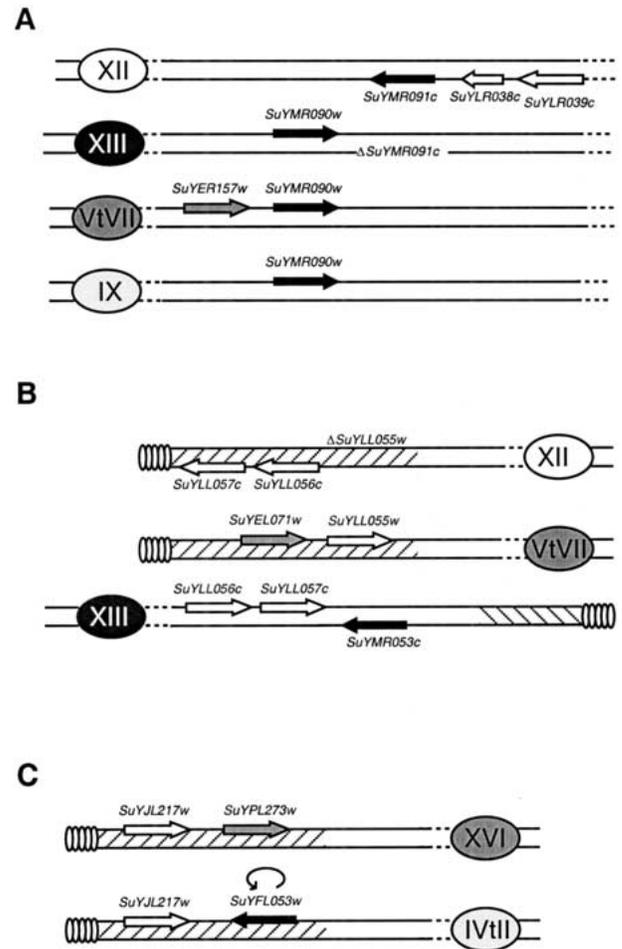


Figure 8 Composite rearrangements. Symbols are the same as in Fig. 1. The shading of the arrows corresponds to the shading of the centromeres. (A) Nonsynthetic gene couples *SuYER157w-SuYMR090w* and *SuYMR091c-SuYLR039c* (Δ *SuYMR091c*). The absence of hybridization of the corresponding probe onto chromosome SuXIII. (B) Nonsynthetic gene couples *SuYLL055w-SuYEL071w* and *SuYLL057c-SuYMR053c*. The *S. uvarum* ORFs homologous with *S. cerevisiae* subtelomeric genes lie in hatched areas that represent, by analogy with *S. cerevisiae*, the subtelomeric regions in *S. uvarum*. Similarly, the contiguous ovals symbolize *S. uvarum* telomeres. *SuYLL056c* and *SuYLL057c* are not represented in a hatched area on chromosome SuXIII because they were associated to *SuYMR053c* whose ortholog in *S. cerevisiae* is not localized in the subtelomeric regions. (C) Nonsynthetic gene couples *SuYJL217w-SuYPL273w* and *SuYJL217w-SuYFL053w*. Same representation for subtelomeres and telomeres as in (B). (Curved arrow) Inversion of the orientation of *SuYFL053w*.

position of individual synteny breakpoints, most of which, if not all, are explainable by the above mechanism of duplication loss. However, it is difficult to discriminate between an accumulation of successive rearrangements and a burst of simultaneous rearrangements in a given chromosomal region. Note that even between two genomes with a highly similar genetic organization some cases of accumulation of rearrangements impede to retrace precisely the primary events leading to a loss of synteny.

DISCUSSION

From a $0.4\times$ random sequencing coverage of the *S. uvarum* genome, a total of 35 synteny breakpoints were identified among 1810 gene couples examined. This figure when extrapolated to the whole genome predicts a total of approximately 80 synteny breakpoints between the genomes of *S. cerevisiae* and *S. uvarum*. The overall conservation of synteny between these two species then could be estimated at 98% (35 of 1810 gene couples in total).

It is commonly accepted that gene order along chromosomes is reshuffled by chromosomal rearrangements such as translocations, duplications, deletions, and inversions. These chromosomal rearrangements physically affect the presence, the orientation, and/or the localization of a DNA segment within the chromosomes. On the contrary, differential gene loss within a previously duplicated segment does not involve any recombination mechanism except for the initial duplication event. As described in this work, gene loss is mainly caused by the accumulation of mutations within the coding sequences. In some cases, traces of an ancient presence of a copy of a gene could still be detected at the nucleotide level by DNA dot-matrix analyses but not at the amino acid level by BLASTX comparisons as it is classically the case for pseudogenes. These traces were named relics rather than pseudogenes because all the characteristics of an ORF have been erased by the high number of mutations accumulated in these sequences. This mechanism of gene erasing was found to affect one copy of an anciently duplicated gene (or possibly one member of a gene family). Sequence conservation between the relic and the present-day active copy of the anciently duplicated gene is variable (see Figs. 2 and 5 for comparison). In some cases, we were not able to detect any relic despite large intergenic regions at the synteny breakpoints. This may be because of an accumulation of mutations in these regions to such an extent that there is not enough resemblance left with the ancestral gene to be detected by dot matrix. The inactivation of one copy of a duplicated gene, presumably by a nonsense mutation, would not be counterselected, and the subsequent accumulation of base substitutions would follow the mutation rate. Duplication creates an unstable transient stage; one of the two copies will disappear. This idea is fully compatible with the prediction based on the degree of nucleotide divergence between duplicated genes that most duplicates are silenced by accumulation of mutations very early after the duplication event (Lynch and Conery 2000).

One can ask what the relative contribution of duplications followed by differential gene loss compared with the other chromosomal rearrangements in the evolution of gene order between *S. cerevisiae* and *S. uvarum* is. Except for the duplication events that underlie most of the changes in gene order, the contribution of chromosomal rearrangements appeared to be limited to three translocations. It is noteworthy that no case of large inversion has been found among the

1776 nonambiguous gene couples indicating that inversion of large DNA segments is rare within the evolutionary distance between *S. cerevisiae* and *S. uvarum*. This might be a general difference between eukaryotes and prokaryotes in which inversions are predominantly large (Huynen et al. 2001). Contrary to what is commonly reported, chromosomal rearrangements played only a minor role in gene order evolution. The 34 remaining events (32 couples of nonsyntenic genes plus two cases of local gene inversion) resulted from or were compatible with a segmental duplication followed by differential gene loss (or divergence) of the duplicated genes.

During the Génolevures program, the proportion of local gene inversions with conservation of synteny was calculated for the 13 species and revealed that this phenomenon remains rare over relatively long evolutionary distances (from *S. cerevisiae* to most *Kluyveromyces* species) but becomes prominent over longer evolutionary distances (between *S. cerevisiae* and *Pichia*, *Candida*, *Debaryomyces*, and *Yarrowia* species; Llorente et al. 2000). This is in good agreement with comparative studies on gene order/orientation evolution between *S. cerevisiae* and *S. bayanus*, *S. servazzii*, and *S. kluyveri*, on one hand (Langkjaer et al. 2000) and between *S. cerevisiae* and *Candida albicans*, on the other hand (Seoighe et al. 2000). The former showed that the impact of gene inversion was very limited between closely related species whereas the latter showed that small size inversions were a major cause of genome reorganization between distantly related species. Our results call for an important consideration regarding the mechanism by which small inversions occur. The characterization of tandemly inverted duplicated genes at the place where local gene inversions occurred supports a model based on an initial inverted duplication event followed by differential divergence or loss of the two copies of the duplicated gene in two different species (Fig. 7).

Surprisingly, 16 of 35 (46%) nonsyntenic gene couples comprised ORFs homologous with *S. cerevisiae* subtelomeric genes whereas the subtelomeric regions represent less than 10% of the nuclear DNA in *S. cerevisiae*. This overrepresentation of subtelomeres within the nonsyntenic gene couples is largely attributable to the pairs obtained from ambiguous matches (Table 1). The reason for this is that subtelomeric regions in *S. cerevisiae* are composed of a variety of tandem and dispersed repeated sequences as well as several large gene families (Louis 1995). The average sequence similarity between the different members is much higher in the subtelomeric families than in the internal ones (except for the ribosomal protein genes). Thus, the high proportion of synteny breakpoints in the subtelomeric regions could be because of the large size of the families that would provide numerous possibilities to differential gene loss leading to synteny breakpoints possibly because of a low selection pressure on the copy number within large families and because the subtelomeric genes are not essential. This is supported by the large proportion of nonsyntenic gene couples found among the ambiguous couples (16 of 34 couples with a least one ambiguous match), which reflects a significantly lower conservation of synteny within gene families than average (53% compared with 98%). Concomitantly, the low level of sequence divergence within members of the subtelomeric families would permit a high level of recombination leading to changes in the order of flanking genes without detrimental effects because of the subtelomeric localization of these sequences.

In conclusion, our results showed that at the macroscopic level, the genomes of *S. cerevisiae* and *S. uvarum* are

mainly colinear, few translocations being the only large chromosomal rearrangements detectable (Fischer et al. 2000). However, if one looks at a higher magnification, numerous synteny breakpoints are present between these genomes, but they correspond to local rearrangements of gene order most of which result from ancient duplication events. These findings lead us to distinguish between microsynteny and macrosynteny breakpoints. The former is restricted to events encompassing only a few genes such as segmental duplication followed by differential gene loss whereas the latter corresponds to chromosomal rearrangements such as translocations encompassing many genes. Evolution of gene order in the yeast genome is mainly caused by the accumulation of numerous microsynteny breakpoints. Macrosynteny breakpoints could be either disadvantaged because of mechanistic constraints or counter-selected because of chromosomal mis-segregation at meiosis. Differences between macro- and microsynteny could also be important in speciation. It has been shown that macrosyntenic rearrangements are not a prerequisite for speciation in yeast (Fischer et al. 2000). However, the microsyntenic rearrangement induced by recurrent gene losses within ancestral duplications would provide an efficient way to reproductive isolation. If gene duplications are followed by geographic separation and subsequent alternative losses of the duplicated copies in the two populations, mating of the previously isolated populations will produce a double-null homozygote nonviable progeny (Lynch and Conery 2000). In this regard, microsyntenic rearrangements could be more effective than the macrosyntenic changes in establishing a postmating reproductive barrier between isolated populations.

METHODS

Computational Analyses and Reexamination of the Original Sequence Data Set

All the sequence data utilized in this work are directly accessible via the Génolevures web site: <http://cbl.labri.u-bordeaux.fr/Genolevures/Genolevures.php3>, except for the sequences of the translocation junctions determined in this work (accession nos. AJ316068 and AJ316069). The paired-end sequence data from the Génolevures project consist of very long sequence tags (RSTs) of 910 bp on average from both ends of the 4–5-kb plasmid inserts (Artiguenave et al. 2000). Annotation of the paired-end sequences by comparison to *S. cerevisiae* allowed the identification of 1810 pairs of neighboring genes in *S. uvarum* (Bon et al. 2000). The BLASTX annotations of the 38 nonsyntenic genes couple previously identified were rechecked. This control revealed that three of the 38 gene couples corresponded to incorrect validation of non-significant hits against the *S. cerevisiae* proteome (matches with *YOR022c*, *YPR194c*, and *YBL082c* in the gene couples *SuYHR176w-SuYOR022c*, *SuYPR194c-SuYCR014c*, and *SuYPR072w-SuYBL082c* were not significant). Two other *S. uvarum* ORFs (*SuYJR045c* and *SuYOL130w*), initially annotated as nonambiguous homologs to *S. cerevisiae* genes, are each related to a paralogous gene in *S. cerevisiae*, which preserves the synteny with the rest of the insert. Thus, *SuYEL031w-SuYJR045c* and *SuYFL048c-SuYOL130w* correspond to the syntenic couples, *SuYEL031w-SuYEL030w* and *SuYFL048c-SuYFL050c*. In addition, homologies with the two paralogous genes *SuYCR106w* and *SuYLL054c* were defined as a nonsyntenic gene couple whereas they represent in fact two overlapping regions of the same ORF (either *SuYCR106w* or *SuYLL054c*). Two other ORFs (*SuYBL017c* and *SuYOL130w*) were annotated as clear homologs with *S. cerevisiae* genes

whereas each of them significantly matched to several members of a gene family, none of which were syntenic with the rest of the inserts. Therefore, these pairs belong to the ambiguous match category defined in the first section of Results (Table 1).

We identified two cases of local gene inversion within the set of syntenic couples (Table 2). The inverted gene of the couple was identified using the rationale defined in Llorente et al. (2000).

In the *S. cerevisiae* genome, we sought traces of ancient duplicated copies of genes (called relics) by aligning the *S. cerevisiae* sequence corresponding to the synteny breakpoint in *S. uvarum* with the sequence of the *S. cerevisiae* gene orthologous with the *S. uvarum* nonsyntenic gene. These alignments were realized by DNA dot matrix (DNA Strider 1.3f11), which allowed us to detect contiguous series of a very short stretch of sequence similarity. Parameters of the matrices are indicated in the legends to the figures.

Experimental Methods

The *S. uvarum* strain from the Génolevures program 623–6C *ura3–1* (or CLIB533) is derived from NCYC 623 (NRRL Y11845, CBS 7001; Bon et al. 2000). *S. uvarum* total genomic DNA was extracted according to Johnston (1988) and the nonchimeric nature of the plasmid inserts containing nonsyntenic gene couples was shown by long-range PCR from total DNA with the Ex-Taq kit (Takara) using the conditions recommended by the supplier and oligonucleotide primers (sequences available on request).

Chromosome plugs were prepared as described in Louis (1998). PFGE karyotypes were performed in a Rotaphor R23 tank (Biometra) using the following program: run time 65 h, pulse time from 140 to 180 sec (linear ramping), angle 110°, 140 volts, 0.9% agarose gel (Seakem GTG) in Tris-Borate-EDTA buffer 0.25×.

S. uvarum ORFs used as probes were PCR-amplified from plasmid DNA of the *S. uvarum* library (Bon et al. 2000) clones using the Wizard Plus SV minipreps kit (Promega) with primers internal to the coding regions (sequences available on request). These PCR products were gel-purified with the Nucleo-spin Extract kit (Macherey-Nagel) and nonradioactively labeled with the Gene Images kit (Amersham). Southern transfers of PFGE karyotypes were performed onto Hybond N+ membrane (Amersham), probed, and detected according to the Gene Images manual. A total of 12 chimeric clones were identified among the gene couples originally annotated as nonsyntenic by hybridization of each of the two probes from the same gene couple onto different *S. uvarum* chromosomes (*SuYOR304w-SuYPR160w*, *SuYPL002c-SuYML075c*, *SuYPR162c-SuYML002w*, *SuYLR392c-SuYER111c* *SuYJL046w-SuYOR119c*, *SuYPL216w-SuYJL099w*, *SuYLL003w-SuYER080w*, *SuYCL031c-SuYBR177c*, *SuYBR269c-SuYJR152w*, *SuYAL028w-SuYPR015c*, *SuYNL059c-SuYDR177w*, and *SuYLL029w-SuYOR049c*).

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