

Extensive Copy Number Variation in Fermentation-Related Genes Among Saccharomyces cerevisiae Wine Strains

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ABSTRACT Due to the importance of Saccharomyces cerevisiae in wine-making, the genomic variation of wine yeast strains has been extensively studied. One of the major insights stemming from these studies is that wine yeast strains harbor low levels of genetic diversity in the form of single nucleotide polymorphisms (SNPs). Genomic structural variants, such as copy number (CN) variants, are another major type of variation segregating in natural populations. To test whether genetic diversity in CN variation is also low across wine yeast strains, we examined genome-wide levels of CN variation in 132 whole-genome sequences of S. cerevisiae wine strains. We found an average of 97.8 CN variable regions (CNVRs) affecting ~4% of the genome per strain. Using two different measures of CN diversity, we found that gene families involved in fermentation-related processes such as copper resistance (CUP), flocculation (FLO), and glucose metabolism (HXT), as well as the SNO gene family whose members are expressed before or during the diauxic shift, showed substantial CN diversity across the 132 strains examined. Importantly, these same gene families have been shown, through comparative transcriptomic and functional assays, to be associated with adaptation to the wine fermentation environment. Our results suggest that CN variation is a substantial contributor to the genomic diversity of wine yeast strains, and identify several candidate loci whose levels of CN variation may affect the adaptation and performance of wine yeast strains during fermentation.

KEYWORDS

domestication genomics structural variation carbohydrate metabolism alcoholic fermentation

Saccharomyces cerevisiae, commonly known as baker's or brewer's yeast, has been utilized by humans for the production of fermented beverages since at least 1350 B.C.E. but may go as far back as the Neolithic period 7000 yr ago (Mortimer 2000; Cavalieri et al. 2003). Phylogenetic analyses and archaeological evidence suggest wine strains originated from Mesopotamia (Bisson 2012), and were domesticated in a single event around the same time as the domestication of grapes (Schacherer et al. 2009; Sicard and Legras 2011). Further phylogenetic, population structure and identity-by-state analyses of single nucleotide

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polymorphism (SNP) data reveal close affinity and low genetic diversity among wine yeast strains across the globe, consistent with a domestication-driven population bottleneck (Liti *et al.* 2009; Schacherer *et al.* 2009; Sicard and Legras 2011; Cromie *et al.* 2013; Borneman *et al.* 2016). These low levels of genetic diversity have led some to suggest that further wine strain development should be focused on introducing new variation into wine yeasts rather than exploiting their standing variation (Borneman *et al.* 2016).

Many wine strains have characteristic variants that have presumably been favored in the wine-making environment (Marsit and Dequin 2015). For example, adaptive point mutations, deletions, and rearrangements in the promoter and coding sequence of *FLO11* contribute to flocculation and floating, thereby increasing yeast cells' ability to obtain oxygen in the hypoxic environment of liquid fermentations (Fidalgo *et al.* 2006). Similarly, duplications of *CUP1* are strongly associated with resistance to copper (Warringer *et al.* 2011), which, at high concentrations, can cause stuck fermentations, and *THI5*, a gene involved in thiamine metabolism whose expression is associated with an undesirable rotten-egg sensory perception in wine, is absent or downregulated among wine strains and their derivatives (Bartra *et al.* 2010; Brion *et al.*

2014). As these examples illustrate, the mutations underlying these, as well as many other, presumably adaptive, traits are not only SNPs, but also genomic structural variants, such as duplications, insertions, inversions, and translocations (Pretorius 2000; Marsit and Dequin 2015).

Copy number (CN) variants, a class of structural variants defined as duplicated or deleted loci ranging from 50 bp to whole chromosomes (Zhang et al. 2009; Arlt et al. 2014), have received considerable attention due to their widespread occurrence (Sudmant et al. 2010; Bickhart et al. 2012; Axelsson et al. 2013; Pezer et al. 2015) as well as their influence on gene expression and phenotypic diversity (Freeman et al. 2006; Henrichsen et al. 2009). Mechanisms of CN variant evolution include nonallelic homologous recombination (Lupski and Stankiewicz 2005) and retrotransposition (Kaessmann et al. 2009). CN variants are well studied in various mammals, including humans (Homo sapiens; Sudmant et al. 2015), cattle (Bos taurus; Bickhart et al. 2012), the house mouse (Mus musculus; Pezer et al. 2015), and the domestic dog (Canis lupus familiaris; Axelsson et al. 2013), where they are important contributors to genetic and phenotypic diversity.

Relatively few studies have investigated whole-genome CN profiles in fungi (Hu et al. 2011; Farrer et al. 2013; Steenwyk et al. 2016). For example, the observed CN variation of chromosome 1 in the human pathogen Cryptococcus neoformans results in the duplications of ERG11, a lanosterol-14- α -demethylase and target of the triazole antifungal drug fluconazole (Lupetti et al. 2002), and AFR1, an ATP binding cassette (ABC) transporter (Sanguinetti et al. 2006), leading to increased fluconazole resistance (Sionov et al. 2010). Similarly, resistance to itraconazole, a triazole antifungal drug, is attributed to the duplication of cytochrome P-450-depdendent C-14 lanosterol α -demethylase (pdmA)—a gene whose product is essential for ergosterol biosynthesis—in the human pathogen Aspergillus fumigatus (Osherov et al. 2001). Finally, in the animal pathogen Batrachochytrium dendrobatidis, the duplication of Supercontig V is associated with increased fitness in the presence of resistance to an antimicrobial peptide, although the underlying genetic elements involved remain elusive (Farrer et al. 2013).

Similarly understudied is the contribution of CN variation to fungal domestication (Gibbons and Rinker 2015; Gallone et al. 2016). Notable examples of gene duplication being associated with microbial domestication include those of α -amylase in Aspergillus oryzae, which is instrumental in starch saccharification during the production of sake (Hunter et al. 2011; Gibbons et al. 2012), and of the MAL1 and MAL3 loci in beer-associated strains of S. cerevisiae that metabolize maltose—the most abundant sugar in the beer wort (Gallone et al. 2016; Gonçalves et al. 2016). Beer strains of S. cerevisiae often contain additional duplicated genes associated with maltose metabolism, including MPH2 and MPH3, two maltose permeases, and the putative maltose-responsive transcription factor, YPR196W (Gonçalves et al. 2016). Adaptive gene duplication in S. cerevisiae has also been detected in experimentally evolved populations (Dunham et al. 2002; Gresham et al. 2008; Dunn et al. 2012). Specifically, duplication of the locus containing the high affinity glucose transporters HXT6 and HXT7 has been observed in adaptively evolved asexual strains (Kao and Sherlock 2008), as well as in populations grown in a glucose-limited environment (Brown et al. 1998; Dunham et al. 2002; Gresham et al. 2008). Altogether, these studies suggest that CN variation is a significant contributor to S. cerevisiae evolution and adaptation.

To determine the contribution of CN variation to genome evolution in wine strains of *S. cerevisiae*, we characterized patterns of CN variation across the genomes of 132 wine strains, and determined the functional impact of CN variable genes in environments reflective of winemaking. Our results suggest that there is substantial CN variation

among wine yeast strains, including in gene families (such as *CUP*, *FLO*, *HXT*, and *MAL*) known to be associated with adaptation in the fermentation environment. More generally, it raises the hypothesis that CN variation is an important contributor to adaptation during microbial domestication.

MATERIALS AND METHODS

Data mining, quality control, and mapping

Raw sequence data for 132 *S. cerevisiae* wine strains were obtained from three studies (Borneman *et al.* 2016, 127 strains, Bioproject ID: PRJNA303109; Dunn *et al.* 2012, two strains, Bioproject ID: SRA049752; Skelly *et al.* 2013, three strains, Bioproject ID: PRJNA186707) (Supplemental Material, File S1 and Figure S1 in File S2). Altogether, these 132 strains represent a diverse set of commercial and noncommercial isolates from the "wine" yeast clade (Borneman *et al.* 2016).

Sequence reads were quality-trimmed using Trimmomatic, version 0.36 (Bolger *et al.* 2014), with the following parameters and values: leading:10, trailing:10, slidingwindow:4:20, minlen:50. Reads were then mapped to the genome sequence of the *S. cerevisiae* strain S288c (annotation release: R64.2.1; http://www.yeastgenome.org/) using Bowtie 2, version 1.1.2 (Langmead and Salzberg 2012), with the "sensitive" parameter on. For each sample, mapped reads were converted to the bam format, sorted and merged using SAMtools, version 1.3.1. Sample depth of coverage was obtained using the SAMtools depth function (Li *et al.* 2009).

CN variant identification

To facilitate the identification of single nucleotide polymorphisms (SNPs), we first generated mpileup files for each strain using SAMtools, version 1.3.1 (Li *et al.* 2009). Using the mpileup files as input to Var-Scan, version 2.3.9 (Koboldt *et al.* 2009, 2012), we next identified all statistically significant SNPs (Fisher's Exact test; P < 0.05) present in the 132 strains that had a read frequency of at least 0.75 and minimum coverage of 8×. This step enabled us to identify 149,782 SNPs. By considering only SNPs that harbored a minor allele frequency of at least 10%, we retained 43,370 SNPs. These SNPs were used to confirm the evolutionary relationships among the strains using Neighbor-Net phylogenetic network analyses in SplitsTree, version 4.14.1 (Huson 1998) as well as the previously reported low levels of SNP diversity (Figure S2 in File S2, and Borneman *et al.* 2016).

To detect and quantify CN variants we used Control-FREEC, version 9.1 (Boeva *et al.* 2011, 2012), which we chose because of its low false positive rate, and high true positive rate (Duan *et al.* 2013). Importantly, the average depth of coverage or read depth of the 132 strains was $30.1 \pm 14.7 \times$ (minimum: $13.0 \times$, maximum: $104.5 \times$; Figure S3 in File S2), which is considered sufficient for robust CNV calling (Sims *et al.* 2014).

Control-FREEC uses LOESS modeling for GC-bias correction and a LASSO-based algorithm for segmentation. Implemented Control-FREEC parameters included window = 250, minExpectedGC = 0.35, maxExpectedGC = 0.55, and telocentromeric = 7000. To identify statistically significant CN variable loci (P < 0.05), we used the Wilcoxon Rank Sum test. The same Control-FREEC parameters, but with a window size of 25 bp, were used to examine CN variation within the intragenic Serine/Threonine-rich sequences of *FLO11* (Lo and Dranginis 1996). Bedtools, version 2.25 (Quinlan and Hall 2010) was used to identify duplicated or deleted genic loci (*i.e.*, CN variable loci) that overlapped with genes by at least one nucleotide. The CN of each gene (genic CN) was then calculated as the average CN of the 250 bp windows that overlapped with the gene's location coordinates in the genome. The same

method was used to determine nongenic CN for loci that did not overlap with genes (i.e., nongenic CN variable loci). To identify statistically significant differences between CN variable loci that were duplicated vs. those that were deleted, we employed the Mann-Whitney U-test (Wilcoxon rank-sum test) with continuity correction (Wallace 2004).

Diversity in CN variation and GO enrichment

To identify CN diverse loci across strains, we used two different measures. The first measure calculates the statistical variance (s^2) for each locus where CN variants were identified in one or more strains; s² values were subsequently log₁₀ normalized. Log₁₀(s²) accounts for diversity in raw CN values, but not for diversity in CN allele frequencies. Thus, we also employed a second measure based on the Polymorphic Index Content (PIC) algorithm, which has previously been used to identify informative microsatellite markers for linkage analyses by taking into account both the number of alleles present and their frequencies (Keith et al. 1990; Risch 1990). PIC has also been used to quantify population-level diversity of simple sequence repeat loci and restriction fragment length polymorphisms in maize (Smith et al. 1997). PIC values were calculated for each locus harboring at least one CN variant based on the following formula:

$$PIC = 1 - \sum_{i=a}^{z} i^2$$

where i^2 is the squared frequency of a to z CN values (Smith et al. 1997). PIC values may range from 0 (no CN diversity) to 1 (all CN alleles are unique). Both $log_{10}(s^2)$ and PIC are measurements of CN diversity between strains, and do not account for any sequence variation between copies of the same locus.

To create a list of loci exhibiting high CN diversity for downstream analyses, we retained only those loci that fell within the 50th percentile of $\log_{10}(s^2)$ values (min = -2.12, median = -1.02, and max = 2.40), or the 50th percentile of PIC values (min = 0.02, median = 0.14, and max = 0.96).

Genes overlapping with loci exhibiting high CN diversity were used for Gene ontology (GO) enrichment analysis with AmiGO2, version 2.4.24 (Carbon et al. 2009) using the PANTHER Overrepresentation Test (release 20160715) with default settings. This test uses the PANTHER GO database, version 11.0 (Thomas et al. 2003; release date July 15, 2016), which is directly imported from the GO Ontology database, version 1.2 (Gene Ontology Consortium2004; release date 27 October, 2016), a reference gene list from S. cerevisiae, and a Mann-Whitney U-test (Wilcoxon rank-sum test) with Bonferroni multi-test corrected P-values to identify over- and under-represented GO terms (Mi et al. 2013). Statistical analyses and figures were created using pheatmap, version 1.0.8 (Kolde 2012), gplots, version 3.0.1, ggplot2 (Wickham 2009), or standard functions in R, version 3.2.2 (R Development Core Team 2011).

Identifying loci absent in the reference strain

To identify loci absent from the reference strain but present in other strains, we assembled unmapped reads from the 20 strains with the lowest percentage of mapped reads. The percentage of mapped reads was determined using SAMtools (Li et al. 2009); its average across strains was 96% (min = 70.5% and max = 99%; Figure S4 in File S2). Unmapped reads from the 20 strains with the lowest percentage of mapped reads were assembled using SPAdes, version 3.8.1 (Bankevich et al. 2012). The identity of scaffolds longer than the average length of a S. cerevisiae's gene (~1400 bp) was determined using blastx from NCBI's BLAST, version 2.3.0 (Madden 2013) against a local copy of

the GenBank nonredundant protein database (downloaded on January

Data availability

The authors state that all data necessary for confirming the conclusions presented in the article are represented fully within the article.

RESULTS

Descriptive statistics of CN variation

To examine CN variation across wine yeasts, we generated whole genome CN profiles for 132 strains (File S1 and Figure S5 in File S2). Across all strains, we identified a total of 2820 CNVRs that overlapped with 2061 genes and spanned 3.7 Mb. The size distribution of CNVRs was skewed toward CN variants that were <1 kb in length (Figure 1A, and Figure S6A and Table S1 in File S2). Most CNVRs stemming from duplications were <1 kb in size, whereas most CNVRs stemming from deletions were between 5 and 7 kb (Figure S7 in File S2). These deletions were flanked by Ty transposable elements, which have been shown to frequently induce deletions (Xu and Boeke 1987). Strains had an average of 97.8 \pm 9.5 CNVRs (median = 86) (Figure S6B in File S2) that affected an average of 4.3 \pm 0.1% of the genome (median = 4.1%) (Figure S6C in File S2).

Due to the known influence of CN variable genes (Henrichsen et al. 2009; Orozco et al. 2009), we next quantified the number of genic and nongenic CNVRs (Figure 1, B and C). We found statistically significant differences in the number of duplicated and deleted loci that are genic or nongenic (Mann-Whitney *U*-test; P < 0.01 for both genic and nongenic comparisons), revealing that there were significantly more deleted genic and nongenic CNVRs than duplicated ones.

CN diversity in subtelomeres

To identify loci that exhibited high CN diversity, we retained only those loci that fell within the 50th percentile of at least one of our two different measures $[\log_{10}(s^2)]$ and PIC across the 132 strains. These loci covered ~6% of the yeast genome. The distributions of the two measures (Figure S8 in File S2) were similar, with 1326 loci (Figure S8C in File S2) and 291 genes (Figure S8D in File S2) identified in the top 50% of CN diverse genes by both measures.

In addition, the $log_{10}(s^2)$ measure identified an additional 85 loci and 54 genes in its set of top 50% genes, and PIC an additional 85 loci and 18 genes. In total, our analyses identified 1502 loci and 363 genes showing high CN diversity. Among the genes harboring the highest log₁₀ (s²) and PIC values were YLR154C-G [PIC = 0.96; $\log_{10}(s^2) = 2.16$], YLR154W-A [PIC = 0.96; $\log_{10}(s^2) = 2.16$], YLR154W-B [PIC = 0.96; $\log_{10}(s^2) = 2.16$, YLR154W-C [PIC = 0.96; $\log_{10}(s^2) = 2.16$], YLR154W-E [PIC = 0.96; $\log_{10}(s^2) = 2.16$], YLR154W-F [PIC = 0.96; $\log_{10}(s^2) = 2.16$] and YLR154C-H [PIC = 0.93; $\log_{10}(s^2) = 2.40$]; these genes are all encoded within the 25S rDNA or 35S rDNA locus. The rDNA locus is known to be highly CN diverse (Gibbons et al. 2015), thereby demonstrating the utility and efficacy of our CN calling protocol as well as our two measures of CN diversity. We next generated CN diversity maps for all 16 S. cerevisiae chromosomes (Figure 1D; Figure S9 in File S2). CN diversity was higher in loci and genes located in subtelomeres (defined as the 25 kb of DNA immediately adjacent to the chromosome ends; Barton et al. 2003). Specifically, 684/1502 (45.5%) of CN diverse loci and 243/363 (66.9%) CN diverse genes were located in the subtelomeric regions. Conducting the same analysis using an alternative definition of subtelomere (defined as the DNA between the chromosome's end to the first essential gene; Winzeler et al. 1999) showed similar results.

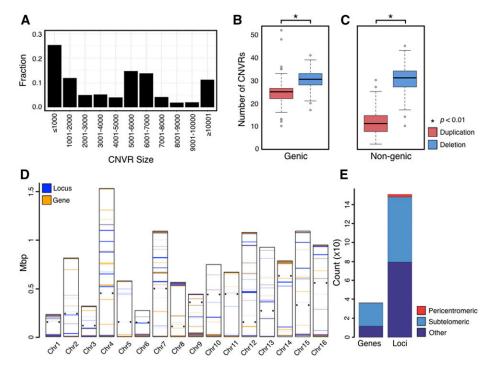


Figure 1 Size distribution and location of CN variable loci. (A) The fraction of CNVRs (y-axis) for a given size range. Most CNVRs are ≤1000 bp. (B, C) Deleted genic (B) and nongenic (C) CNVRs are more prevalent than duplicated ones (P < 0.01 for both comparisons). Note that 26.23% of genic duplications occurred in multiples of three. (D) Location of CN variable loci across the 16 yeast chromosomes. The small, black squares on either side of each chromosome denote centromere location. Chromosomes are oriented with the start of the chromosome on the bottom and the end on top. Loci (blue bars) and genes (orange bars) harboring high log₁₀(s²) or PIC values are shown. (E) A total of 684 of the 1502 CN diverse loci and 243 of the 363 CN diverse genes reside in subtelomeric regions of the yeast genome; in contrast, very few are found in pericentromeric regions (28 loci and three genes).

Specifically, 721/1502 (48%) of CN diverse loci and 233/363 (64.2%) of CN diverse genes were located in the subtelomeric regions.

GO enrichment of CN diverse genes

To determine the functional categories over- and under-represented in the 363 genes showing high CN diversity, we performed GO enrichment analysis. The majority of enriched GO terms were associated with metabolic functions such as α -Glucosidase activity (P < 0.01) and Carbohydrate transporter activity (P < 0.01) (Figure 2 and File S3 in File S1).

Genes associated with these GO terms include SUC2 (YIL162W, involved in hydrolyzing sucrose), all six members from the MAL gene family (involved in the fermentation of maltose and other carbohydrates), and all five members of the IMA gene family (involved in isomaltose, sucrose, and turanose metabolism). Other enriched categories were associated with multi-cellular processes such as the FLOCULATION (P < 0.01) and AGGREGATION OF UNICELLULAR ORGANISMS (P = 0.03). All members of the FLO gene family (involved in flocculation) and YHR213W (a flocculin-like gene) were associated with these GO enriched terms.

Contrary to over-represented GO terms, under-represented terms were associated with genes whose protein products are part of the interactome or protein–protein interactions such as protein complex (P < 0.01), Macromolecular complex assembly (P = 0.03), transferase complex (P < 0.01), and ribonucleoprotein complex biogenesis (P = 0.04). Our finding of under-represented GO terms being associated with multi-unit protein complexes supports the gene balance hypothesis, which states that the stoichiometry of genes contributing to multi-subunit complexes must be maintained to conserve kinetics and assembly properties (Birchler and Veitia 2010, 2012). Thus, genes associated with multi-unit protein complexes are unlikely to exhibit CN variation.

Genic CN diversity

To further understand the structure of CN variation in highly diverse CN genes, we first calculated the absolute CN of 23 genes associated with GO enriched terms related to wine fermentation processes (*e.g.*, metabolic functions; Figure 2 and File S3 in File S1) as well as 57 genes with

the highest PIC or $\log_{10}(s^2)$ values (File S4 in File S1 and Figure S10 in File S2; 69 total unique genes). Among these 69 genes, gene CN ranged from 0 to 92; both the highest CN diversity and absolute CN values were observed in segments of the rDNA locus (mentioned above).

Importantly, 35 of the 69 genes have also been reported to have functional roles in fermentation-related processes. The remaining 34 genes with high scores for CN diversity, to our knowledge, have no known association with wine fermentation (e.g., YAL064W-B, FRK1/ YPL141C, and ENA5/YDR038C among others). All genes with high CN diversity scores are listed in File S4 in File S1 and summarized in Figure S10 in File S2. For the purposes of this manuscript, we chose to focus on genes related to fermentation. For example, the CNs of PAU3 (YCR104W), a gene active during alcoholic fermentation, and its gene neighbor ADH7 (YCR105W), an alcohol dehydrogenase, both varied between zero and three. Similarly, the absolute CN of the locus containing both CUP1-1 (YHR053C; PIC = 0.868) and its paralog CUP1-2(YHR055C; PIC = 0.879) ranged from 0 and 14 (Figure 3 and File S4 in File S1), with 90 strains (68.2%) showing duplications (i.e., a CN > 1), and another 11 strains (8.3%) a deletion (i.e., a CN of 0). Interestingly, multiple copies of CUP1 confer copper resistance to wine strains of S. cerevisiae, with CN variation at this locus thought to be associated with domestication (Warringer et al. 2011; Marsit and Dequin 2015).

The expression of SNO family members is induced just prior to, or after, the diauxic shift as a response to nutrient limitation, and is associated with vitamin B acquisition (Padilla *et al.* 1998; Rodríguez-Navarro *et al.* 2002). We found that SNO2 (YNL334C) and SNO3 (YFL060C) were among the 363 genes with highest CN diversity. SNO2 was duplicated in 14 strains (10.6%) and deleted in nine strains (6.8%), while SNO3 was deleted in 117 strains (88.6%) (Figure 3). The other two members of the SNO gene family, SNO1 (YMR095C) and SNO4 (YMR322C), both showed a CN of 1 in all strains.

Another gene family whose members show high CN diversity is the *THI* gene family, which is responsible for thiamine metabolism, and is activated at the end of the growth phase during fermentation

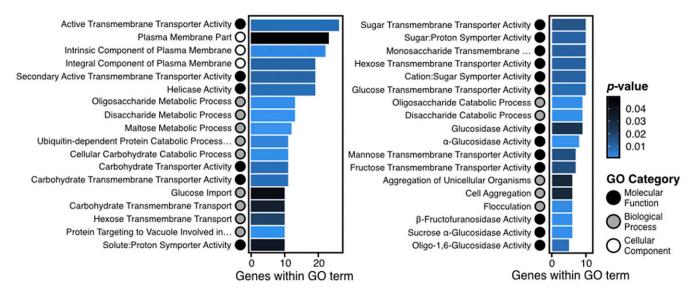


Figure 2 GO enriched terms from high CN diverse genes. Molecular function (black), biological process (gray), and cellular component (white) GO categories are represented by circles, and are enriched among the 363 genes that overlap with CN diverse loci. Enriched terms are primarily related to metabolic function, such as α -glucosidase activity (P < 0.01), carbohydrate transporter activity (P < 0.01) and flocculation (P < 0.01).

(Brion et al. 2014). Specifically, THI13 (YDL244W; PIC = 0.759) was among the 57 genes with the highest CN diversity (File S4 in File S1), and THI5 (YFL058W) and THI12 (YNL332W) among the 363 most CN diverse genes (File S3 in File S1). THI13 was duplicated in 82 strains (62.1%) and deleted in two strains (1.5%) (Figure 3). In contrast, THI5 was deleted in 121 strains (91.67%), whereas THI12 was deleted in 23 strains (17.42%), and duplicated in only three strains (2.27%). Lastly, the CN of the last THI gene family member, THI11 (YJR156C), did not exhibit CN variation.

In addition to the high CN diversity observed in all six members of the MAL1 and MAL3 loci responsible for maltose metabolism and growth on sucrose (Stambuk et al. 2000; Gallone et al. 2016), MAL13 (YGR288W; PIC = 0.53) was among the 57 genes with the highest CN diversity (File S4 in File S1). Evaluation of the absolute CN of all MAL1 locus genes (Figure 3) showed that MAL11, MAL12 (YGR292W), and MAL13 were deleted in 65 (49.2%), 86 (65.2%), and 61 strains (46.2%), respectively. In contrast, the MAL3 locus genes MAL31 (YBR298C), MAL32 (YBR299W), and MAL33 (YBR297W) were duplicated in 100 (75.8%), 99 (75%), and 98 strains (74.2%), respectively. Interestingly, we did not observe any deletions in any of the MAL3 locus genes across the 132 strains. When considering all members of the MAL gene family, we found that the 132 strains differed widely in their degree to which the locus had undergone expansion or contraction (Figure S11 in File S2).

All members of the IMA gene family, composed of genes aiding in sugar fermentation (Teste et al. 2010), were among the 363 genes with high CN diversity (File S3 in File S1) and IMA1 (YGR287C; PIC = 0.87) was among the top 57 genes with the highest CN diversity (File S4 in File S1). IMA1 was deleted in 54 strains (40.9%) and duplicated in 50 strains (37.9%) (Figure 3). Although many duplications or deletions did not span the entirety of IMA1, there were four strains that harbored high CNs between four and six. These same four strains also had similar and unique duplications of MAL11 and MAL13, suggesting that IMA1, MAL11, and MAL13, which are adjacent to each other in the genome, may have been duplicated as one locus. The other isomaltases (IMA2-5; YOL157C, YIL172C, YJL221C, and YJL216C) were deleted in at least 11 strains (8.3%) and at most 55 strains (41.7%). No duplications in IMA2-5 were detected, and only rarely in IMA3 (five strains, 3.8%).

Altogether, the 132 strains exhibited both expansions and contractions of the IMA gene family (Figure S11 in File S2).

We identified seven members of the HXT gene family (HXT6/ YDR343C, HXT7/YDR342C, HXT9/YJL219W, HXT11/YOL156W, HXT13/YEL069C, HXT15/YDL245C, and HXT17/YNR072W), which is involved in sugar transport, that were among the 363 CN diverse genes (File S3 in File S1). Members of the HXT gene family were duplicated, deleted, or had mosaic absolute CN values across the 132 strains. For example, HXT6 and HXT7 were primarily duplicated in 25 (18.9%) and 22 strains (16.7%), respectively, while only three strains (2.3%) had deletions in either gene (Figure 3). HXT9, HXT11, and HXT15 were deleted in 32 (24.2%), 57 (43.2%), and 53 strains (40.2%), respectively, while no strains had duplications. Finally, HXT13 was duplicated in 12 strains (9.1%) and deleted in 17 strains (12.9%), and HXT17 was duplicated in 37 strains (28%) and deleted in nine strains (6.8%).

As expansions in the HXT gene family are positively correlated with aerobic fermentation in S. paradoxus and S. cerevisiae (Lin and Li 2011), we also examined the absolute CN of all other 10 members (GAL2/YLR081W, HXT1/YHR094C, HXT2/YMR011W, HXT4/ YHR092C, HXT5/YHR096C, HXT8/YJL214W, HXT10/YFL011W, HXT16/YJR158W, RGT2/YDL138W, and SNF3/YDL194W) of the HXT gene family (Figure 3). Interestingly, all remaining 10 members of the HXT gene family were not CN variable. Altogether, examination of the HXT family CN diversity patterns across the 132 strains suggests that wine yeast strains typically exhibit minor contractions (i.e., HXT gene deletions exceed those of duplications) relative to the S288c reference strain (Figure S11 in File S2).

All five members of the FLO gene family, which is responsible for flocculation (Govender et al. 2008), a trait shown to aid in the escape of oxygen limited environments during liquid fermentation (Fidalgo et al. 2006; Govender et al. 2008), were found to be among the 363 most CN diverse genes. Furthermore, FLO5 (YHR211W; PIC = 0.82) and FLO11 (YIR019C; PIC = 0.88) were among the 57 genes with the highest CN diversity (File S4 in File S1). Due to the importance of site-directed CN variation in FLO family genes (Fidalgo et al. 2006), we modified our representation of CN variation to display intragenic

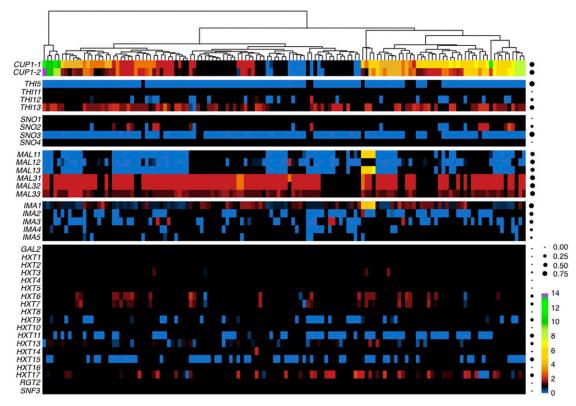


Figure 3 CN variation of genes and gene families. Heat map of the CN profiles the *CUP*, *THI*, *SNO*, *MAL*, *IMA*, and *HXT* gene families; rows correspond to genes and columns to strains. Blue-colored cells correspond to deletions, black-colored cells to no CN variation and red-to-purple-colored cells to duplications (ranging from 2 to 14). Dots on the right side of the figure represent the proportion of individual strains that harbor CN variation in that gene—the larger the dot, the greater the proportion of the strains that is CN variable for that gene.

CN variation using a 250 bp window (Figure S12 in File S2). FLO5 was partially duplicated in 57 strains (43.2%), partially deleted in 47 strains (35.6%), and 115 strains (87.1%) had at least one region of the gene unaffected by CN variation. Duplications and deletions were primarily observed in the Threonine-rich region or Serine/Threonine-rich region located in the center or end of the FLO5 gene, respectively. To better resolve intragenic CN variation of FLO11, whose repeat unit is shorter than that of FLO5, we recalled CN variants with a smaller window size of 25 bp and re-evaluated CN variation (Figure S13 in File S2). Using this window size, we found extensive duplications in 97 strains (73.5%) between gene coordinates 250–350 bp. Furthermore, duplications were observed in the hydrophobic Serine/Threonine-rich regions (Figure S13 in File S2), which are associated with the flocculation phenotype (Fidalgo $et\ al.\ 2006$; Ramsook $et\ al.\ 2010$).

In contrast to *FLO5* and *FLO11*, other members of the *FLO* gene family did not exhibit intragenic CN variation. For example, CN variation in *FLO1* (YAR050W) and FLO9 (YAL063C) typically spanned most or all of the sequence of each gene. Specifically, 125 strains (99.2%) had deletions spanning \geq 80% of the gene in *FLO1*, and only two strains (1.5%) had the entirety of the gene intact. *FLO9* had deletions in 99 strains (75%) that spanned \geq 75% of the gene, 11 strains (8.3%) that had a partial deletion spanning <75% of the gene, whereas one strain (0.8%) had a CN of two, and the remaining 21 strains (15.9%) had a CN of one. In contrast, *FLO10* (YKR102W) showed limited CN variation. Specifically, 108 strains (81.8%) had no CN variation while six strains (4.5%) had deletions spanning the entirety of the gene. No duplications spanned the entirety of the gene but partial

duplications were observed in 17 strains (12.9%) and were located in, or just before, the Serine/Threonine-rich region.

Functional implications CN variable genes

To determine the functional impact of deleted CN variable genes, we examined the relative growth of deleted CN variable genes (denoted with the Δ symbol) relative to the wild-type (WT) *S. cerevisiae* strain S288c across 418 conditions using the Hillenmeyer *et al.* (2008) data (File S5 in File S1 and Figure S14 in File S2). To determine the impact of duplicated genes, we examined growth fitness of the WT strain with low (\sim 2–3 gene copies) or high (\sim 8–24 gene copies) plasmid CN, where each plasmid contained a single gene of interest from previously published data, relative to WT (File S6 in File S1, Figure S15 in File S2, and Payen *et al.* 2016).

Among deleted genes, 42/69 genes for which data exist showed negative and positive fitness effects in at least one tested condition in the S288c genetic background. Furthermore, we found that 12/42 genes that are commonly deleted among wine strains typically resulted in a fitness gain in conditions that resembled the fermentation environment. These conditions include growth at 23° and at 25°, temperatures within the 15–28° range in which wine is fermented (Molina *et al.* 2007), and growth in minimal media, which is commonly used to understand fermentation-related processes (Seki *et al.* 1985; Govender *et al.* 2008; Vilela-Moura *et al.* 2008).

When examining fitness effects when grown at 23° or at 25° for five or 15 generations for the 12 commonly deleted genes, we observed at least one deletion that resulted in a fitness gain or loss for each condition. However, we observed extensive deletions in the MAL1 locus (Figure 3), and therefore prioritized reporting the fitness impact of deletions in MAL11, MAL12, and MAL13. \(\Delta MAL11 \) resulted in a fitness gain for growth at 23° and 25° for 5 (0.45× and 0.27×, respectively) and 15 generations (0.20× and 0.52×, respectively). $\Delta MAL12$ resulted in a gain of fitness at only 25° after 15 generations (0.46×) and in a loss of fitness ranging from $-0.36 \times$ to $-1.29 \times$ in the other temperature conditions. Similarly, $\Delta MAL13$ resulted in fitness gains and losses dependent on the number of generations. For example, when grown for 15 generations at 25° a fitness gain of 0.50× was observed, while a fitness loss of $-0.82\times$ was observed at 23°.

We next determined the fitness effect of deleted genes in minimal media after 0, 5, and 10 generations. Similar patterns of complex fitness gain and loss were observed as for the other conditions. For example, $\Delta THI12$ resulted in a loss of fitness of $-4.13\times$ and $-1.97\times$ after 0 and 5 generations, but a fitness gain of 0.63× after 10 generations. In contrast, other genes resulted in positive fitness effects. For example, $\Delta MAL12$ resulted in a fitness gain of 7.25× and 10.41× for 0 generations and 10 generations.

Among duplicated genes, we focused on growth in glucose- and phosphate-limited conditions because glucose becomes scarce toward the end of fermentation prior to the diauxic shift and phosphate limitation is thought to contribute to stuck fermentations (Bisson 1999; Marsit and Dequin 2015). Among the 35 of the 69 genes where data were available, 14 genes had duplications among the 132 strains.

When examining the fitness effects of duplicated genes in a glucoselimited environment in the S288c background, we found that fitness effects were small in magnitude, and dependent on condition and plasmid CN (File S6 in File S1). For example, MAL32 low CN increased growth fitness by $0.02\times$ but decreased fitness by $-0.01\times$ at a high CN (Figure S15 in File S2). Interestingly, the most prevalent CN for MAL32 across the 132 strains was two (96 strains, 72.7%), with only three strains showing a CN of three and none a higher CN. Another gene found at low CN in 37 strains (28%) was HXT17. Low plasmid CN in a glucose-limited conditions resulted in a fitness gain of 0.06x. In contrast, MAL13 low or high plasmid CN resulted in a negative growth fitness of $-0.02\times$ and $-0.01\times$, respectively. Interestingly, MAL13 duplication is observed in only four strains (3%), and deletions are observed in 61 strains (46.2%).

Similar to the glucose-limited condition, we found fitness was dependent on high or low plasmid CN in the phosphate-limited condition. For example, MAL31, a gene present at low CN in 100 strains, had a fitness gain of 0.04× at high plasmid CN, but low plasmid CN resulted in a fitness loss of $-0.02\times$. In contrast, MAL32, which was present at low CN in 99 strains, had a small fitness gain of 0.002× at low plasmid CN, and a fitness loss at a high plasmid CN of $-0.02\times$. A total of six genes resulted in a disadvantageous growth effect when present at low CN, such as DDR48, which resulted in a fitness loss of $-0.04\times$. Altogether, our results suggest that the deleted and duplicated CN variable genes we observe (Figure 4) modulate cellular processes that result in advantageous fitness effects in conditions that resemble the fermentation environment.

Identifying loci absent from CN variation analysis

The present study was able to capture loci represented in the WT/S288c laboratory strain. To identify loci absent from the reference strain, we assembled unmapped reads for 20 strains with the lowest percentage of reads mapped and determined their identity (see Materials and Methods; Figure S4 in File S2). Across the 20 strains, we identified 429 loci absent from S288c but present in other sequenced S. cerevisiae strains.

These loci had an average length of 6.9 kb and an average coverage of 107.2×. The 20 loci with the highest bitscore alongside with the number of strains containing the locus are shown in Table S2 in File S2. All but two of these loci were present only in one of the 20 strains we examined. The two exceptions were the EC1118_1N26_0012p locus, which we found in 8/20 strains, which originates from horizontal gene transfer from Zygosaccharomyces rouxii to the commercial EC1118 wine strain of S. cerevisiae (Novo et al. 2009); and the EC1118_1O4_6656p locus, which we found in 7/20 strains. This locus was also originally found in the EC1118 strain (Novo et al. 2009), and contains a gene similar to a conserved hypothetical protein found in S. cerevisiae strain AWRI1631 (Borneman et al. 2008).

DISCUSSION

CN variant loci are known to contribute to genomic and phenotypic diversity (Perry et al. 2007; Cutler and Kassner 2008; Orozco et al. 2009). However, the extent of CN variation in wine strains of S. cerevisiae, and its impact on phenotypic variation remains less understood. Our examination of structural variation in 132 yeast strains representative of the "wine clade" showed that CN variants are a significant contributor to the genomic diversity of wine strains of S. cerevisiae. Importantly, CN variant loci overlap with diverse genes and gene families functionally related to the fermentation environment such as CUP, FLO, THI, MAL, IMA, and HXT (summarized in Figure 4).

The characteristics of CN variation in wine yeast (Figure 1A, and Figure S6 and Table S1 in File S2) were found to be similar to those of the recently described beer yeast lineage (Gallone et al. 2016). For example, both lineages exhibited a similar size range of CNVRs (Figure 1A, and Figure S6 and Table S1 in File S2), as well as a higher prevalence of CNVRs in the subtelomeric regions (Figure 1D). However, wine strains had a smaller fraction of their genome affected by CN variation (Figure S6 in File S2) than beer strains (Gallone et al. 2016).

Wine yeast strains are thought to be partially domesticated due to the seasonal nature of wine-making, which allows for outcrossing with wild populations (Marsit and Dequin 2015; Gallone et al. 2016; Gonçalves et al. 2016). One human-driven signature of domestication is thought to be the duplication of the CUP1 locus, because multiple copies confer copper resistance and copper sulfates have been used to combat powdery mildews in vineyards since the early 1800s (Warringer et al. 2011; Marsit and Dequin 2015). Consistent with this "partial domestication" view (Marsit and Dequin 2015; Gallone et al. 2016; Gonçalves et al. 2016), many wine strains were not CN variable for CUP1-1 and CUP1-2, or had one or both genes deleted (Figure 3).

An alternative, albeit not necessarily conflicting, hypothesis is that wine yeasts underwent domestication for specific but diverse wine flavor profiles (Hyma et al. 2011). Consistent with this view is the deletion (in >90% of the strains) of the *THI5* gene (Figure 3), whose activity is known to produce an undesirable rotten-egg sensory perception via higher SH₂ production and is associated with sluggish fermentations (Bartra et al. 2010). In contrast to wine strains, duplications of THI5 have been observed across the Saccharomyces genus, including in several strains of S. cerevisiae (CBS1171, two copies; S288c, four copies; EM93, five copies), S. paradoxus (five copies), and the lager brewing yeast hybrid S. pastorianus (syn. S. carlsbergensis; 2+ copies) (Wightman and Meacock 2003). In contrast, THI13, which is duplicated in 62.1% of strains, shows an increase in its expression of 6- to 100-fold in S. cerevisiae when grown on medium containing low concentrations of thiamine, allowing for the compensation of low thiamine levels (Li et al. 2010). Low levels of thiamine in wine fermentation have been associated with stuck or slow fermentations (Ough et al. 1989;

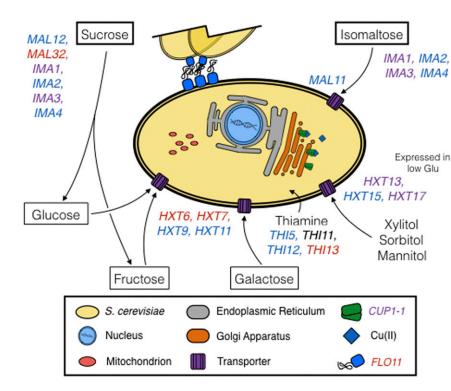


Figure 4 Model summary of CN variable genes in wine yeast strains and their cellular functions. Genes that are deleted among wine strains are blue, whereas those that are duplicated are in red. Genes that were observed to be both duplicated and deleted (IMA1, IMA3, HXT13, and CUP1-1) are purple. Disaccharides are in thick-lined boxes, monosaccharides in thin-lined boxes, and alcohols are unboxed.

Bataillon et al. 1996). Similar to THI5 deletions, THI13 duplications may have also been driven by human activity due to the advantageous effect of increased expression within the fermentation environment.

Two other gene families subject to CN variation were the MAL and HXT gene families. The S288c strain that we used as a reference contained two MAL loci (MAL1 and MAL3), each containing three genes—a maltose permease (MALx1), a maltase (MALx2), and an MAL trans-activator (MALx3)—and located near the ends of different chromosomes (Michels et al. 1992). MAL1 has been observed to be duplicated in beer strains of S. cerevisiae (Gallone et al. 2016; Gonçalves et al. 2016), while wine strains primarily lack this locus (Figure 3; Gonçalves et al. 2016). In contrast to the deletion of the MAL1 locus, MAL3 duplication in wine yeasts (Figure 3; Gonçalves et al. 2016) is surprising because maltose is absent from the grape must (Gallone et al. 2016). However, knockout studies have demonstrated MAL32 is necessary for growth on turanose, maltotriose, and sucrose (Brown et al. 2010), which are present in small quantities in wines (Victoria and Carmen 2013). Due to the prominent duplication of MAL3, in particular the enzymatic genes MAL31 and MAL32, we speculate that the MAL3 locus may be utilized to obtain sugars less prevalent in the wine environment, or serve other purposes.

The HXT gene family in the S288c strain that we used as a reference contains 16 HXT paralogs, GAL2, SNF3, and RGT2. The expansion of the HXT gene family is positively correlated with aerobic fermentation in S. paradoxus and S. cerevisiae (Lin and Li 2011). HXT6 and HXT7 are high-affinity glucose transporters expressed at low glucose levels, and repressed at high glucose levels (Reifenberger et al. 1995). In contrast to the recently described Asia (Sake), Britain (Beer) and Mosaic lineages (Gallone et al. 2016), we detected duplications in the HXT6 and HXT7 genes in wine yeasts (Figure 3). This may confer an advantage toward the end of fermentation and before the diauxic shift when glucose becomes a scarce resource. Evidence potentially supporting this hypothesis is that HXT6 and HXT7 are upregulated by 9.8- and 5.6-fold, respectively, through wine fermentation in the S. cerevisiae strain Vin13 (Marks et al. 2008). Furthermore, HXT6 or HXT7 is found

to be duplicated in experimentally evolved populations in glucoselimited environments (Dunham et al. 2002; Gresham et al. 2008; Dunn et al. 2012).

In summary, these results, together with recent studies of CN variation in beer yeast strains (Gallone et al. 2016; Gonçalves et al. 2016), suggest that this type of variation significantly contributes to the genomic diversity of domesticated yeast strains. Furthermore, as most studies of CN variation, including ours, use reference strains, they are likely conservative in estimating the amount of CN variation present in populations. This caveat notwithstanding, examination of publically available data regarding the functional impact of duplicated or deleted genes (again in the context provided by the reference strain's genetic background) suggests that CN variation in several, but not all, of the wine yeast genes confer fitness advantages in conditions that resemble the fermentation environment. Our results raise the questions of the extent to which CN variation contributes to fungal, and more generally microbial, domestication as well as whether the importance of CN variants in natural yeast populations, including those of other Saccharomyces yeasts, is on par to their importance in domestication environments.

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