Revisiting the *Saccharomyces cerevisiae* predicted ORFeome

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Accurately defining the coding potential of an organism, i.e., all protein-encoding open reading frames (ORFs) or “ORFeome,” is a prerequisite to fully understand its biology. ORFeome annotation involves iterative computational predictions from genome sequences combined with experimental verifications. Here we reexamine a set of *Saccharomyces cerevisiae* “orphan” ORFs recently removed from the original ORFeome annotation due to lack of conservation across evolutionarily related yeast species. We show that many orphan ORFs produce detectable transcripts and/or translated products in various functional genomics and proteomics experiments. By combining a naive Bayes model that predicts the likelihood of an ORF to encode a functional product with experimental verification of strand-specific transcripts, we argue that orphan ORFs should still remain candidates for functional ORFs. In support of this model, interstrain intraspecies genome sequence variation is lower across orphan ORFs than in intergenic regions, indicating that orphan ORFs endure functional constraints and resist deleterious mutations. We conclude that ORFs should be evaluated based on multiple levels of evidence and not be removed from ORFeome annotation solely based on low sequence conservation in other species. Rather, such ORFs might be important for micro-evolutionary divergence between species.

[Supplemental material is available online at www.genome.org.]
sively for functional genomics and proteomics studies, providing valuable functional evidence that allow further evaluation of coding potential of the orphan ORFs.

Using currently available functional genomics and proteomics data sets, we collate functional evidence for a significant portion of *S. cerevisiae* orphan ORFs, finding that many orphan ORFs produce detectable transcripts and/or translated products. Using a naïve Bayes model, we predict the likelihood that any *S. cerevisiae* ORF encodes a functional product and show that the number of orphan ORFs with potential functional significance is higher than expected by chance. Notably, we provide experimental verification for strand-specific transcription of many orphan ORFs. Finally, we report that interstrain intraspecies genome sequence variation is lower across orphan ORFs than in intergenic regions. Altogether our results demonstrate that orphan ORFs should not be excluded from current ORFeome annotation simply because they fail to show interspecies sequence conservation. We suggest that orphan ORFs should be included in future genome-wide experimental studies to reveal their bona fide identity either as functional ORFs or as randomly occurring misannotated ORFs.

Results

Evidence for biological significance of *S. cerevisiae* orphan ORFs

The genome annotation of *S. cerevisiae* has undergone continuous modification through computational and experimental efforts since the original release in 1996 (Goffeau et al. 1996; Fisk et al. 2006). Three independent comparative genomic analyses compared the conservation of DNA or predicted protein sequences among several ascomycete species (Brachat et al. 2003; Cliften et al. 2003; Kellis et al. 2003), recommending that 402, 513, and 495 ORFs, respectively, be removed from the *S. cerevisiae* predicted ORFeome because their putative counterparts in other yeast species accumulate stop codons and frame-shift mutations (Fig. 1A). The union of these three comparative analyses is a set of 648 orphan ORFs called “spurious” or “false” in these studies (Fig. 1A).

High-throughput functional genomics and proteomics approaches have recently accelerated functional characterization of predicted ORFs. Several of these genome-wide approaches, such as gene-expression profiling or in vivo characterization of protein complexes, have detected transcripts or translated products of orphan ORFs. For example, in a proteome-wide purification of yeast protein complexes (Krogan et al. 2006), 85 proteins identified by mass spectrometry were encoded by orphan ORFs.

To provide a systematic reanalysis of *S. cerevisiae* orphan
ORFs, we collected 13 large-scale studies (Table 1) informing on either transcription or translation of orphan ORFs. The transcriptome studies included tiling arrays (David et al. 2006), high-density Affymetrix chip analysis (Holstege et al. 1998), SAGE analysis (Velculescu et al. 1997), and cDNA sequencing (Miura et al. 2006). Because many (69%) of the orphan ORFs overlap with another annotated ORF, we only included transcriptome studies able to detect strand-specific transcripts. Protein–protein interaction studies included proteome-scale yeast two-hybrid screens (Uetz et al. 2000; Ito et al. 2001) and affinity pull-downs of tagged proteins followed by mass spectrometry (Gavin et al. 2002, 2006; Ho et al. 2002; Krogan et al. 2006). For yeast two-hybrid studies, we considered an ORF being translated only if its product was involved in a protein–protein interaction as a prey. Protein expression studies included global surveys of protein abundance (Ghaemmaghami et al. 2003) and subcellular localization (Kumar et al. 2002; Huh et al. 2003).

Out of the 648 orphan ORFs, most (79%) have been detected in at least one of these data sets. The proportion of orphan ORFs detected was nearly the same for ORFs rejected by each of the three comparative genomics analyses independently (80% for Brachat, 79% for Cliften, and 79% for Kellis) and for the 276 orphan ORFs discarded by all three (79%) (Fig. 1A). Among the 648 orphan ORFs, many were detected by more than one approach. In total, 145 orphan ORFs (22%) were both detected as transcripts and translated products (Fig. 1B). A similar distribution of functional evidence was observed for the orphan ORFs rejected by all three comparative genomic analyses (Supplemental Fig. 1).

Evaluating biological significance of S. cerevisiae ORFs by a naïve Bayes approach

High-throughput approaches have inherently limited coverage (not all ORFs are detectable) and precision (detection of some ORFs might be artifactual). Therefore information from large-scale data sets needs to be accepted cautiously. We chose a naïve Bayes model to quantify the observations reported above, because this approach can integrate dissimilar types of data sets into a common probabilistic framework with maximal coverage and precision (Jansen et al. 2003; Yu et al. 2004). By use of such an integration scheme, evidence (i.e., features) from several data types can be accumulated to estimate with increasing confidence the likelihood that an ORF encodes a functional product. As with any machine learning algorithm, naïve Bayes models need a training set of gold standard positives (GSPs) and negatives (GSNs). The Saccharomyces Genome Database (SGD), the arbiter of genome annotation for budding yeasts, has categorized all S. cerevisiae ORFs into three major groups based on conservation across species and on available experimental characterization: “verified” (4449 ORFs), “uncharacterized” (1333 ORFs), and “dubious” (823 ORFs) (Fisk et al. 2006). Both verified ORFs and uncharacterized ORFs are conserved across species. Verified ORFs have clear small-scale experimental evidence for the existence of functional ORF products, but uncharacterized ORFs do not. Dubious ORFs are thought not to encode a functional product due to (1) lack of conservation across species, and/or (2) absence of any small-scale experiment demonstrating detectable mRNA or protein production or phenotypic effects. We used all 4449 verified ORFs as the GSPs and all 823 dubious ORFs as the GSNs. Although ideally the GSNs should be depleted of functional ORFs, this cannot exactly be true for the dubious set. However, the dubious set is likely enriched with nonfunctional ORFs. It is common practice to use an “enriched” set of negatives in training data sets (Miller et al. 2005; Xia et al. 2006).

We calculated the ratio of the fraction of GSPs present in each of the 13 functional genomics and proteomics data sets divided by the fraction of GSNs present in each data set, which measures the confidence levels (Supplemental Table 1). The product of these ratios of the 13 data sets for each ORF is defined as the likelihood ratio (LR) of an ORF, i.e., the likelihood of each ORF to encode a functional product (see Methods). We used the base 10 logarithmic form of LR (LLR) as final prediction scores (Supplemental Table 2). Out of the large-scale studies integrated, several did measure similar biological features of ORFs and ORF products. However, we treated all 13 data sets as independent features, due to the low correlation between them (Supplemental Tables 3, 4).

To evaluate the performance of the naïve Bayes model, we used threefold cross-validation (see Methods). After randomly dividing both the GSPs and GSNs into three separate equal sets, we used two of the three sets as the training set to calculate LLRs and the remaining set as the test set to identify positives and negatives. The true-positive rate (TP rate: fraction of GSPs that are predicted to be functional) and the false-positive rate (FP rate: fraction of GSNs that are predicted to be functional) were calculated at different LLR cutoffs. The resulting couplets (TP rate–FP rate) were used to plot a receiver operating characteristic (ROC) curve. We ran this process three times so that each of the three sets was a test set and the remaining two constituted the training set. Each ROC curve looked similar (Supplemental Fig. 2), which
validated the overall quality of our training set. A final ROC curve was plotted by using potential LLR cutoffs from all three training subsets and their associated TP rate and FP rate based on the predictions from the complete training set (Fig. 2A). The significant deviation of the final ROC curve from the 45° random ROC line indicates that our model has substantial predictive value (area under ROC curve = 0.982). To assess the contribution of each data set to the final prediction scores, we successively omitted one data set and repeated the training and cross-validation procedures. We plotted ROC curves for all procedures (Suppl-
mental Fig. 3) and observed little difference when excluding any single data set. Thus it seems that no single data set dominates the prediction.

We divided all 6718 S. cerevisiae ORFs into 20 bins ranked by decreasing LLR, with each bin containing similar numbers of ORFs. Verified ORFs localized mostly in the higher LLR bins (92.5% of all verified ORFs distributed between bin 1 and bin 15), while dubious ORFs localized in lower LLR bins (only 4.98% of dubious ORFs distributed between bin 1 and bin 15) (Fig. 2B). Such segregation between verified ORFs and dubious ORFs was expected, given that the ORFs used in the training as GSNs (verified ORFs) are bound to have a higher LLR than the ones used in the training as GSNs (dubious ORFs). An unanticipated result of the naïve Bayes predictions is that orphan dubious ORFs have overall higher LLR ($P < 10^{-15}$ by Mann-Whitney U test) (Fig. 2B) than ORFs classified as dubious for reasons other than strict lack of introns. Notably, out of 49 orphan ORFs tested that had not been detected by any of the 13 data sets (Table 1), 29 were expressed (Supplemental Table 2), among which YPR096C was recently found to encode a ribosome-interacting protein (Fleischer et al. 2006) and YOR235W was shown through a genome-wide phenotypic analysis to be involved in DNA recombination events (Alvaro et al. 2007). Therefore, we suggest that more experimentation is needed before rejecting ORFs from the S. cerevisiae ORFeome annotation.

**Interstrain intraspecies sequence conservation for S. cerevisiae orphan ORFs**

The available experimental evidence from large-scale data sets, combined with our experimental support for many orphan ORFs, implies that lack of interspecies conservation does not necessarily dispel the bona fide functionality of an ORF. Functional orphan ORFs may have a relaxed selective constraint due to their dispensable roles in other species and may therefore rapidly lose sequence similarity even in closely related species (Schmid and Aquadro 2001). However, select species–specific functions may stringently constrain sequence divergence of functional orphan ORFs within species (Domazet-Loso and Tautz 2003). Therefore, we examined the intraspecies conservation of orphan ORFs in S. cerevisiae, using single nucleotide polymorphism (SNP) information from genome resequencing of multiple strains of S. cerevisiae by the Saccharomyces Genome Resequencing Project (SGRP) (http://www.sanger.ac.uk/Teams/Team71/durbin/sgrp/index.shtml). Among the 37 currently available strain sequences, four (SK1, W303, Y55, and DBVPG6765) have been sequenced at twofold coverage or higher. We used the SNP data from these four genomes to assess nucleotide variation in different genomic regions across S. cerevisiae strains. We compared nucleotide divergence among these genomic features: orphan ORFs, nonorphan ORFs, and intergenic regions, considering only the regions that do not overlap with any other annotated ORF (see Methods).
Two-step strand-specific RT-PCR. (A) Schematic diagram of the strand-specific RT-PCR procedure. Reverse ORF-specific primers (OSP), with sequences complementary to the ORF-coding strand, were used for first-strand cDNA synthesis. Second-step PCR amplifications used a pair of forward (OSP) and reverse ORF-specific primers (OSP). As controls, the first step of RT-PCR was performed without reverse transcriptase for detecting contamination by genomic DNA, or without the OSP primer for detecting residual reverse transcriptase activity in second-step PCR reactions. Two intron-containing verified ORFs, YER133W (genomic DNA length: 1464 bp; coding sequence length: 939 bp) and YBR078W (genomic DNA length: 1737 bp; coding sequence length: 1407 bp), were used to test the strand specificity. An extra control for these two verified ORFs was a standard PCR action using yeast genomic DNA as template and the same pair of ORF-specific primers. The observed difference in the length of PCR products amplified from genomic DNA versus poly(A) mRNA manifested the strand specificity. Strand-specific RT-PCR results of 201 nonoverlapping orphan ORFs were analyzed on 1% agarose E-gel (Invitrogen). Of the reactions 53% (105 ORFs) gave rise to visible RT-PCR products of the expected sizes. Three orphan ORFs, YJL199C (327 bp), YJR108W (372 bp), and YDR344C (444 bp), are shown as examples of successful RT-PCR reactions. (B) Comparison of the average LLR between nonoverlapping ORFs detected and undetected by strand-specific RT-PCR. Error bars, SEM.
Across the four strains analyzed, orphan ORFs showed higher nucleotide divergence (7.0 ± 0.4 SNPs per kb) than did nonorphan ORFs (3.7 ± 0.1 SNPs per kb, \( P < 10^{-5} \) by Mann-Whitney U test), but less than intergenic regions (15.5 ± 0.2 SNPs per kb, \( P < 10^{-15} \) by Mann-Whitney U test) (Fig. 4A). Such intermediate nucleotide divergence for orphan ORFs suggests that at least a portion of them are subject to significant intraspecies evolutionary constraints. Such “interstrain intraspecies” conservation of orphan ORFs indicates potential functionality of an ORF in addition to experimental evidence.

Among the 648 orphan ORFs, the most-likely functional ones displayed a significantly lower nucleotide divergence (3.8 ± 0.7 SNPs per kb) than both moderately-likely (6.4 ± 0.8 SNPs per kb, \( P = 0.016 \) by Mann-Whitney U test) and least-likely ORFs (7.7 ± 0.6 SNPs per kb, \( P = 0.005 \) by Mann-Whitney U test) (Fig. 4B). Although the moderately-likely category does have a lower nucleotide divergence than least-likely category, the difference is not significant (\( P > 0.05 \) by Mann-Whitney U test). Because different types of SNPs, such as synonymous or nonsynonymous substitutions, could have distinct effects on an ORF product, we applied another test to compare sequence conservation among the three groups, measuring the percentage of ORFs with preserved reading frames (absence of stop codons or frame-shift mutations) across all four \( S. cerevisiae \) strains. A decreasing trend was observed from most-likely to least-likely ORFs (Fig. 4C), with significant differences among the three categories.

**Figure 4.** Interstrain intraspecies sequence conservation for orphan ORFs. (A) Distribution of nucleotide divergence in different genomic features. We binned three types of genomic features, (1) non-orphan ORFs (red curve), (2) orphan ORFs predicted by three comparative genomic analyses (blue curve) (Brachat et al. 2003; Cliften et al. 2003; Kellis et al. 2003), and (3) intergenic regions (green curve), using a window of an average three SNPs per kb across four \( S. cerevisiae \) strains. Each dot represents the fraction of genomic features in each bin. Numbers on the X-axis represent the maximum number of SNPs per kb in each bin. For instance the first bin collects the genomic regions that have between zero and three SNPs per kb in four strains. The inset zooms in on the 0–21 SNPs per kb range with SEM displayed. (B) Comparison of nucleotide divergence among three predicted categories of orphan ORFs based on their LLRs. Error bars, SEM in each category. (C) Comparison of the percentage of ORFs among the three predicted categories of orphan ORFs that have reading frames preserved across four \( S. cerevisiae \) strains.
(P = 0.03 by χ² test). The coexistence of high interstrain intra-
species conservation with high likelihood of functionality dem-
strates that some orphan ORFs face functional constraints that
protect them from deleterious interspecies mutations.

In summary, analysis of nucleotide variation in multiple S. cere-
visiae strains, combined with multiple lines of experimental
evidence, suggest that reevaluation of the functionality of all
ORFs, especially orphan ORFs, is warranted.

Discussion

We report here that many interspecies nonconserved ORFs or
orphan ORFs predicted by comparative genomic analyses in S.
cerevisiae show evidence of transcription or translation, as re-
ported in various functional genomics or proteomics data sets.
We used a naïve Bayes probabilistic integration of a heteroge-
neous set of large-scale data sets to predict the likelihood that a
predicted ORF encodes a functional product. Threefold cross-
validation demonstrated high performance for this approach,
which revealed that orphan ORFs are more likely functional than
are ORFs classified as dubious for reasons other than strict lack of
sequence conservation across species. Independent strain-
specific RT-PCR confirmed that many orphan ORFs are indeed
expressed. Although presence of transcripts is not sufficient by
itself to conclude that an ORF encodes a functional product, the
correspondence between our RT-PCR results and naïve Bayes pre-
diction scores demonstrated both the potential functionality of
orphan ORFs and the robustness of our prediction method. Con-
firming that orphan ORFs could be functional, many show signs
of interstrain interspecies negative selection, such as lower
nucleotide divergence than intergenic regions and retaining an
intact reading frame in multiple S. cerevisiae strains.

Collectively our findings argue that the likelihood that an
ORF encodes a functional product is best evaluated by combining
multiple lines of experimental and evolutionary evidence
(Snyder and Gerstein 2003). The potential functionality of or-
phan ORFs in S. cerevisiae suggests that experimentally verified
functional sequences are not always conserved across species.
Such nonconserved functional sequences might be responsible
for species-specific phenotypic differences, making S. cerevisiae
“cerevisiae” and not some other species in the Saccharomyces
genus. An alternative explanation is that there are some functional
elements evolving neutrally and conferring no specific benefit to
the organism (Rinney et al. 2007). Either way, experimental in-
vestigation has an irreplaceable role in determining biologically
relevant DNA sequences. Comparative genomics has demon-
strated analytic power in predicting functional regions before
availability of any experimental information (Hardison 2003).
When experimental information does become available (mainly
from high-throughput functional genomics and proteomics
analyses), then its integration should revise the genome annota-
tion accordingly. The naïve Bayes model implemented here can
be readily applied to all organisms.

Although we provide confidence scores about the likelihood
of a predicted ORF to encode a functional product, compre-
prehensive functional characterization of an ORF needs more concrete
evidence from genetics, cell biology, and biochemistry than
simple evidence of transcription or translation. The functional
genomics or proteomics data sets used in our naïve Bayes predic-
tions only investigated a few growth conditions, generally
growth on rich media, limiting investigation of functions unique
to the development and physiology of S. cerevisiae. Given the
limited functional information obtained so far under laboratory
conditions and uncharacterized ORFs (Pena-Castillo and
Hughes 2007), perhaps what is needed are studies of yeast cells
outside the laboratory. Upon such a shift, data sets generated
under diverse conditions will become available, and our ap-
proach will then be available to aid precise and powerful anno-
tation of genomes.

Methods

Large-scale data sets analysis

We collected 13 published functional genomics and proteomics
data sets of S. cerevisiae, summarized in Table 1 with references
to the data sources. Only ORFs identified by the same primary
SGCID in the publication and in the January 2007 version of
SGD annotation were included. We assigned “presence” or “ab-

cence” of transcript or translated product of every ORF in each
data set. For protein complexes characterization data sets (Gavin
et al. 2002, 2006; Ho et al. 2002; Krokog et al. 2006) all proteins
that were identified as peptides were considered “present,” inde-
pendent of further filtration by the investigators. For high-
throughput yeast two-hybrid (Uetz et al. 2000; Ito et al. 2001),
only proteins identified as preys were considered present. Only
protein–protein interactions classified as “core” by Ito et al.
(2001) were included. Transcripts identified by SAGE (Velculescu
et al. 1997) and assigned to “class 1” by the investigators were
considered present; all others, absent. We divided the Affymetrix
Genechip data (Holstege et al. 1998) into two groups: intensity of
expression strictly positive but less than or equal to 1, and inten-
sity strictly more than 1. These two groups were treated sepa-
ately in the naïve Bayes model. The normalized intensity of
expression per probe (David et al. 2006) was averaged, and the
percentage of probes whose intensity was higher than this aver-
age was considered as the intensity of expression of each ORF.
We then extracted four groups (undetected, intensity strictly
positive but less than 0.4, intensity strictly more than or equal to
0.4 but less than 0.8, and intensity strictly more than or equal to
0.8) that were treated separately in the naïve Bayes model. The
remaining data sets were not reprocessed.

The naïve Bayes model

If the numbers of positives are known among the total number of
ORFs, the “prior” odds of finding a positive are

\[
O_{\text{prior}} = \frac{P(\text{pos})}{P(\text{neg})} = \frac{P(\text{pos})}{1 - P(\text{pos})}.
\]

The “posterior” odds are the odds of finding a positive after con-

\[
O_{\text{post}} = \frac{P(\text{pos}|f_1 \ldots f_N)}{P(\text{neg}|f_1 \ldots f_N)}.
\]

The likelihood ratio LR is defined as

\[
LR(f_1 \ldots f_N) = \frac{P(f_1 \ldots f_N|\text{pos})}{P(f_1 \ldots f_N|\text{neg})}.
\]

According to Bayes rule, the posterior odds can be expressed as

\[
O_{\text{post}} = LR(f_1 \ldots f_N)O_{\text{prior}}.
\]

If the N features are conditionally independent, LR can be sim-

\[
LR(f_1 \ldots f_N)O_{\text{prior}}.
\]

\[
\text{N} \quad \text{1301}
\]
LR (1) can be computed from contingency tables relating positive and negative examples with the N features (we binned the feature values f1, . . . , fN into discrete intervals). Since 0 < P(f1, . . . , fN) is a fixed value, 0 LR is determined by LR. We used log-likelihood ratio (log10 LR or LLR) as the final prediction score. The higher the LLR of a certain ORF, the more likely it is a functional ORF.

Threefold cross-validation
We divided the whole training set into three subsets randomly. We then trained the model with two subsets and tested its performance on the third subset. We repeated this step three times so that each subset was used once to test the performance. We calculated the ROC curve with the predictions from the three repeated tests.

Strand-specific RT-PCR
*S. cerevisiae* strain S288C was grown in yeast extract-yeast-dextrose (YPD) medium at 30°C to mid-exponential phase. Yeast cells were then harvested and used for total RNA isolation with an RNeasy kit (Qiagen). Poly(A) RNA was subsequently enriched by Oligotex mRNA kit (Qiagen). Before RT-PCR experiments, Poly(A) RNA was subjected to DNA-free DNase treatment (Ambion) to eliminate genomic DNA contamination. Genomic DNA was extracted from yeast culture by the DNeasy blood and tissue kit (Qiagen). We modified a strand-specific RT-PCR method previously described (Craggs et al. 2001), using the GeneAmp thermostable rTth reverse transcriptase RNA PCR kit (Applied Biosystems). DNase-treated poly(A) RNA sample (25 ng) was denatured for 5 min at 70°C with 2 μL of 10× rTth reverse transcriptase buffer and 1 μL of 10 μM reverse ORF-specific primer complementary to the ORF-coding strand (OSP). While the template and the primer were still incubating at 70°C, a preheated reaction mixture was added consisting of 2 μL of 10 mM MnCl2 solution, 1.6 μL of 10 mM dNTP mix, and 2.5U of rTth polymerase. The temperature was lowered for 2 min to 55°C for annealing and then raised for 30 min to 70°C for the first-strand cDNA synthesis. After the cDNA synthesis, 20 μL of prewarmed 1× chelating buffer was added to chelate Mn2+ followed by heating the mixture for 30 min at 98°C to inactivate the reverse transcriptase activity of rTth. Second-step PCR reactions were performed in a 50-μL reaction volume using one-tenth of the synthesized first-strand cDNA as template, forward ORF-specific primer (OSP) and OSPp as primers, and one unit of High Fidelity Platinum Taq polymerase (Invitrogen). The OSPp complementary to the ORF-coding strand was used in both first-strand cDNA synthesis and second-step PCR amplification. The OSPp complementary to the opposite strand was used only in the second-step PCR amplification. Both OSP and OSPp were designed using the OSP Program (Hillier and Green 1991). The OSPp starts from the last nucleotide of the termination codon, while the OSPp starts from A of the ATG initiation codon. Primers used for RT-PCR of 201 nonoverlapping orphan ORFs are listed in Supplemental Table S.

Interstrain intraspecies conservation analysis
SNP information from the four strains SK1, Y55, DBVPG7675, and W303 were extracted from the website of the Sanger Institute Saccharomyces Genome Resequencing Project (http://www.sanger.ac.uk/Projects/S288C/) on September 18, 2007 (R. Durbin and E. Louis, pers. comm.). The preassembly SNPs were taken into account only when their quality was “con-


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