Supplemental Material:

Eisosomes and plasma membrane organization

Molecular Genetics and Genomics

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Phylogenetic analysis:

To determine homology relationships of *S. cerevisiae*, *A. nidulans*, *A. gossypii*, *C. albicans* and *S. pombe* eisosomal proteins we performed a phylogenetic analysis across 16 fungal genomes encompassing all ascomycota subphyla and two basidiomycota subphyla. Eisosomal proteins amino acid sequences from *S. cerevisiae* S288c strain were obtained from SGD (http://www.yeastgenome.org/). These sequences were used as queries to perform genomic psi-blast searches (Altschul et al. 1997) using NCBI web-server (http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi?organism=fungi). The analyzed fungal genomes were: *Aspergillus nidulans*, *Aspergillus terreus*, *Coccidioides immitis*, *Neurospora crassa*, *Sclerotinia sclerotiorum*, *Ashbya gossypii*, *Candida albicans*, *Candida tropicalis*, *Clavispora lusitaniae*, *Kluyveromyces lactis*, *Saccharomyces cerevisiae*, *Yarrowia lipolytica*, *Schizosaccharomyces japonicus*, *Schizosaccharomyces pombe*, *Cryptococcus neoformans* and *Ustilago maydis*. Subsequent multiple sequence alignments were done using Mafft employing both L-INS-i and G-INS-i methods (Katoh et al. 2002; Katoh and Toh 2010). Ensuing alginent editions were done with trimal using the gappyout method (Capella-Gutierrez et al. 2009). Evolution models were selected using ProtTest (Darriba et al. 2011). Phylogenetic reconstructions were inferred with phym using the SPR algorithm (Guindon et al. 2005; Guindon et al. 2010). Tree nodes with a SH-like branch support grater than 75 were considered for homology determination.

Phylogenetic tree images:

One phylogenetic tree is presented for each *S. cerevisiae* eisosomal protein or protein group analyzed. Proteins in bold red letters correspond to Table 2. Numbers correspond to SH-like branch support. Proteins were named by systematic name for *A. gossypii*, *C. albicans*, *A. nidulans* and *S. pombe*, whereas the standard name was used for *S. cerevisiae* and GI number of NCBI
protein database for the remaining organisms. When a clear out-group appears in the tree it is indicated in green. When evident, gene clades were shaded in grey.

References:


Sur7-Fmp45-Ynl194c-Pun1

Ecm7

Rim9

Fig1

Sur7-Fmp45-Ynl194c