**File S1**

**Identification of the *ICL1*, *FOX2* and *PXA1* genes in the genome of *C. lusitaniae***. The genes *ICL1* encoding the isocitrate lyase*, FOX2* encoding the multifunctional protein of β-oxidation*,* and *PXA1* encoding part of an ABC transporter responsible for peroxisomal long chain FA uptake*,* were identified in the genome of *C. lusitaniae* (http://www.broadinstitute.org/) with a BLAST analysis [1] using as query the orthologous proteins of *C. albicans* (*Candida* Genome Database, http://www.candidagenome.org/). This *in silico* analysis allowed us to identify: **i/** the 1650-bp ORF CLUG\_01411.1 encoding a predicted protein of 549 amino acids (61 kDa) having 79% identity and 89% similarity with Icl1p (orf19.6844) of *C. albicans*, **ii/** the 2709-bp ORF CLUG\_01348.1 encoding a predicted protein of 902 amino acids (98 kDa) having 71% identity and 85% similarity with Fox2p (orf19.1288) of *C. albicans*, **iii/** the 2430-bp ORF CLUG\_01238.1 encoding a predicted protein of 809 amino acids having 66% identity and 79% similarity with Pxa1p (orf19.7500) of *C. albicans*. The nucleotide sequences of *ICL1*, *FOX2* and *PXA1* were determined for the strain CBS6936 and were deposited in GenBank under the accession number JQ710936, JQ710937, and JQ710938, respectively. The *C. lusitaniae* Icl1p putative protein showed conservation of the K208, K209, C210, H212 amino acids, which were previously identified as the catalytic residues in the isocitrate lyase of *Escherichia coli* [2]. As in other yeasts, the *C. lusitaniae* Fox2p contains two dehydrogenase domains (DHaseA at aa 24-180, and DHaseB at aa 323-485), which are shortchain alcohol dehydrogenase/reductase superfamily members, and one enoyl-CoA hydratase domain (aa 780-895) [3]. Both Icl1p and Fox2p of *C. lusitaniae* contain a type I peroxisomal targeting signal (-GKL) at the COOH extremity of the protein [4], [5]. Synteny was conserved in the close vicinity of CLUG\_01411.1 and CLUG\_01348.1 in *C. lusitaniae* and in *C. albicans*, which reinforced the idea that these ORF are the true orthologs of the *ICL1* gene and *FOX2* gene of *C. albicans*. Furthermore, other paralog genes having significant homology with *ICL1* and *FOX2* could not be detected in the genome of *C. lusitaniae*. Pxa1p belongs to the superfamily of ATP-binding cassette (ABC) proteins, and to the adrenoleukodystrophy protein (ALDp) subfamily [6]. The *C. lusitaniae* Pxa1p putative protein have highly conserved residues corresponding to the Walker A (aa 566–589) and Walker B (aa 687-734) domains, possess an ABC signature (aa 668-716) and a motif that resembles (aa 603-635) a sequence described as “new motif” for the ALDp subfamily [7]. Synteny was partially conserved in the close vicinity of Pxa1p in *C. lusitaniae* and in *C. albicans.*

**Result S1 references**

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