



Putative protein motifs of 8 members of the proline-rich protein (Prp) family of *Coccidioides posadasii*

Blastp was used to search the genome database of *C. posadasii* (isolate C735) (www.broad.mit.edu/annotation/genome/coccidioides) for additional paralogs of Prp1 and Prp2 (Herr. et al., 2007). Prp1 has previously been referred to as proline-rich antigen 2 (Ag2/Pra; Cox and Magee, 2004). Six additional members of the Prp family were identified and designated Prp3 - Prp8. Genomic DNA and cDNA versions of each of the 8 *PRP* genes of *C. posadasii* have been cloned and subjected to nucleotide sequence analysis. The number of residues of each Prp is indicated. SignalP, DGPI, and PROSITE algorithms were used to evaluate the amino acid sequences of the individual paralogs for predicted signal peptides, GPI anchor sequences, and conserved protein domains, respectively. All but Prp3 were predicted to have a signal peptide. All members of the Prp family contain two or more TXX'P repeats and, except for Prp2 and Prp7, the C-terminal region includes a GPI anchor consensus sequence. The structurally-conserved cysteine-rich fungal extracellular membrane (CFEM) domain (Kulkarni et al., 2003) was present in each of the newly discovered proline-rich proteins. The CFEM domain of Prp1 has been reported to contain B cell epitopes (Zhu et al., 1997). CLUSTAL W alignment of the translated sequences of the Prp family revealed that Prp2 shows the highest sequence homology with Prp1 (Herr et al, 2007).

Putative protein motifs of 8 members of the proline-rich protein (Prp) family of *Coccidioides posadasii*

Blastp was used to search the genome database of *C. posadasii* (isolate C735) (www.broad.mit.edu/annotation/genome/coccidioides) for additional paralogs of Prp1 and Prp2 (Herr. et al., 2007). Prp1 has previously been referred to as proline-rich antigen 2 (Ag2/Pra; Cox and Magee, 2004). Six additional members of the Prp family were identified and designated Prp3 - Prp8. Genomic DNA and cDNA versions of each of the 8 *PRP* genes of *C. posadasii* have been cloned and subjected to nucleotide sequence analysis. The number of residues of each Prp is indicated. SignalP, DGPI, and PROSITE algorithms were used to evaluate the amino acid sequences of the individual paralogs for predicted signal peptides, GPI anchor sequences, and conserved protein domains, respectively. All but Prp3 were predicted to have a signal peptide. All members of the Prp family contain two or more TXX'P repeats and, except for Prp2 and Prp7, the C-terminal region includes a GPI anchor consensus sequence. The structurally-conserved cysteine-rich fungal extracellular membrane (CFEM) domain (Kulkarni et al., 2003) was present in each of the newly discovered proline-rich proteins. The CFEM domain of Prp1 has been reported to contain B cell epitopes (Zhu et al., 1997). CLUSTAL W alignment of the translated sequences of the Prp family revealed that Prp2 shows the highest sequence homology with Prp1 (Herr et al, 2007).