

Computacional Prediction of Protein-Coding Gene and Annotation of DNA Sequences with Agronomic Interest in *Pleurotus ostreatus* (Oyster Mushroom)

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Pleurotus ostreatus, commonly known as oyster mushroom, is a commercially important edible fungus with interesting biotechnological properties. Quantitative trait loci (QTL) analyses are rare in fungi and little is known about their number, position, and genetic structure. Previous studies of our group have allowed the construction of a genetic linkage map of *P. ostreatus* var. *florida*, which has provided the basis for performing an efficient QTL analysis. In fact, there is a region of the chromosome VII of *P. ostreatus* where the most QTLs related to the production and precocity characters have been mapped. These quantitative traits are presumably under the control of a polygenic genetic system and could be associated with some chromosomal regions. The hypothesis of this work is that there is a region in the chromosome VII of protoclon PC15 (monokaryotic parental of the N001 dikaryotic strain) where exist genes which are responsible for the QTLs mentioned above. In order to test this hypothesis, we are developing a molecular QTL analysis through the sequencing of a region with an approximated size of 320 Kbp in chromosome VII (protoclon PC15). For this purpose, a BAC genomic library was constructed and two BAC clones spanning the region of interest are being sequenced. To carry out an efficient computational prediction of protein-coding genes and its annotation on the partial sequences obtained up to date, we have used different Internet resources such as BLASTx, BLASTp, BLASTn, and FGENESH trained on some basidiomycetes genomic data like *Phanerochaete chrysosporium* and *Cryptococcus neoformans* (SoftBerry). To our knowledge, this is the first molecular QTL analysis performed on this edible mushroom.