In silico prediction and comparative studies on plant GPCRs

Natália F. Martins, Emmanuel Bresso, Priscila Grynberg, Roberto C. Togawa, Deisy X. Amora and Bernard Maigret

EMBRAPA Recursos Genéticos e Biotecnologia, Parque Estação Biológica, Brasília, DF,Brazil; CNRS, LORIA, UMR 7503, Lorraine University, Vandoeuvre-lès-Nancy, France

G-protein coupled receptors (GPCRs) is the largest family of membrane proteins, as key components of signal transduction pathways. They are activated by diverse ligands, including odorants, fatty acids, peptides and neurotransmitters, across cell membranes. The identification of novel G protein-coupled receptors (GPCRs) from genome analysis allowed the prediction of new important receptors in several species. Despite the current knowledge, GPCRs in plants are not well characterized if compared to animals. The availability of plant genomes allowed the prediction and characterization of diverse GPCRs as well as a comparative analysis of the GPCR structure-function relationship. In plants, the repertoire of GPCRs remains unclear. Therefore, in silico analyses of candidates from Arabidopsis, *Capsicum annum*, *Glycine max, Manihot esculenta, Medicago trunculata, Oryza sativa, Phaseolus vulgaris, Populus tricocarpa, Ricinus communis, Solanum lycopersicum, Solanum tuberosum, Sorghum bicolor, Theodroma cacau, Triticum aestivum, Vitis vinifera* and *Zea mays* describes the comparative survey for GPCRs with a total amount of 997,435 proteins. Following a logic pipeline the proteins were filtered by length resulting in 487,012 proteins between 250 and 1000 AA. Another trimming round of candidates with seven transmembrane segments revealed 4,878 possible proteins which were, therefore, submitted to the GPCRpipe program. This software predicted 60 GPCRs candidates, ranging from none (*Capsicum annuum*) to 12 candidates (*Populus trichocarpa*) (median = 3 ± 2.90). Comparative studies based on structure, sequence, ontology and phylogeny showed a low diversity in genes if compared to humans GPCR's classification. The Neighbor joining dendrogram of the 60 predicted GPCR candidates grouped the proteins in three groups. The first are similar to A Rhodopsin like, the second has similarity with GPCRs with Lung seven transmembrane receptor family protein and the third one was identified as GCR1 orthologs. These findings may indicate that GPCR in plants can be involved in drought stress responses, specially related to cytosolic calcium concentration changes in response to several stimuli, including light, pressure, gravity, and hormones.