Identification of non-homologous isofunctional enzymes in the antioxidant system of plants and phytopathogens

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In plants, the antioxidant system is responsible for the hypersensitive response, elicited when hosts are infected by pathogenic strains of bacteria or biotrophic fungi. It is composed of several enzymes such as catalase (CAT), peroxidase (POX), superoxide dismutase (SOD), Glutationa peroxidase (Gprx), Peroxiredoxin (Prxs), among others. This arsenal plays a critical role in the detoxification of reactive oxygen species during host–pathogen interactions. Blocking or inhibiting these enzymes would, in principle, decrease the virulence of the pathogen and/or delay the defense against free radicals used by the plant as defense mechanisms during the raids, debilitating the pathogen. Recently, researchers identified and characterized non-homologous isofunctional enzymes (NISEs), enzymes that perform the same biochemical function but have different evolutionary origins, which are reflected in differences between their primary and tertiary structures. These differences may be exploited for the development of specific blocking or inhibiting agents, resulting in a diminished virulence or pathogenicity. The objective of this study was to identify NISES in the antioxidant system, using as model *Glicine max* and some of its pathogens, like *Aspergillus flavus*, *Fusarium oxysporum*, *Phytophthora sojae*, *Sclerotinia sclerotiorum, Xanthomonas axonopodis.* We have also included *Appis melifera* (pollinator), *Bacillus subtilis* (soil bacteria), *Azobacter chroococcum* and *Trichoderma arzianum* (soil fungi) and *Homo sapiens* in the analysis, for applications in a ecologycal context. Files containing information about active proteins in metabolic pathways were obtained from KEGG, and datasets of predicted proteins of *G. max* and its pathogens were downloaded from UniprotKB and RefSeq. The AnEnPi pipeline was used for clustering, by comparing the primary structures of enzymes previously annotated with the same Enzyme Commission number. The BLASTP was used to analyze the difference between the primary structures of the enzymes within each EC, on this step the activities were compared all against all. After clustering, enzymes grouped in the same cluster were considered homologous (score above 120), while enzymes allocated in different clusters were considered potential analogous enzymes (score under 120). The identified NISES had their folds sorted using the SCOP and SUPERFAMILY databases. In this work, we have been able to identify several NISEs candidates belonging to the antioxidant system between *G. max* and its pathogens: 9 for CAT, 7 for POX, 6 for SOD e and 1 Prxs. These results show that it may be possible to exploit differences in the enzymes belonging to the antioxidant system to develop specific inhibitor molecules.

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