Bioinformatic Analysis of Ubiquitin-Specific Protease Genes in Genome of Phaseoulus vulgaris L.

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Abstract

The Bean is a leguminous plant with high protein value, nutritional and heme iron donor widely consumed. The ubiquitin-proteasome is a pathway responsible controls many cellular processes able controlled such as degraded of proteins flawed, with error of synthesis, and that are no longer necessary. Once they were marked with ubiquitin protein, they are degraded by the protein complex proteasome 26S. The complex ubiquitin-proteasome regulation is one mechanism of control post- translational regulatory of many proteins important, but also able to be controlled by other proteins, which are called Deubiquitinating enzymes DUB and their function control the ubiquitin binding, off and clear the programmed degradation. The DUBs are composed by five super families of proteins such as JAMMs (metaloproteases), Ubiquitin C-terminal Hydrolases - UCHs, Machado-Joseph Domain MJD, Ovarian Tumor Proteases - OTU and Ubiquitin-Specific Proteases-USPs (UBPs in plants). The UBPs are specific proteins which degraded ubiquitin and therefore the study of these proteins is very important for understanding the regulation of many cellular functions and physiological in plants. Thus, the aim of this study, was to identify, annotate, characterize and classify putative UBP proteins in the genome of Phaseolus Vulgaris L.. Genome sequence of Phaseolus Vulgaris L. deposited in the public database Phytozome was used as queries in BLAST tool (Basic Local Search Alignment Tool). Conserved domains, amino acid residues from active sites were retrieved through the predicted proteins using PFAM database (http://pfam.sanger.ac.uk/) and CDD. Phylogenetic analysis was conducted in Mega5.2 program. We found 15 putative proteins UBPs in P. vulgaris among 12 subfamilies: UBP2-like; UBP4-like; UBP6-like; UBP8, UBP9-like; UBP13-like; UBP15, UBP17 and UBP18-like; UBP20-like; UBP22-like; UBP23-like; UBP25-like; UBP26-like. The putative UBP proteins showed conserved domains UCH containing significant and conserved residues at critical positions on the protein (putative active sites). The putative conserved catalytic site comprised (C/D/H) which divided into cys box and his box. The putative proteins UBP clustered on the phylogenetic tree in distinct clades agreeing with the predicted paralogous sub-families. Therefore, this study expanded the knowledge of the Ubiquitin-specific protease in P. vulgaris and it is the starting point for new challenges that pathway can help for produces, in future, cultivars genetically modified, with best growing, adaptation and production.

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