

## عنوان مقاله:

Comparative coexpressed network study of phenylalanine ammonialyase in *Brachypodium distachyon* and *Glycine max*

## محل انتشار:

هفتمین همایش بیوانفورماتیک ایران (سال: 1396)

تعداد صفحات اصل مقاله: 1

## نویسندگان:

S Mousavi Fard - *Department of Cell & Molecular Biology, Faculty of Life Sciences & Biotechnology, Shahid Beheshti University G.C., Evin, Tehran, Iran, ۱۹۸۳۹۶۳۱۱۳*

N Farrokhi - *Department of Cell & Molecular Biology, Faculty of Life Sciences & Biotechnology, Shahid Beheshti University G.C., Evin, Tehran, Iran, ۱۹۸۳۹۶۳۱۱۳*

S Gharanjik - *Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahrood University of Technology, Shahrood, Iran, ۳۶۱۹۹۹۵۱۶۱*

M Parsaeyan - *Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahrood University of Technology, Shahrood, Iran, ۳۶۱۹۹۹۵۱۶۱*

## خلاصه مقاله:

Lignin is a complex and heterogeneous phenolic polymer comprising of monolignols, namely guaiacyl, syringyl and p-hydroxyphenyl [1]. Lignin cross-links with other polysaccharids in secondary cell wall for hardening the corresponding structure and improving the resilience of plant against both biotic and abiotic stresses [2,3]. Phenylalanine ammonia lyase (PAL) is the first enzyme in phenylpropanoid pathway [4], catalyzing the conversion of L-phenylalanine to cinnamic acid and ammonia were carried out [2,5]. Here Comparative coexpressed network study of PAL in *Brachypodium distachyon* and *Glycine max* were carried out. Gene coexpression network (GCN) for PAL genes were predicted via PlaNet and Phytozome for *B. distachyon* and Phytozome for *Glycine max*. Plantpan 2.0 was implemented to look for the co-occurrence of transcription factor binding sites (TFBSs) in the promoter sequences of the coexpressed genes to further confirm what was obtained in GCN. GCN analyses revealed that there are 33 and 27 genes in 6 sub-networks for *G. max* and *B. distachyon*, respectively. Our results were definitively led to the identification of some more genes in addition to what was characterized earlier [1,2]. Analyses of upstream sequences of the genes ORFs via plantpan 2.0 were revealed many co-occurred TFBSs in each sub-network, and common co-occurrence TFBS between sub-networks in each plant. Interestingly, some TFBSs were common between some sub-networks of the two plants that were examined.

## کلمات کلیدی:

Lignin biosynthesis; Transcription factor binding site; Gene coexpressed network; PAL

## لینک ثابت مقاله در پایگاه سیویلیکا:

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