

# Plant Polyprenol Reductase in the Database

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**Abstract:** Chemical constituents such as polyprenols and dolichols are known to generate higher plants. The present document discusses the database search (<https://www.ncbi.nlm.nih.gov/>) or GQuery on plant polyprenol reductase from the National Center for Biotechnology Information (NCBI). A amount of useful data was searched for NCBI databases. Results developed for plant polyprenol reductase in 10 databases. All polyprenol reductase plant databases consisting of source literature, genes, genetics, protein, genomes, and chemical characteristics. It is noteworthy that plant polyprenol reductase has complete information. The literature comprised of PubMed and PubMed Central. Gene consisted of Gene, GEO Profiles, and UniGene. Genetics data was available for plant polyprenol reductases such as dbGap and MedGen. Proteins feature contained four protein sequences. Genomes encompassed one BioSample and 365 Nucleotides. The chemicals property denoted 3392 BioSystems. The present study affords indispensable information concerning biotechnology of plant polyprenol reductase.

## 1 INTRODUCTION

Higher plants are well known to produce short to lengthy polyisoprenoids, which are classified into polyprenol and dolichol (Sagami et al., 2018). The occurrence of polyisoprenoids in the tropical, subtropical and temperate areas was outlined in different plant organs (Skorupins-Tudek et al., 2008; Surmacz and Swiezewska, 2011; Basyuni et al., 2016, 2017 Arifiyanto et al., 2017; Basyuni and Wati, 2017). These reports demonstrated the extensive distribution in the plant kingdom of polyisoprenoids. In plant leaves, polyprenols are defined and minor dolichols are identified (Skorupins-Tudek et al., 2008; Surmacz and Swiezewska, 2011; Arifiyanto et al., 2017; Basyuni and Wati, 2017). Otherwise, dolichols in plant roots, yeast and animal tissues were identified extensively (Grabińska. and Palamarczyk 2002; Ishiguro et al., 2014; Basyuni et al., 2016, 2017; Sagami et al., 2018). By contrast to these studies, it is noteworthy that the primary structure of polyisoprenoids in

mangroves and coastal plant leaves and roots was dolichols (Basyuni et al., 2016, 2017).

The presence of adequate dolichols in these plants leaves suggests that the polyprenol reductase enzyme worked (Basyuni et al., 2018a,b,c). It has also been reported the presence of polyprenol reductase enzyme in *Arabidopsis thaliana* (Jozwiak et al., 2015) and other higher plants (Basyuni and Wati, 2018). This enzyme connected with the SRD5A3 protein in animals has been revealed to catalyze the final step in the dolichol biosynthetic of polyprenol converted to dolichols (Rosenwald et al., 1993; Cantagrel et al., 2010; Gründahl et al., 2012; Sagami et al., 2018). Limited work focused on the biotechnology data investigated from all earlier accessible NCBI databases in the plant polyprenol reductase. Here, through a search engine, we report a quick and simple technique to collect useful data needed in latest biotechnology-related science studies. The aim of this research is to describe the implementation of the National Center for Biotechnology Information (NCBI) databases in

order to obtain more insight into useful data on updated biotechnology on polyphenol reductase in plants.

## 2 MATERIAL AND METHOD

The online search engine for NCBI databases (<https://www.ncbi.nlm.nih.gov/>) has been used to produce useful data about polyphenol reductase in the plant. As stated previously on 19 February 2018, databases were accessed by typing plant and polyphenol reductase in all NCBI databases. The characteristic was all databases made using GQuery that consisted of the literature, genes, protein, genomes and chemical characteristics of plant polyphenol reductase. The considerations for data included the PubMed, PubMed Central, GEO (Gene Expression Omnibus) profiles, UniGene, dbGaP (database of Genotypes and Phenotypes), MedGen, Protein, Assembly, BioCollections, BioSamples, Clone, GSS (Genome Survey Sequences), Nucleotide, and BioSystems.

## 3 RESULTS AND DISCUSSION

The search for plant polyphenol reductase led ten databases for plant polyphenol reductase in the NCBI database. Table 1 demonstrates the literature on plant polyphenol reductase available in the NCBI. Two biographies deposited with countless figures. The online NCBI literature provides online libraries and free access to two PubMed papers consisting of science and medical abstracts / citations and 23 PubMed Central articles.

Table 1: Literature source NCBI database for plant and polyphenol reductase

Literature	Number	Description
PubMed	2	Abstracts/quotations from science and medicine
PubMed Central	23	Articles in full-text journals

Information on sources of genes is shown in Table 2. This information includes plant-related polyphenol reductase genes than consisting of one gene, namely TNF receptor-associated factor 6 [*Harpegnathos saltator* (Jerdon's jumping ant)]. Table 2 shows 20 GEO profiles and three unigenes. *Arabidopsis thaliana* species dominated the Geo profiles. The Geo profiles are AT1G72590-Red light effect on the root, AT2G16530-Diurnal and

circadian-regulated genes (II), AT1G72590-Necrosis- and ethylene-inducing peptide effect on dicots, AT1G72590-Leaf Response to Aphid Feeding, AT1G72590-MicroRNA miR159a overexpression effect on flower, AT1G72590-MicroRNA miR319a overexpression effect on the leaf, AT1G72590-Vier F-Box VFB triple mutant seedlings, AT1G72590-Chitin oligomer chitooctase effect on seedlings, the effect of AT1G72590-MicroRNA miR156b and miR164b on floral apex, AT1G72590- MicroRNA miR164b and miR172a on vegetative apex, DFG10-Saponin treatment effect: time course, AT2G16530-Indole acetic acid treatment time course (AG), AT1G72590- the impact of salt stress on mannitol-producing M6PR transgenic plant with salt tolerance: leaf, AT1G72590-Indole acetic acid treatment time course (ATH1), AT1G72590- mRNA cap-binding protein ABH1 mutant response to abscisic acid, AT1G72590-Salt stress effect on multiple genotypes: leaf, LOC4336740-Cytokinin effect on rice roots and leaves: time course, AT1G72590 Ozone impact on double-null mutant leaves of G-protein: time span, AT1G72590-Pollinated pistils: time span, and AT1G72590-Indole acetic acid therapy: time span and time span (Table 2).

The UniGene consisted of 3 clusters of expressed transcripts. They are Putative polyphenol reductase 2 (AT2G16530), represented by 11 ESTs from 5 cDNA libraries. This gene corresponds to 2 reference sequences (different isoforms) (Joswiak et al., 2015). The 2<sup>nd</sup> UniGene was Probable polyphenol reductase 2-like, Soybean protein-encoding gene LOC100814660. Displayed by 13 ESTs from 8 cDNA libraries and Transcribed locus, moderately similar to XP\_003537828.1 predicted: probable polyphenol reductase 2-like *Glycine max*. This unigene was represented by *Lotus japonicus* putative protein-coding gene and represented by 4 ESTs from 3 cDNA libraries.

Table 2: Genes source NCBI database for plant polyphenol reductase

Genes	Total	Information
Gene	1	Collected gene loci data
GEO Profiles	20	Gene expression and profiles of molecular abundance
UniGene	3	Expressed transcript clusters

Furthermore, the genetics source NCBI database comprises of 8 dbGaP and 2 MedGen. The study of the database of Genotypes and Phenotypes consist of phs000287.v6.p1 Cardiovascular Health Study (CHS) Cohort, phs000280.v5.p1 Atherosclerosis

Risk in Communities (ARIC) Cohort, phs000209.v13.p3 Multi-Ethnic Study of Atherosclerosis (MESA) Cohort, phs001496.v1.p1 A genomic approach to the prescription of warfarin in Hispanics of the Admixed Caribbean, phs000007.v30.p11 Framingham Cohort, phs000309.v3.p2 The CARDIA-GENEVA Study, phs000090.v5.p1 GENEVA: The Atherosclerosis Risk in Communities (ARIC) Study, and phs000547.v1.p1 A Study of the Genome-Wide Association in SUCCESS Trial Breast Cancer Patients. Regarding with protein for plant polyprenol reductase observed in the database, 55 proteins were recorded.

The biological and pharmacological function of polyisoprenoids especially dolichols have been well documented (Tao et al., 2016; Illian et al., 2018; Sari et al., 2018). Furthermore, the role of dolichols for the clinical and biochemical phenotypes in dolichol-linked Congenital disorders of glycosylation (CDG) has been described (Buczowska et al., 2015).

Table 3: Genetics source NCBI database for plant and polyprenol reductase

Genetics	Number	Explanation
dbGaP	8	Genotype/phenotype interaction studies
MedGen	2	Medicinal genetics literature and links

Table 4: Protein source NCBI database and plant polyprenol reductase

Proteins	Number	Description
Protein	55	Protein sequence

Table 5: Genomes source NCBI database for plant polyprenol reductase

Genomes	Number	Information
Assembly	24	Information on assembly of genomes
BioCollections	149	Museum, herbarium and other collections of biorepository
BioSample	1	Information of of materials from biological sources
Clone	12	cDNA and genomic clones
GSS	2	Genome search sequences
Nucleotide	266	RNA and DNA sequences

The MedGene has two kinds of Glycyrrhetic acid product and High-Selenium *Brassica juncea* (Table 3). Table 4 shows 55 protein sequences that consist of 39 eudicots and 16 monocots. The top plant species for protein sequence in the plant polyprenol reductases are *Noccaea caerulea*

(12), *Vitis vinifera* (6), *Arachis ipaensis* (6), *Ananas comosus* (5), *Dendrobium catenatum* (5), and *Dichantherium oligosanthes* (3), and others (18).

Furthermore, it has been shown from Table 5; there are 266 nucleotides from plant polyprenol reductase, which classified from molecular type as 227 from genomic/RNA and only 22 from mRNA. While from the sources database of nucleotide are derived from INSDC (International Nucleotide Sequence Database Collaboration)/Genbank (109) and RefSeq (157). The mRNA molecule type of plant polyprenol reductase is derived from *Arachis ipaensis* (6), *Ananas comosus* (5), *Dendrobium catenatum* (4), *Arachis duranensis* (2), *Juglans regia* (2), and all other taxa (3).

Recently three predicted polyprenol reductases from *K. obovata* had been described (Basyuni et al., 2018a,b,c) to add previous information on polyprenol reductase from *A. thaliana* (Jozwiak et al., 2015). The position of predicted polyprenol reductase *K. obovata* existed together with *Ricinus communis* and *Iopoea nil* (Basyuni et al., 2018b,c; Basyuni and Wati, 2018). Polyprenol reductase also occurred in yeast *Saccharomyces cerevisiae* (Szkopinska et al., 2006).

Table 6: Chemicals source NCBI database for plant and polyprenol reductase

Chemicals	Total	Explanation
BioSystems	3392	Gene, protein and chemicals linked molecular pathways

No variation of chemical features of the plant polyprenol reductase as was displayed in Table 5, in this report only BioSystems were detected. Biosystems contained two types, conserved biosystems (135) and organism-specific biosystems (3257). According to a record type, 3,359 pathways, 28 structural complexes, five working sets. Concerning to source name consisting of GO (135) and KEGG (3,255). The BioAssays comprised BioAssays via Actives (3,255) and BioAssays via Target (157).

## 4 CONCLUSIONS

The web NCBI supplied countless data on plant polyphenol reductase in biology and biotechnology. The current research encouraged researchers in the field of biotechnology to obtain more advantages using the NCBI search engine. The present study also delivers crucial data regarding biotechnology of plant polyphenol reductase.

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