Information on Polyprenol Reductase Enzyme in the NCBI Online

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Abstract: Polyprenol reductase an enzyme is necessary to convert polyprenol to dolichol in the last phase of dolichol biosynthesis. The present work reports search result of National Center for Biotechnology Information (NCBI) databases on polyprenol reductase. To produce some useful data, the search for NCBI databases (https:/www.ncbi.nlm.nih.gov/) was used. Results detected in 16 databases for polyprenol reductase. The databases of the polyprenol reductase consist of literature, health, genomes, genes, protein, and chemical features. The literature contained 16 bookshelves, 1 MeSH (Medical Subject Headings), 16 PubMed, and 58 PubMed Central. Health comprised 3532 Clincar documents, 163 dbGap, 899 GTR, 257 MedGen, 3 OMIM (Online Mendelian Inheritance in Man database). Gene involves of 681 Genes, 303 GEO profiles, 1 HomoloGene, and 20 UniGenes. Proteins properties contained 933 Identical Protein Groups, 1,208 Proteins, and 4 Protein Clusters. Genomes included 37,135 nucleotides, which are derived from 34,821 bacteria, 1,151 animals, 603 plants, 340 archaea, 141 fungi, and 7 viruses. The chemicals property represented 3648 BioSystems and five bioactivity screening studies. The present data provides indispensable information about biotechnology of polyprenol reductase enzyme.

1 INTRODUCTION

Polyprenol reductase is an enzyme that stimulates the reduction of polyprenols into dolichols in the dolichol biosynthesis (Rosenwald et al., 1993; Quellhorst Jr et al. 1997; Sagami et al. 2018). The occurrence of polyprenol reductase has been described as various organisms. In the plant kingdom, for example, has been described in *Arabidopsis thaliana* (Jozwiak et al., 2015), *Kandelia obovata* leaves (Basyuni et al., 2018a,b,c), spinach leaves (Sakaihara et al., 2000). Polyprenol reductase has been shown in *Haloferax volcani*, a halophilic archeon (Naparstek et al., 2012), mammalian (Dsouzaschorey et al., 1994), yeasts (Tateyama and Sagami, 2001; Szkapinska et al., 2006), hamster (Chaves et al., 2015), and human (Cantegral et al., 2010).

The biological and pharmacological activity of polyprenol reductase has been described, such as prostate cancer prevention (Nacusi and Tindall, 2011; Schmidt and Tindall, 2011). Polyprenol reductase has been shown to play a role in congenital disorders of glycosylation (CDG) (Gründahl et al., 2012) and genetic defects of dolichol metabolism in dolichol-related CDGs for clinical and biochemical phenotypes (Buczkowska et al., 2015).

In this context, it is essential to understand further the polyprenol reductase enzyme relating biotechnology from all databases available. Here we report a brief review via a search engine to gather useful data in biotechnology-related science studies. Therefore, the present study aimed to report the use of the databases of the National Center for Biotechnology Information (NCBI) search to obtain more insight on updated biotechnology related to polyprenol reductase enzyme.

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2 MATERIALS AND METHOD

The material of this work applied databases of polyprenol reductase that were used to produce some valuable information biotechnology can be conducted using NCBI databases search engine online (https://www.ncbi.nlm.nih.gov/). The material was derived from typing on all database search as mentioned earlier on January 22, 2019. Information features include the Bookshelf, MeSH (Medical Subject Headings), NLM (National Library of Medicine) Catalog, PubMed, PubMed Central, Clinvar, a database of Genotypes and Phenotypes (dbGap), Genetic Testing Registry (GTR). MedGen, Online Mendelian Inheritance in Man (OMIM), BioSample, Clone, database of human genomic structural variation (dbVar), Genome, GSS (Genome Survey Sequences), Nucleotide, Probe, EST, Gene, Gene Expression Omnibus (GEO) Profiles, HomoloGene, UniGene, Identical Protein Groups, Protein, Protein Clusters, Biosystems, and PubChem BioAssay.

3 RESULT AND DISCUSSION

The exploration for the polyprenol reductase enzyme showed sixteen databases in the NCBI database. Table 1 depicts the literature available in the NCBI concerning polyprenol reductase. Four biographies, namely bookshelf, MeSH, PubMed, and PubMed Central with a number of deposited documents. The online NCBI literature provides online libraries and free access to bookshelf data (sixteen books and reports). MeSH contained one ontology used for Pubmed indexing. PubMed covered the publication year 1990-2018.

Table 1: Literature source NCBI database for polyprenol Reductase.

Literature	Sum	Information
Bookshelf	16	Books and reports
MeSH	1	The ontology used to index Pubmed
PubMed	16	Abstracts/quotations from science and medicine
PubMed Central	58	Full-text journal articles

Table 2: Health source NCBI database for polyprenol reductase.

Health	Total	Definition
Clinvar	3532	variations in human clinical importance
dbGap	163	genotype/phenotype interaction issues
GTR	899	genetic testing registry
MedGen	257	Medical genetics literature and links
OMIM	3	online mendelian inheritance in man

Information on health sources is displayed in Table 2. This data is including 3,532 ClinVar relating to individual variations of clinical significance, 163 dbGap, 899 GTR, 257 MedGen. It is important to mention that this research (Table 2) identified the OMIM (Online Mendelian Inheritance in Man). The OMIM consisted of Steroid 5-alpha-reductase 3, SRD5A3, Steroid 5-alpha-reductase 1, SRD5A1, and Congenital disorder of glycosylation (CDG), CDG1Q as previously was reported ((Gründahl et al., 2012; Buczkowska et al., 2015).

Table 3: Genomes source NCBI database for polyprenol reductase.

Genomes	Number	Explanation
BioSample	302	descriptions of materials from biological sources
Clone	12	genomic and cDNA clones
dbVar	21,375	studies of structural genome variation
Genome	4	organizational genome sequencing projects
GSS	1,514	genome project sequences
Nucleotide	37,135	DNA and RNA sequences
Probe	18	samples and primers based on sequences

Furthermore, genome source for polyprenol reductase enzyme namely 302 BioSample, 12 clones of genomic and cDNA, 21,375 trials of structural genome variability, 4 projects of genome sequencing, 1514 GSS, 37,135 DNA and RNA sequences, and 18 Probes. It is intersting that from 37,135 nucleotides in the databases comprised of 1,151 animals, 603 plants, 141 fungi, 78 protists, 34,821 bacteria, 340 archea, and 7 viruses while the molecular type contained 36,192 DNA/RNA and 851 mRNA.

The Genes collection consisted of 1 Expressed sequence tag (EST), 681 information about gene loci, 303 gene expressions, one homologene, and 20 Unigenes as depicted in Table 4. Table 5 shows the protein source for 933 identical protein groups, 1,208 protein, and 4 protein clusters. Four protein

clusters are 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal domain containing Embryophyte protein (Accession: PLN03164), 3-oxo-5-alpha-steroid 4-dehydrogenase family protein conserved in *Arabidopsis thaliana* (Accession: CLSN2912717), probable polyprenol reductase 1-like conserved in BOP clade, and probable polyprenol reductase 2-like conserved in *Glycine max* (Accession: CLSN2960920).

Table 4: Genes source NCBI database for polyprenol Reductase.

Genes	Number	Definition
EST	1	expressed sequence tag sequences
Gene	681	collected gene loci data
GEO Profiles	303	gene expression and profiles of molecular abundance
HomoloGene	1	homologous gene
UniGene	20	sets of expressed transcripts for chosen organisms

Table 5: Proteins source NCBI database for polyprenol reductase.

Proteins	Number	Explanation
Identical Protein Groups	933	identity grouped protein sequences
Protein	1,208	protein sequences
Protein Clusters	4	Sequence of protein clusters based on similarity

Table 6: Chemicals source NCBI database for polyprenol reductase.

Chemicals	Amount	Information
BioSystems	3,648	gene, protein and chemicals linked molecular pathways
PubChem BioAssay	5	screening of bioactivity

The biological activities have been well documented (Nacusi and Tindall, 2011; Schmidt and Tindall, 2011Buczkowska et al., 2015; Tao et al., 2016). Polyprenol reductase has been reported to play an essential role in CDG (Gründahl et al., 2012) and the clinical and biochemical phenotypes in dolichol-concerning CDG (Buczkowska et al., 2015).

Probable polyprenol reductases from *K. obovata* had been reported (Basyuni et al., 2018a,b,c) to different previous data on polyprenol reductase from *A. thaliana* (Jozwiak et al., 2015). The position of predicted polyprenol reductase from *K. obovata* sit together with *Ricinus communis* and *Iopoea nil* (Basyuni et al., 2018b,c; Basyuni and Wati, 2018).

Variation of chemical features of the polyprenol reductase as was displayed in Table 6, in this report only BioSystems and PubChem BioAssay were detected. Biosystems contained two types, conserved biosystems (206) and organism-specific biosystems (3442). According to a record type, 3,608 pathways, 28 structural complexes, 12 functional sets. Relating to source name consisting of BioCyc (2), GO (196) and KEGG (3,337). Whereas the source of databases derived from INSDC/GenBank was 24,798 and RefSeq was 12,331. The PubChem BioAssays comprised 5 bioactivities screening studies (Table 6). These five Assays are Upregulation of NADH-cytochrome b5 reductase expression in Candida albicans SC5314 at 200 uM after 24 hrs by MALDI-TOF MS, Upregulation of Glutathione reductase expression in Candida albicans SC5314 at 200 uM after 24 hrs by MALDI-TOF MS, Upregulation of Mitochondrial 2-enoyl thioester reductase expression in Candida albicans SC5314 at 200 uM after 24 hrs by MALDI-TOF MS, Upregulation of Aldose reductase expression in Candida albicans SC5314 at 200 uM after 24 hrs by MALDI-TOF MS, and Inhibition of 5alpha-reductase in human epidermis assessed as inhibition of [14C]testosterone to DHT after 24 hrs.

4 CONCLUSIONS

The NCBI online discusses different data about polyprenol reductase enzyme in biology and biotechnology. The current study also delivers important data regarding biotechnology of polyprenol reductase.

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