

NCBI Database on Cycloartenol Synthase

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Keywords: Abiotic stress, cycloartenol, isoprenoid, oxidosqualene

Abstract: Cycloartenol synthase (EC 5.4.99.8) is a cycloartenol-converting enzyme. The current research describes the search of cycloartenol synthase databases from the National Center for Biotechnology Information (NCBI). A amount of precious information was generated by NCBI database search (<https://www.ncbi.nlm.nih.gov/>). Results discovered in 22 cycloartenol synthase databases. All literature, genes, genetics, protein, genomes, and chemical features of cycloartenol synthase databases. Bookshelf, MeSH (Medical Subject Headings) and PubMed Central were discussed in the literature. Gene was made up of profiles from Gene, Gene Expression Omnibus (GEO), HomoloGene, PopSet, and UniGene. Data on genetics such as MedGen was available for cycloartenol synthase. Proteins characteristic comprised Conserved Domains, Identical groups of proteins, clusters of proteins, sparcle, and structure. Nucleotide and sample were engaged in genomes. BioSystems, PubChem BioAssay, PubChem Compound, and PubChem Substance are the chemical properties. The present work affords vital information in term biotechnology of cycloartenol synthase.

1 INTRODUCTION

Phytosterol including cycloartenol is ordinary chemical constituents in higher plants (Augustin et al., 2011; Uddin et al., 2015). Phytosterols serve as chemotaxonomy markers also have been shown (Koch et al., 2011). Many phylogenetic analyses have been suggested that plant oxidosqualene cyclases (OSCs) are generally evolutionarily derived from cycloartenol synthase (Zhang et al., 2003; Basyuni et al., 2007a,b). More than thousands different OSC genes together with cycloartenol have been reported from plant kingdom, which are expanded from a shared 2,3-oxidosqualene substrate via OSCs, they separate in the cyclization of this intermediacy into each of phytosterol of cycloartenol and lanosterol or a diversity of triterpenes (Augustin et al., 2011). In plantae, cycloartenol synthase (CAS) along with lanosterol synthase (LAS), family member of OSC

are accountable for biosynthesis of phytosterol, and more OSCs are committed for triterpene synthesis (Thimmappa et al., 2014).

Lanosterol and cycloartenol are significant elements of the membrane and can provide substrates for hormones of sterols (Bloch 1983). Our previous studies have shown that membrane lipids (triterpenoids and phytosterols) have an evident role in mangrove modification to salinity stress (Oku et al., 2003; Basyuni et al., 2009, 2012a,b), *Saccharomyces cerevisiae*, GIL77, modulated the salt tolerance of lanosterol synthase deficient (Inafuku et al., 2018). Even though a significant number of studies in cycloartenol synthases have been well documented (Augustin et al., 2011; Xue et al., 2012; Gas-Pascual et al., 2014; Moses et al., 2014; Thimmappa et al., 2014;), Limited work concentrated on biotechnology data from all accessible databases in cycloartenol synthases. Here we report an alternative technique

to collect useful data needed in latest biotechnology-related science studies on cycloartenol synthase through a preferred search engine. Therefore, the aim of this research was to explain the implementation of the National Center for Biotechnology Information (NCBI) databases (GQuery) search to gain more deepful information on updated cycloartenol synthesis biotechnology.

2 MATERIALS AND METHODE

The search engine for NCBI databases (<https://www.ncbi.nlm.nih.gov/>) was used to produce a amount of useful rubber plant data biotechnology. As stated previously on September 19, 2018, data bases were obtained by writing *Hevea brasiliensis* in all database searches. All databases composed of literature, health, genes, protein, genomes, and chemical properties were featured. Cycloartenol synthase (GQuery) was performed. The bookshelf, MeSH (Medical Subject Headings), NLM (National Medicine Library) Catalog, PubMed, PubMed Central, EST, Gene, GEO datasets, PopSet, Identical Protein Groups, Protein, Sparde, Structure, Assembly, BioProject, BioSample, Genome, GSS, Nucleotide, Probe, SRA, Taxonomy, Biosystems, and PubChem BioAssay were the data variables.

3 RESULTS AND DISCUSSIONS

Table 1 demonstrates the literature on cycloartenol synthase available in the NCBI. Four biographies stored in countless numbers. The web NCBI literature provides internet libraries and free access to bookshelf data (two reports and books), 2 MeSH (Medical Subject Headings), namely cycloartenol synthase [Supplementary Concept] and 3-beta-(2-(diethylamino) ethoxy) androst-5-en-17-one [Additional Concept], ontology used to index PubMed papers.

Table 1: Literature source NCBI database for cycloartenol synthase

Literature	Total	Information
Bookshelf	2	Reports and books
Mesh	2	Medical topic in the collections of the NLM
PubMed	312	Scientific and medical abstracts/quotations
PubMed Central	584	Articles in full-text journals

Furthermore, 87 Pubmed and 232 PubMed Central documentations were stored as called the plant cycloartenol synthase (Table 1). The PubMed database includes quotes derived different topics in many connections to reports of full-text papers on rubber plants open access.

Table 2: Genes source NCBI database for cycloartenol synthase

Health	Amount	Explanation
Gene	242	Gathered data about the gene loci
GEO Profiles	116	Gene profile and molecular abundance patterns
HomoloGene	2	Homologous gene sets for chosen organisms
PopSet	3	Sets of phylogenetic and population studies sequences
UniGene	66	Groups of transcripts conveyed

Table 3: Genetics source NCBI database for cycloartenol synthase

Genetics	Total	Information
MedGen	1	Literature and connections in medical genetics

Table 4: Proteins source NCBI database for cycloartenol synthase

Proteins	Number	Explanation
Conserved Domains	1	Preserved protein domains
Identical Protein Groups	723	Sequences of proteins classified by similarity
Protein	976	Sequences of proteins
Protein Clusters	17	Sequence of protein clusters based on similarity
Structure	2	Experimentally determined biomolecular structures

Table 5: Genomes source NCBI database for Plant and cycloartenol synthase

Genomes	Number	Description
Nucleotide	1583	RNA and DNA sequences
Probe	92	Biomolecular structures experimentally determined

Information on genes sources is displayed in Table 2. This data is as well as genes associated to cycloartenol synthase than consisting of 242 genes with top organisms are *Rosa chinensis* (15), *Malus domestica* (14), *Camellia sinensis* (11), *Zea mays* (10), *Pyrus x bretschneideri* (10), *Gossypium hirsutum* (10), *G. raimondii* (10), *Vitis vinifera* (10), *Aegilops tauschii* (8), *Arachis hypogaea* (8),

Brachypodium distachyon (7), *Phoenix dactylifera* (7), *Nicotiana tabacum* (7), and all other taxa. Table 2 shows there is 116 GEO profiles, one homologene, three popset, and 66 uniges. It is important to note that top organisms for unigene are *Malus domestica* (5), *Zea mays* (5), *Panicum virgatum* (4), *Brassica napus* (3), *Arabidopsis thaliana* (3), *Citrus sinensis* (3), *Medicago truncatula* (3), *Vitis vinifera* (3), *Triticum aestivum* (3), and *Pinus taeda* (3). The three popsets are *Nicotiana tabacum* cycloartenol synthase (CAS1) mRNA, complete cds, Bacillariophyta cycloartenol synthase gene, partial cds, and *Avena* cycloartenol synthase gene, complete cds.

Table 3 shows one genetics information on medical genetics literature and links. On the other hand, Table 4 depicts protein source from NCBI database for there are five sources for protein that consists of one conserved domain, 723 identical protein groups, 976 proteins, 17 protein clusters, and two structures. The conserved domains comprise C-terminal domain of squalene-hopene cyclase. EC:5.4.99.17 registered as squalene-hopene cyclase, in bacteria activates the cyclisation of squalene into hopene. This response is partly cationic cyclisation cascade, to be similar to a critical level in cholesterol biosynthesis. The C-terminal half of the molecule belongs to this family (Marchler-Bauer et al., 2016).

The same protein groups combined from 13 invertebrates, 437 plants and fungi, and 26 prokaryotes. It is interesting to note that 976 proteins are consisting of animals (2), plants (797), fungi (1), protists (85), bacteria (90) and archaea (1). Top organism for plants are 51 *Oryza sativa* (International Rice Genome Sequencing Project, 2005), 46 *Vitis vinifera* (Roach et al., 2018) and 46 *Zea mays* (Soderlund et al., 2009), 21 *Medicago truncatula* (Young et al., 2011), and 20 *Arabidopsis thaliana* (Corey et al., 1993).

The two structures of cycloartenol are structure of human OSC in complex with Ro 48-8071 [Isomerase, EC: 5.4.99.7] and Human OSC structure in lanosterol complex [Isomerase, EC: 5.4.99.7].

Table 5 displays 1583 nucleotides that comprising of Animals(6), Plants(1,294), Fungi(1), Protists(111), Bacteria(171), Archaea(1). The top plant species as following *Oryza sativa* (55), *Malus domestica* (45), *Zea mays* (43), *Glycine max* (27), *Vitis vinifera* (27), and all other taxa (1097). There are 92 probes in the cycloartenol synthase. Table 6 describes the chemical source of the NCBI database that consists of 10234

Biosystems, 107 PubChem bioassay, 22 PubChem compound, and 58 PubChem substance.

Table 6: Chemicals source NCBI database for cycloartenol synthase

Chemicals	Total	Information
BioSystems	10234	Molecular pathways associated to genes, proteins and chemicals
PubChem BioAssay	107	Bioactivity screening
PubChem Compound	22	Chemical data with systems, experience and relationships
PubChem Substance	58	Substance stored and chemical data

Protein modeling of cycloartenol synthase from mangrove trees has recently been defined (Basyuni et al. 2018). The protein modeling for KcCAS in *Kandelia candel* and RsCAS of *Rhizophora stylosa* cycloartenol synthases was analyzed by Pyre2 showed homologous results with lightly divergent in sequence similarity. By disparity, the Swiss model for KcCAS had marginally greater sequence homology (47.3%) and differentiated Qmean (0.70) from RsCAS.

4 CONCLUSIONS

The web NCBI defines multiple biological and biotechnology data on cycloartenol synthase. The current work motivated scientists in the field of biotechnology to obtain more advantages using the NCBI search engine. The present study also delivers crucial data regarding biotechnology of triterpene synthases.

ACKNOWLEDGMENTS

This work was in part assisted by an International Research Collaboration and Scientific Publication Grant 2019 from Universitas Sumatera Utara.

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