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National Center for Biotechnology Information (NCBI) database for *Pseudomonas aeruginosa*

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ABSTRACT

The present study describes search National Centre for Biotechnology Information (NCBI) databases (GQuery) on Pseudomonas aeruginosa. NCBI databases search (https://www.ncbi.nlm.nih.gov/) was employed to generate a number of valuable information. Results found in 31 databases for Pseudomonas aeruginosa. All databases of Pseudomonas aeruginosa consist of literature, genes, protein, genomes, clinical and pubchem. The literature contained bookshelf, MeSH (Medical Subject Headings), National Library of Medicine Catalogue, PubMed, and PubMed Central. The genes consists of gene, geo datasets,gep profiles, popset. Proteins feature contained conserved domains, identical protein groups, protein, protein family models and structure. Genomes included Assembly, BioProject, BioSample, Genome, Nucleotide, SRA, and Taxonomy. The clinical contained clinicaltrials.gov, clinvar, dbgap, gtr, medgen and imim. The pubchem consist of bioassays, compunds, pathways, substances. The present work provides essential information relating to biotechnology of Pseudomonas aeruginosa.

Keywords: *pseudomonas; aeruginosa; NCBI; oil palm; biotechnology*

INTRODUCTION

The potential biodegradation of crude oil was assessed based on the development of a fermentative process with a strain of *Pseudomonas aeruginosa* was initially added into the medium to facilitate the biodegradation of crude oil. These results suggest that *Pseudomonas aeruginosa* could degrade most of crude oil with direct or indirect addition of rhamnolipid. And this conclusion was further supported by another adsorption experiment, where the adsorption capacity of crude oil by killed cell biomass was negligible in comparison with the biologic activities of live cell biomass (Zhang *et al* 2005). These oil palm biomass wastes are generated during the milling processes, and they are mainly composed of empty fruit bunches (EFB), oil palm shells, palm kernel shells, and palm oil sludge (Wang *et al* 2022; Lee *at al* 2023). In this study wil show the useful of NCBI database in collecting so many information about *Pseudomonas aeruginosa*.

METHOD

NCBI databases search engine (https://www.ncbi.nlm.nih.gov/) (https://www.ncbi.nlm.nih.gov/search/all/?term=Pseudomonas+aeruginosa) was employed to generate a number of valuable information biotechnology about the *Pseudomonas aeruginosa*. Databases were accessed by writing *Pseudomonas aeruginosa* in all databases search as mentioned earlier on May 10, 2024 The feature was all databases consisting of the literature, health, genes, protein, genomes and chemical properties of *Pseudomonas aeruginosa* was carried out using (GQuery) (Pratomo *et al* 2021; Basyuni *et al* 2019).

The information factors contained All databases of *Pseudomonas aeruginosa* consist of literature, genes, protein, genomes, clinical and pubchem. The literature contained bookshelf, MeSH (Medical Subject Headings), National Library of Medicine Catalogue, PubMed, and PubMed Central. The genes consists of gene, geo datasets,gep profiles, popset. Proteins feature contained conserved domains, identical protein groups, protein, protein family models and structure. Genomes included Assembly, BioProject, BioSample, Genome, Nucleotide, SRA, and Taxonomy. The clinical contained clinicaltrials.gov, clinvar, dbgap, gtr, medgen and imim. The pubchem consist of bioassays, compunds, pathways, substances.

Table 1. Literature of *Pseudomonas aeruginosa* in NCBI database

Booshelf	1.329
MeSH	214
NLM Catalog	124
PubMed	84.003
PubMed Central	182.792

Table 2. Genes of Pseudomonas aeruginosa in NCBI database

Gene	36.692
GEO DataSets	9.894
GEO Profiles	352.804
PopSet	1.391

Table 3. Proteins of Pseudomonas aeruginosa in NCBI database

Conserved Domains	329
Identical Protein Groups	4.010.929
Protein	26.208.618
Protein Family Models	1.188
Structure	3.531

Table 4. Genoms of Pseudomonas aeruginosa in NCBI database

Assembly	30.634
BioProject	3.684
BioSample	75
Genome	2
Nucleotide	3.214.258
SRA	66.078
Taxonomy	1

Table 5. Clinicals of Pseudomonas aeruginosa in NCBI database

ClinicalTrials.gov	424
ClinVar	15
dbGaP	2
GTR	3
MedGen	25
OMIM	51

Table 6. PubChem of Pseudomonas aeruginosa in NCBI database

BioAssays	24.345
Compounds	5
Pathways	1.008
Substances	96

RESULTS AND DISCUSSION

Table 1 show about NCBI's Literature resources include the world's largest repository of medical and scientific abstracts, full-text articles, books, and reports. Let me break down some of the key components PubMed Citations & Abstracts. PubMed is a widely used database for scientific and medical literature. It contains citations and abstracts from various sources, including journals, conference proceedings, and more. Researchers, clinicians, and students often rely on PubMed to find relevant articles and stay up-to-date with the latest research. We can search PubMed using keywords, author names, or specific topics. PMC (PubMed Central) Articles & Books consist of PMC hosts full-text journal articles and books. It's an open-access repository, meaning that many articles are freely available to the public. Researchers can access complete articles on PMC, making it a valuable resource for scientific literature. The NLM Catalog provides information about journals referenced in NCBI databases. We can search for specific journals by topic, title, abbreviation, or ISSN. It's a useful tool for identifying journals related to specific fields of study. MEDLINE content is searchable via PubMed and constitutes the primary component of PubMed. It includes citations from biomedical and life sciences journals. Researchers often rely on MEDLINE for comprehensive literature searches.

From table 2 there are information about NCBI's Gene resources include several valuable components related to genes and their study. Gene Loci. This collection provides gene summary information, including links to clusters of expressed sequences. Researchers can explore details about specific genes, their chromosomal localization, and associated markers. It's a great starting point for understanding the function and context of individual genes. Nucleotide Gene and Transcript Sequences. Curated nucleotide sequences are available for various genes. These sequences serve as references and are essential for understanding gene structure and function. Homologs (HomoloGene) : HomoloGene offers sets of homologous genes across different organisms. Researchers can predict and study gene homologs, which are genes with similar functions in related species. Gene Expression (GEO Profiles) : GEO Profiles provide expression profiles for individual genes. Scientists can explore how gene expression varies across tissues, conditions, and developmental stages. Additional Resources : Taxonomy: Explore taxonomic classification and nomenclature related to genes. GenBank: Access the primary nucleotide sequence repository. RefSeq: Curated, non-redundant biological sequence sets. BioProject: A catalog of high-throughput genome-wide studies. BioSample: A sample repository linked to BioProject data. Clone : Genomic and cDNA clone repository. Probe : Sequence-based probe and primer repository. Tools : BLAST: Finds regions of local similarity between biological sequences. GEO2R: Identifies differentially expressed genes in GEO datasets. Map Viewer: Browses and displays genomic maps. ORF Finder: Suggests potential open reading frames in DNA sequences.

Table 3 and table 4 provides a comprehensive collection of resources related to proteins and genomes. Here are some key features of NCBI's Protein resources : **Protein Sequences** : The protein sequence repository includes protein sequences from various organisms. You can retrieve all protein sequences for a specific organism or taxon. Use the **BLASTp** tool for protein sequence similarity searches. Explore the **Protein Clusters** for sequence similarity-based protein clusters. **Functional Domains**. **Supporting Resources**. **Genome List** : The NCBI Genome resource includes information on large-scale genomics projects, genome sequences, and assemblies. It covers a wide range of organisms, including eukaryotes, prokaryotes, viruses, plasmids, and organelles. As of now, there are over 87,000 genomes available in the NCBI Genome database. **Genome Data Viewer (GDV)** : GDV displays biological information mapped to a genome, including gene annotations, variation data, BLAST alignments, and experimental study data from the NCBI GEO and dbGaP. Currently, GDV provides access to assemblies from more than 2,730 organisms.

Table 5 and Table 6 are the clinical resources available in the National Center for Biotechnology Information (NCBI)**.** ClinVar aggregates information about genomic variation and its relationship to human health. It provides data on variations, classifications, and their impact on health. ClinVar is a valuable resource for understanding the clinical significance of genetic variants. ClinicalTrials.gov **:** While not directly part of NCBI, ClinicalTrials.gov is a registry and results database for publicly and privately supported clinical studies involving human participants. It includes information about ongoing and completed clinical trials worldwide. Genome Data Viewer (GDV) :The NCBI Genome Data Viewer (GDV) is a genome browser that supports the exploration and analysis of annotated eukaryotic genome assemblies. GDV displays biological information mapped to genomes, including gene annotations, variation data, BLAST alignments, and experimental study data from NCBI GEO and dbGaP. Although GDV primarily focuses on genome data, it indirectly supports clinical research by providing insights into genomic variations.

CONCLUSION

The NCBI online describes various biological and biotechnology information on the *Pseudomonas aeruginosa*. The present work encouraged researchers in the biotechnology field to gain more benefits using the NCBI search engine.

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