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Abstract Topic:- Genetic, genome and epigenome databases and resources

Abstract Title:- From genetics to epigenetics, journey of GeMemiOM- the first curated database of Genes, putative Methylation targets and miRNA targets for Otitis Media

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Aims:-Otitis media (OM), the complex middle ear disorder onsets during childhood and recurs till it perplexes in susceptible patients leading to chronicity with disabling hearing loss. Though a complex disease, its epigenetic aspects are unexplored. Hence to provide open-access processed/annotated information and, prospect new avenues on genetic-epigenetic aspect on otitis media, GeMemiOM (<https://www.gememiom.org>) was established.

Methods:- Post literature survey, the OM associated gene set (80+genes) was subjected to enrichment analysis, these promoter sequences were extracted using the EPDnew-UCSC genome browser-dbSNP (v.151) default pipeline and were oriented/annotated for SNVs harbouring in the CpG islands (CGIs). The CGI status and transcription factor (TF) binding analysis was performed for all the reported alleles. Functional enrichment and interaction analyses were completed for the OM gene set using Genemania, HIPPIE, miRwalk and Reactome which were visualized by Cytoscape. The database was constructed using ReactJS v18.2.0, Tailwind CSS and FramerMotion v6.5.1 and is hosted at in-premises Ubuntu server v22.04 using NGINX v1.18. The scenario in the patient and control samples are being investigated.

Results:- The annotated promoter sequences from this database can be used for context specific methylation primer designing. SNVs harbouring in the CGIs were analysed, some of these SNVs, when altered from wild type, changed the status of CGIs existence (size change, splitting, and abolishment of CGIs) and were also found to create/abolish binding sites for important TFs which may affect the downstream pathways. The functional enrichment and interactions are represented as primary node-node interactions. The FDR filtered pathways are also hosted in the database. Every results can be viewed/downloaded in form of image or csv files by the users.

Conclusions:- GeMemiOM, a first of its kind database, provides a comprehensive dataset of OM associated genes with a possible implication of genetic/epigenetic perspective for the resolution of the disease. This distinctive database for otitis media provides the associated genes, putative methylation study targets (SNVs in CGIs and their possible impact on CGI status and TF binding), protein-protein interaction, co-expression, genetic interaction, miRNA targets, lncRNA-miRNA interactions and possibly involved pathways. This majorly aids the decision of candidate gene selection by researchers/clinicians studying various OM populations across the globe.

Keywords:- Otitis media, Short nucleotide variations, CpG islands, Transcription factor, miRNA, Database