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Genetic Variation And Relationship Of Three Dimensional Structure Like Human Liver, Evaluation Method Of Hepatotoxicity And Conjugate Like Human Liver

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Background : Genetic variation is an important force in evolution as it allows natural selection to increase or decrease frequency of alleles already in the population. Genetic disease is mostly caused by familiarity in the genetic code. DNA arrays capable of simultaneously measuring expression of thousands of genes in clinical specimens from affected and normal individuals have the potential to provide information about superior characteristics gene from organism. Genes can be used as markers for cell recruitment and activation molecules. This study aims to evaluate the variation and relationship of variation and relationship of three dimensional structure like human liver, evaluation method of hepatotoxicity and conjugate like human liver.

Methods : Data obtained from 8 nucleotide sequences of three dimensional structure like human liver, evaluation method of hepatotoxicity and conjugate like human liver sequence on secondary data form on https://www.ncbi.nlm.nih.gov/ and selected articles journal evaluated by searching in PubMed, EMBASE, and the Cochrane Library database that have been carried out in the last 5 years (2017–2021). The phylogeny analysis of variations and relationships of DNA sequences was inferred using the UPGMA method and the evolutionary distances were computed using the Maximum Composite Likelihood method using MEGA7 software.

Results : Based on the analysis of variations and relationships, it is known that on the dendogram, 8 sequences were divided into 2 main groups, namely groups A consisting of 7 specimens and groups B consisting of 1 specimens. The optimal tree with the sum of branch length = 7.53041418 is shown. The tree is drawn to scale, with branch lengths (next to the branches) in the same units as those of the evolutionary distances used to infer the phylogenetic tree. This grouping is based on the existence of a similar genetic makeup equation with a high bootstrap value indicating the degree of kinship between specimens and the strength of the philogenous trees. Specimens that are in the same sub–groups show a degree of close kinship. On the other hand, specimens from different sub–groupss display distant kinship. Grouping was achieved on the basis of differences in expression levels across individual specimens.

Conclusions : It can be concluded that the variation and relationship of three dimensional structure like human liver, evaluation method of hepatotoxicity and conjugate like human liver sequence have highly variation. Information about kinship can be used as an informative source to assembly of superior genes in living of human cells.

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