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Computational Profiling of Deleterious Non-Synonymous SNP's in *HFE*

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Abstract

Liver cirrhosis describes a condition where scar tissue gradually replaces healthy cells in liver. The main causes are sustained, excessive alcohol consumption, viral hepatitis B and C, and fatty liver disease - however, there are other possible causes. Hemochromatosis is most common form of iron overload disease. Three types of hemochromatosis are primary hemochromatosis, also called hereditary hemochromatosis; secondary hemochromatosis; and neonatal hemochromatosis. The *HFE* gene helps regulate the amount of iron absorbed from food and inherited genetic defects or mutation in *HFE* [C282Y] cause primary hemochromatosis. Computational approach is sought to determine other similar mutations in this gene. *In-silico* tools such as SIFT, Polyphen 2.0, and PROVEAN were employed to determine the various deleterious ns-SNPs of *HFE* that may influence cystic fibrosis.

Keywords: Cystic Fibrosis, HFE, ns-SNP's, In-silico analysis

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