Research Article
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In silico analysis of nsSNPs in *CYP19A1* gene affecting breast cancer associated aromatase enzyme

Honey Pavithran & Ranjith Kumavath

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Abstract

The human aromatase protein encoded by *CYP19A1* gene is the principle enzyme involved in the biogenesis of oestrogen in adipose tissues. An excessive exposure to endogenous oestrogen is regarded as an important determinant in the risk of breast cancer. Thus, in the present study we have used multiple computational methods to identify the most deleterious nonsynonymous SNPs in *CYP19A1* gene that caused probable genotypic–phenotypic alterations susceptible to breast cancer malignancy. In this study, a total of 338 nsSNPs were screened using 12 *in silico* tools including SIFT, PROVEAN, PolyPhene-2, SNAP2, I Mutant 3.0, MuPro, mCSM, PhD SNP, SNP&GO, P-Mut, Dr Cancer, and, CScape. Additionally the structural and functional consequences of missense mutations were validated using Consurf,