Commentary: Deciphering the association of intronic single-nucleotide polymorphisms of crystallin gene family with congenital cataract

Congenital cataract is an opacification in the crystalline lens and leads to *loss of transparency*, which cause blindness in the early stages of childhood.[1] This childhood cataract is highly prevalent in India.[2] It has been shown that congenital cataract is genetically heterogeneous and associated with genetic mutations in various human genes. Importantly, proteins are associated with crystallins, gap junction, cytoskeleton, and membrane transport channel, transcriptional regulation. Almost 360 human genes are accountable for the reason of nonsyndromic congenital cataract patients.[3] Noncoding introns are essential because it maintains the protein repertoire significantly through the regulation of alternative splicing.[4] Apart from genetic mutation, intronic single-nucleotide polymorphisms (SNPs) also the risk factor for disease susceptibility further implicated in genotype/phenotype correlation.[5] Due to genetic heterogeneity in congenital cataract disease, it is important to identify new genetic factors, which might be helpful for diagnosis and clinical management. Studies have shown the contribution of genetic factors in congenital cataract patients from Indian population.[6] Interestingly, this genetic study was carried out[7] in congenital cataract patients from Western India region. Ophthalmic examination or clinical evaluation of patients (141 congenital cataract and 107 healthy controls), enrolled in this study, was used an appropriate methods. Genetic association study of intronic SNPs [*CRYAA* (rs3788059), *CRYAB* (rs2070894), *CRYBA4* (rs2071861), and *CRYBB2* (rs5752083, 5996863)] was done in 141 congenital cataract and 107 healthy controls. The authors showed that "A" allele of rs3788059 (*CRYAA*) was linked to an increased risk of developing congenital cataract, whereas "G" allele was found to be protective (AA + AG vs GG; OR [95% CI]; 3.73 [1.71–8.15], $P = 0.0009$) using the dominant model. On the other hand, "A" allele of both rs2070894 (AA + AG vs GG; OR [95% CI]; 0.49 [0.29–0.84], $P = 0.012$) and (*CRYBB2*) rs5752083 (AA + AC vs CC; OR [95% CI] =0.25 [0.08–0.76], $P = 0.016$) were shown to have a protective function by using the dominant model. Additionally, haplotype analysis of A-C-T (rs2071861, rs5752083, and rs5996863) was a predominant risk factor involved in the development of congenital cataract patients. This study may be hampered due to limitations of sample size, but increasing large cohorts and meta-analyses might help to reach the strong statistical significance or overcome the study limiting factors. Altogether, the study concludes that genetic predisposition of noncoding SNPs in crystallin genes was associated with the development of congenital cataract in Western India region.

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Conflicts of interest

There are no conflicts of interest.

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