

EVALUATION OF THE SINGLE NUCLEOTIDE POLYMORPHISM'S IN KIAA GENE CONTRIBUTING TO DYSLEXIA SUSCEPTIBILITY IN SOUTH INDIAN POPULATION

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ABSTRACT

INTRODUCTION: Dyslexia is a hereditary neurological disorder that manifests as an unexpected difficulty in learning to read despite adequate intelligence, education, and normal senses. The prevalence of dyslexia ranges from 3 to 15% for the school aged children.

BACKGROUND: Studies in different populations have established associations between Dyslexia and single nucleotide polymorphisms (SNPs) in a number of candidate genes like DYX1C1, KIAA0319. Very few studies are done in India.

METHODS: 100 dyslexic individuals and 100 controls in the age group between 6 to 11 years were taken. 13 SNPs in KIAA gene were analyzed by Mass Array technique.

RESULTS: The Male predominance was noted in dyslexia cases (P value <0.0001) in the Telangana population. There is significant association of dyslexia with increase in unconjugated bilirubin levels (in the first 3 weeks of life) with P value of <0.0001. Allelic association of 13 SNPs in KIAA gene was done. The association of dyslexia with SNPs rs 3756821, rs 6935076, rs 4576240 was found significant with P value.

CONCLUSION: The present study is the first study on the genetic markers (SNPs) associated with dyslexia in the state of Telangana and the second study in India. The importance of this study is that 100 dyslexic children and 100 controls are taken which has given a statistically significant association with SNPs of KIAA gene. Since dyslexia is a major educational problem, there is a need for detailed genetic analysis to find out the genes in the ethnic population which are responsible for dyslexia.

KEYWORDS: Evaluation of the Single Nucleotide Polymorphism's

INTRODUCTION

LANGUAGE is a unique human gift. It is a complex process that enables communication and social functioning. Language gave humans an increased chance of survival thus giving the humans an enormous edge over others [1]. Most children acquire language naturally in the sequence of listening, speaking, reading and writing. Failure in any of these processes may lead to lifelong socioeconomic and mental health consequences [2].

Dyslexia is a difficulty in learning to read and spell despite adequate education, intelligence and socio-cultural

opportunities and without any obvious sensory deficits [3]. Dyslexia accounts for 80% of learning disabilities. Prevalence of the trait ranges from 3 to 17.5% of school-age children [3]

Hormonal factors such as fetal testosterone levels during late pregnancy may play a critical role and this is possibly reflected in the large male predominance of dyslexia boys [4] more often than girls are affected by all the cognitive developmental disorders of childhood. Dyslexia has a complex link with immune diseases and sex hormones especially with testosterone [5].

The incidence of neurological, allergic, and immune reactive conditions such as dyslexia, allergies, asthma, eczema, psoriasis, childhood diabetes, etc. have been increasing rapidly in recent years [6]. A report by the National Research Council in 2000 found that 50% of all pregnancies in the U.S. were resulting in prenatal or postnatal mortality, significant birth defects, developmental disabilities or otherwise chronically unhealthy babies. Recent studies published in JAMA report (JAMA, 2007, Jun 27, pg 297(24)) found similar trends continuing with huge increases in children's chronic conditions.

Incidence of chronic developmental conditions in infants more than doubled between 1988 and 2006, especially asthma, learning and behavioral problems, and obesity. There has been a similar sharp increase in developmental disabilities in Canadian children over the last 2 decades (CICH; 2000), including learning disabilities and behavioral problems, asthma and allergies, and childhood cancer. Studies have documented that the primary cause of the increased developmental conditions are increased toxic exposures, including increased use of vaccines with toxic and inflammatory ingredients (Windham).

Pushpa savior et al 2009, showed that Allergy, migraine, delayed milestones, low level of blood cholesterol and certain fatty acid deficiency signs were found to be associated with dyslexia. Since complex array of symptoms are associated with dyslexia an integrated research approach is needed for effective diagnosis and remediation of dyslexia.

Based on the literature kernicterus and high levels of unconjugated bilirubin affects the basal ganglia and the formation of astrocytes, and possibly also the hippocampus, the thalamus and central parts of the cerebellum. The hippocampus has important functions in the storing of new information in forms that can be used in long-term memory. Damage to the left region of the hippocampus impairs verbal memory in all its modalities.

Impaired formation of astrocytes associated with high levels of unconjugated bilirubin should be considered as an etiological factor in poor memory. It is recommended that pediatricians should suggest early screening procedures to infants at risk. With early screening for possible deficiencies of attention, memory, and visual-motor integration functioning as well as intervention programs the learning difficulties can be addressed and remediation started earlier in life (10.1080/03004430212714 E. Pretorius^a, H. Naude^b & P. J. Becker^c pages 391-404)

Evidences for origin of dyslexia have been increasingly accumulating during the last two decades. Although multiple etiologies are proposed for this complex trait, the exact cause still remains unknown; but substantial evidence from genetic and neurological studies suggests that dyslexia is a disorder which is influenced by genetic factors and the underlying deficit is in the language areas of the brain. Many theories are put forward to explain the etiology of dyslexia.

Twin studies have shown a concordance rate of 68% in monozygotic twins versus 38% in dizygotic twins [7]. An autosomal dominant pattern of inheritance of dyslexia has been hypothesized in families collected in southern India. [8]. [9], performed a genome scan with 320 markers showing a novel dominant locus linked to dyslexia in the

pericentromeric region of chromosome 3 with a multipoint lod score of 3.84. Nineteen out of 21 affected pedigree members shared this region identical by descent (corrected $p < 0.001$).

Numerous candidate genes have emerged from genetic association studies and the characterization of chromosomal translocations in individuals with Dyslexia, including DYX1C1 on 15q21 [10], ROBO1 on 3p12 [11] DCDC2 [12] and KIAA0319 [13] on 6p22, and MRPL19 and C2ORF3 on 2p12 [14]. Several of these genes have been implicated in brain development [15]. In particular, RNAi-knockdown studies suggest that DYX1C1 [16], DCDC2 [12], and KIAA0319 [17] play a role in neuronal migration during the development of the rat cortex. Interestingly, altered neuronal migration has been implicated in Dyslexia based on the only post-mortem anatomical study conducted to date [15]; specifically, the brains of dyslexic individuals were found to have subtle structural anomalies consistent with defective neuronal migration.

In individuals with dyslexia, Francks et al. (2004) found an association between dyslexia and a 77-kb region on chromosome 6p22.2 spanning the TTRAP gene (605764) and the first 4 exons of KIAA0319. One main risk haplotype (1-1-2) for reading disability (frequency of approximately 12%) was found in both U.K. and U.S. samples: the 1-1-2 haplotype comprised rs4504469, rs2038137, and rs2143340.

Cope et al. (2005) found that 6 SNPs in the 6p22.2 region showed significant evidence of association with dyslexia, including a SNP in exon 4 of the KIAA0319 gene that changed an amino acid (A311T, rs4504469). Haplotype data implicated KIAA0319 as a susceptibility gene for dyslexia.

Paracchini et al. (2006) noted that reading disability may be related to irregularities in neuronal migration, and suggested that down regulation of KIAA0319 may be a susceptibility factor in the development of dyslexia when combined with other genetic and environmental factors. KIAA0319 has turned out to be involved with controlling the early development of the brain. It may also underlie the unfortunate tendency of the immune system of dyslexics to cause allergies, eczema etc.

Silvia Paracchini *et al.*, (2006) identified a risk haplotype associated with dyslexia on chromosome 6p22.2 which spans the TTRAP gene and portions of THEM2 and KIAA0319.

A pathophysiological correlates of dyslexia of the candidate genes discussed to date, shows the most convincing evidence for DCDC2 and KIAA0319 on chromosome 6. With DCDC2, as with KIAA0319, inhibition leads to poorer neuronal migration in the neo cortex of fetal rats through specific small interfering RNAs (Meng *et al.*, 2005 Parachini *et al.*, 2006).

Megan et al 2009, showed that (1) a dyslexia associated haplotype has been implicated in the reduced expression of KIAA0319, and (2) the strongest association has been found for the region spanning exon 1 of KIAA0319. The variant(s) responsible for reduced KIAA0319 expression resides on the risk haplotype close to the gene's transcription start site. Seven single nucleotide polymorphisms on the risk haplotype immediately upstream of KIAA0319, were determined that three of these are strongly associated with multiple reading-related traits.

Megan Y. Dennis et al 2009, functionally characterized one such gene (KIAA0319) to identify variant(s) that might affect gene expression and contribute to the disorder. They discovered a variant residing outside of the protein-coding region of KIAA0319 that reduces expression of the gene. This variant creates a binding site for the transcription factor OCT-1. In this case, reduced KIAA0319 expression could lead to improper development of regions of the brain

involved in reading ability. This is the first study to identify a functional variant implicated in dyslexia.

Using luciferase-expressing constructs containing the KIAA0319 upstream region, Adrienne Elbert et al 2011, characterized the minimal promoter and additional putative transcriptional regulator regions. This revealed that the minor allele of rs9461045, which shows the strongest association with dyslexia in the sample (max pvalue = 0.0001), confers reduced luciferase expression in both neuronal and non-neuronal cell lines.

Adrienne Elbert et al 2011, found several putative functional variants including a microsatellite (JA04) and rs71815143, of which JA04 showed evidence for association to Dyslexia. The microsatellite may create risk for Dyslexia by transitioning from B to Z-DNA, which can increase or decrease gene expression, depending on the gene context.

T. M. Centanni et al, 2013 results provide the first evidence that decreased expression of the dyslexia-associated gene KIAA0319 can alter cortical responses and impair phoneme processing in auditory cortex.

Shyamala K , venkatesh et al 2011, screened twenty SNPs located within the coding region of these three candidate genes (KIAA, DCDC2, DYX1C1) by mass ARRAY technique. At this point, there was no statistical evidence of association between the allelic variation in the three candidate genes and Dyslexia in the sample.

Venkatesh SK et al 2013, has showed the most consistent evidence of linkage for Dyslexia and two susceptible genes KIAA0319 and DCDC2 at DYX2 locus which showed significant association. Specific candidate gene-association studies have identified variants, risk haplotypes and microsatellites of KIAA0319 and DCDC2 correlated with wide range of reading-related traits. In this study, a case-control approach for analyzing single-nucleotide polymorphisms (SNPs) in KIAA0319 and DCDC2 was done. The study demonstrated the association of Dyslexia with SNP rs4504469 of KIAA0319 and not with any SNPs of DCDC2.

Even though interest and knowledge about dyslexia is increasing, decades of multidisciplinary research in this area in different parts of the world does not provide proper diagnostic criteria. In this regard, genetic analysis promises some insights into the problem. Several phenotypes have been found in dyslexia, but the etiological link between these related phenotypes and genotype is yet to be established. Much study is needed in this area to prove a definitive relationship between phenotype and genotype of dyslexia. Thus, isolation and analysis of the genetic variants will initiate a new phase of research which will provide a more fundamental understanding of the nature of dyslexia, eventually leading to early diagnosis, risk estimation, better methods of treatment and prevention.

Dyslexia is a major educational problem in our country and its wide presence has to be acknowledged and dealt with. Pupils with dyslexia are generally ignored and passed unnoticed in schools, until they become dropouts or delinquents. There is a great dearth of proper statistical data to show the incidence of dyslexia among pupils in India. No substantial and significant research work has been undertaken in our country in this regard.

If this area is neglected any more, our country may face a high dropout rate of pupils at the elementary stage of education. There should be implementation of legislation in the country to take utmost care of these children, because dyslexia is an invisible handicap.

So far, no studies have been conducted in Telangana population, regarding the association of four candidate genes for Dyslexia. Except, for one study from India (Pushpa Saviour *et al.*, 2008), who have conducted a study regarding the association of KIAA gene with only 50 Dyslexia cases (not statistically significant). They found a negative

association for this gene. Our study will be the first of its kind in India to carry out screening of SNPs in statistically significant number of 100 for Dyslexia. This will identify the Single Nucleotide Polymorphisms which are associated with Dyslexia.

The present study also shows the association of dyslexia with allergy, eczema and increased unconjugated bilirubin. This study is the first of its kind to find the association of dyslexia with increased unconjugated bilirubin.

The present study may reveal the complex molecular mechanisms behind the development of the brain and lead to new treatments in the future.

METHODOLOGY

Study Subjects

The study samples were selected from the Department of Child Psychiatry, Niloufer Hospital & Institute of Child and Health, Hyderabad. With the help of psychiatrists and psychologists 103 samples and 100 control samples have been selected for the study subject. All the samples and controls are matched with age and sex. All the affected individuals were assessed by the psychiatrist and psychologist by taking clinical history, family history and age at diagnosis. Also consent of each individual (parent) has been taken in the prescribed format for the study. Care was taken to avoid population admixture and only unrelated subjects from Indian origin was considered for the study.

INCLUSION CRITERIA

Dyslexic subjects were selected based on the following criteria: Age between 6-15 years, IQ >90, Discrepancy between ability and achievements, IQ test (Binet Kamath); Malin's Intelligence Scale for Indian children (MISIC)

Diagnostic criteria based on DSM IV-R criteria for reading and spelling was followed. Schonell's Graded word reading ability test, Schonell's Graded word spelling test were done.

Exclusion Criteria

Acquired Dyslexia, Dyscalculia, Dysphasia (articulation difficulty), Speech sound disorder (SSD), Specific language disorder (SLI), Mental retardation due to birth trauma, epilepsy and infections, like meningitis and encephalitis

Emotional, environmental and educational causes were excluded.

Controls

Controls were collected from Niloufer Hospital, children in the age group of 6 to 15 years without learning difficulty.

Measurement of Clinical and Biochemical Variables

History of birth weight, swallowing of meconium, birth cry delay, nausea and vomiting during pregnancy was taken. History of unconjugated bilirubin levels (cases with values between 10 -15 mg/ dl) after birth to 3 weeks was taken. History of phototherapy given was taken. History of allergy and eczema in the first 3 years was taken.

DNA was extracted from EDTA anticoagulated whole blood by Quiagen Blood DNA Extraction Kit. The quantity and purity of each sample were determined by ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, USA). After quantitation, the genomic DNA was diluted in to a concentration of 20 ng/ L in 96 well plate for all mass array

(Sequenom) based genotyping.

Genotyping was performed using Sequenom's newly developed genotyping assay termed iPLEX Gold chemistry (www.sequenom.com). Briefly, the assay consists of an initial locus-specific PCR reaction, followed by single base extension using mass-modified dideoxynucleotide terminators of an oligonucleotide primer which anneals immediately upstream of the polymorphic site of interest

The MassARRAY Designer software can automatically design both PCR and Mass EXTEND primers for multiplexed assays. The software checks for and avoids primer combinations and non-template extension products that could possibly result in nonspecific extension. Briefly the flanking sequence (FASTA file) was retrieved from <http://www.ncbi.nlm.nih.gov/snp/> and the input FASTA file includes 500 base pairs of specific genomic sequences, 250 upstream and downstream from the SNP of interest.

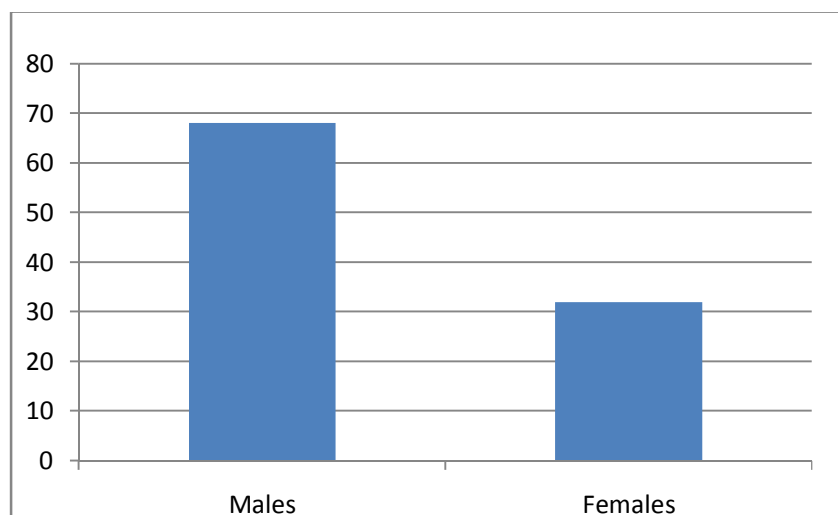
The mass array genotyping involve the following steps a) Assay Design b) PCR Amplification, c) SAP Treatment, d) iPLEX Reaction, e) Clean Resin, f) Dispensing to SpectroCHIP and g) MALDI-TOF MS Analysis.

RESULTS

The present study included 103 Dyslexic subjects and 100 controls. The gender wise association with dyslexia, is done in the study. Association with unconjugated bilirubin levels and allergy is done statistically. The results of the molecular study in the patients are presented. The association analysis was carried out in this study by using Chi-square test and odd's ratio.

Table 1: Showing the Gender Distribution in Dyslexia

Cases male	Cases Female	p-value
68	32	<0.0001



The above table shows the gender distribution in dyslexia. The number of male cases is significantly high in dyslexia

Table 2: Showing Increased Unconjugated Bilurubin Levels (Upto 3 Weeks of Birth)in Cases & Controls

	Cases (103)	Controls (100)	Z Test (p-value)
Unconjugated bilurubin levels(10-15 mg/dl)	29(29%)	6(6%)	4.28 (<0.0001)

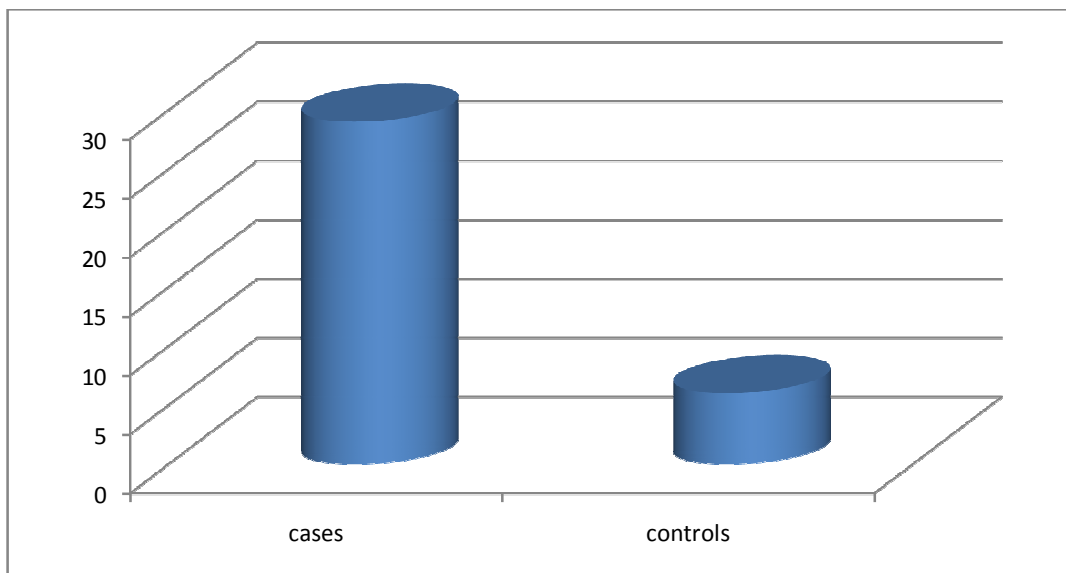


Table showing the unconjugated bilirubin levels in cases and controls in the first 3 weeks of neonatal period. This shows that there is significant association of dyslexia with increased unconjugated bilirubin levels.

Table 3: Showing History of Allergy in Cases & Controls (< 3 Years of Birth)

	Cases (100)	Controls (100)	Z Test (p-value)
History of allergy (< 3 Years of Age)	41(41%)	10(10%)	5.02 (<0.0001)

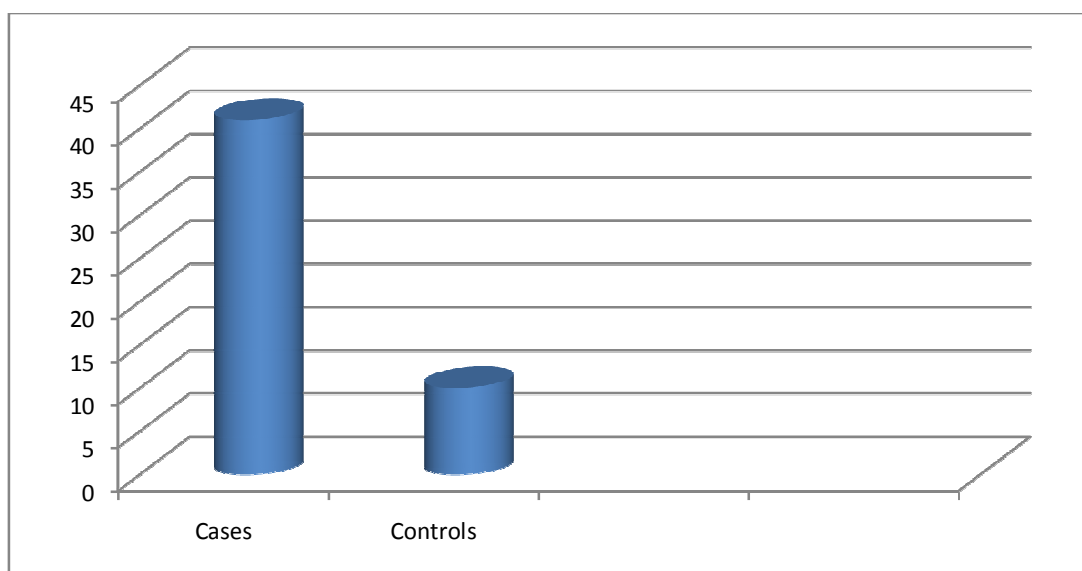
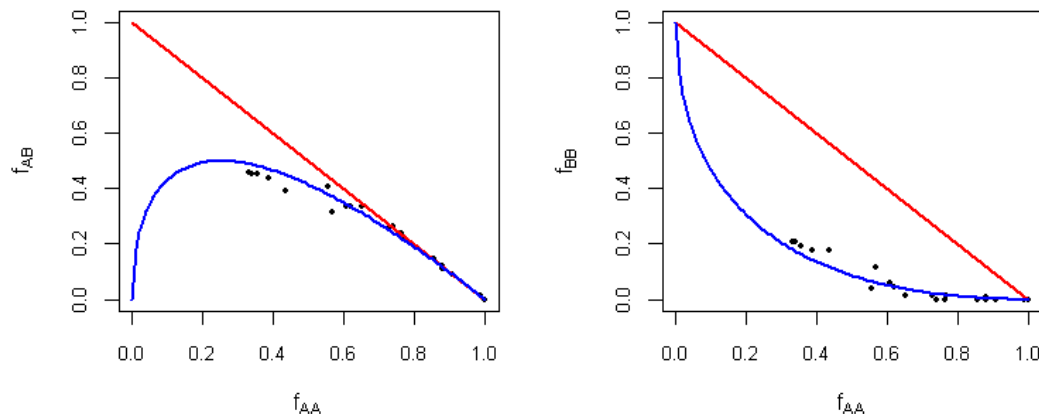
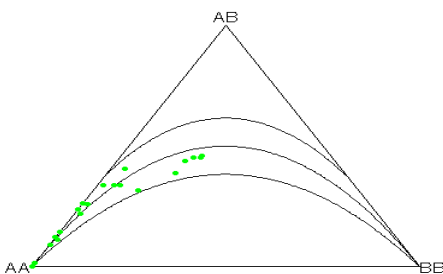


Table showing the history of Allergy level in cases and controls in the first 3 Years of Birth. This shows that there is significant association of dyslexia with history of allergy.

HARDY WEINBERG



The above graphs are scattered plots which help to explore the relationship between genotype frequencies, such as f_{AB} versus f_{AA} or f_{BB} versus f_{AA} . In these scattered plots, genetic markers tend to follow a particular curve described by the Hardy-Weinberg law (blue curve). If there are any markers that do not fall in HW equilibrium, they are shown by red points. Both the plots generated from the sample dataset indicate that SNPs fall closely around HWE curve.



The above plot is the ternary plot it is an information-rich graphical display, which helps to recover genotype frequencies, allele frequencies, and infer the equilibrium status of a genetic marker at a glance. The HWE condition and acceptance region for chi-square test are shown as parabolas in the plot. Markers deviating from HWE are shown with red points. In the ternary plot generated from the sample dataset, all the SNPs fall closely around HWE parabola within the acceptance region i.e. p-value of 0.001.

Allele Frequencies

SNP	GENES	A1	A2	MAF	NCHRO BS	Chromosome	chromo position	aa_change
rs2143340	KIAA0319	C	T	0.2122	410			
rs2744550	KIAA0319	0	T	0	410	chr6	24576631	558
rs2744559	KIAA0319	0	C	0	410	chr6	24576631	522
rs28501680	KIAA0319	0	G	0	410			
rs3212236	KIAA0319	G	A	0.4366	410	chr6	24648455	

rs3756821	KIAA0319	A	G	0.2756	410	chr6	24646821	
rs4576240	KIAA0319	T	G	0.04634	410	chr6	24596472	133
rs807535	KIAA0319	C	T	0.07317	410	chr6	24551729	982
rs807541	KIAA0319	C	T	0.2415	410	chr6	24559281	889
rs9461045	KIAA0319	T	C	0.439	410	chr6	24649061	
rs9467247	KIAA0319	A	C	0.4171	410	Chr6	26467219	

A1	Minor Allele
A2	Major Allele
MAF	Minor Allele Frequency
NCHROBS	Non-missing allele count

This table indicates the frequency of minor allele calculated from the samples considered in the study.

Zero MAF value indicates the presence of only one allele in the entire set of samples. SNPs with MAF < 0.01 can be deleted from further analysis (highlighted in red).

ALLELIC ASSOCIATION

Genes	SNP	A1	F_A	F_U	A2	OR	L95	U95	CHISQ	P	FDR_BH	
KIAA0319	rs3212236	G	0.4429	0.43	A	1.054	0.713	1.557	0.0688	0.793	0.9066	
KIAA0319	rs3756821	A	0.3429	0.205	G	2.023	1.295	3.161	9.751	0.0018	0.03353	*
KIAA0319	rs4576240	T	0.0714	0.02	G	3.769	1.229	11.56	6.131	0.0133	0.0631	*
KIAA0319	rs6935076	T	0.2857	0.165	C	2.024	1.254	3.267	8.512	0.0035	0.03353	*
KIAA0319	rs807534	C	0.0714	0.06	T	1.205	0.5496	2.642	0.2175	0.641	0.9066	
KIAA0319	rs807535	C	0.0714	0.075	T	0.9487	0.4511	1.995	0.0193	0.8896	0.9066	
KIAA0319	rs807541	C	0.2143	0.27	T	0.7374	0.4683	1.161	1.736	0.1876	0.4456	
KIAA0319	rs9461045	T	0.4429	0.435	C	1.032	0.6988	1.525	0.0257	0.8727	0.9066	

A1	Minor allele name (based on whole sample)
F_A	Frequency of minor allele in cases
F_U	Frequency of minor allele in controls
A2	Major allele name
OR	Estimated odds ratio (for A1, i.e. A2 is reference)
L95	Lower bound of 95% confidence interval for odds ratio
U95	Upper bound of 95% confidence interval for odds ratio
CHISQ	Basic allelic test chi-square (1df)
P	p-value of chi-square test
FDR_BH	Benjamini & Hochberg FDR Corrected p-values

The table shows Allelic association between cases and controls. OR are calculated for minors alleles with reference to the major alleles. SNP's which Odd's Ratio >1.2 are highlighted in Red.

SNP's with FD adjusted P value for chisquare <0.1 are marked. There are 3 SNP's which are significant, highlighted in Red

GENOTYPIC DISTRIBUTION

SNP	A1	A2	TEST	CASES	CONTROLS	CHISQ	P	FDR_BH
rs3756821	A	G	GENO	18/36/51	6/29/65	8.327	0.01556	0.09336
rs4576240	T	G	GENO	0/15/90	0/4/96	NA	NA	NA
rs6935076	T	C	GENO	12/36/57	0/33/67	NA	NA	NA
rs807534	C	T	GENO	0/15/90	2/8/90	NA	NA	NA
rs807535	C	T	GENO	0/15/90	0/15/85	NA	NA	NA
rs807541	C	T	GENO	3/39/63	5/44/51	NA	NA	NA
rs9461045	T	C	GENO	24/45/36	19/49/32	0.8655	0.6487	0.7602
rs3212236	G	A	GENO	24/45/36	19/48/33	0.6871	0.7093	0.7602
rs9467247	A	C	GENO	21/45/39	18/48/34	0.5484	0.7602	0.7602

SNPs with FDR_BH less than 0.1 can be considered as significantly associated with the disease (denoted with *)

This table shows the Genotypic distribution between affected & Controls. The Genotypes are compared and P Value significant for rs 3786821

For Example

For the SNP's Rs 3756821, the distribution of genotypes in cases and controls is given below

The conclusion from the above table for the SNP's Rs 3756821, is that there is significant genotypic association between Dyslexia cases and controls.

	Cases	Controls
AA	18	6
AG	36	29
GG	51	65

DISCUSSIONS

The present study showed a male preponderance for dyslexia with significant P – value in 100 dyslexic individuals from the state of Telangana. This is the first study with statistical evidence to show the male preponderance in the state of Telangana.

The present study shows association of allergy and eczema in the first 3 years of life with dyslexia (p value < 0.0001) . This study also correlates with the only Indian study done on 50 dyslexic patients by Pushpa savior et al 2009, which showed that Allergy, migraine, delayed milestones, low level of blood cholesterol and certain fatty acid deficiency signs were found to be associated with dyslexia. Since complex array of symptoms are associated with dyslexia an integrated research approach is needed for effective diagnosis and remediation of dyslexia.

The present study was done on 100 dyslexic individuals in the state of Telangana and statistical association was found between history of allergy and dyslexia.

In the present study an association of dyslexic cases with increased unconjugated bilirubin (first 3 weeks of birth

in the range of 10 to 15 mg/dl) was found to be significant with p value of <0.001. The present study is the only study which shows the positive association of increased unconjugated bilirubin levels with dyslexia worldwide .

The present study is the first study on the genetic markers (SNPs) associated with dyslexia in the state of Telangana and the second study in India..

In the present study 13 SNPs from KIAA0319 gene (rs 2744559, rs 28501680, rs 28501680, rs2744550, rs6935076, rs807534, rs9467247, rs10946705, rs807541, rs3212236, rs4576240, rs9461045, rs807535) were analysed. Significant association was found with SNPs rs 3756821, rs 6935076, rs 4576240 and dyslexia .

Linkage disequilibrium showed, that the significant SNPs rs 6935076, rs 3756821 are linked together.

Shyamala K Venkatesh et al 2011, analysed 20 coding SNPs located within the three candidate genes KIAA0319, DCDC2, DYX1C1 and found no association. but this study was done on only 50 dyslexics which is not statistically significant and the study does not fall in the Hardy Weinberg equilibrium. Whereas the present study has 100 dyslexic individuals and 100 controls which is statistically significant. The present study falls in the Hardy Weinberg equilibrium.

The present study is the first study on the genetic markers (SNPs) associated with dyslexia in the state of Telangana and the second study in India. The importance of this study is that 100 dyslexic children and 100 controls are taken which has given a statistically significant result unlike the first study from Mysore which had only 50 dyslexic children and Hardy Weinberg equilibrium is not mentioned.

Since dyslexia is a major educational problem, there is a need for detailed genetic analysis to find out the genes in the ethnic population which are responsible for dyslexia . This will in turn provide simple diagnostic tools to ease the clinicians for early diagnosis of the disorder and treatment. An attempt is made to verify whether allelic variants of *candidate genes* are responsible for dyslexia in 100 dyslexic children of Indian population.

Because SNPs are inherited and do not change much from generation to generation, analysis of SNPs is essential for finding genes that predispose people to more common conditions in which inheritance patterns are complex . This will have a wide range of applications for developing diagnostic, therapeutic, and preventative strategies.

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