



Received on 09 September 2022; received in revised form, 11 November 2022; accepted 18 November 2022; published 01 June 2023

IMPACT OF GENETICS IN NEURODEVELOPMENTAL DISORDERS

Aritraa Das, Sutripto Ghosh and Tamalika Chakraborty *

Department of Biotechnology, Guru Nanak Institute of Pharmaceutical Science and Technology, 157/F, Nilgunj Rd, Sahid Colony, Panihati, Kolkata - 700114, West Bengal, India.

Keywords:

Neurodevelopmental Disorders,
Neuropsychotic Development,
Orthologous Genes

Correspondence to Author:

Ms. Tamalika Chakraborty

Assistant Professor,
Department of Biotechnology, Guru
Nanak Institute of Pharmaceutical
Science and Technology, 157/F,
Nilgunj Rd, Sahid Colony, Panihati,
Kolkata - 700114, West Bengal, India.

E-mail: tamalika.chakraborty@gnipst.ac.in

ABSTRACT: A category of illnesses known as neurodevelopmental disorders is predominantly linked to neurodevelopmental dysfunctions. The two most prevalent neurodevelopmental disorders, “Attention Deficit/Hyperactivity Disorders (ADHD)” as well as “Autism Spectrum Disorders (ASD)”, affect both humans and lower-class species like rats, mice and zebra fish. The purpose of this review is to identify the behavioral changes brought on by certain Neurodevelopmental disorders-Risk genes, such as CHD8, SHANK3, LPHN3, SLC6A3, *etc.*, and to summarize their genetic screening and epidemiological researches, which directed various neurodevelopmental disorders in various organisms brought on by the interaction of genetic and environmental factors, as well as their genetic screening, which can be used to identify those diseases in humans by this orthologous gene that are present in humans. The majority of genes linked to neurodevelopment disorders were shown to have an excess of de novo mutations (DNMs), but case-control mutation burden research has not been able to prove their importance. We could identify the behavioral anomalies caused by these genes in different species for the development of neuropsychotic disorders by integrating the published scientific data. We have indeed been able to include the several genetic tests available to diagnose the diseases, as well as the various newly discovered genes that cause ADHD and ASD.

INTRODUCTION: Neurodevelopmental disorders (NDD) are primarily linked to the brain's and nervous system's dysfunction⁵⁻⁸. Changes in communication, behavior, cognition and/or motor function during development characterize this group of illnesses. These are clinically and etiologically diverse disorders that are seen in infancy, childhood and adolescence as a sign of altered brain development.

“Attention Deficit/Hyperactivity Disorders (ADHD)”, “Autism Spectrum Disorders (ASD)”, learning challenges, and intellectual impairments in vision and hearing are examples of NDDs in children¹⁻³. Children who are afflicted by these illnesses may experience difficulty with their motor abilities, behavior, memory, learning, and other brain functions.

According to survey research, it is the most common pediatric serious medical illness that typically affects children aged 3 to 17 around the world². The vast majority of these patients have been classified as having neurodevelopmental disorders, which include ADHD, ASD, Fragile X syndromes, cerebral palsy, global developmental delays (GDD), seizures, stuttering or stammering,

QUICK RESPONSE CODE 	DOI: 10.13040/IJPSR.0975-8232.14(6).2658-69
	This article can be accessed online on www.ijpsr.com
DOI link: http://doi.org/10.13040/IJPSR.0975-8232.14(6).2658-69	

etc. in the “Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition”². Each of these illnesses is defined by a certain set of characteristics. While ADHD patients often exhibit hyperactivity and impulsivity along with a decreased attention span, ASD is defined as impaired sociability along with communication problems in addition to repeated activities⁶. Neurological studies have shown that ASD is associated with changes in various neuronal types, including glutamatergic, GABAergic, and aminergic neurons as well as reduced glycine sensitivity. These changes can affect the cerebellum, temporal lobes, hippocampus, and frontal lobes, among other brain regions⁶. Contrarily, it has been shown that dopamine, noradrenaline, and signaling are hampered in ADHD in the prefrontal cortex, striatum, and cerebellum⁶. When it comes to neurological developmental issues, genes can be very essential. It has been discovered that a particular collection of genes, such as CHD8⁹, Multiple Ankyrin Repeat Domain Protein 3 (SHANK3)¹⁰⁻¹², LPH3³⁸, SLC6A3³⁶, etc., are to blame for some specific situations, such as intellectual impairments, Autism, and ADHD. These genes are orthologous genes that may be found in various species, and

they serve the same function in the human body in addition to many lower-class organisms including zebrafish, mice, and rats, among others. This gene normally regulates neuropsychiatric processes and brain activity, but when a mutation occurs in one of its several areas, it takes on the role of an antipsychotic regulator. For instance, a mutation (CGG repeat expansion) in the fragile X mental retardation gene FMR1, which is situated on the X chromosome, causes the hereditary neuropsychiatric disorder known as fragile X syndromes⁸. In addition, Down's syndrome, which is brought on by a trisomy of chromosome 21, is the most well-known NDDs. These genes are therefore referred to as NDDs-risk genes since they can lead to NDDs in a variety of species⁸. As a result, various genetic, neurological, psychological and environmental risk factors are linked to these illnesses⁸. Effect of different genes responsible for autism spectrum disorder and their phenotypic expression in various organisms. Our next goal is to identify the several genes involved in ASD as well as their phenotypic manifestation in various organisms. In various organisms, a certain gene exhibits phenotypic expression. A list of these genes can be found in **Table 1**.

TABLE 1: EFFECT OF AUTISM SPECTRUM DISORDER RISK GENES ON DIFFERENT ORGANISMS AND THEIR PHENOTYPIC EXPRESSION

Name of ASD-risk Genes	Effected organisms	Phenotypic expressions in various organisms
CHD8 ^{9,59,60}	Human	Sleep issues, a speech delay, distinctive facial traits, and macrocephaly
	Mice	Deformities of the face and skull, impairments associated with learning and memory, and macrocephaly
	Zebra Fish	Complications associated with gastrointestinal motivity along with increase in the overall head size as a result of growth of frontal or midbrain
CNTNAP2 ^{21,22,27}	Zebra Fish	Deficits in GABAergic transmission, especially in the frontal region of the brain, and vulnerability to drug-induced convulsions
	Mouse	Abnormal neural development, diminished GABAergic neurons, unprovoked convulsions, restlessness, social impairments, and an increase in repetitive behavioral tendencies
	Human	Delays in speech and language, linguistic impairment, mood changes, distress, and recklessness
SHANK ^{11,19,20}	Human	Hypotonia, general developmental retardation, significant speech and language impediment, and behavior related to autism.
	Zebra Fish	Rise in developmental anomalies, an increase in atypical tail bending, a weakened sense of social choice, an increase in swimming behavior, and a general drop-in fish locomotor activity.
	Mouse	Decreased scent marking, elevated anxiousness, and hampered nesting
DYRK1A ^{14,23,24}	Zebra Fish	Reduction in forebrain size along with diminished midbrain activity
	Mouse	Increased hyperthermia-induced convulsions as well as significant cognitive difficulties, impairment of ultra - sonic vocalizations

TBR1 ^{25,26,61,62}	Human	utilized for communication, and social interactions Usual facial gestalt, feeding difficulties, seizures, muscle rigidity, gait abnormalities, foot abnormalities, and intellectual deficits such as delayed speech, anxiousness as well as stereotypical behavioral issues, and microcephaly
	Zebra Fish	More daytime activity compared to other fish used as a comparison.
	Mice	Reduced social interaction, a modest rise in anxiety-related behavior, and increased self-care

The various common genes responsible for ASD in several model organisms are identified and enlisted in **Table 1**. The next progressive objective of this review to comprehend and address the unresolved

queries is to find the numerous tests that are available for the detection and characterization of ASD in different model organisms.

TABLE 2: GENETIC TESTS TO DETERMINE ASD IN MODEL ORGANISMS

Genetic test	Organism	Test Description	Behavior for ASD	Behavior for no ASD
Test to determine social interactions ^{67,68}	Mouse	Comparing a mouse's preference for an object or another mouse	Preference shown for object	Preference shown for Mouse
Test to determine preference for social novelty ^{67,68}	Mouse	Contrasting a mouse's preference for a familiar mouse and another new mouse	Preference shown for familiar mouse	Preference shown for new mouse
Ultrasonic vocalization test ^{67,68}	Mouse	Mice use their ultrasonic vocalizations to find their young and other family members and detecting them by placing a microphone inside the cage	No Ultrasonic Vocalization detected	Ultrasonic vocalizations detected
Self grooming ⁶⁹	Mouse	Calculating the selfgrooming time of mice.	Repetitive grooming lasting for more than two minutes	Grooming not lasting for more than ten seconds
Olfactory Senses of a mouse as a tool for socialization ⁷⁰	Mouse	By sensing the unique urine pheromones of other mice, mice can mark their territory and identify their mate for mating. A cotton swab carrying the urine pheromones of other mice inside the mouse's cage	As evidence of the impaired socializing abilities in ASD, mice prefer not to sniff following novel odors	Mice often sniff new smells as a sign of social interaction or emit pheromones to find a mate or mark their territory
Assessment of social interaction ⁶⁷	Zebra Fish	Three sections of a fish tank are separated from one another, and all three sections are transparent. Two of the tank's compartments are filled with two different kinds of zebrafish, while the third is left vacant. The target fish was compared to a group of zebrafish and a single zebrafish using the same setup. They were both distinct species from the fish that was the target	The center compartment's zebra fish swims toward the vacant compartment and prefers to remain there rather than moving toward the chamber containing the other fish. The fish of interest swam toward the individual fish or avoided swimming toward any of the compartments	The central compartment's zebrafish makes a move toward the compartment housing the other zebrafish, displaying symptoms of social behaviour. The fish of interest swam primarily in the direction of the school of zebrafish.
Test for Socialization ⁶⁷	Zebra Fish	Zebrafish were tested using the Shaolin method to determine their preference to swim alone, in small or large groups, or alone, or polarization	Zebra fishes tends to swim alone with opposite polarization or in very large groups	As a sign of social behavior, the fishes will frequently swim in small groups along the same direction

The tests for identifying and characterizing the disorder and the disease-causing genes are identified together with the primitive genes responsible for ASD. However, as time goes on, current improvements in genome sequencing methods have also been developed, along with the identification of novel genes that are engaged in the induction of ASD. The following section of this review will focus on the recently discovered genes that cause ASD. The identification of whole genome sequencing as a next generation sequencing method for identifying gene variants

and mutations that cause ASD, has made significant improvements in autism research. It identifies inherited or spontaneous mutations in the gene's coding region, which further aided in discovering new unique genes linked to ASD. **Table 3** covers each new potential gene for ASD along with how it manifests. Consequently, the various newly discovered genes and mutations have been identified as collectively responsible for ASD. The different genes which drive the induction of ASD are enlisted in **Table 3**.

TABLE 3: RECENTLY IDENTIFIED GENES AND THEIR MUTATION WHICH INDUCES ASD

Name of Gene	Location on chromosome	Mutation
MYO1A ⁷⁸	12:55,708,658	3'UTR
TGM3 ⁷⁸	20:2,239,665	Missense
LAMC3 ⁷⁸	9:132,904,111	Missense
FOXP1 ⁷⁸	3:71,132,860	Frameshift
TTN ⁷⁸	2:179,145,956	Synonymous
DCTN5 ⁷⁸	16:23,585,994	3'UTR
AFF4 ⁷⁸	5:132:251,451	Synonymous
TLK2 ⁷⁸	17:58,033,198	Missense
EPHB2 ⁷⁸	7:142,274,902	Synonymous
XIRP1 ⁷⁸	3:39,204,494	Missense
ANK3 ⁷⁹	10q21	Missense
SLIT3 ⁷⁹	5q35	Missense
HTR3A ⁷⁹	11q23.1	Missense
UNC13B ⁷⁹	9p13.3	Missense
RAB2A ⁸⁰	8:60,516,910	Nonsense
PPM1D ⁸⁰	17q23.2	Nonsense
SCP2 ⁸⁰	1p32.3	Frameshift
ADAM33 ⁸⁰	20p13	Nonsense
FCRL6 ⁸⁰	1q23.2	Splice site

Therefore, with the zeal to identify and characterize ASD in model organisms, an outmost necessary point of view, many genes are discovered and genetic testing are described. This review shall further address another set of genes as well as genetic tests to determine, describe and characterize ADHD disorders in model organisms.

Effect of Different Genes Responsible for Attention Deficit/ Hyperactivity Disorder and their Phenotypic Expression in Various Organisms: The phenotypic expression of many

ASD genes in various organisms has been documented. Similar to how distinct ADHD risk genes are expressed in various organisms, the host is affected by these disorders. The identification of many ADHD risk genes in various creatures and their phenotypic manifestation in their hosts will be our next area of focus as we proceed. As a result, **Table 3** includes a list of many ADHD risk genes expressed in various organisms and information on how they express phenotypically.

TABLE 4: EFFECT OF DIFFERENT ATTENTION-DEFICIT/HYPERACTIVITY DISORDERS-RISK GENES ON DIFFERENT ORGANISMS AND THEIR PHENOTYPIC EXPRESSION

Name of ADHD-risk genes	Effected organisms	Phenotypic expressions in effected organisms
SLC6A3 ^{36,37,63}	Human	Impact on the frontal cortex, striatum, and cerebellum as well as functional hyperactivity, altered dopamine system, and decreased thickness of cortex
	Zebra Fish	Hovers close to the tank's bottom, loss of immunoactivity neurons, and behavioral problems have been identified

LPHN3 ^{38,47,50,52}	Mice	Delay in cortical mutagenesis, altered neuronal structure and function, and altered timing of brain development
	Zebrafish	Hyperactive/impulsive motor phenotype with a reduction in dopamine-positive neurons in the ventral diencephalon
DRD4 & DRD5 ^{39,48,57,58}	Human	Anger, irritability, and attention-seeking behaviors such as dopamine-regulated aggression
	Zebrafish	Interference with dopaminergic signaling pathways of the fish
5HT1B ^{40,44,49,53}	Mouse	Phenotypes brought on by the expression of gene include increase in impulsivity and aggression
	Human	Increase in depression among young people followed by rise in suicide attempts along with obesity

Several genes causing ADHD in various model species have been found and defined, much as the genes causing ASD. As we proceed, we will

examine the various genetic tests available for detecting ADHD in the various model organisms.

TABLE 5: GENETIC TESTS TO DETERMINE ADHD IN MODEL ORGANISMS

Genetic test	Organism	Test Description	Behavior for ADHD	Behavior for no ADHD
Test to assess impulsivity and attentiveness ⁷¹	Zebrafish	“Five choice serial reaction time task”: Assessing the capacity of a zebrafish to react to one among the five similar stimuli, randomly after a variable interval time.	Increased impulsivity of the zebrafish	Normal impulsivity of the Zebrafish; “noradrenergic control of impulsivity”
Test for assessing hyperactivity ⁷¹	Zebrafish	Zebrafish larvae were observed for five to ten minutes to measure their swimming abilities, such as speed, distance travelled, frequency of swimming, duration of swimming, etc	An increase in every parameter taken into account; regular, frequent swimming activities if seen	Normal parameters evaluated over time
Test to determine hyperactivity, anxiety ^{71,72}	Zebrafish	“Novel tank test”: An individual fish is placed within a fish tank, and their performance is evaluated based on how much time they spend swimming in their favorite zones, how far they go between the top and bottom of the tank, and how many times they enter the top of the tank	The longer it takes to reach the top of the tank, the more anxious the fish is. If the bottom of the tank is the preferred swimming spot, anxiety levels are higher. Greater travel distance at the bottom suggests greater anxiety	Contrarily, shorter time required to reach the top, preferred swimming spot is at the top of the tank, greater travel distances at the top, all suggests lower anxiety levels and points to the absence of ADHD symptoms.
Test for behavioral symptoms relating to ADHD ^{73,74}	Mouse	Dopamine transporter knockout mice used to assess the symptoms of ADHD.	Comparison between the diseased and control mice, an excessive activity, spontaneous behavior, and very slow or impaired learning was noted.	Symptoms similar to the control mouse, hence no indication of ADHD.
Test for impulsiveness ⁷⁷	Mouse	“Cliff Avoidance Reaction test”, the mice were positioned so that their forelimbs touched the edge of a round, elevated wooden block in order to test the impulsiveness of NURR1 knockout mice. For one hour, both the number and timing of the mice falls were recorded.	Compared to the control mice, impulsive mice are more likely to fall from the wooden cliff. In the experiment performed by Montarolo et al. in 2019, the majority of the mice (-85.7%) fell from the wooden cliff in comparison to control mice, whose rate was substantially lower (11.7 %).	Mice that didn’t descend the wooden cliff exhibited no evidence of impulsivity or ADHD.

According to published scientific literature, there have been far fewer novel genes found for ADHD

than for ASD. However, the many novel genes identified are mentioned in **Table 6**.

TABLE 6: NEWLY IDENTIFIED GENES RESPONSIBLE FOR INDUCING ADHD ⁸¹

Name of Gene	Location on Chromosome	Gene Function
FOXP2	7q31.1	Establishing neural connections in people that will support language and learning skills ⁸¹
DUSP6	12q21.33	A crucial component of ADHD that is involved in the dopamine-mediated neuronal activity ⁸¹
SEMA6D	15q21.1	Expression in the brain during embryogenesis is responsible for processes like neuronal branching ⁸¹

DISCUSSION: The heterogeneous neuro-developmental disorder known as ASD is characterized by the presence of abnormalities in brain development and is dependent on the expression of a number of mutated orthologous genes, including CHD8 ^{9, 59, 60}, SHANK3 ¹¹, CNTNAP2 ²¹, DYRK1A ¹⁴, and TBR ^{25, 26}, which are found in both humans and other model organisms like mice and zebrafish. Below is a description of several instances of these mutant genes' regulation.

The “Chromodomain helicase DNA-binding protein 8” or CHD8 gene mutations are associated with the typical form of ASD ⁹. Further, a protein that is responsible for blocking catenin's transactivation activity and serves as a regulator of the Wnt β -catenin signaling pathway is made as a result of CDH8 gene on human chromosome 14q11.2. It may control Wnt signaling, which is crucial for the growth and morphogenesis of vertebrates ⁹. During brain development, the co-expression of additional ASD-risk genes is likewise regulated by the CHD8 gene. For instance, a patient with a CHD8 gene mutation noticed autistic behavior and other phenotypic characteristics such as macrocephaly, rapid postnatal development, distinctive facial features, and insomnia ⁹.

Additionally, mutation in the SHANK family (SHANK1, SHANK2, and SHANK3) genes are also linked with syndromic and idiopathic autisms as a result of anxiety-like behavior in humans and other organisms ^{12, 31}. In the human postsynaptic site at 22q13.3, SHANK proteins serve as the “master” scaffolding proteins ¹⁰. This protein family as a result of the expression of the gene interacts with several glutamate receptors at the Post Synaptic Density (PSD) region, including the NMDA and AMP receptors ¹³. On the other hand, deletion of both SHANK alleles reduces synaptic

basal transmissions, which showed high hyperactivities, by up regulating ionotropic glutamate receptors at synapses in certain brain regions ¹². Synaptic proteins, in particular SH3 and SHANK3, are encoded by mutant genes, which causes changes in the number, size, shape, and strength of neural synapses ^{13, 33}. Recent research in mice with the SHANK gene mutation revealed that disrupted GABA circuits in the brain may influence the social drives of these mice, leading to problems at the synaptic, circuit, behavioral, and molecular levels ^{20, 32}.

Therefore, these genes play a significant influence on cognitive and emotional health, as well as social behavior in ASD. Another gene, CNTNAP2 (Contactin-Associated Protein 2), is situated at 7q35-q36.1 on chromosome 7, designated as the master gene for ASD. The expression of this gene results in speech-language delay by altering the Epithelial Growth Factor (EGF) protein region, which is essential in the origin of aberrant behavior in autism and the downstream cascade. CAM and expressed language control are controlled by CNTNAP2, which controls neuron signaling ²⁷.

The CNTNAP2 gene mutation hinders language development by concentrating voltage-gated potassium ion channels present at the Nodes of Ranvier. It has a high level of expression in the cortico-striato-thalamic circuit, which is involved in language development defects in autism¹⁶. Further, through the deletion or duplication of regulatory miRNA, CNTNAP2 gene disruption can influence the expression of genes ²⁸⁻³⁰. It works by reducing RNA degradation caused by genes important in neurodevelopment in neuronal cells ²⁷. Additionally, on chromosome 21 at position 21q22.13 in the human body, the “tyrosine-(Y) phosphorylation-regulated kinase 1A” (DYRK1A) gene with dual specificity has also been identified

as an ASD risk gene¹². DYRK1A protein is essential for several aspects of postnatal brain development in autistic patients¹². This gene is crucial for the growth of the nervous system and phosphorylates a wide range of substrates, such as transcription factors, splicing factors, and synaptic factors. The tau protein and Neuronal Wiskott-Aldrich Syndrome Protein (N-WASP) are DYRK1A phosphorylated proteins and affect microscopic fibers and actin outgrowth, passively regulating the development of dendritic spines and neuronal dendrites. Gain-of-function in mutant mice with overexpressed DYRK1A gene exhibit memory deficits due to cortical neurons' reduced total neurite and axon length. This mutation affects cortical development and defective brain growth in autistic patients. The TBR1 gene, another ASD-risk gene, controls the molecular, synaptic, neural, and behavioral abnormalities associated with ASD^{17, 18, 25}.

It is a neuron-specific T-box transcription factor that cannot bind to target DNA and is found at 2q24.2 on chromosome 2. It controls the laminar identity of neocortical areas during brain development. As a result of anxiety-like behavior and aggressiveness in autistic patients, the layer 6 deletion of TBR1 gene in 6 pyramidal neurons, expression of TBR1 is increased with CASK (a synaptic PDZ protein) and CINAP (a nucleosome assembly protein), which are involved in brain development and intellectual abilities^{15, 62}. This is how these genes regulate the disorders associated with autism. Humans and several other creatures have shown various phenotype traits due to the expression of the mutant gene, which is described in **Table 1**.

In addition to being a well-known critical heterogeneous neuropsychotic and behavioral condition, ADHD is also recognized to cause abnormal social behaviors and developmental inadequacies and impairing inattention and overactivity^{34, 35}. Additionally, it may be heritable due to an orthologous gene mutation. Recent research has demonstrated the importance of many genes in the genesis of ADHD and its comorbidities, including DRD4 and DRD5^{39, 48, 57, 58}, SLC6A3 (DAT1)^{36, 37, 63}, LPH3^{38, 51}, etc. Therefore, ADHD is now thought of as a genetic-environmental developmental condition. **Table 2**

enlists the description of these genes' traits in different organisms. Because changes in the dopamine system cause attention difficulties, they carry a high risk of developing ADHD. By altering the brain, a mutation in the SLC6A3 gene, a Dopamine Transporter (DAT) factor gene found in the human body's synaptic cleft on 5p15.33 chromosome 5, is directly connected to ADHD³⁶. A variable number tandem repeat (VNTR) polymorphism in the 3' non-translated region of SLC6A3 regulates the aging factors by those risk alleles (10R, 9R, 6R)⁶⁴⁻⁶⁶. These genes show how cocaine abuse reduces the expression of these genes⁶⁵. The DAT inhibitor changed the mRNA levels in the animal model. This gene also controls the signaling pathway through polymorphic regulatory regions and cis-acting elements. These are the rules that this haplotype-dependent gene uses to govern ADHD⁴⁶.

Additionally, higher amounts of dopamine are seen in the brain's striatum of DAT knockout mice. These mice also exhibit dopamine auto receptor dysfunction and a decrease in the production of the tyrosine hydroxylase protein, which together makes them useful for studying the behaviors associated with ADHD^{75, 76}. The mutation in the "Adhesion G-protein coupled receptor L3 gene" (LPHN3 or ADGRL3), also known as "Latrophilin 3", acts as a reporter for latrotoxin, a component of black spider venom is also recognized as an ADHD risk factor gene³⁸. According to a recent study, the family of leucine-rich repeat transmembrane proteins acts as a ligand for the LPH3 gene, which can lower the density of excitatory synapses in neurons and lower the strength and quantity of afferent input into dentate granule cells.

Additionally, this combination controls the growth and transmission of glutamatergic synapses as well as the transmission of nerve impulses. It controls the pathophysiology of ADHD in humans and other creatures in this way⁴⁷. "Dopamine Receptor D4 (DRD4)" gene polymorphism, found at 11q15.5 of chromosome 11, also affects parenting and marital conflict on ADHD among humans. This gene promoter allele increases parental susceptibility and the likelihood that children would blame their parents for marital problems. Therefore, the DRD4 and DRD5 protein families were recognized as environmental risk factors. The reciprocal striatal-

thalamo-cortical and ascending limbic-frontal circuits in the brain, which may be sensitive to changes in behavior in the environment, are regulated by dopaminergic receptor genes. The number of perceptual experiences, such as sensitivity to pain and responsiveness to acute psychosocial stressors, are moderated by DRD genes in an adult. It can reduce the impact of dopaminergic neurotransmission in the case of ADHD by making highly emotive stimuli with immediate, rapidly changing, or unexpected outcomes more salient⁴⁸.

Another one is the “serotonin receptor gene 5HT1B (5-Hydroxytryptamine receptor 1B)”, a regulatory element for ADHD found on chromosome 6 between 6q13 and 6q26. Reduced transcriptional activity is caused by polymorphisms in various transcription factor binding sites in risk alleles as a result of the 5HT1B gene mutation. By reducing transcription activity, the haplotype H5 allele affects the genetic expression of the 5HT1B gene, increasing the quantity of receptors^{49, 54, 55}. These polymorphisms altered the gene expression of several mutant genes that are genetically associated. **Table 2** lists a few phenotypic traits of these genes in various species.

Limitations and Future Aspects: Examination of the functional effects of related genetic variations at the level of molecules, cells, neural systems, and circuits as well as their effects on brain development, more advanced research employing bioinformatics and experimental designs should be focused more.

A deeper and more critical understanding of the pathophysiology of how ADHD or ASD affects a patient's cognitive abilities and thus establishing a better diagnostic test, screening on model organism, for the same extensive research focusing on this area is the demand of the era. Funders and researchers carrying out clinical trials must understand that developmental research necessitates long-term follow-up, which is costly and time-consuming yet crucial to science. Hence, the focus should be shifted to assessment based on traits, rather than individual patients' data, making them useful for genetic investigation and providing further valuable developmental information.

Additionally, attention should be paid to gene therapy-based treatments for such NDD. No common or rare gene variants have yet been identified that are significantly associated with the effectiveness of treatment for ADHD. Extensive research will be required to identify any relevant genome-wide sites. A proper solution to unsolved problems related to what ramifications genetic discoveries have for ASD or ADHD is the demand for society. It is also important to consider medical professionals because of its two major implications.

Firstly, there is an increased risk of neurodevelopmental disorders like ADHD, ASD, and learning disabilities in parents and other family members of people with ADHD, and secondly, there is also an increased risk of developing other neuropsychiatric conditions, most commonly major depression, which may impair a person's ability to be evaluated, receive treatment, or be treated effectively⁸²⁻⁸⁸. As a result, attention should be given to gene therapy-based treatment alternatives or routine patient counseling for NDD and its accompanying issues, such as depression.

CONCLUSION: It is clear to us that the neurodevelopmental disorders in the class of attention deficit hyperactivity disorders and autism spectrum disorders, are brought on by several genes. As a result, many genes linked to these illnesses need to be identified and characterized for the prevention of the disease. Thus, this may lead to the scope of opening a new horizon for genetic screening for neuro-developmental disorders and its therapeutic intervention.

ACKNOWLEDGEMENT: I would like to show my sincere gratitude and respect to my mentor Ms. Tamalika Chakraborty, Assistant Professor, Department of Biotechnology, Guru Nanak Institute of Pharmaceutical Science and Technology for providing me with the necessary guidance and helping me throughout my work. I would also express my gratitude to Guru Nanak Institute of Pharmaceutical Science and Technology for providing me with the necessary resources throughout my work.

CONFLICTS OF INTEREST: The authors have no conflicts of interest.

REFERENCES:

- Jackson, LP: America's Children and the Environment. U.S. Environmental Protection Agency, Third Edition 2013.
- Savatt JM and Myers SM: Genetic Testing in Neurodevelopmental Disorders. *Frontiers in pediatrics* 2021; 9: 526779. <https://doi.org/10.3389/fped.2021.526779>.
- Ismail FY and Shapiro BK: What are neurodevelopmental disorders?. *Current opinion in neurology* 2019; 32(4): 611–616. <https://doi.org/10.1097/WCO.0000000000000710>.
- Brentani H, Paula CS, Bordini D, Rolim D, Sato F, Portolese J, Pacifico MC and McCracken JT: Autism spectrum disorders: an overview on diagnosis and treatment. *Revistabrasileira de psiquiatria (Sao Paulo, Brazil: 1999)* 2013; 35(1): S62–S72. <https://doi.org/10.1590/1516-4446-2013-S104>.
- Sakai C, Ijaz S and Hoffman EJ: Zebrafish Models of Neurodevelopmental Disorders: Past, Present, and Future. *Frontiers in molecular neuroscience* 2018; 11:294. <https://doi.org/10.3389/fnmol.2018.00294>.
- Vaz R, Hofmeister W and Lindstrand A: Zebrafish Models of Neurodevelopmental Disorders: Limitations and Benefits of Current Tools and Techniques. *International Journal of Molecular Sciences* 2019; 20(6): 1296. <https://doi.org/10.3390/ijms20061296>.
- Grove J, Ripke S, Als TD, Mattheisen M, Walters RK, Won H, Pallesen J, Agerbo E, Andreassen OA, Anney R, Awasthi S, Belliveau R, Bettella F, Buxbaum JD, Bybjerg-Grauholm J, Bækvad-Hansen M, Cerrato F, Chambert K, Christensen JH, Churchhouse C and Børglum AD: Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics* 2019; 51(3): 431–444. <https://doi.org/10.1038/s41588-019-0344-8>.
- van Loo KM and Martens GJ: Genetic and environmental factors in complex neurodevelopmental disorders. *Current genomics* 2007; 8(7): 429–444. <https://doi.org/10.2174/138920207783591717>.
- Alotaibi M and Ramzan K: A de novo variant of CHD8 in a patient with autism spectrum disorder. *Discoveries (Craiova, Romania)* 2020; 8(1): e107. <https://doi.org/10.15190/d.2020.4>.
- Monteiro P and Feng G: SHANK proteins: roles at the synapse and in autism spectrum disorder. *Nature reviews Neuroscience* 2017; 18(3): 147–157. <https://doi.org/10.1038/nrn.2016.183>.
- Uchino S and Waga C: SHANK3 as an autism spectrum disorder-associated gene. *Brain and development* 2013; 35(2): 106–110. <https://doi.org/10.1016/j.braindev.2012.05.013>.
- Poot M: SHANK Mutations May Disorder Brain Development. *Molecular syndromology* 2015; 6(1): 1–3. <https://doi.org/10.1159/000368949>.
- Ma SL, Chen LH, Lee CC, Lai KYC, Hung SF, Tang CP, Ho TP, Shea C, Mo F, Mak TSH, Sham PC and Leung PWL: Genetic Overlap Between Attention Deficit/Hyperactivity Disorder and Autism Spectrum Disorder in SHANK2 Gene. *Frontier Neuroscience* 2021; 15: 649588. doi: 10.3389/fnins.2021.649588.
- Dang T, Duan WY, Yu B, Tong DL, Cheng C, Zhang YF, Wu, W, Ye, K, Zhang WX, Wu M, Wu, B. B, AnY, Qiu Z L, Wu and BL: Autism-associated Dyrk1a truncation mutants impair neuronal dendritic and spine growth and interfere with postnatal cortical development. *Molecular psychiatry* 2018; 23(3): 747–758. <https://doi.org/10.1038/mp.2016.253>.
- Yook C, Kim K, Kim D, Kang H, Kim SG, Kim and E, Kim SY: A TBR1-K228E Mutation Induces Tbr1 Upregulation, Altered Cortical Distribution of Interneurons, Increased Inhibitory Synaptic Transmission, and Autistic-Like Behavioral Deficits in Mice. *Frontiers in molecular neuroscience* 2019; 12: 241. <https://doi.org/10.3389/fnmol.2019.00241>.
- Satterstrom FK, Kosmicki JA, Wang J, Breen MS, De Rubeis S, An JY, Peng M, Collins R, Grove J, Klei L, Stevens C, Reichert J, Mulhern MS, Artomov M, Gerges S Sheppard B, Xu X, Bhaduri A, Norman U, Brand H and Buxbaum JD: Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. *Cell* 2020; 180(3): 568–584.e23. <https://doi.org/10.1016/j.cell.2019.12.036>.
- Sener E: Association of Copy Number Variations In Autism Spectrum Disorders: A Systematic Review. *Chinese Journal of Biology* 2021; 10.1155/2014/713109.
- Cheroni C, Caporale N and Testa G: Autism spectrum disorder at the crossroad between genes and environment: contributions, convergences, and interactions in ASD developmental pathophysiology. *Molecular Autism* 2021; 11(1). <https://doi.org/10.1186/s13229-020-00370-1>.
- Liu C, Wang Y, Deng J, Lin J, Hu C, Li Q and Xu X: Social Deficits and Repetitive Behaviors Are Improved by Early Postnatal Low-Dose VPA Intervention in a Novel shank3-Deficient Zebrafish Model. *Frontiers in neuroscience* 2021; 15: 682054. <https://doi.org/10.3389/fnins.2021.682054>.
- Jiang YH and Ehlers MD: Modeling autism by SHANK gene mutations in mice. *Neuron* 2013; 78(1): 8–27. <https://doi.org/10.1016/j.neuron.2013.03.016>.
- Hoffman EJ, Turner KJ, Fernandez JM, Cifuentes D, Ghosh M, Ijaz, S, Jain RA, Kubo, F, Bill, BR, Baier H, Granato M, Barresi MJ, Wilson SW, Rihel J, State MW and Giraldez AJ: Estrogens Suppress a Behavioral Phenotype in Zebrafish Mutants of the Autism Risk Gene, CNTNAP2. *Neuron* 2016; 89(4): 725–733. <https://doi.org/10.1016/j.neuron.2015.12.039>.
- Toma C, Pierce KD, Shaw AD, Heath A, Mitchell PB, Schofield PR and Fullerton JM: Comprehensive cross-disorder analyses of CNTNAP2 suggest it is unlikely to be a primary risk gene for psychiatric disorders. *PLoS Genetics* 2018; 14(12): e1007535. <https://doi.org/10.1371/journal.pgen.1007535>.
- Raveau M, Shimohata A, Amano K, Miyamoto H and Yamakawa K: DYRK1A-haploinsufficiency in mice causes autistic-like features and febrile seizures. *Neurobiology of disease* 2018; 110: 180–191. <https://doi.org/10.1016/j.nbd.2017.12.003>.
- van Bon BWM, Coe BP and de Vries BBA: DYRK1A Syndrome. University of Washington, Seattle; 1993-2022. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK333438/>.
- Liu J, Reggiani JDS, Laboulaye MA, Pandey S, Chen B, Rubenstein JLR, Krishnaswamy A and Sanes JR: Tbr1 instructs laminar patterning of retinal ganglion cell dendrites. *Natural Neuroscience* 2018; 21(5): 659-670. doi: 10.1038/s41593-018-0127-z.
- Mione M, Shanmugalingam S, Kimelman D and Griffin K: Overlapping expression of zebrafish T-brain-1 and eomesodermin during forebrain development. *Mechanisms of development* 2001; 100(1): 93–97. [https://doi.org/10.1016/s0925-4773\(00\)00501-3](https://doi.org/10.1016/s0925-4773(00)00501-3).

27. Agarwala S and Ramachandra NB: Role of CNTNAP2 in autism manifestation outlines the regulation of signaling between neurons at the synapse. *Egyptian Journal of Medical Human Genetics* 2021; 22: 22.
28. Tong DL, Chen RG, LY L, Li WK, Zhang YF, Lin JK, He LJ, Dang T, Shan SF, Xu XH, Zhang Y, Zhang C, Du YS, Zhou WH, Wang X and Qiu Z: The critical role of ASD-related gene CNTNAP3 in regulating synaptic development and social behavior in mice. *Neurobiology of Disease* 2019; 130: 104486. <https://doi.org/10.1016/j.nbd.2019.104486>.
29. Fuller ZL, Berg JJ, Mostafavi H, Sella G and Przeworski M: Measuring intolerance to mutation in human genetics. *Nature genetics* 2019; 51(5): 772–776. <https://doi.org/10.1038/s41588-019-0383-1>.
30. Alonso-Gonzalez A, Rodriguez-Fontenla C and Carracedo A: De novo Mutations (DNMs) in Autism Spectrum Disorder (ASD): Pathway and Network Analysis. *Frontiers in genetics* 2018; 9: 406. <https://doi.org/10.3389/fgene.2018.00406>.
31. Waga C, Asano H, Sanagi T, Suzuki E, Nakamura Y, Tsuchiya A, Itoh M, Goto Y, Kohsaka S and Uchino S: Identification of two novel Shank3 transcripts in the developing mouse neocortex. *Journal of neurochemistry* 2014; 128(2): 280–293. <https://doi.org/10.1111/jnc.12505>.
32. Schmeisser MJ: Translational neurobiology in Shank mutant mice--model systems for neuropsychiatric disorders. *Annals of anatomy = Anatomischer Anzeiger: official organ of the Anatomische Gesellschaft* 2015; 200: 115–117. <https://doi.org/10.1016/j.aanat.2015.03.006>.
33. Rylaarsdam L and Guemez-Gamboa A: Genetic Causes and Modifiers of Autism Spectrum Disorder. *Frontiers in Cellular Neuroscience* 2019; 13: 385. <https://doi.org/10.3389/fncel.2019.00385>.
34. Thapar A and Stergiakouli E: An Overview on the Genetics of ADHD. *Xin li xue bao. Acta psychological Sinica* 2008; 40(10): 1088–1098. <https://doi.org/10.3724/SP.J.1041.2008.01088>.
35. Faraone SV and Larsson H: Genetics of attention deficit hyperactivity disorder. *Molecular Psychiatry* 2019; 24(4): 562–575. <https://doi.org/10.1038/s41380-018-0070-0>.
36. Brown AB, Biederman J, Valera EM, Doyle AE, Bush G, Spencer T, Monuteaux MC, Mick E, Whitfield-Gabrieli S, Makris N, LaViolette PS, Oscar-Berman M, Faraone SV and Seidman LJ: Effect of dopamine transporter gene (SLC6A3) variation on dorsal anterior cingulate function in attention-deficit/hyperactivity disorder. *American journal of medical genetics. Part B, Neuropsychiatric genetics: the official publication of the International Society of Psychiatric Genetics* 2010; 153(2): 365–375. <https://doi.org/10.1002/ajmg.b.31022>.
37. Wang G, Zhang G, Li Z, Fawcett CH, Coble M, Sosa MX, Tsai T, Malesky K, Thibodeaux SJ, Zhu P, Glass DJ and Fishman MC: Abnormal Behavior of Zebrafish Mutant in Dopamine Transporter Is Rescued by Clozapine. *iScience* 2019; 17: 325-333. doi: 10.1016/j.isci.2019.06.039.
38. Orsini CA, Setlow B, DeJesus M, Galaviz S, Loesch K, Ioerger T and Wallis D: Behavioral and transcriptomic profiling of mice null for Lphn3, a gene implicated in ADHD and addiction. *Molecular genetics and genomic medicine* 2016; 4(3): 322–343. <https://doi.org/10.1002/mgg3.207>.
39. Ptáček R, Kuzelová H and Stefano GB: Dopamine D4 receptor gene DRD4 and its association with psychiatric disorders. *Medical science monitor: international medical journal of experimental and clinical research* 2011; 17(9): RA215–RA220. <https://doi.org/10.12659/msm.881925>.
40. Wasel O and Freeman JL: Chemical and Genetic Zebrafish Models to Define Mechanisms of and Treatments for Dopaminergic Neurodegeneration. *International journal of molecular sciences* 2020; 21(17): 5981. <https://doi.org/10.3390/ijms21175981>.
41. Kalyan M, Hua K, Mohd Noor S, Wong C and Ekker M: Comprehensive Analysis of Neurotoxin-Induced Ablation of Dopaminergic Neurons in Zebrafish Larvae. *Biomedicines* 2019; 8(1): 1. <https://doi.org/10.3390/biomedicines8010001>.
42. Vijayanathan Y, Lim FT, Lim SM, Long CM, Tan MP, Majeed A and Ramasamy K: 6-OHDA-Lesioned Adult Zebrafish as a Useful Parkinson's Disease Model for Dopaminergic Neuroregeneration. *Neurotoxicity Research* 2017; 32(3): 496–508. <https://doi.org/10.1007/s12640-017-9778-x>.
43. Oliveri AN and Levin ED: Dopamine D1 and D2 receptor antagonism during development alters later behavior in zebrafish. *Behavioural Brain Research* 2019; 356: 250–256. <https://doi.org/10.1016/j.bbr.2018.08.028>.
44. Stepień A, Chalimoniuk M and Strosznajder J: Serotonin 5HT1B/1D receptor agonists abolish NMDA receptor-evoked enhancement of nitric oxide synthase activity and cGMP concentration in brain cortex slices. *Cephalalgia: an International Journal of Headache* 1999; 19(10): 859–865. <https://doi.org/10.1046/j.1468-2982.1999.1910859.x>.
45. Vaz RL, Outeiro TF and Ferreira JJ: Zebrafish as an Animal Model for Drug Discovery in Parkinson's Disease and Other Movement Disorders: A Systematic Review. *Frontiers in Neurology* 2018; 9: 347. <https://doi.org/10.3389/fneur.2018.00347>.
46. Zhao Y, Xiong N, Liu Y, Zhou Y, Li N, Qing H and Lin Z: Human dopamine transporter gene: differential regulation of 18-kb haplotypes. *Pharmacogenomics* 2013; 14(12): 1481–1494. <https://doi.org/10.2217/pgs.13.141>.
47. Acosta MT, Swanson J, Stehli A, Molina BS, MTA Team, Martinez AF, Arcos-Burgos M and Muenke M: ADGRL3 (LPHN3) variants are associated with a refined phenotype of ADHD in the MTA study. *Molecular genetics and genomic medicine* 2016; 4(5): 540–547. <https://doi.org/10.1002/mgg3.230>.
48. Martel MM, Nikolas M, Jernigan K, Friderici K, Waldman I and Nigg JT: The dopamine receptor D4 gene (DRD4) moderates family environmental effects on ADHD. *Journal of abnormal child Psychology* 2011; 39(1): 1–10. <https://doi.org/10.1007/s10802-010-9439-5>.
49. Xia X, Ding M, Xuan JF, Xing JX, Yao J, Wu X and Wang BJ: Functional polymorphisms and transcriptional analysis in the 5' region of the human serotonin receptor 1B gene (HTR1B) and their associations with psychiatric disorders. *BMC psychiatry* 2020; 20(1): 499. <https://doi.org/10.1186/s12888-020-02906-4>.
50. Acosta MT, Vélez JI, Bustamante ML, Balog JZ, Arcos-Burgos M and Muenke M: A two-locus genetic interaction between LPHN3 and 11q predicts ADHD severity and long-term outcome. *Translational psychiatry* 2011; 1(7): e17. <https://doi.org/10.1038/tp.2011.14>.
51. Hwang IW, Lim MH, Kwon, HJ and Jin HJ: Association of LPHN3 rs6551665 A/G polymorphism with attention deficit and hyperactivity disorder in Korean children. *Gene* 2015; 566(1): 68–73. <https://doi.org/10.1016/j.gene.2015.04.033>.
52. Bruxel EM, Salatino-Oliveira A, Akutagava-Martins GC, Tovo-Rodrigues L, Genro JP, Zeni CP, Polanczyk GV, Chazan R, Schmitz M, Arcos-Burgos M, Rohde LA and Hutz MH: LPHN3 and attention-deficit/hyperactivity disorder: a susceptibility and pharmacogenetic study.

- Genes, brain, and behavior 2015; 14(5): 419–427. <https://doi.org/10.1111/gbb.12224>.
53. Wu X, Yao J, Ding M, Shi ZS, Xu FL, Zhang JJ and Wang BJ: 5-HT1A receptor (HTR1A) 5' region haplotypes significantly affect protein expression in vitro. *Neuroscience letters* 2017; 638: 51–54. <https://doi.org/10.1016/j.neulet.2016.12.011>.
 54. SvobStrac D, Nedic Erjavec G, NikolacPerkovic M, Nenadic-Sviglin K, Konjevod M, Grubor M and Pivac N: The association between HTR1B gene rs13212041 polymorphism and onset of alcohol abuse. *Neuropsychiatric disease and treatment* 2019; 15: 339–347. <https://doi.org/10.2147/NDT.S191457>.
 55. Conner TS, Jensen KP, Tennen H, Furneaux HM, Kranzler HR and Covault J: Functional polymorphisms in the serotonin 1B receptor gene (HTR1B) predict self-reported anger and hostility among young men. *American journal of medical genetics. Part B, Neuropsychiatric genetics: the official publication of the International Society of Psychiatric Genetics* 2010; 153(1): 67–78. <https://doi.org/10.1002/ajmg.b.30955>.
 56. Muller D, Grevet EH, Panzenhagen AC, Cupertino RB, da Silva BS, Kappel DB, Mota NR, Blaya-Rocha P, Teche SP, Vitola ES, Rohde LA, Contini V, Rovaris DL, Schuch JB and Bau C: Evidence of sexual dimorphism of HTR1B gene on major adult ADHD co-morbidities. *Journal of Psychiatric Research* 2017; 95: 269–275. <https://doi.org/10.1016/j.jpsychires.2017.09.011>.
 57. Nikolaidis A and Gray JR: ADHD and the DRD4 exon III 7-repeat polymorphism: an international meta-analysis. *Social cognitive and affective neuroscience* 2010; 5(2-3): 188–193. <https://doi.org/10.1093/scan/nsp049>.
 58. Grady DL, Thanos PK, Corrada MM, Barnett JC Jr, Ciobanu V, Shustarovich D, Napoli A, Moyzis AG, Grandy D, Rubinstein M, Wang GJ, Kawas CH, Chen C, Dong Q, Wang E, Volkow ND and Moyzis RK: DRD4 genotype predicts longevity in mouse and human. *The Journal of neuroscience: the official journal of the Society for Neuroscience* 2013; 33(1): 286–291. <https://doi.org/10.1523/JNEUROSCI.3515-12.2013>.
 59. Weissberg O and Elliott E: The Mechanisms of CHD8 in Neurodevelopment and Autism Spectrum Disorders. *Genes* 2021; 12(8): 1133. <https://doi.org/10.3390/genes12081133>.
 60. Sugathan A, Biagioli M, Golzio C, Erdin S, Blumenthal I, Manavalan P, Ragavendr A, Brand H, Lucente D, Miles J, Sheridan SD, Stortchevoi A, Kellis M, Haggarty SJ, Katsanis N, Gusella JF and Talkowski ME: CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. *Proceedings of the National Academy of Sciences of the United States of America* 2014; 111(42): E4468–E4477. <https://doi.org/10.1073/pnas.1405266111>.
 61. Huang TN, Yen TL, Qiu LR, Chuang HC, Lerch JP and Hsueh YP: Haploinsufficiency of autism causative gene Tbr1 impairs olfactory discrimination and neuronal activation of the olfactory system in mice. *Mol Autism* 2019; 10: 5. doi: 10.1186/s13229-019-0257-5.
 62. Notwell JH, Heavner WE, Darbandi SF, Katzman S, McKenna WL, Ortiz-Londono CF, Tastad D, Eckler MJ, Rubenstein JL, McConnell SK, Chen B and Bejerano G: TBR1 regulates autism risk genes in the developing neocortex. *Genome research* 2016; 26(8): 1013–1022. <https://doi.org/10.1101/gr.203612.115>.
 63. Reith M, Kortagere S, Wiers CE, Sun H, Kurian MA, Galli A, Volkow ND and Lin Z: The dopamine transporter gene SLC6A3: multidisease risks. *Molecular psychiatry* 2022; 27(2): 1031–1046. <https://doi.org/10.1038/s41380-021-01341-5>.
 64. Zhao Y, Yu J, Zhao J, Chen X, Xiong N, Wang T, Qing H and Lin Z: Intragenic Transcriptional cis-Antagonism Across SLC6A3. *Molecular neurobiology* 2019; 56(6): 4051–4060. <https://doi.org/10.1007/s12035-018-1357-5>.
 65. Kampangkaew JP, Spellicy CJ, Nielsen EM, Harding MJ, Ye A, Hamon SC, Kosten TR, Nielsen, DA: Pharmacogenetic role of dopamine transporter (SLC6A3) variation on response to disulfiram treatment for cocaine addiction. *The American journal on addictions* 2019; 28(4): 311–317. <https://doi.org/10.1111/ajad.12891>.
 66. Fuke S, Suo S, Takahashi N, Koike H, Sasagawa N and Ishiura S: The VNTR polymorphism of the human dopamine transporter (DAT1) gene affects gene expression. *The pharmacogenomics journal* 2001; 1(2): 152–156. <https://doi.org/10.1038/sj.tpj.6500026>.
 67. Stewart AM, Nguyen M, Wong K, Poudel MK and Kalueff AV: Developing zebrafish models of autism spectrum disorder (ASD). *Progress in neuro-psychopharmacology and biological psychiatry* 2014; 50: 27–36. <https://doi.org/10.1016/j.pnpbp.2013.11.014>.
 68. Roulet FI and Crawley JN: Mouse models of autism: testing hypotheses about molecular mechanisms. *Current topics in behavioral neurosciences* 2011; 7: 187–212. https://doi.org/10.1007/7854_2010_113.
 69. Silverman JL, Yang M, Lord C and Crawley JN: Behavioural phenotyping assays for mouse models of autism. *Nature reviews. Neuroscience* 2010; 11(7): 490–502. <https://doi.org/10.1038/nrn2851>.
 70. Roulet FI and Crawley JN: Mouse models of autism: testing hypotheses about molecular mechanisms. *Current topics in behavioral neurosciences* 2011; 7: 187–212. https://doi.org/10.1007/7854_2010_113.
 71. Norton W, Lange M, Bally-Cuif L and Lesch KP: Zebrafish Models of Attention-Deficit/Hyperactivity Disorder (ADHD). In: Kalueff, A. (eds) *The rights and wrongs of zebrafish: Behavioral phenotyping of zebrafish*. Springer, Cham 2017. https://doi.org/10.1007/978-3-319-33774-6_7.
 72. Adam D, Collier AD, Kalueff AV and Echevarria DJ: Zebrafish models of anxiety-like behaviours. In A.V. Kalueff (Ed.), *The Rights and Wrongs of Zebrafish: Behavioral phenotyping of zebrafish*. Switzerland: Springer International Publishing 2017: 45–72.
 73. Leo D and Gainetdinov RR: Transgenic mouse models for ADHD. *Cell and tissue research* 2013; 354(1): 259–271. <https://doi.org/10.1007/s00441-013-1639-1>.
 74. Kasahara Y, Kubo Y and Sora I: *Nihon shinkeiseishinyakurigakuzasshi = Japanese journal of psycho pharmacology* 2013; 33(5-6):185–189.
 75. Giros B, Jaber M, Jones SR, Wightman RM and Caron MG: Hyperlocomotion and indifference to cocaine and amphetamine in mice lacking the dopamine transporter. *Nature* 1996; 379(6566): 606–612. <https://doi.org/10.1038/379606a0>.
 76. Jaber M, Dumartin B, Sagné C, Haycock JW, Roubert C, Giros B, Bloch B and Caron MG: Differential regulation of tyrosine hydroxylase in the basal ganglia of mice lacking the dopamine transporter. *The European journal of neuroscience* 1999; 11(10): 3499–3511. <https://doi.org/10.1046/j.1460-9568.1999.00764.x>.
 77. Montarolo F, Martire S, Perga S, Spadaro M, Brescia I, Allegra S, De Francia S and Bertolotto A: NURR1 deficiency is associated to ADHD-like phenotypes in mice. *Translational psychiatry* 2019; 9(1): 207. <https://doi.org/10.1038/s41398-019-0544-0>.

78. O'Roak BJ, Deriziotis P, Lee C, Vives L, Schwartz JJ, Girirajan S, Karakoc E, Mackenzie AP, Ng SB, Baker C, Rieder MJ, Nickerson DA, Bernier R, Fisher SE, Shendure J and Eichler EE: Exome sequencing in sporadic autism spectrum disorders identifies severe de novo mutations. *Nature genetics* 2011; 43(6): 585–589.
79. Bi C, Wu J, Jiang T, Liu Q, Cai W, Yu P, Cai T, Zhao M, Jiang YH and Sun ZS: Mutations of ANK3 identified by exome sequencing are associated with autism susceptibility. *Human mutation* 2012; 33(12): 1635–1638. <https://doi.org/10.1002/humu.22174>.
80. Sanders SJ, Murtha MT, Gupta AR, Murdoch JD, Raubeson MJ, Willsey AJ, Ercan-Sencicek AG, DiLullo NM, Parikshak NN, Stein JL, Walker MF, Ober GT, Teran NA, Song Y, El-Fishawy P, Murtha RC, Choi M, Overton JD, Bjornson RD, Carriero NJ and State MW: De novo mutations revealed by whole-exome sequencing are strongly associated with autism. *Nature* 2012; 485(7397): 237–241. <https://doi.org/10.1038/nature10945>.
81. University of Barcelona: First genetic map of Attention Deficit Hyperactivity Disorder. *Science Daily* 2018; Retrieved August 10, 2022 from www.sciencedaily.com/releases/2018/11/181126123334.htm.
82. Thapar A: Discoveries on the Genetics of ADHD in the 21st Century: New Findings and Their Implications. *The American journal of psychiatry* 2018; 175(10): 943–950. <https://doi.org/10.1176/appi.ajp.2018.18040383>.
83. Rajaprakash M and Leppert ML: Attention-Deficit/Hyperactivity Disorder. *Pediatr Rev.* 2022; 43(3): 135-147. doi: 10.1542/pir.2020-000612.
84. Leffa DT, Caye A and Rohde LA and ADHD in Children and Adults: Diagnosis and Prognosis. *Curr Top BehavNeurosci.* 2022; 57: 1-18. doi: 10.1007/7854_2022_329.
85. Weibel S, Menard O, Ionita A, Boumendjel M, Cabelguen C, Kraemer C, Micoulaud-Franchi JA, Bioulac S, Perroud N, Sauvaget A, Carton L, Gachet M and Lopez R: Practical considerations for the evaluation and management of Attention Deficit Hyperactivity Disorder (ADHD) in adults. *Encephale* 2020; 46(1): 30-40. doi: 10.1016/j.encep.2019.06.005.
86. Lam AP, Matthies S, Graf E, Colla M, Jacob C, Sobanski E, Alm B, Rösler M, Retz W, Retz-Junginger P, Kis B, Abdel-Hamid M, Müller HHO, Lücke C, Huss M, Jans T, Berger M, Tebartz van Elst L and Philippsen A: Comparison of Methylphenidate and Psychotherapy in Adult ADHD Study (COMPAS) Consortium. Long-term Effects of Multimodal Treatment on Adult Attention-Deficit/Hyperactivity Disorder Symptoms: Follow-up Analysis of the COMPAS Trial. *JAMA Netw Open.* 2019; 2(5): 194980. doi: 10.1001/jamanetworkopen.2019.4980.
87. Roy A, Garner AA, Epstein JN, Hoza B, Nichols JQ, Molina BSG, Swanson JM, Arnold LE and Hechtman L: Effects of Childhood and Adult Persistent Attention-Deficit/Hyperactivity Disorder on Risk of Motor Vehicle Crashes: Results From the Multimodal Treatment Study of Children With Attention-Deficit/Hyperactivity Disorder. *J Am Acad Child Adolesc Psychiatry* 2020; 59(8): 952-963. doi: 10.1016/j.jaac.2019.08.007.
88. Curry AE, Power TJ and Editorial: Paving the Way Toward Improving Safety Among Drivers With Attention-Deficit/Hyperactivity Disorder. *J Am Acad Child Adolesc Psychiatry* 2020; 59(8): 923-925. doi: 10.1016/j.jaac.2020.02.012.

How to cite this article:

Das A, Ghosh S and Chakraborty T: Impact of genetics in neurodevelopmental disorders. *Int J Pharm Sci & Res* 2023; 14(6): 2658-69. doi: 10.13040/IJPSR.0975-8232.14(6).2658-69.

All © 2023 are reserved by International Journal of Pharmaceutical Sciences and Research. This Journal licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 3.0 Unported License.

This article can be downloaded to **Android OS** based mobile. Scan QR Code using Code/Bar Scanner from your mobile. (Scanners are available on Google Playstore)