

Whole Exome Sequencing Analysis

Patient name	: Mr. XXX	PIN	: XX
Gender/ Age	: Male/ 31 Years	Sample number	: XX
Referring clinician	: XX	Sample collection date	: XX
Specimen	: Peripheral Blood	Sample receipt date	: XX
		Report date	: XX

Clinical history

Proband, Mr. XXX is presented with a 1.5 year history of insidious onset and progressively worsening hyperkinetic movement in the form of generalized Chorea, oromandibular dystonia, swallowing dystonia and vocal tics (grunting) with generalized hyporeflexia with normal HMF, sensory and cerebellar examination with no bowel/bladder involvement and no associated systemic disorders. He is suspected to be affected with Neuroacanthocytosis. Proband, Mr. XXX has been evaluated for pathogenic variations.

Results

Variant of uncertain significance related to the given phenotype was detected

List of uncertain significant variant identified related to the phenotype:

Gene	Region	Variant*	Allele Status	Disease	Classification*	Inheritance pattern
VPS13A (+)	Exon 63	c.8666A>G (p.Gln2889Arg)	Homozygous	Choreoacanthocytosis (OMIM#200150)	Uncertain Significance	Autosomal Recessive

*Genetic test results are based on the recommendation of American college of Medical Genetics [1].
No other variant that warrants to be reported for the given clinical indication was identified.

Interpretation

VPS13A: c.8666A>G

Variant summary: A homozygous missense variation in exon 63 of the *VPS13A* gene (chr9:g.77369411A>G, NM_033305.3, Depth: 59x) that results in the amino acid substitution of Arginine for Glutamine at codon 2889 (p.Gln2889Arg) was detected.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes database.

In-silico prediction: The in-silico predictions of the variant are damaging by SIFT, PolyPhen-2 (HumDiv), LRT and MutationTaster2. The reference codon is conserved across PhyloP and GERP++ tools.

OMIM phenotype: Choreoacanthocytosis (OMIM#200150) can be caused by homozygous or compound heterozygous mutation in the *VPS13A* gene (OMIM*605978). This disease follows autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as variant of uncertain significance. In this view, clinical correlation and familial segregation analysis is strongly recommended to establish the significance of the finding. If the results do not correlate, additional testing may be considered based on the phenotype observed.

Additional Variant(s)

List of additional carrier variant identified:

Gene	Region	Variant*	Allele Status	Disease	Classification*	Inheritance pattern	ClinVar
SACS (-)	Exon 10	c.13132C>T (p.Arg4378Ter)	Heterozygous	Spastic ataxia, Charlevoix-Saguenay type (OMIM#270550)	Likely Pathogenic	Autosomal Recessive	370756

Recommendations

- Sequencing the variant(s) in the parents and the other affected and unaffected members of the family is recommended to confirm the significance.
- Alternative test is strongly recommended to rule out the deletion/duplication.
- Genetic counselling is advised.

Methodology

DNA extracted from the blood was used to perform whole exome using whole exome capture kit. The targeted libraries were sequenced to a targeted depth of 80 to 100X using GenoLab M sequencing platform. This kit has deep exonic coverage of all the coding regions including the difficult to cover regions. The sequences obtained are aligned to human reference genome (GRCh38.p13) using Sentieon aligner and analyzed using Sentieon for removing duplicates, recalibration and re-alignment of indels. Sentieon DNAscope has been used to call the variants. Detected variants were annotated and filtered using the VarSeq software with the workflow implementing the ACMG guidelines for variant classification. The variants were annotated using 1000 genomes (V2), gnomAD (v3.1.2.1.1), ClinVar, OMIM, dbSNP, NCBI RefSeq Genes. *In-silico* predictions of the variant was carried out using VS-SIFT, VS-PolyPhen2, PhyloP, GERP++, GeneSplicer, MaxEntScan, NNSplice, PWM Splice Predictor. Only non-synonymous and splice site variants found in the coding regions were used for clinical interpretation. Silent variations that do not result in any change in amino acid in the coding region are not reported.

Sequence data attributes

Total reads generated	9.22 Gb
Data ≥ Q30	93.02%

Genetic test results are reported based on the recommendations of American College of Medical Genetics [1], as described below:

Classification	Interpretation
Pathogenic	A disease-causing variation in a gene which can explain the patients' symptoms has been detected. This usually means that a suspected disorder for which testing had been requested has been confirmed
Likely Pathogenic	A variant which is very likely to contribute to the development of disease however, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity.
Variant of Uncertain Significance	A variant has been detected, but it is difficult to classify it as either pathogenic (disease causing) or benign (non- disease causing) based on current available scientific evidence. Further testing of the patient or family members as recommended by your clinician may be needed. It is probable that their significance can be assessed only with time, subject to availability of scientific evidence.

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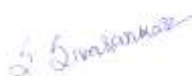
Disclaimer

- The classification of variants of unknown significance can change over time. Anderson Diagnostics and Labs cannot be held responsible for it.
- Intronic variants, UTR, Promoter region variants and CNV are not assessed using this assay.
- Certain genes may not be covered completely, and few mutations could be missed. Variants not detected by this assay may impact the phenotype.
- The variations have not been validated by Sanger sequencing.
- The above findings and result interpretation was done based on the clinical indication provided at the time of reporting.
- It is also possible that a pathogenic variant is present in a gene that was not selected for analysis and/or interpretation in cases where insufficient phenotypic information is available.
- Genes with pseudogenes, paralog genes and genes with low complexity may have decreased sensitivity and specificity of variant detection and interpretation due to inability of the data and analysis tools to unambiguously determine the origin of the sequence data in such regions.
- Incidental or secondary findings that meet the ACMG guidelines can be given upon request [3].

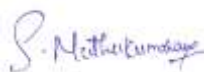
References

1. Richards, S, et al. Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genetics in medicine: official journal of the American College of Medical Genetics. 17.5 (2015): 405-424.
2. Amberger J, Bocchini CA, Scott AF, Hamosh A. McKusick's Online Mendelian Inheritance in Man (OMIM). Nucleic Acids Res. 2009 Jan;37(Database issue):D793-6. doi: 10.1093/nar/gkn665. Epub 2008 Oct 8.
3. Kalia S.S. et al., Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2016 update (ACMG SF v2.0): a policy statement of the American College of Medical Genetics and Genomics. Genet Med., 19(2):249-255, 2017.

This report has been reviewed and approved by:



Sivasankar.S, Ph.D
Molecular Biologist



Muthukumaran. S, Ph.D
Clinical Bioinformatician



Sachin. D.Honguntikar, Ph.D,
Molecular Geneticist



Dr. G. Suriyakumar
Director