Whole Genome CGH+SNP Array, Methylation Analysis, UBE3A Gene Analysis for Angelman Syndrome, SLC9A6 Gene Analysis for Angelman-Like (Christianson) Syndrome / X-Linked Intellectual Disability

Clinical Features:
Angelman syndrome (AS) is a neurological disorder affecting development and behavior. Individuals with Angelman syndrome exhibit developmental and cognitive delays typically noted in the first year of life, including absent or significantly impaired speech. Neurological features include seizures, ataxia, and characteristic electroencephalogram (EEG) abnormalities. Characteristic behavioral features include sleep disorders and a happy demeanor with recurrent laughter, smiling, and excitability. Individuals with AS are typically noted to have prominent chin, small head circumference and a wide mouth with protruding tongue. The presence and severity of the clinical features can vary among individuals with AS.[1]

Males with Angelman-like (Christianson) syndrome may exhibit many clinical features suggestive of Angelman syndrome such as intellectual disability, ataxia, severe speech and language impairment, a happy demeanor with frequent smiling or spontaneous laughter, epilepsy, and microcephaly.[2,3] Variants in the SLC9A6 gene have also been identified in families with nonsyndromic X-linked intellectual disability.[10,11]

Genetics:
AS is an imprinting disorder caused by one of four known mechanisms that result in absence of expression of the UBE3A gene on the maternally derived chromosome 15 within 15q11.2-q13.1. The majority (65-75%) of patients with AS have a large recurrent microdeletion extending from 15q11.2 to 15q13.1 on the maternally inherited chromosome.[4] Paternal UPD accounts for 3-7% of patients with AS.[4] Approximately 3% of patients have an imprinting error that establishes a paternal chromosome-specific methylation pattern despite the presence of both parental alleles, and these imprinting errors can be caused by a microdeletion within the imprinting center in 15q11.2 (0.5% of all AS cases) or by an unknown mechanism that inappropriately silences genes regardless of the parental origin of the chromosome (2.5% of all AS cases).[1,2,4] UBE3A variants detectable by sequencing are responsible for 5-11% of AS cases, while rare patients have been reported to harbor a partial deletion of the UBE3A gene.[4]

The *UBE3A* gene encodes an E3 ligase in the ubiquitin proteasome pathway and functions as a transcriptional coactivator. The UBE3A gene consists of 13 exons with three alternatively spliced transcripts.[8] Most pathogenic variants are private and include missense and nonsense

changes, small deletions/insertions, splice site alterations, and large deletions.[1,8,9] Mutations have been found throughout the coding region, with a somewhat higher concentration in exon 9 (typically reported as exon 6 using the naming convention that is common in the published literature).[9]

The majority of cases of genetically confirmed AS are de novo with a recurrence risk of <1%; however, the recurrence is 50% for an inherited imprinting center deletion, a maternally inherited UBE3A variant or partial deletion, or for microdeletions inherited from a mother with a balanced chromosome rearrangement.[4] Patients with Angelman syndrome who have large deletions have the most severe phenotype, with severe seizures, cognitive delays and an absence of speech.[8] Patients with AS due to paternal UPD and imprinting errors tend to have the least severe presentation, with a lower occurrence of seizures and better cognitive and speech development. Intermediate severity of the phenotype has been reported in patients with AS due to mutations in the UBE3A gene, who have better cognitive and speech development than those with a gene deletion.[8]

The etiology of the remaining AS cases is unknown; however, the differential diagnosis of AS includes Angelman-like (Christianson) syndrome, a disorder caused by pathogenic variants in the SLC9A6 gene located on chromosome Xq26.3.[4] Multiple pathogenic variants that introduce a premature stop codon and a few missense changes in the SLC9A6 gene have been reported in association with an Angelman-like syndrome. A few partial gene deletions have been reported to date in males with X-linked intellectual disability.[11,12] Angelman-like syndrome is an X-linked disorder that affects males. Most females who are heterozygous carriers of SLC9A6 variants have normal intelligence, although some carrier females have been reported with learning disabilities and/or mild behavioral abnormalities. [2,13]

GeneDx test methods and sensitivity for Angelman syndrome:

Test	Abnormalities Identified	Detection Rate	Comments
Whole genome CGH+SNP array	- common 15q11.2-15q13.1 deletion - UPD - imprinting center deletions - intragenic UBE3A deletion/duplication	~76% AS	can detect other genomic imbalances with features overlapping with AS
Methylation-specific MLPA (MS-MLPA)	- common 15q11.2-15q13.1 deletion - paternal UPD - all types of imprinting abnormalities	~78% AS	can confirm AS diagnosis and determine mechanism

UBE3A Sequencing and Del/Dup Testing	- intragenic variants in UBE3A gene - intragenic deletions/duplications of an exon or larger in UBE3A gene	5-11% AS Rare in AS	for patients with clinical suspicion of AS and normal whole genome CGH+SNP array OR MS-MLPA
SLC9A6 Sequencing and Del/Dup Testing	- intragenic variants in SLC9A6 gene - intragenic deletions/duplication of an exon or larger in SLC9A6 gene	~6% AS-like	for males with clinical features of AS and no detectable UBE3A abnormalities
Rett/Angelman Syndrome Panel	- intragenic variants, deletions, and duplications of UBE3A, SLC9A6, and 9 other genes	See website	cannot detect UPD or imprinting abnormalities

Whole-genome CGH+SNP array is available to detect the common 15q11.2-15q13.1 deletion, paternal UPD, imprinting center deletions (but not other types of imprinting errors), and intragenic deletions or duplications of the UBE3A gene. Together, these four causes account for an estimated 76% of patients with AS. The array contains 118,000 oligonucleotide probes for detection of copy number variants (CNVs) in the unique sequence of the genome and can therefore identify other genomic imbalances that may produce an AS-like phenotype (e.g., 2q23 or 17q21.31 deletions). In addition, it contains 66,000 SNP probes throughout the genome and can detect stretches of homozygosity extending 5 Mb or longer.

Methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA) can determine the parent-specific methylation imprint. An abnormal MS-MLPA result can confirm a diagnosis of AS and reveal the mechanism (deletion, UPD, or imprinting error). Methylation analysis is available as reflex testing following normal array results for individuals with a high suspicion of AS to identify UPD or imprinting errors, or as a first-line test for patients with a suspected diagnosis of AS. GeneDx does not offer imprinting center sequence analysis. However, patients with abnormal methylation studies but normal whole-genome CGH+SNP array are assumed to have an imprinting error.

UBE3A and SLC9A6 gene sequencing and deletion/duplication testing are offered as separate tests or are also available as part of a panel of genes causing Rett/Angelman syndrome and other related disorders. Among patients with normal methylation patterns, FISH results, and UPD studies, UBE3A variants are detected by DNA sequencing in 50-80% of familial cases and in 10-44% of de novo cases of AS.[1,5,6,7] Variants in SLC9A6 are rare in patients with an Angelman-like phenotype, accounting for 4 out of 73 (~6%) probands with an AS-like presentation in one study.[2] Variants in the SLC9A6 gene have also been identified in families with nonsyndromic X-linked intellectual disability.[10,11]

Using genomic DNA from the submitted specimen, the coding regions and splice junctions of the requested gene are PCR amplified and capillary sequencing is performed. Bi-directional sequence is assembled, aligned to reference gene sequences based on NCBI RefSeq transcript and human genome build GRCh37/UCSC hg19, and analyzed for sequence variants. Concurrent deletion/duplication testing is performed for most, if not all, of the coding exons using exon-level oligo array CGH (ExonArrayDx), and data analysis is performed using gene-specific filtering. Probe sequences and locations are based on human genome build GRCh37/UCSC hg19. Reported clinically significant variants are confirmed by an appropriate method. Sequence and copy number variants are reported according to the Human Genome Variation Society (HGVS) or International System for Human Cytogenetic Nomenclature (ISCN) guidelines, respectively. Reportable variants include pathogenic variants, likely pathogenic variants and variants of uncertain significance. Likely benign and benign variants, if present, are not routinely reported but are available upon request.

The Rett/Angelman Syndrome Panel includes Next Generation sequencing and deletion/duplication analysis of a panel of genes causing Rett/Angelman syndrome and other related disorders with overlapping clinical phenotypes, including epilepsy, developmental delay and intellectual disability. Additional information about the panel is available on the website https://www.genedx.com/test-catalog/available-tests/rettangelman-syndrome-panel/

References:

1. Malzac, P., et al. (1998) Am J Hum Genet. 62(6):1353-1360.
2. Gillfillan G., et al. (2008) Am. J. Hum. Genet. 82(4): 1003-1010.
3. Christianson A., et al. (1999) Am J. Hum Genet. 36:759-766.
4. Dagli AI, Mueller J, Williams CA. Angelman Syndrome. 1998 Sep 15 [Updated 2015 May 14]. In: Pagon RA, Adam MP, Ardinger HH, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2017. Available from: https://www.ncbi.nlm.nih.gov/books/NBK1144/
5. Hitchins, M.P., et al. (2004) Am J Med Genet. 125A(2):167-172.
6. Lossie, A.C., et al. (2001) J Med Genet. 38(12):834-845.
7. Fang, P., et al. (1991) Hum Molec Genet. 8(1):129-135.
8. Clayton-Smith, J., et al. (2003) J Med Genet. 40(2):87-95.
9. Russo, S., et al. (2000) Hum Mutat. 15(4):387-393.
10. Hu, et al. (2009) HUGO J. 3:41-49.
11. Whibley, et al. (2010) Am J Hum Genet. 87:173-188.
12. Tzschach, A, et al. (2015) Eur J Med Genet. 23(11):1513-1518.
13. Schroer R., et al. (2010) Am J Med Genet. 152A:2775-2783.
14. Boyes L., et al. (2006) Eur J Med Genet. 49(6):472-80.
15. Beleza-Meireles et al. (2011) Eur J Med Genet 54:348-350.
16. Piard et al. (2011) Am J Med Genet 155:3170-3173.