

Angelman Syndrome and Prader-Willi Syndrome Testing

Angelman syndrome (AS) and Prader-Willi syndrome (PWS) are complex neurodevelopmental disorders characterized by developmental delay and intellectual disability, as well as symptoms unique to each disorder (eg, unique happy demeanor in AS, excessive eating in PWS). Both conditions are linked to loss of function of genes in the 15q11.2-q13 region.

Disease Overview

Prevalence

- AS: 1 in 12,000-24,000
- PWS: 1 in 10,000-30,000

Age of Onset

- AS: 6-12 months
- PWS: Neonatal

For more information about the clinical characteristics of AS and PWS, see the [Angelman Syndrome and Prader-Willi Syndrome Consult](#) topic.

Genetics

Genes

15q11.2-q13 region

Etiologies

- Deletion of 15q11.2-q13 (AS: maternal; PWS: paternal)
- Uniparental disomy (UPD) for chromosome 15 (AS: paternal; PWS: maternal)
- *UBE3A* gene mutation (AS only)
- Imprinting center defect
- Unbalanced chromosome translocation
- Unidentified (AS only)

For more information about the underlying mechanisms of AS and PWS, see the [Angelman Syndrome and Prader-Willi Syndrome Consult](#) topic.

Prenatal Screening

- Prenatal testing is recommended for subsequent pregnancies of couples who have a previous child with AS or PWS.
- Parental testing does not exclude somatic and/or germline mosaicism.
- Methylation testing is not offered on chorionic villus samples.
- Incomplete methylation in early embryonic development may cause false-positive results.

Test Interpretation

Sensitivity

Tests to Consider

[Angelman Syndrome and Prader-Willi Syndrome by Methylation-Sensitive PCR 2005077](#)

Method: Methylation Sensitive Polymerase Chain Reaction/Fluorescence Monitoring

- Preferred initial diagnostic test for AS or PWS
- Use to establish a diagnosis in individuals with clinical symptoms

[Angelman Syndrome and Prader-Willi Syndrome by Methylation-Sensitive PCR, Fetal 2012232](#)

Method: Methylation Sensitive Polymerase Chain Reaction/Fluorescence Monitoring

- Prenatal testing for AS or PWS
- Use to identify cases resulting from molecular mechanisms that produce abnormal methylation patterns

Related Tests

[Chromosome FISH, Metaphase \(Temporary Delay as of 09/21/21\) 2002299](#)

Method: Fluorescence in situ Hybridization (FISH)

Follow-up for abnormal methylation test for AS

[Cytogenomic SNP Microarray 2003414](#)

Method: Genomic Microarray (Oligo-SNP Array)

Follow-up for abnormal methylation test for AS

	DNA Methylation	UBE3A Gene Sequencing ^a
Clinical sensitivity	AS: ~80%	AS: 11%
	PWS: >99%	PWS: n/a
Analytical sensitivity	99%	99%

^aTest is not performed at ARUP Laboratories.

Results

DNA Methylation	
Positive result	<p>Abnormal methylation pattern of maternally (PWS) or paternally (AS) contributed AS/PWS critical region is present</p> <p>Confirms diagnosis of AS or PWS</p> <p>Follow up with fluorescence in situ hybridization (FISH) or array comparative genomic hybridization (CGH) to determine whether deletion is present</p> <ul style="list-style-type: none"> • If large deletion is present <ul style="list-style-type: none"> ◦ Order chromosome analysis in parent to exclude rearrangement (alters recurrence risk; see AS and PWS Consult topic) • If FISH is normal <ul style="list-style-type: none"> ◦ Order DNA polymorphism analysis to distinguish between UPD and imprinting defect • If no UPD <ul style="list-style-type: none"> ◦ Order further DNA studies to detect imprinting defect <p>Testing of both parents may be necessary</p>
Inconclusive result	n/a
Negative result	<p>Normal methylation pattern of both maternally and paternally contributed AS/PWS critical regions</p> <p>Reduces, but does not exclude, the probability of an AS diagnosis (~20% of individuals with AS have normal methylation patterns)</p> <p>Greatly reduces the probability of a PWS diagnosis (99% of individuals with PWS have abnormal methylation patterns)</p>

n/a, not applicable

Limitations

DNA Methylation

- Specific molecular mechanism responsible for abnormal methylation results cannot be determined via this test alone.
- AS or PWS resulting from molecular mechanisms that do not affect methylation patterns will not be identified.

Additional Resources

Beygo J, Buiting K, Ramsden SC, et al. [Update of the EMQN/ACGS best practice guidelines for molecular analysis of Prader-Willi and Angelman syndromes](#). *Eur J Hum Genet*. 2019;27(9):1326-1340.

Dagli AI, Mueller J, Williams CA. [Angelman syndrome](#). In: Adam MP, Ardinger HH, Pagon RA, et al, eds. GeneReviews, University of Washington; 1993-2020. [Last Revision: Dec 2017; Accessed: Sep 2020]

[Diagnostic testing for Prader-Willi and Angelman syndromes: report of the ASHG/ACMG Test and Technology Transfer Committee](#). *Am J Hum Genet*. 1996;58(5):1085-1088.

Driscoll DJ, Miller JL, Schwartz S, et al. [Prader-Willi syndrome](#). In: Adam MP, Ardinger HH, Pagon RA, et al, editors. GeneReviews, University of Washington; 1993-2020. [Last Update: Dec 2017; Accessed: Sep 2020]

Goldstone AP, Holland AJ, Hauffa BP, et al. [Recommendations for the diagnosis and management of Prader-Willi syndrome](#). *J Clin Endocrinol Metab*. 2008;93(11):4183-4197.

Related Information

[Angelman Syndrome and Prader-Willi Syndrome](#)

[Laboratory Testing for Developmental Delay, Intellectual Disability, and Autism Spectrum Disorder](#)

[Testing for Genetic Syndromes Related to Developmental Delay \(DD\), Intellectual Disability \(ID\), and Autism Spectrum Disorder \(ASD\)](#)

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