Beckwith-Wiedemann Syndrome: H19 Methylation

**Condition Description**

Beckwith-Wiedemann syndrome (BWS) is a growth disorder and clinical features commonly include: macrosomia (large body size), macroglossia (enlarged tongue), visceromegaly, omphalocele, neonatal hypoglycemia, ear creases/pts, adrenocortical cytomegaly, and renal abnormalities (e.g., medullary dysplasia, nephrocalcinosis, medullary sponge kidney, and nephromegaly). Polyhydramnios may be identified during pregnancy. Infants with BWS have an approximately 20% mortality rate, mainly caused by complications of prematurely, omphalocele, and/or hypoglycemia. Macroglossia and macrosomia are generally present at birth but may have postnatal onset. The growth rate slows around seven to eight years of age. Hemihyperplasia may affect segmental regions of the body or selected organs and tissues. In addition, individuals with BWS are at an increased risk of developing embryonal tumors (e.g., Wilms tumor, hepatoblastoma, neuroblastoma, rhabdomyosarcoma). Development and intelligence are typically unaffected, with the exception of mild speech delay in some individuals with severe macroglossia.

Defects in imprinted gene expression at 11p15 are associated with BWS [1]. Greater than 70% of cases are found to have alterations in DNA methylation at two distinct differentially methylated regions (DMRs) at 11p15. DMR1 is located within the telomeric domain (also known as ICR1) and controls the expression of two genes, IGF2 and H19. DMR2 is located within the centromeric domain (also known as ICR2) and controls the expression of KCNQ1, CDKN1C, SLC22A1L and the TSSC3 genes. Alterations in DNA methylation at either of these DMRs causes aberrant expression of these imprinted genes leading to Beckwith-Wiedemann Syndrome.

BWS is typically sporadic, though inheritance has also been reported in an autosomal dominant pattern, due to other mutations. No single explanation can account for the phenotypic heterogeneity seen in patients with BWS. The recurrence risk due to methylation defects is estimated to be low.

References:

**Genes**

H19

**Indications**

This test is indicated for:
- Individuals with a clinical diagnosis of Beckwith-Wiedemann syndrome.
- Individuals with isolated segmental hemihyperplasia.

**Methodology**

Methylation-specific MLPA (MS-MLPA) is used to test for BWS. One advantage of MS-MLPA is that in addition to detecting DNA methylation abnormalities (epimutations), similar to Southern blot and quantitative methylation sensitive PCR, it also detects deletions and duplications (CNVs) of the 11p15 region. CNVs are estimated to be present in ~10% of patients with BWS. The presence of a CNV can increase the recurrence risk from that of the general population up to a 50% risk. Both methylation and CNVs will be reported from this analysis.

**Detection**

Hypermethylation of DMR1 (H19 gene) is expected to detect an additional 2-13% of individuals with BWS.

**Reference Range**

For DMR1 (H19 gene), an increase in DNA methylation of greater than two standard deviations above the mean of normal is consistent with BWS. See Coffee et al. for explanation of reference range [3].

**Specimen Requirements**

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) tube:
- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml
Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Related Tests**

- Chromosome analysis (CA, CB) and array CGH is available for children with growth disorders and congenital anomalies with or without mental retardation.
- Methylation for DMR1 (H19 gene) combined with methylation for DMR2 (Lit1 gene) is offered as a separate panel when no previous studies have been performed.