CARRIER GENETIC TESTING (CGT 600) v1.2

Patient Information		Sample Information		Clinic Information	
Unique pat id.:	0083148 - 15420713	**Sample type:**	Blood (EDTA)	**Clinic:**	IVI BUENOS AIRES
Patient name:		**Date of draw:**	24/08/2020	**Doctor:**	FLORENCIA D'ATRI
Patient DOB:		**Date of receipt:**	27/08/2020		
Sex:	Female	**Report date/time:**	06/04/2026 12:39		
Ethnic group:	Caucasian				
Indication:	No family history				

TEST RESULTS

POSITIVE

The individual is carrier of:

Deafness type 1A, autosomal recessive

Gene :	GJB2	**Allele:**	Het
DNA Change:	NM_004004.5:c.503A>G	**Inheritance:**	AR
Protein change:	p.Lys168Arg		
Variant classification:	pathogenic		

INTERPRETATION OF TEST RESULTS

This result does not have direct clinical consequences for the carrier individual; there is another normal gene copy for all positive autosomal recessive (AR) gene/s indicated in the table which provide normal biological information. The likelihood of transmission of the variant/s is 50%, independently for each one. To have a reduced risk of having affected offspring, the partner or gamete donor must be negative for the positive gene/s included in the table. Please be aware that family members may also carry some of the AR variants and this information maybe significant for them and for their offspring.

LOW COVERAGE VARIANTS

There are no low coverage variants.

TEST DESCRIPTION

The Carrier Genetic Test (CGT) is a preconception DNA screening test that aims to identify individuals and couples at increased risk of conceiving children affected by a monogenic disease. Knowledge of this risk may influence a couple's decision to conceive or encourage the couple to adopt preventive measures, including preimplantation genetic testing for the at risk disease (PGT-M) prenatal genetic testing, or to use donated gametes. The multigene CGT interrogates thousands of DNA variants using a high-throughput technology (Next Generation Sequencing, NGS).

COMMENTS

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TEST METHODOLOGY

1.DNA extraction from the biological sample. 2. Next Generation Sequencing of gene regions where known mutations are located (list available at https://cgt.igenomix.com/diseases-list/). 3. Raw data analysis using bioinformatics. QC parameters require that more than 99.7% of the tested variants have coverage greater than the minimum read depth (10x). 4. Complementary testing by other techniques for: a) SMN1 gene: exon 7 deletion; exon 7-8 deletion; b) CYP21A2 gene: frequent mutations (https://cgt.igenomix.com/diseases-list/); c) HBA1/HBA2 genes: frequent deletions (https://cgt.igenomix.com/diseases-list/); d) FMR1 gene: CGG repeat sizing (females only); e) DMD gene: frequent deletions and duplications (females only); f) F8 gene: intron 22 inversion (females only).

TEST LIMITATIONS

The CGT test only includes analysis of the specific variants included into the list at https://cgt.igenomix.com/diseases-list/, and no others. Therefore, the CGT test does not cover all monogenic diseases nor 100% of disease-causing mutations for each tested gene. The test does not include the analysis of conditions associated with mitochondrial DNA, multifactorial, digenic or dominant inheritance. The test does not detect large rearrangements (inversions, deletions and duplications more than 15 nucleotides), mutations located in regulatory regions or intronic regions outside the +/-3bp cut off or in low sequence coverage areas. DNA changes caused by trinucleotide repeat expansions are not detected, except those indicated in the methodology section. Finally, if our assessment of a variant fails to meet our QC parameters due to low coverage, a result for the variant(s) will not be issued. The analytical detection rate is higher than 99%. The clinical sensitivity varies among conditions (e.g.: for HEXB gene, 30% of affected patients are carriers of a 16 kb deletion that is not included in the test). The sensitivity for SMN1 is approximately 96% because point mutations or small ins/del are not analyzed and, for a normal result (2 copies detected), it is not possible to be certain that the two copies are each in one of the two alleles (non-carrier) or if both are in the same allele (cis) and no copies in the other (carrier).
A negative result for the variants included in CGT does not exclude the possibility of being a carrier. The presence of pseudogenes and/or rare polymorphisms and/or homopolymers may lead to false negative or false positive results. A negative result for the CGT variants does not exclude the possibility of a de novo mutation being present in the offspring. Germline mosaicism or low-level somatic mosaicism cannot be detected. As with any laboratory test, there is a small chance that this result may be inaccurate for a procedural reason such as an error during sample collection, labelling, processing, data collection or interpretation. Please note that the classification of variants can change over time. To check whether there have been any changes to the classification of reported variants, please contact IGENOMIX.

LEGAL/QUALITY

This test was developed, and its performance characteristics determined by Igenomix Group. It has not been cleared or approved by the US Food and Drug Administration. The test is used as a laboratory developed test for clinical purposes. *IGENOMIX SPAIN holds CLIA Certificate of Compliance: #99D2146167. Part of this test has been outsourced to a referral laboratory whose QMS is based on high Quality Standards, periodically monitored by Igenomix SPAIN and audited by independent external parties.

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EXEMPTION CLAUSE OF DIAGNOSTIC LIABILITY

The genetic diagnosis services carried out by IGENOMIX LATAM are exclusively intended to be interpreted by qualified/certified health professionals.

The result obtained by this test and the information that could be derived from it, cannot be considered in any case as substitute of genetic counselling or medical treatment by a trained professional neither represent itself a medical enquiry. We recommend that you consult your physician for genetic testing & counselling upon reception of your results.

Any result should be interpreted in the context of all available clinical findings, within the general context of a medical investigation, which must be conducted by clinically trained professionals. IGENOMIX LATAM is not responsible for any decisions made or actions undertaken by the contracting party based on the results provided by IGENOMIX LATAM or otherwise., nor the harmful temporary consequences diverted by its use, making specific discretion of taking appropriate legal measures assuming an improper use of those mentioned studies and analysis.

SIGNED	COUNTERSIGNED
	
Ana Cervero PhD	**ADEDOYIN OPEYEMI AKINWOLE MSc**
2703-CV Laboratory Director	Sr. Laboratory Manager

Si reside en ARGENTINA puede realizar cualquier consulta u obtener asistencia a través de los teléfonos +54 11 2000-3107 /11 5984-2420 o a través del mail de contacto infoargentina@igenomix.com

This test or part of this test has been outsourced to a referral Laboratory (IGENOMIX Group) Lab CLIA No.: 99D2146167

Deafness type 1A, autosomal recessive

What is Deafness type 1A, autosomal recessive?

Deafness, autosomal recessive type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GJB2 and GJB3 genes located on chromosomal regions 13q12.11 and 1p34.3 respectively. The age of onset is infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment. No other associated medical findings are present.

What is the next step if I am a carrier of Deafness type 1A, autosomal recessive?

If you are a carrier of Deafness type 1A, autosomal recessive it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

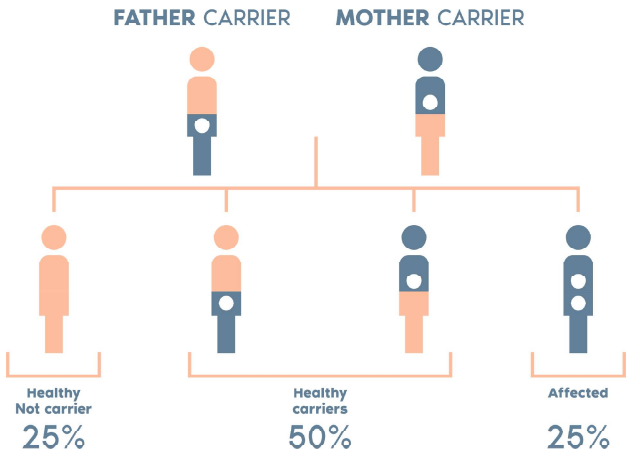
If your partner tests negative for Deafness type 1A, autosomal recessive, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Deafness type 1A, autosomal recessive?

When both parents are carriers of Deafness type 1A, autosomal recessive, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

GLOSSARY

TYPES OF INHERITANCE:

- AR: Autosomal recessive

  Inherited conditions that require two pathogenic variants (one from each parent) in a given gene to display symptoms.

- XR: X-linked recessive

  The gene is located on the X chromosome. Men with a pathogenic variant have the disease. Women with a pathogenic variant are carriers and generally asymptomatic or may mild symptoms.

- Digenic inheritance

  In some diseases, the symptoms could be explained by the coexistence of pathogenic variants in two different genes related with the disease instead of two pathogenic variants in the same gene.

ALLELES:

Pathogenic variants present in the two copies of a gene.

- Homozygous pathogenic variant (Hom.):

  Each copy of the gene has the same pathogenic variant. Generally, this is associated with clinical symptoms.

- Compound heterozygous (Het.):

  Each copy of the gene has a different pathogenic variant. Generally, this is associated with clinical symptoms. This situation is referred as having variants "in trans".

Pathogenic variant present in one copy of a gene.

- Heterozygous pathogenic variant (Het.):
  Only one copy of a gene has a pathogenic variant. There is another normal gene copy.

Note: Sometimes an individual has two pathogenic variants in the same gene copy. This situation is referred as having variants in cis and it is considered as a single pathogenic variant.

CNV:

Refers to copy number variation (deletion or duplication), i.e., the number of copies of a particular gene (or gene region) is different from the usual two copies.

LARGE GENE CONVERSION:

Refers to pathogenic variants caused by gene sequence exchange or replacement between a normal functional gene and a quasi-identical non-functional gene (pseudogene).