ABOUT MACULAR DYSTROPHIES AND STARGARDT DISEASE

Macular dystrophy exhibits autosomal dominant, autosomal recessive and X-linked pattern of inheritance. It is characterized by a localized impairment in the macula of the retina, which causes a loss of visual acuity. The most common pathology in this group is Stargardt disease, or juvenile macular dystrophy, with a prevalence of 1:10,000. Clinically it is characterized by the appearance of bronze-colored pigment deposits in the macula. Most of these cases are caused by recessive mutations in the ABC4A gene.

PATHOLOGIES

The panel includes the genes most often responsible for the following disorders:

- Bestrophinopathy
- Bothnia retinal dystrophy
- Doyne honeycomb degeneration of retina
- Fundus Albinipunctatus
- Pigmented paravenous choroidal atrophy
- Retinoschisis
- Sorsby Fundus Dystrophy
- Stargardt disease
- Vitelliform macular dystrophy type I
- Vitelliform macular dystrophy type II
- Vitreoretinoidopathy

GENES ANALYZED

ABCA4, BEST1, CIOTNFS, CDH3, CERK1, CFH, CNGB3, CRB3, DNM1L, EFEMP1, ELOVL4, FSCN2, GUCA1B, IMPG1, IMPG2, IRX1, KCNJ13, PROM1, PRPH2, RAX2, RBP3, RHDS, RLBP1, RPL1, RPGR, RPGRIP1, RSI, TIMP3

Non-coding regions included: ABCA4 all introns, RPGRIP1 promoter

PRICE

From €825. Please contact us to know the options that best suit your needs.

RESULTS

A detailed genetic report that includes the genetic variants identified and genetic counseling will be provided. Supporting information will be exhaustive based on bibliographical studies and database analyses and, especially, on our 25 years of experience researching the genetics of hereditary eye diseases. The test will be performed once payment is made and the signed informed consent and the sample are received. The report will be delivered 12 to 14 weeks after the above conditions are satisfied.

METHODOLOGY

The diagnostic strategy relies on the automated sequencing of DNA on Illumina HiSeq 2000 sequencers that are specially designed for this kind of high-performance analysis. Our panels have been designed to prioritize the genomic regions associated with the hereditary eye diseases indicated in this text.

The likely pathogenic nucleotide variants are verified using Sanger sequencing. We check that their frequency in the control population is below 1% and that they meet the pathogenicity predictions as per established bioinformatics algorithms (SIFT, LRT, MutationTaster, PolyPhen2, CADD and NetGene2).

RECOMMENDED FOR

This test is recommended when the clinical diagnosis indicates one of the pathologies previously listed and when the clinical condition is clearly defined.

This panel offers a high diagnostic performance because it includes all of the genes known to cause these diseases and because the method used allows identifying certain structural genomic alterations that are difficult to detect with other test types.