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### Miscarriage and thrombosis risk



WOMAM®<sub>MTR</sub> allows determining a woman's genetic risk of miscarriage and other thrombosisassociated pregnancy complications

This type of thrombophilia has a prevalence of up to 10% of the population depending on the affected gene.

WOMAM®<sub>MTR</sub> is a genetic test specifically designed to assess the risk of thrombophilia and reproductive complications in women with gestational desire in both, natural and assisted reproduction processes.

#### The process



#### Thrombophilia and its hereditary variant

Thrombophilia is a disease caused by the alteration of blood clotting mechanisms, which predisposes to developing thrombotic phenomena, such as the formation of clots that can obstruct the blood vessels. In many cases, women are unaware that they have thrombophilia until it manifests a related symptom, such as repeated miscarriages. Thrombophilia is one of the main causes of repeated pregnancy loss.

In pregnancy, the risk of thrombosis increases due to natural physiological phenomena. However, pregnant women suffering from thrombophilia have an increased risk. These women are more likely to develop clots that obstruct blood vessels and make it difficult for oxygen and nutrients to reach the fetus, risking the continuation of the pregnancy.

Hereditary or genetic thrombophilia is a genetic predisposition to abnormal blood clotting. It is a type of thrombophilia whose cause lies in the presence of genetic variants in the genes of the clotting proteins that alter their function, increasing the risk of developing clots.

Thrombosis is a complex disease and, as such, it is the result of the interaction between environmental factors, genetic predisposition and risk factors of the patient. However, genetics contributes in approximately 60% to the development of thromboembolic events. Therefore, the genetic study is key for the diagnosis of thrombophilia.

#### **WOMAM®**<sub>MTR</sub> test description

WOMAM®<sub>MTR</sub> is a genetic study that includes the analysis of 9 polymorphic variants of 7 genes (F2, F5, F12, F13A1, FGB, MTHFR, SERPINE1) that constitute a risk factor for thrombophilia and have been associated with pregnancy complications such as spontaneous abortion, recurrent fetal loss, preeclampsia, intrauterine growth restriction and/or placental insufficiency.

In this test, the polymorphisms and genes of interest are genotyped through an analysis of SNPs by quantitative PCR. It is therefore possible to determine the presence of risk allelic variants for a particular patient and, consequently, to establish the risks of thrombophilia and associated pregnancy complications.

#### **Benefits & value-added**

WOMAM®<sub>MTR</sub> is the first genetic panel for thrombophilia specifically designed for the analysis of the most informative gene variants responsible for hereditary thrombophilia and reproductive risk. Genetic variants classified as pathological and influencing human reproduction have been carefully selected, including variants associated with recurrent miscarriage preeclampsia, intrauterine fetal growth retardation, placental abruption, or intrauterine fetal death. The WOMAM®<sub>MTR</sub> panel can help in the diagnosis and orientation of the most indicated treatment in women who are experiencing difficulties in conceiving and want to avoid pregnancy risks and complications.

## Indications

Most women are unaware that they suffer from thrombophilia. This test is indicated for:

- Women who have experienced pregnancy loss, fetal growth retardation or intrauterine fetal death.
- Women who have experienced placental abruption, preeclampsia or implantation failure.
- Women exposed to risk factors such as muscle and blood vessel injuries, obesity, tobacco use, chronic diseases or major surgeries.
- Women who are experiencing difficulties to conceive.

#### **Process details**

A blood sample from the patient is required to perform the test. This sample is sent to our laboratory at room temperature where we will extract the DNA from the sample and analyse the genetic variants selected in the panel.



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