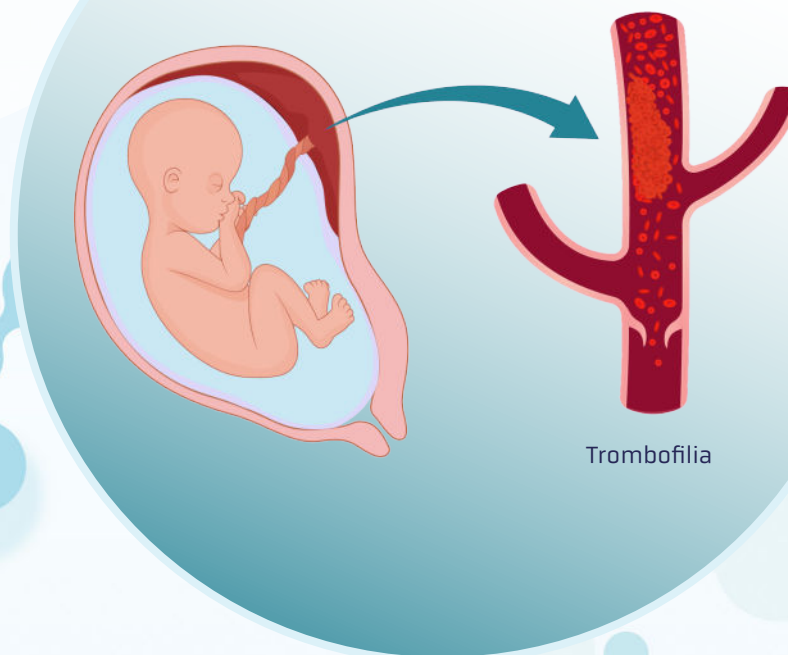


WOMAM[®]_{MTR} allows to establish the risk of miscarriage or other pregnancy complications associated with hereditary thrombophilia.

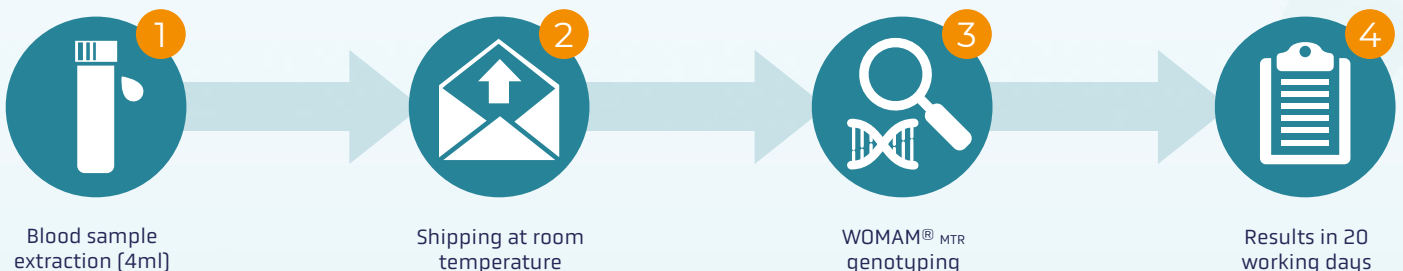


Thrombophilia has a prevalence of up to 10% of the population, depending on the affected gene.

WOMAM[®]_{MTR} is a genetic study specifically designed to assess the risk of thrombosis with reproductive impact in women with natural gestational desire or undergoing assisted reproduction treatment.

WOMAM[®]_{MTR} analyses 9 variants of 7 genes that have been associated with pregnancy complications such as miscarriage and pre-eclampsia.

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[®]MTR test description

WOMAM[®]MTR 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

The WOMAM[®]MTR panel can help in the diagnosis and guidance of the most indicated treatment for women who are experiencing difficulties in conceiving and want to avoid the risks and complications associated with pregnancy.

WOMAM[®]MTR is the first thrombophilia gene panel specifically designed for the analysis of the most informative gene variants responsible for inherited thrombophilia and reproductive risk. Genetic variants classified as pathological and with influence on human reproduction have been carefully selected, including variants associated with recurrent miscarriage, pre-eclampsia, intrauterine fetal growth retardation, placental abruption or intrauterine fetal death.

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

To perform the test, a blood sample from the patient is required. 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 using high-throughput quantitative PCR.

