



Effect of polymorphic variants of hereditary thrombophilia genes on the risk of early pregnancy loss for married couples

Liliya Fishchuk^{a,b,*}, Zoia Rossokha^a, Nataliia Medvedieva^a, Viktoriia Vershyhora^a, Larisa Sheyko^{b,c}, Ljudmila Brisevac^{b,c}, Nataliia Gorovenko^{b,c}

^a State Institution Reference-centre for molecular diagnostic of Public Health Ministry of Ukraine, Kyiv, Ukraine

^b State Institute of Genetic and Regenerative Medicine National Academy of Medical Sciences of Ukraine, Kyiv, Ukraine

^c Shupyk National Medical Academy of Postgraduate Education, Kyiv, Ukraine

ARTICLE INFO

Keywords:

Married couples
Early pregnancy loss
Hereditary thrombophilia
Gene

ABSTRACT

Background: Recent data demonstrate that hereditary thrombophilia may amount to 40–50% from all the early pregnancy loss (EPL) cases. However, the discrepancies in the results of different studies have not allowed for a categorical view on the role of hereditary thrombophilia in EPL development. The *aim* of this study was to assess the genetic risk of EPL in married couples, conditioned by variants of hereditary thrombophilia genes.

Materials: 137 married Caucasian couples (137 males and 137 females) from central regions of Ukraine with early pregnancy losses in the anamnesis were involved in the study. The comparison group consisted of 503 (240 males and 263 females) Caucasians enrolled in the 1000 Genomes Project.

Results: The study demonstrated a lower risk for men: in the recessive model, genotype 148TT of *FGB* gene; in the recessive model, genotype 455AA of *FGB* gene; in the dominant model, genotype 807CT and 807TT of *ITGA2* gene. The increased risk for women was observed: in the dominant model, genotype 148CT and 148TT of *FGB* gene; in the dominant model, genotype 455GA and 455AA of *FGB* gene; in the dominant model, genotype 1565TC and 1565CC of *ITGB3b* gene. There were no statistically significant differences between comparison groups for variants G20210A of *FII* gene and G1691A of *FV* gene. No statistically significant differences for investigated variants of genes were detected between the groups of men and women.

Conclusion: Our results demonstrate that the hereditary thrombophilia genes are associated with the risk of developing of early pregnancy loss for married couple, both for women and men.

Capsule.

Our results demonstrate that the hereditary thrombophilia genes are associated with the risk of developing of early pregnancy loss for married couple, both for women and men.

1. Introduction

Early pregnancy loss (EPL) – the loss of a pregnancy during the first 13 weeks of pregnancy – is among the most urgent problems of modern obstetrics and gynecology. The incidence of this pathology is up to 10–20% from the total number of pregnancies and does not tend to decrease (Vovk et al., 2015). In recent years, the understanding of reasons for EPL has changed considerably. It was previously believed that this pathological condition was caused by genetic, anatomic, endocrine, infectious, and immune factors, whereas recently the impairments in

homeostasis system have been separated into a special group. In particular, the researchers have turned their attention to hereditary thrombophilia as one of the events, leading to the EPL development (Bates, 2010; Carbone and Rampersad, 2010; Middeldorp, 2016). Recent data demonstrate that hereditary thrombophilia may amount to 40–50% from all the EPL cases (Nassour-Mokhtari et al., 2020).

During pregnancy, the changes in the mother's body lead to altered homeostasis (Ishida et al., 2011). Thus, there is a higher risk of thrombophilia owing to many genetic factors, including the later effect of gene variants on the coagulation and fibrinolytic systems (Barut et al., 2018; Kiseleva et al., 2017a, 2017b). On the other hand, many studies demonstrate a significant contribution of paternal thrombophilia into the increased risk of EPL (Udry et al., 2014).

Many thrombophilic gene variants, deemed to associate with EPL, have been reported (Coulam et al., 2006; Kamali et al., 2018). The most

* Corresponding author at: State Institution Reference-centre for molecular diagnostic of Public Health Ministry of Ukraine, Kyiv, Ukraine.

E-mail address: medgen@ukr.net (L. Fishchuk).

<https://doi.org/10.1016/j.mgene.2021.100902>

Received 3 September 2020; Received in revised form 26 March 2021; Accepted 10 April 2021

Available online 16 April 2021

2214-5400/© 2021 Elsevier B.V. All rights reserved.