DISTRIBUTION OF FOLLICLE-STIMULATING HORMONE RECEPTOR (*FSHR*) POLYMORPHISMS IN LITHUANIAN WOMEN

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Objectives: To our knowledge, this is the first study that observes FSHR Asn680Ser and Thr307Ala polymorphisms in Lithuanian women. The aim of this study is to investigate *FSHR* (follicle-stimulating hormone receptor) Asn680Ser and Thr307Ala polymorphisms and their association with clinical data in women undergoing assisted reproductive procedures at Fertility Center Santara. Ovarian stimulation is one of the most important steps in assisted reproductive procedures, amount and quality of retrieved oocytes often determines pregnancy success. FSHR polymorphisms could be biological markers for ovarian stimulation prediction and outcome prognosis.

Keywords: FSH receptor, DNA polymorphism, Ovarian stimulation, Asn680Ser, Thr680Ala, SNP, Assisted reproductive procedures.

Materials and methods: 66 women were included in this study. All women signed Informed consent (permission of Vilnius Regional Committee of Bioethics No 158200-14-743-260). Follicular fluid with remaining granulosa cells were collected after ultrasound controlled ovarian punction procedure and transported to Biobank (Vilnius, Lithuania), where DNA was extracted. Asn680Ser polymorphism was determined by PCR-RFLP and Thr307Ala – by nested PCR-RFLP. Age, amount and quality of retrieved oocytes, zygotes, embryos and procedure outcome (pregnancy) was registered in each woman.

Results: The frequency of Ser680Ser, Asn680Ser and Asn680Asn variants in women was 38, 45, and 17%, respectively, distribution of Thr307Thr, Thr307Ala and Ala307Ala variants was 30, 50 and 20%, respectively. Asn680Asn carriers provided more oocytes than other allelic variants – 12,60±8,49, Asn680Ser carriers provided 10,23±5,23 oocytes and Ser680Ser carriers provided less than other allelic varients – 9,36±5,70 oocytes, however differences were not statistically significant.

Conclution: Although Ser680Ser carriers provided less oocytes than other allelic variants, the differences were not statistically significant. Regardless statistically significance the further analysis of various SNP and their combination is needed to find the biological markers for the ovarian stimulation prediction.