GENETIC INFLUENCES ON ENDOCRINE SIGNALING IN WOMEN

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Objective: The hypothalamic-pituitary-ovarian (HPO) axis signaling pathway in female reproduction includes reproductive hormones GnRH, FSH, LH, estradiol, and progesterone. Studies have shown that endocrine levels in women are affected by single nucleotide polymorphisms (SNPs). This study aimed to identify SNPs impacting the HPO by exploring links between SNPs and baseline serum hormone levels in women.

Methods: Clinical and genetic data was collected for 143 women. AMH levels and day 2/3 serum FSH, LH, estradiol, and progesterone levels were collected by chart review. Genetic polymorphisms within FSHR, FSHB, AMH, and AMHR2 were genotyped. Welch’s t-test tested 150 associations between hormone levels and SNPs. A p-value of p<0.05 was considered significant. Documented informed consent was obtained.

Results: FSH levels were associated with two FSHR variants: p.S680N (rs6166; p=0.002) & p.A307T (rs6165; p=0.0065). Progesterone levels were associated with an FSHB variant: c.-280G>T (rs10835638; p=0.034). LH levels were associated with two AMH variants: c.-649C>T (rs4807216; p=0.019) and p.S49I (rs10407022; p=0.03).

Conclusions: We identified a novel interaction between LH levels and AMH, indicating a potential interaction between AMH and LH not yet characterized. The links between FSH levels and FSHR and between progesterone levels and FSHB have been shown before, demonstrating our ability to validate previous findings. Further studies designed to investigate multifactorial influences on endocrine signaling in female reproduction will lead to a deeper understanding of the clinical implications of hormone levels on fertility.