Docket #: S19-444

Predicting Male and Female Testosterone Levels from Genetic Data

Researchers at Stanford have developed a genetics-based approach that uses sex-specific genetic effects to predict testosterone levels in males and females. The new model outperforms all others and improves the ability to detect individuals likely to have abnormal testosterone levels in the population. Levels of the hormone are heritable and play an essential role in the health of both sexes. Problematic levels (over or underproduction) have been linked to infertility, cancer and other issues. However, to date no predictive models have been developed using genetic data to identify individuals likely to have abnormal levels. Understanding and predicting sex hormones from birth could provide significant insights into the physiological underpinnings of testosterone (and perhaps other sex hormones) in development and aging, and even present therapeutic opportunities.

Stage of Development
Successfully demonstrated. Future models will be improved using whole genome and exome sequencing data.

Applications

- Treatment of adrenal disorders
- Fertility prediction
- Sex drive prediction and treatment

Advantages

- No genetic methods exist for prediction of testosterone levels in females and males

Publications

- Emily Flynn, Yosuke Tanigawa, Fatima Rodriguez, Russ B. Altman, Nasa Sinnott-Armstrong, Manuel A. Rivas. Sex-Specific Genetic Effects Across Biomarkers bioRxiv 2019 doi: https://doi.org/10.1101/837021

Patents

- Published Application: 20210123932

Innovators

- Manuel Rivas
- Emily Flynn
- Yosuke Tanigawa

Licensing Contact

Imelda Oropeza

Senior Licensing Manager, Physcial Sciences

Email