Pharmacogenomics is undoubtedly a promising field in optimizing fertility treatment. Several polymorphisms in FSH and estrogen receptor genes have been detected so far but although it would be beneficial to predict accurately the response of patients to FSH, unfortunately we cannot yet rely on absolute predictors of ovarian performance.

The ovarian response to FSH stimulation is variable. Patients who undergo IVF/ICSI cycles tend to present with different responses to exogenous gonadotrophin administration probably due to the various single nucleotide polymorphisms (SNPs) in their receptor genes. We have now a large number of studies on the effect of single-nucleotide polymorphisms (SNPs) in the FSH receptor gene and its predictability in ovarian response to FSH stimulation. However, larger studies are needed to move on to clinical practice as other genes related to the FSH hormone mechanism of action may participate along with other factors to the control of ovarian response to FSH and until now, there is no clear clinical benefit in the screening for SNP before IVF treatment. Moreover, most of the available studies are retrospective, observational.

Identifying potential genetic markers that could predict ovarian response and implementing them in routine screening tests would allow to tailor fertility treatment, maximizing the success rate and eliminating potential side effects. However, there is the prospect of devising mathematical models using a group of polymorphisms to provide an important tool for improving ovulation induction, especially in poor responders.