

Περίληψη Αγγλικά

Infertility now affects 15% of couples worldwide, with the male factor being responsible for 50% of cases. Male infertility includes cases of oligozoospermia, asthenozoospermia, teratozoospermia, their combination and azoospermia which is divided into two categories, non-obstructive azoospermia and obstructive azoospermia. Infertility, a condition that affects a large percentage of the population, has been thoroughly investigated along with all the parameters that contribute to the manifestation of the condition, such as environmental effects, aging, daily habits and the genetic landscape of each individual. Regarding the genetic landscape specifically, there have been numerous studies that have used techniques such as the analysis of Y chromosome microdeletions in AZF regions, exome sequencing to investigate the coding regions of the genome, and sequencing of RNA molecules, both miRNAs and lncRNAs, molecules whose role in the occurrence of male infertility pose as a wide scientific field. The rapid development of new generation techniques has allowed an even more penetrating look at the exploration of the genetic causes of male infertility, with the use of genome wide association studies. GWAS contributed to the discovery of new markers responsible for a number of diseases that had not been analyzed until now, through the analysis of the frequencies of polymorphisms in two groups of individuals. The present study is the first attempt to carry out a genome-wide association study using the genotyping technique, in samples of fertile and infertile men in the Greek population.

The markers, as well as those in linkage disequilibrium with them, were categorized based on their functional role, thus highlighting the existence of many EQTLs, actively affecting the regulation of the expression of nearby (cis-EQTL) or distant (trans-EQTL) genes. The collection of all genes that EQTLs affect revealed numerous lncRNAs whose expression is regulated by them.

The role of lncRNAs in fertility is multifaceted as they are known to interact with miRNAs which in turn affect the expression of many mRNAs, silencing them. The collection of the complete list of interactions between lncRNAs-miRNAs-mRNAs leads to the understanding of the mechanisms through which RNA molecules can lead to the manifestation of male infertility and the discovery of new markers.

Overall, this thesis managed to obtain a fairly significant sample for the Greek population and creates a genetic and epidemiological data base, which is the foundation for subsequent studies, with an even larger number of individuals and more analytical power.