

Whole Exome Sequencing and Whole Genome Sequencing for Investigation of the Genetic Basis of Obesity: A Rapid Review

Roghayeh Dehghan* Mansoor Salehi***

ABSTRACT

Objective: In recent decades, the prevalence of obesity has reached a global epidemic level. This study was done to assess the whole exome sequencing and whole genome sequencing methods used to investigate the genetic basis of obesity.

Materials and Methods: Different studies on Pubmed, Scopus, Google Scholar and other data bases were extracted and their findings were analyzed.

Results: Childhood obesity has risen to alarming levels as World Health Organization (WHO) estimates that there were 38.2 million children under the age of 5 years with overweight or obesity in 2019. It has been shown that genetic factors also play a key role in the risk of obesity, and strong evidence suggests that BMI is highly heritable. However, in both adults and children, a major part of the genetic aetiology of obesity is still unknown. Recent advances and increasing affordability of whole exome sequencing (WES) and/or whole genome sequencing (WGS) have provided a rapid and comprehensive method for identifying the novel genes in obesity, particularly in children with severe early-onset obesity. **Conclusion:** This rapid review aimed to review a variety of literature reporting novel candidate genes for non-syndromic obesity identified through applying WES and WGS techniques in humans.

Keywords: Genetic Research, Obesity, Whole Exome Sequencing, Whole Genome Sequencing

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* Department of Genetics and Molecular Biology
School of Medicine
Isfahan University of Medical Science, Isfahan, Iran.

** Department of Genetics and Molecular Biology, School of Medicine
Pediatric Inherited Diseases Research Center
Child Growth and Development Research Center
Research Institute for Primordial Prevention of Non-Communicable Disease
Isfahan University of Medical Sciences, Isfahan, Iran.
E-mail: m.salehii@med.mui.ac.ir