

Editorial

Epigenetics of Obesity and Diabetes: Emerging Roles and Mechanisms of Non-coding RNAs

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Obesity is a chronic metabolic disorder affecting adults and children in developed and developing countries [1]. The World Health organization (WHO) considers that obesity has now reached epidemic proportions and continues to be a health concern worldwide. The pathogenesis of obesity is also an important driving factor for the development of type 2 diabetes mellitus (T2DM). The strong relationship between obesity and diabetes is of such interdependence that the term 'diabesity' was coined [2], suggesting a causal pathophysiological link between both diseases [3, 4]. Evidence suggests that both obesity and diabetes predispose to cardiovascular abnormalities [3, 5]. Multiple genetic, epigenetic and environment factors have been shown to play crucial roles in obesity and related vascular complications [6]. In spite of efforts in characterizing obesity at the genetics level and advanced clinical treatments, mortality in patients with obesity and diabetes remains high. In addition, the molecular mechanisms underlying these



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complications are still poorly understood. Hence, promising search for additional clinically relevant treatments as well as potential biomarkers with precise prognostic and diagnostic value may come from the ongoing clinical epigenetics research.

Epigenetics is defined as heritable changes in gene activity and expression that take place without a change in the DNA sequence. This process is now considered to be an intrinsic mechanism that bridges the two major disease-causing factors, environmental and genetic (Figure 1) [7]. In this respect, the recently unveiled epigenetic regulatory mechanisms are probably the most relevant finding to explain how genome interact with environment factors to alter gene expression and ultimately affect a phenotype. The epigenome includes DNA methylation, histone modifications and the most recently discovered class of noncoding RNAs (ncRNAs), particularly microRNAs (miRNAs), long noncoding RNAs (lncRNAs) and circular RNAs (circRNAs) [8]. They are shown to regulate various processes such as cell differentiation, cell-specific gene expression, posttranslational modifications and chromatin stability and structure [9]. In addition, they are now well characterized and incorporated as important epigenetic players in epigenetic-based diseases [10].

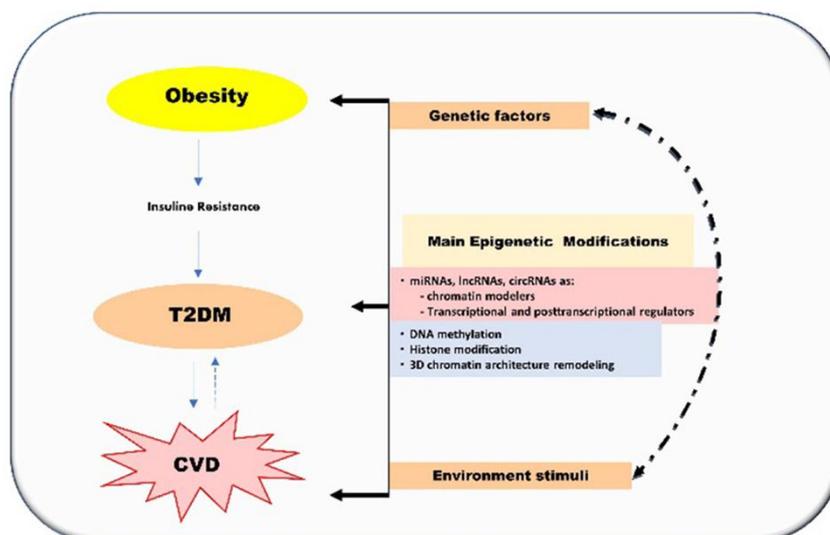


Figure 1 A simplified schematic diagram of the most studied epigenetic regulators that may mediate genetics and environment factors interaction in obesity and type 2 diabetes mellitus (T2DM). Epigenetics is now considered to be an intrinsic mechanism that bridges the gap between genetic and environmental factors to cause diseases. In addition to DNA methylation, histone post-transcriptional modifications, and chromatin remodeling, some dysregulated RNA transcripts, including long noncoding RNAs (lncRNAs), microRNAs (miRNAs) and circular RNAs (circRNAs) are also suggested to regulate gene transcription and mRNA processing and modifications. By these mechanisms, ncRNAs are supposed to mediate the effects of genetic and environment factors interaction to shape obesity and its related complications phenotype.

Although epigenetic has offered valuable tools for the understanding of obesity, most available studies in the field have focused only on DNA methylation [11]. Recently, reports have highlighted the relevance of ncRNAs to the development and progression of obesity and diabetes, supporting the importance of epigenomics in the pathogenesis of metabolic disorders [12-16]. However,

researchers remain challenged with many open questions: “How ncRNAs are engaged in networks that control the pathogenesis of obesity and related diabetes and by which mechanisms they can play a role in consequent risk of cardiovascular and metabolic problems?”

Answers to these questions may come from advances in knowing epigenetic mechanisms which will provide new opportunities for predicting, preventing, diagnosing and treating complex diseases such as obesity and diabetes. Thus, it is of significance to publish this Special Issue of *OBM Genetics* that focuses on “Epigenetics of Obesity and Diabetes: Emerging roles and mechanisms of noncoding RNAs”. This issue serves to highlight some of the latest and outstanding developments in the field of obesity and DM, specifically in the context of the emerging epigenetics regulatory mechanisms. Additionally, the current issue represents a great opportunity for researchers around the world to cover various research topics related to ncRNAs as epigenetic regulators not only in obesity but also in its main complications, T2DM and cardiovascular diseases. The papers gathered in here might provide readers with comprehensive overview and update on the status studies of ncRNAs as they may also help them gain a better understanding on epigenetics mechanisms and develop strategies that targets RNA transcripts to prevent obesity and obesity-promoted diabetes and other vascular complications. Such knowledge could pave a way to discover novel biomarkers for early detection of obesity and diabetes and reveal the underlying mechanisms.

I hope that research presented here will not only provide researchers with new insights and viewpoints on the epigenetic regulatory role of ncRNAs in obesity and diabetes states but also trigger some hypothesis and novel directions for further work on this topic. I am grateful to the Editor-in-Chief, Dr. Joep Geraedts, and Editorial members of *OBM Genetics* for giving me this opportunity to publish this special issue on this special and relevant topic.

Author Contributions

Mohamed Zaiou is the sole contributor to this work.

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