# Hereditary component analysis for ms

The family and twin studies provide evidence of the presence of an important hereditary component in the etiology of MS, with percentages of heritability ranging from 24% to 31. 6% (Bellia et al., 2009; Lin et al. ., 2005; O'neill et al., 2015). Among the etiopathogenic models to explain the origin of MS, partial lipodystrophy, which results from mutations in the LAMINA A / C (LMNA) genes or the peroxisomal proliferator activated receptor (PPARg) gene, is a paradigm of genetic processes Involved (Hegele and Pollex, 2005). The PPARg gene, which is involved in the processes of differentiation and functioning of adipocytes, is believed to be related to the etiopathogenesis of obesity (Ristow et al., 1998; Moustafa and Froguel, 2013). Specifically, the α-form of PPAR is believed to play an essential role in the origin of MS, since it regulates the oxidation and transport of fatty acids and the generation of lipoproteins (Guan and Breyer 2001, Tan, Zhuang and Wahli, 2017). PPARγ is a key regulator in the process of adipogenesis and its increased function results in increased body mass, whereas decreased activity induces weight loss and the development of IR ( Deeb et al., 1998, Majid et al., 2016).

The adiponectin regulatory gene (APN gene), a hormone involved in the regulation of energy homeostasis, and glucose and lipid metabolism, could induce IR by reducing the synthesis of this hormone (Maeda et al. , 2002; Yamauchi et al., 2003). Plasma adiponectin levels are inversely related to body mass and may have an important protective role against MS because of its anti-inflammatory, antioxidant and antiatherogenic effects (Esfahani et al., 2015). In addition, certain genetic polymorphisms have been identified for this gene that are related to the synthesis of insulin, IR and DM (Filippi et al., 2004).

The CD36 receptor gene for thrombospondin, whose function is to bind and capture fatty acids to be used by other tissues, is also a candidate in the etiopathogenesis of MS (Love-Gregory et al., 2008; Zhou et al., 2016 ), Since we know that fatty acids induce IR, obesity and inflammation (Roden, 2007). It is described that CD36 deficiency causes an imbalance in glucose levels in response to insulin, as well as higher levels of fatty acids, TR, fasting glucose and blood pressure (MA) (Ma et al., 2004: Pioltine et al. Al., 2017).

The enzyme 11 beta-hydroxysteroid dehydrogenase type 1 (11β-HSD1), whose function is to interconvert 11-inert ketosteroids, cortisone and 11-dehydrocorticosterone (11-DHC), to its 11-hydroxy active forms, cortisol and corticosterone. 11β-HSD1 is considered to have an important etiological factor in obesity. Although circulating concentrations of glucocorticoids are not elevated in prevalent forms of human obesity, locally enhanced glucocorticoid response in skeletal muscle and adipose tissue has been implicated in MS (Walker, 2007; Cai et al., 2016) . Clinically, RI and HT are associated with increased messenger RNA alpha glucocorticoid receptors (GRα) and the number of receptors in skeletal muscle, and a positive association between messenger RNA levels for both GR Such as 11β-HSD1 in skeletal muscle for the condition of insulin resistance (Seckl, Morton and Chapman 2004; Freude et al., 2016).

B-adrenergic receptors regulate the lipolysis and metabolism of free fatty acids. The β3-adrenergic receptor (β3AR) is a candidate gene for abdominal obesity and is related to visceral fat (Krief et al., 1993; Chen et al., 2015). Increased β3AR function leads to increased catecholamine-induced lipolysis in the visceral fat of subjects with abdominal obesity, as well as to a lower

metabolic rate and a lower activity of the resting sympathetic nervous system, all of them characteristics of MS (Shihara et al. Groop and Orho-Melander, 2001, Luglio, Sulistyoningrum and Susilowati, 2015)

The Calpain-10 gene (CAPN10), which encodes the corresponding protein, has been associated with an increased risk of DM and RI becoming a strong candidate in the pathogenesis of MS (Orho-Melander et al., 2002; Loya Méndez Et al., 2014). It is also related to hypertension (Chen et al., 2007), overweight and obesity (Orozco et al., 2014), high cholesterol (Wu et al., 2005) and elevated triglyceride levels (Carlsson, Fredriksson et al. Groop, 2004), all components of the syndrome being analyzed. Another scientific work found in a haplotype of the polymorphism of this gene a risk factor for MS in patients with DM (Kang et al., 2006). It also establishes association with two indicators of the presence of IR, such as high glucose levels after a tolerance test and with HOMA values of RI (Saez et al., 2008).

Other genes possibly implicated are those that encode the C-reactive protein, the best inflammatory biomarker, a characteristic of MS and also a predictor of CVR (Devaraj, Singh and Jialal, 2009), as well as the encoder of substrate 1 Of the insulin receptor (IRS1), whose mutations are associated with DM and IR (Kubota et al., 2000). In any case, the genetic ethiopatology leaves unresolved the controversy regarding the predisposing causative factor of MS, since in the scientific community there are defenders of the IR as the main factor involved, while others are inclined to obesity and metabolic dysfunction Of lipids as the most important agent (Alberti et al., 2009; Dragsbæk et al., 2016; Gluvic et al., 2017).