Differences in circulating microRNA signature in Prader-Willi syndrome and non-syndromic obesity

D. Pascut, S. Tamini, S. Bresolin, P. Giraudi, G. Basso, A. Minocci, C. Tiribelli, G. Grugni, A. Sartorio

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Prader-Willi syndrome (PWS) represents the most common genetic-derived obesity disorder caused by the loss of expression of genes located on the paternal chromosome 15q11.2-q13. The PWS phenotype shows peculiar physical, endocrine and metabolic characteristics compared to those observed in non-syndromic essential obesity. Since miRNAs have now a well-established role in many molecular pathways, including regulatory networks related to obesity, this pilot study was aimed to characterize the expression of circulating miRNAs in PWS compared to essential obesity. The circulating miRNome of 10 PWS and 10 obese subjects, adequately matched for age, BMI and sex, was profiled throughout Genechip miRNA 4.0 microarray analysis. We identified 362 out of 2578 mature miRNAs to be expressed in serum of the studied population. The circulating miRNA signature significantly characterising the two populations include 34 differently expressed RNAs. Among them, miR-24-3p, miR-122 and miR-23a-3p highly differ between the two groups with a FC >10 in obese compared to PWS. In the obese subjects, miR-7107-5p, miR-6880-3p, miR-6793-3p and miR-4258 were associated to the presence of steatosis. A different signature of miRNAs significantly distinguished PWS with steatosis from PWS without steatosis, involving miR-619-5p, miR-4507, miR-4656, miR-7847-3p and miR-6782-5p. The miRNA target GO enrichment analysis showed the different pathway involved in these two different forms of obesity. Although the rarity of PWS actually represents a limitation to the availability of large series, the present study provides novel hints on the molecular pathogenesis of syndromic and non-syndromic obesity.