Mitochondrial genetic variants identified to be associated with BMI in adults.

Abstract:
It has been suggested that mitochondrial dysfunction plays a role in metabolic disorders including obesity, diabetes, and hypertension. The fact that mitochondrial defects can be accumulated over time as a normal part of aging may explain why some individuals can eat all sorts of foods and remain at normal weight while they are young. However, around the fourth decade of life there is a trend towards "middle-age spread" with weight gain and the body's decreasing ability to metabolize calories efficiently. To test the hypothesis that mitochondrial variants are associated with BMI in adults, we analyzed a total number of 984 mitochondrial single nucleotide polymorphisms (mtSNPs) in a sample of 6,528 individuals participating in the KORA studies. To assess mtSNP association while taking heteroplasmy into account we used the raw signal intensity values measured on the microarray and applied linear regression. Significant results were obtained for 2 mtSNPs located in the Cytochrome c oxidase subunit genes (MT-CO1: $P_{adj} = 0.0140$ and MT-CO3: $P_{adj} = 0.0286$) and 3 mtSNPs located in the NADH dehydrogenase subunit genes (MT-ND1, MT-ND2 and MT-ND4L: $P_{adj} = 0.0286$). Polymorphisms located in the MT-CO3 and MT-ND4L genes have not been associated with BMI or related phenotypes in the past.
Our results highlight the importance of the mitochondrial genome among the factors that contribute to the risk of high BMI. Focusing on mitochondrial variants may lead to further insights regarding effects of existing medications, or even to the development of innovative treatments.