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Distinct Genetic Susceptibility Patterns of the Obese and Non-obese South Indian Women with Polycystic Ovary Syndrome

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ABSTRACT The researchers studied association of 92 SNPs of the metabolic and reproductive pathways genes in the obesity related cohorts of obese PCOS cases and non-obese controls, and non-obese PCOS cases and non-obese controls and observed eleven SNPs to be significantly associated ($p \leq 0.05$). While eight of those SNPs, five from FTO and one each from MTCH2, DENNDIA and THADA genes, were found to be associated in the first set involving obese PCOS cases, only three SNPs (IRS2-intronic, LOC107984901-intergenic and SUMO1P1-regulatory variants) showed association in the 2nd set involving non-obese cases. The SNPs associated in the two cohorts were distinct and mutually exclusive. However, all the SNPs associated in either obese or non-obese PCOS cohorts were not only risk-prone but also broadly represented a metabolic pathway, involving mostly obesity and T2DM related genes, prompting one to surmise if the recent spurt in PCOS prevalence is not driven by changes in the lifestyles.