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Prospective Study

Epigenetic profiles of pre-diabetes transitioning to type 2 diabetes and nephropathy

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Abstract

Recent studies suggest that gene-environment interactions relevant for diabetes are at least partly regulated by epigenetic mechanisms and may contribute to the progression of pre-diabetes (Pre-DM) to overt type 2 diabetes (T2DM). In this study, DNA methylation profiles were examined in a longitudinal comparison of Pre-DM subjects who transitioned to T2DM. The cohort examined was limited to white non-Hispanic male subjects transitioning from Pre-DM to T2DM who eventually developed diabetic nephropathy. DNA methylation profiling was carried out on bisulphite-converted DNA obtained from controls and from Pre-DM subjects (n=11) at baseline and at their transition to T2DM using the Illumina Infinium® HumanMethylation27 BeadChip. There were 64 CpG sites hypomethylated and 174 CpG sites hypermethylated in progression from Pre-DM to T2DM, representing putative genes involved in glucose

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