

Sequence variation in a microRNA (miRNA) seed region can influence its biogenesis and effects on target mRNAs; however, in mammals, few seed region mutations leading to functional alterations have been reported to date. Here, we report the identification of a single nucleotide polymorphism (SNP) with functional consequence located in the seed region of porcine miR-378. *In vitro* analysis of this rs331295049 A17G SNP showed significantly up-regulated expression of the mature miR-378 (miR-378/G). *In silico* target prediction indicated that the SNP would modulate secondary structure and result in functional loss affecting >85% of the known target genes of the wild-type miR-378 (miR-378/A), and functional gain affecting >700 new target genes, and dual-luciferase reporter assay verified this result. This report of a SNP in the seed region of miR-378 leads to functional alteration and indicates the potential for substantive functional consequences to the molecular physiology of a mammalian organism.

The SNP changed the secondary structure of pre-miR-378 and increased the production of mutant miR-378. Functionally, the SNP lead to loss and gain of miR-378 targets.