

TITLE

THE CAUSE OF CONGENITAL WATTLES IN PIGS

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CONTENT

Background

In some rare breeds of domestic pigs, such as Kunekune from New Zealand or Casertana from Italy, most of the animals show congenital wattles at the base of their throat. Wattles are supposed to be under genetic control with a Mendelian dominant mode of inheritance. This study aims to unravel the molecular genetics of wattles in pigs.

Material & Methods

Hair root samples of 40 Kunekune were collected and the animals were scored for the number of wattles. Most Kunekune (32/40) showed two wattles on their lower jaw, whereas a single animal showed only one wattle and seven pigs showed no wattles. Furthermore, blood samples of 11 Casertana pigs (5 with and 6 without wattles) were collected from Campania in Italy. A total of 35 samples were genotyped with GeneSeek Genomic Profiler Porcine 51k SNP chip for a subsequent genome-wide association study.

Results

A cohort of 23 pigs (18 Kunekune and 5 Casertana) with wattles and 12 pigs (7 Kunekune and 5 Casertana) without wattles was genotyped successfully at 45787 SNP markers. We obtained a single strong genome-wide significant association signal on pig chromosome 1 in a region containing a gene encoding a bone morphogenetic protein (BMP) family member. The associated haplotype is shared across breeds.

Discussion & Conclusion

This is the first report, mapping the most likely dominant inherited wattles locus in the porcine genome. Members of the BMP family have been implicated in setting up patterning of the vertebrate limb and in its outgrowth. Interestingly, the identified association is not located in the genomic region containing the gene associated with wattles in goats indicating genetic heterogeneity causing this phenotype in different domestic animal species. We are currently sequencing the whole genomes of individual pigs with and without wattles from both examined breeds to identify the causative variant.