

Polydactyl Pigs: There's More to the Story Than Just Extra Toes

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Summary and Implications

Several pigs expressing a polydactyl (extra toes) phenotype were identified in the ISU purebred Yorkshire herd. Sires, dams, and littermate sibs to the polydactyl pigs were retained in the herd and planned matings were designed to enlarge the population. In addition to creating 12 pigs with either extra toes or dewclaws, the population also had an extremely high number of stillborn and mummified pigs. Furthermore, this population also showed differences in growth and reproduction. Multiple genes have been implicated in causing extra digits in several other species. Using comparative genomics as a guide many of these genes were expected to map on pig chromosome 18. Pig chromosome 18 is the smallest pig autosome on which there has been limited research. Candidate genes on pig chromosome 18 were mapped to ensure their location using Iowa State University's Berkshire by Yorkshire resource population. Once chromosomal locations were confirmed for each candidate gene, genotypes were obtained for each gene on all pigs in the polydactyl population and were used by a complex statistical method (Elston-Stewart algorithm) to calculate the likelihood that the gene caused the polydactyl phenotype.

Introduction

In November of 2003, two purebred Yorkshire pigs (one gilt and one barrow) from different litters were identified on Iowa State University's swine research farm that possessed what appeared to be extra feet (see Figure 1). The pedigrees of both pigs were analyzed and showed that they in fact shared enough common ancestry to allow for a gene with a recessive mode of inheritance to be the culprit. When the polydactyl pigs were identified, both dams were still on the farm while only one of the sires remained. Therefore the remaining sire was mated to both dams. Littermates (all gilts and intact males) to both affected pigs and pigs resulting from subsequent matings were retained on the farm and were included in this unique population once they reached sexual maturity.

Results and Discussion

We have generated 12 pigs with any one of three distinct phenotypes, being what appeared to be an extra foot with a normal dewclaw (Figure 1), an extra foot minus the normal dewclaw (Figure 2), or an extra dewclaw (Figure 3). These phenotypes have only been seen on the front legs of the individual and can appear on either one or both front legs. Of the 12 pigs generated with these distinct phenotypes, 6 have been alive at birth while 6 were stillborn with no preference for sex. In the 13 litters produced thus far in this population, there have been 40 stillborn pigs and 13 mummies with only 87 live pigs. Additionally, pigs from these litters show a decrease in average daily weight gain with the gilts showing a delayed first estrus and various vulva deformities.



Figure 1.

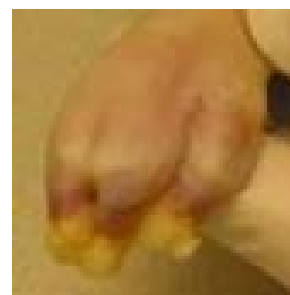


Figure 2.



Figure 3.

Several candidate genes on pig chromosome 18 have been isolated and checked for the mutation(s) causing the polydactyl phenotype. Genes such as LMBR1, WNT, TWIST, and HoxA, which are all known to cause some sort of polydactyl in other species, have all been analyzed though none have shown association with the polydactyl phenotype in this population of pigs. These markers in addition to other markers on pig chromosome 18 (see Figure 4) have been used in conjunction with the Elston-Stewart algorithm to help narrow down the region expected to contain the causative mutation. Through this procedure, we have isolated a small region on chromosome 18 (highlighted in red in Figure 4) that gives a statistically high likelihood of containing the causative mutation. More research in this region is warranted to determine the causative mutation.

Conclusion

Though the polydactyl phenotype is what first led us to examine this population, we strongly feel that the more important story at hand is the other phenotypes that we are witnessing in this population such as the decreased growth, high number of stillborns, and delayed estrus, which are the most pertinent traits in the swine industry. This research, in conjunction with ongoing research, led us to believe that the mutation causing this polydactyl phenotype is at least linked to these additional traits. Though the mutation that causes the polydactyl phenotype eludes us at this time, we feel confident that in the near future we will be able to identify the causative mutation using this unique population and the genetic tools at hand.

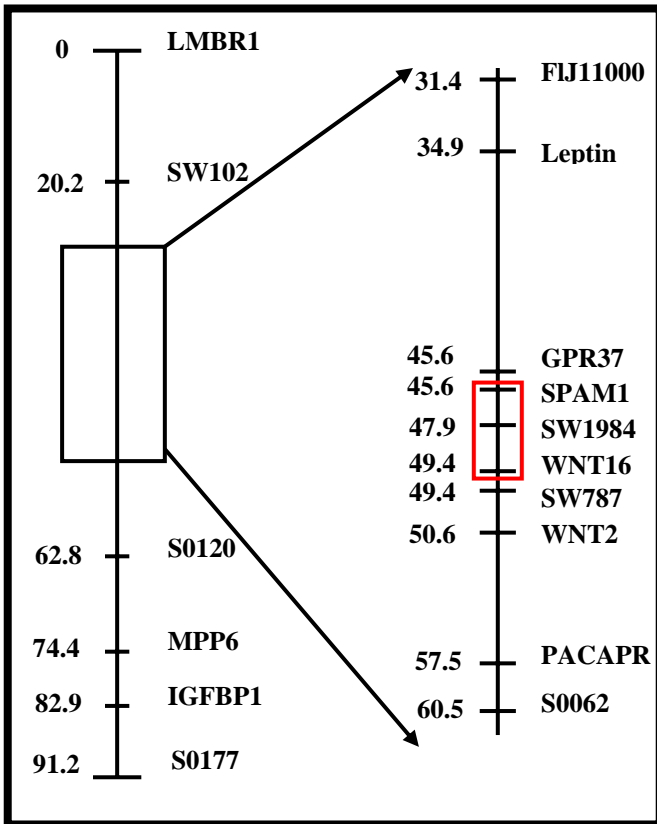


Figure 4.