Maternal Effects on Long Bone Length

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Abstract

Past studies have given the heritability of long bones but have not taken maternal effects into consideration. The goal of this research is to identify the proportion of maternal effects in that heritability and the level of influence that it has on offspring. This will use the information of a parent and offspring generation of mice to create a mixed model that can identify the maternal effects apart from direct effects. The results will give a map for identifying the loci for the maternal effects that indirectly influence long bones. This would overall give estimates and an explanation for variation of offspring for certain populations.

Introduction

Maternal effects are defined as the effects of the genetic and environmental factors acting indirectly through their mother on the offspring's phenotype. These effects are transferred to the offspring in addition to the genes passed from the parents to their offspring. Maternal effects contribute to the risk of many known diseases in their offspring, such as obesity and diabetes. The goal of this research is to identify the influence of such maternal effects on the growth of long bones (the focus being the humerus, ulna, tibia, and femur) and measure their level of influence while excluding the direct effects of genes carried by the offspring on their long bone growth. It is already known that the heritability of long bone growth is high, ranging from 0.68 to 0.85. We were also able to measure the direct effects of the genetic locations and diet of the offspring, but the genetic effects from the maternal generation are still unknown. Maternal effect QTL indicates that the gene activity responsible for variation in offspring long bone lengths resides in the mother, not the offspring

Methodology

The data for the mice from the F33/F34 generation were taken from a study done at Washington University. With this data, we used a program created by R to produce three models: the null, reduced, and full model. The reduced model included the additive, dominance, as well as imprinting effects while the full models included the same traits with the addition of maternal dominance and additive effects. We then looked for locations in which the data exceeded the value for significance for both the full and reduced model to find which parts of which chromosomes were of interest.

Results

Four QTLs across the mouse genome exceeded the 5% threshold in both the full and reduced mode. These chromosomes were 8, 12, 14, 15, and 18. The ulna did not past the threshold for chromosome 8, 15, or 18. Tibia was the only one that was shown to be significant in chromosome 12 and this is paralleled for the ulna in chromosome 14.

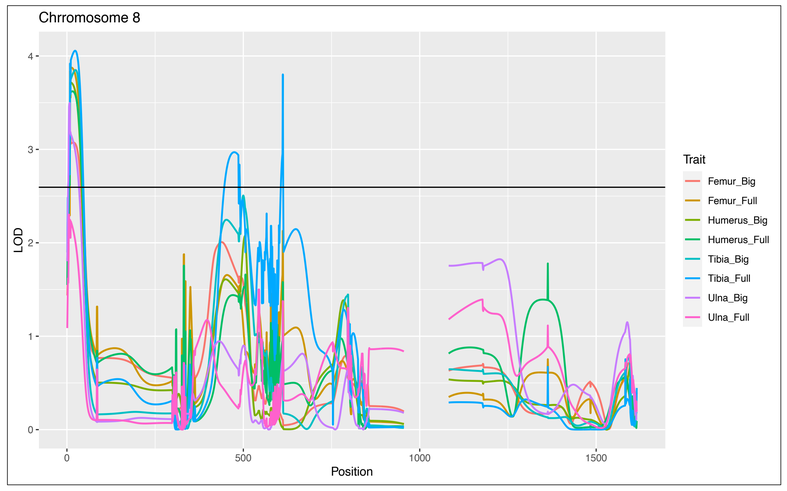

Figure 1. Significance of lod scores in chromosome 8 across 1618 positions. The femur, tibia, and humerus had the greatest significance in the first 40 positions as both the reduced and full model were above the threshold of 2.59467594.

Discussion

It was expected that there would be a few regions that exceed the threshold across the 19 chromosomes, and this is supported by the data. Although five of the chromosomes showed some significance, these regions were small. Each of these chromosomes has a range from 800-1600 positions in which the highest significance range was only 35. It was interesting to see that the ulna was influenced solely by chromosome 12 and not by chromosome 8 as well as 15 since the other long bones were influenced together in those regions. It was anticipated that all four long bones would be influenced by the same regions.

Future Steps

These steps are going to be repeated for the F9/10 and the F2/3 generations. This will help create a map for maternal genetic loci which affect the length of the long bones in the offspring and can tell us how much variation is caused by these indirect effects. Genome databases will also be used to identify the known genes in the regions.

References

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