

Fine-tuning the predicted position of genes associated with economic traits in livestock

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Summary and Implications

Different methods that estimate the position of a gene on a chromosome were tested in computer-simulated populations to determine their accuracy. Given the same amount of genetic information from the animals, one method performed better than the others. In situations where experimental costs were assumed to be equal but genetic information could vary, this method was no longer the most accurate. Further study of this method found that the animals' genetic information must be used in a specific way in order to obtain the most accurate position of the gene. These methods will be useful in identifying genes and the genetic differences between animals that can be used for genetic improvement of livestock.

Introduction

In order to identify the genetic differences that may be useful for genetic improvement, the genes underlying important traits must first be found in the genome. The objective of this study was to determine which of several different methods could best estimate the position of a gene within a small region of a chromosome. These methods all compare animals' genetic markers with their trait measurements and determine which genetic markers are most associated with the trait. The actual gene affecting the trait is assumed to be located closest to the marker(s) that show the strongest statistical association with the trait. The methods differ in the way that they use the animals' genetic information. Determining the best method of analysis is important for locating genes quickly at a minimal cost.

Materials and Methods

Multiple animal populations were generated by computer simulation to test these gene mapping methods under different conditions. In all the populations each animal had one gene that affected a single trait and ten

genetic markers surrounding the gene. Two different statistical methods, Methods A and B, were compared. Method A uses genetic marker information to determine if individuals' genes were inherited from a common founder individual, or are identical by descent (IBD). Method B uses the statistical method of regression (REG) to determine an association between marker genotypes and the trait measurements. The gene affecting the trait is assumed to be closest to the marker with the strongest association. Within each method, the amount of genetic information used from the animals was allowed to vary. Method A was allowed to use information from 1, 2, 4, 6 or 10 genetic markers at a time. Method B was allowed to use 1 or 2 markers at a time. Using Method A for analysis will result in additional genotyping costs for the additional markers compared to Method B. So, Method B was also allowed to use information from 20 total genetic markers, still using 1 or 2 markers at a time.

Results and Discussion

In all populations, Method A using all 10 markers was better than Method B using 10 markers. However, when 20 markers were used for Method B, it was nearly always more accurate than Method A. It was found that Method A using 4 or 6 markers and Method B using 20 markers were comparable and were the most accurate methods in all population types. Generalized results from these comparisons are shown in Table 1.

Conclusions

Additional studies revealed that individual animal's genetic information must be used in a specific way in order to obtain the most accurate estimate of the gene's position. Future studies to identify genes affecting economically important traits in livestock should consider using Methods A or B in the manner described.

Acknowledgements

This work was supported in part by Monsanto Company, Sygen International, the Iowa Agriculture and Home Economics Experiment Station, Ames, Iowa and by Hatch Act and State of Iowa funds. We would like to thank Dr. Dan Nettleton for his comments and suggestions.

Table 1. Method(s) with the highest mapping accuracy (✓) for a given population type.

| Population | Method A (IBD method) ¹ | | | | | Method B (REG method) ¹ | | | |
|------------|------------------------------------|-----------|-----------|-----------|------------|------------------------------------|-----------|------------------|-----------|
| | 1 marker | 2 markers | 4 markers | 6 markers | 10 markers | 10 total markers | | 20 total markers | |
| | | | | | | 1 marker | 2 markers | 1 marker | 2 markers |
| 1 | | | ✓ | | | | | ✓ | |
| 2 | | | ✓ | ✓ | | | | ✓ | |
| 3 | | | ✓ | | | | | ✓ | |
| 4 | | | | | | | | ✓ | |
| 5 | | | ✓ | ✓ | ✓ | | | ✓ | |

¹IBD = identical by decent, REG = regression