

Integrating QTL Mapping Data Across Species: Comparative Genomics Made Quantitative

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Abstract:

Comparative genomics involves using information gained in one or more species to help understand genomic structure or genotype/phenotype connections in other species. The importance of comparative genomics cannot be understated. An example involves the discovery of the “double muscling” (myostatin) gene. This gene was knocked out in mice and found to produce massive muscle hypertrophy. It was subsequently found to be the same gene that produced the double muscling syndrome in cattle. Most examples of comparative genomics are somewhat less dramatic than this. It is extremely common in QTL mapping for investigators to identify a statistically significant linkage in one region of the genome of one species (e.g. human) and point out that sentenic regions of other species (e.g. mouse; rat; pig) have also been shown to harbor putative QTL, thereby strengthening belief in the validity of the linkage finding. This strengthening belief is almost always conducted in a subjective or qualitative manner. However, it may be possible to make this subjective approach objective through the use of methods that incorporate empirical bays methodology. Drawing on the approach cogently articulated by Morris (1983) and the ever-increasing available information about homology between the genomes of organisms such as human, mouse, pig, rat, etc., show how one could approach comparing QTL results from one species to another for a degree of consistency. Moreover, I offer one way in which this approach might be used to provide tighter estimates of QTL effects and, thereby, increase statistical power to detect significant QTL.