Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Precision of distances and ordering of microsatellite markers in consensus linkage maps of chromosomes 1, 3 and 4 from two reciprocal chicken populations using bootstrap sampling

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Genet. Mol. Res. 9 (3): 1357-1376 (2010)
Received March 20, 2010
Accepted May 18, 2010
Published July 13, 2010
DOI 10.4238/vol9-3gmr842

ABSTRACT. Some factors complicate comparisons between linkage maps from different studies. This problem can be resolved if measures of precision, such as confidence intervals and frequency distributions, are associated with markers. We examined the precision of distances and ordering of microsatellite markers in the consensus linkage maps of chromosomes 1, 3 and 4 from two F_2 reciprocal Brazilian chicken populations, using bootstrap sampling. Single and consensus maps were constructed. The consensus map was compared with the International Consensus Linkage Map and with the whole genome sequence. Some

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loci showed segregation distortion and missing data, but this did not affect the analyses negatively. Several inversions and position shifts were detected, based on 95% confidence intervals and frequency distributions of loci. Some discrepancies in distances between loci and in ordering were due to chance, whereas others could be attributed to other effects, including reciprocal crosses, sampling error of the founder animals from the two populations, F_2 population structure, number of and distance between microsatellite markers, number of informative meioses, loci segregation patterns, and sex. In the Brazilian consensus *GGA1*, locus *LEI1038* was in a position closer to the true genome sequence than in the International Consensus Map, whereas for *GGA3* and *GGA4*, no such differences were found. Extending these analyses to the remaining chromosomes should facilitate comparisons and the integration of several available genetic maps, allowing meta-analyses for map construction and quantitative trait loci (QTL) mapping. The precision of the estimates of QTL positions and their effects would be increased with such information.

Key words: Confidence interval; CRI-MAP; Linux; Seriation;
Gallus gallus domesticus