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Bayesian association-based fine mapping in small chromosomal
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Bayesian association-based fine mapping in small chromosomal segments,

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A Bayesian method for fine-scale genetic mapping given a set to closely linked markers is presented (Sillanpää & Bhattacharjee 2004).

The method does not need linkage phases and considers marker locations as putative QTL. The method can handle multi-allelic markers, missing data, and both quantitative and binary traits. We utilize locus-specific indicator variables to select a subset of trait-associated

markers. Covariance between consecutive markers depends on their physical or genetic distance. The estimation of model parameters is based on Markov chain Monte Carlo sampling and is implemented using inBUGS.

We obtain posterior estimates for QTL effects and the time to most recent common ancestor of the causal mutation using cystic fibrosis data set.

REFERENCES

Sillanpää MJ, Bhattacharjee M. 2004. Bayesian association-based fine mapping in small chromosomal segments. (manuscript in preparation).

QTL for primary response to KLH: detection, confirmation, fine mapping

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Improvement of health of chickens by selection for enhanced general resistance to pathogens is an attractive alternative for veterinary health treatments. However, there are many pathogenic organisms to which poultry may be exposed during a lifetime. Also, it is difficult to identify organisms that could serve as the appropriate targets, for selection of improved immune response. Genetic resistance of poultry may be improved by selecting for a generalized improved immune response by selection for immune responses to a complex antigen such as sheep red blood cells (SRBC).

In the present study, keyhole limpet hemocyanin (KLH) was used as antigen to detect QTL controlling antibody responses to T-cell dependent antigens other than SRBC. The KLH antigen is an antigen that birds do not encounter during their lifetime, and thus represents a novel antigen, which is suitable to measure primary immune responses. In mammals, KLH immunization resulted in TH-2 dependent (antibody) immune responses.

In the current study two independent populations were used: The first population was the H/L F2 population that originated from a cross (ISA Warren, medium heavy layers) between two divergently selected lines for either high (H line) or low (L line) primary antibody response to SRBC. Selection was based on the individual antibody titer at 5 d after primary intramuscular immunization with SRBC at 37 d of age. Six half-sib families were created to obtain 672 F2 animals. The F2 chicks were hatched in 6 batches at 2 wk intervals. The second population was the feather pecking (FP) F2 population that was created from a cross between two commercial White Leghorn lines differing strongly in the feather pecking behavior. In brief, reciprocal crosses were made to create F1 animals.

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