Identification of QTL for production traits in chickens.

If the poultry industry hopes to continue to flourish, the identification of potential quantitative trait loci (QTL) for production-related traits must be pursued. This remains true despite the sequencing of the chicken genome. In view of this need, a scan of the chicken genome using 72 microsatellite markers was carried out on a meat-type x egg-type resource population measured for production and egg quality traits. Using a Bayesian analysis, potential QTL for a number of traits were identified on several chromosomes. Evidence of eight QTL regions associated with a total of eight traits (specific gravity, albumin height, Haugh score, shell shape, total number of eggs, final body weight, gain, and feed efficiency) was found. Two of these regions, one spanning the area of 263/287 cM on GAA01 and the other spanning the area of 23/28 cM on GAA02, were associated with multiple QTL.