Additive genetic variability and the Bayesian alphabet.

The use of all available molecular markers in statistical models for prediction of quantitative traits has led to what could be termed a genomic-assisted selection paradigm in animal and plant breeding. This article provides a critical review of some theoretical and statistical concepts in the context of genomic-assisted genetic evaluation of animals and crops. First, relationships between the (Bayesian) variance of marker effects in some regression models and additive genetic variance are examined under standard assumptions. Second, the connection between marker genotypes and resemblance between relatives is explored, and linkages between a marker-based model and the infinitesimal model are reviewed. Third, issues associated with the use of Bayesian models for marker-assisted selection, with a focus on the role of the priors, are examined from a theoretical angle. The sensitivity of a Bayesian specification that has been proposed (called "Bayes A") with respect to priors is illustrated with a simulation. Methods that can solve potential shortcomings of some of these Bayesian regression procedures are discussed briefly.