Predictive ability of alternative models for genetic analysis of clinical mastitis.

Mastitis in cows can be defined as a binary trait, reflecting presence or absence of clinical mastitis (CM), or as a count variable, number of mastitis cases (NCM), within a defined time interval. Many different models have been proposed for genetic analyses of mastitis, and the objective of this study was to evaluate the predictive ability and sire predictions of a set of models for genetic evaluation of CM or NCM. Linear- and threshold liability models for CM, and linear, censored ordinal threshold, and zero-inflated Poisson (ZIP) models for NCM were compared in a cross-validation study. To assess the ability of these models to predict future data, records from 620492 first-lactation Norwegian Red cows, which were daughters of 3064 sires, were evaluated in a fourfold cross-validation scheme. The mean squared error of prediction was used for model comparison. All models but ordinal threshold model equally performed when comparing the overall predictive ability. This result was on average, across sick and healthy cows; however, the models behaved differently for each category of animals. For example, healthy cows were predicted better by the threshold and linear models for binary data and ZIP model, whereas for mastitic cows, the ordinal threshold model was by far the best model. Predicted sire effects and rankings of sires were highly correlated across all models. For practical purposes, the linear models are very competitive with the nonlinear models.