

Genetic evaluation of mastitis liability and recovery using transition probabilities

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Many methods for genetic analyses of mastitis are performed with a cross-sectional approach, leaving out information such as repeated mastitis cases during lactation, somatic cell count fluctuations, and the recovery process. Acknowledging the dynamic behavior of mastitis during lactation and viewing it as more than a binary variable, can enhance the genetic evaluation of mastitis. Genetic evaluation of mastitis was carried out by modeling the dynamic nature of somatic cell count (SCC) within lactations. The SCC patterns were captured by modeling transition probabilities between assumed states of mastitis and non-mastitis. A widely dispersed SCC pattern generates high transition probabilities and vice versa. The method simultaneously models transitions to and from states of infection, i.e. both the mastitis liability and the recovery process are considered. A multilevel discrete time survival model was used for estimation of breeding values (BVs) on simulated data of different sizes, mastitis frequencies, and genetic correlations. The correlation between estimated and simulated breeding values (accuracy) for mastitis liability was similar (0.75-0.77 with 150 daughters/sire) to those from previously tested methods, despite that these methods used data of confirmed cases, while the current method is based on SCC as indicator of mastitis. In addition, this method also generated breeding values for the recovery process. The accuracy of these BVs was, however, lower: 0.38-0.47. The model provides an improved tool for genetic evaluation of mastitis, where both the mastitis liability and the ability to recover from mastitis can be included.