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Czech Journal of Animal Science

Imputation accuracy of bovine spongiform encephalopathy-associated *PRNP* indel polymorphisms from middle-density SNPs arrays

Gurgul A., Sieńko K., Żukowski K., Pawlina K., Bugno-Poniewierska M.:

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Statistical methods of imputation allow predicting genotypes of markers (which were not genotyped in the whole population) based on known linkage disequilibrium relationships between the

flanking polymorphisms and the information obtained from reference datasets used as a pattern. In this study we attempted to predict genotypes of two bovine spongiform encephalopathy (BSE) susceptibility associated indel polymorphisms located in the promoter region of *PRNP* gene relying on the data obtained from middle density SNPs arrays in a sample of the population of Holstein cattle. The two SNPs panels spanning *PRNP* locus were tested in terms of imputation efficiency. Both panels gave satisfactory imputation results showing high accuracy and high probabilities of imputed genotypes. Our results suggest that the approach applied can be used to evaluate the frequency of the disease associated polymorphisms in large populations of animals genotyped with whole-genome SNPs panels based on a limited-size reference population and small financial outlays.

Keywords:

BSE; cattle; indel; prion gene

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