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Accuracy of imputation of single-nucleotide polymorphism marker genotypes for water buffaloes (*Bubalus bubalis*) using different reference population sizes and imputation tools

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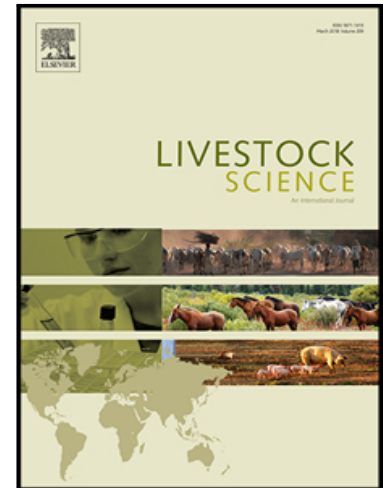
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Highlights

Reasonable imputation accuracy for buffalo can be achieved by imputing from a low-density to 90K SNP BeadChip even using a small reference population size.

With a small reference population size, minimac performed better than the two other imputation tools.

Accurate imputations were obtained using FImpute followed by Beagle and minimac when a relatively large reference population size was used.

Poor imputation for rare alleles could be traced when using the correlation coefficient as a measure of imputation accuracy.

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