

## عنوان مقاله:

Strategies for Genomic Selection in Small Populations

## محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 1

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## خلاصه مقاله:

Genomic selection refers to selection decisions based on genomic breeding values (GEBV), where the GEBV for selection candidates are calculated from single nucleotide polymorphism (SNP) markers and a prediction equation. The prediction equation is derived in a large reference population (training set) where individuals have both marker and phenotypic data. Prediction relies on the assumption that all quantitative trait loci (QTLs) tend to be in strong linkage disequilibrium (LD) with at least one marker. The quality of reference population is fundamental to maximizing the benefits of genomic selection. Genomic selection requires of large datasets to be effective. For that reason, it has been mainly implemented in simple scenarios such as dairy cattle, where one single breed is used worldwide. In many other circumstances, including small populations, evaluation is required across breeds. Number of genotyped individuals for the construction reference population are limited in small populations and therefore the accuracy of predictions is rapidly lost. Moreover, prediction equations derived in one breed do not predict accurate genomic estimated breeding values when applied to other breeds especially when the populations have diverged for many generations. In this study, a joint multi-breed reference population merged with pre-selecting markers was proposed as an ideal strategy, based on 5 breeds of European beef cattle. Criteria for selecting SNPs from Illumina Bovine700K platforms, were based on minor allele frequency (MAF) and minimum  $F_{st}$  in each breed. Results showed that genomic predictions can work across different populations, when SNP selection criteria implemented for genotyping of candidates.

## کلمات کلیدی:

.Reference Population, Feature Selection, Genomic Prediction, Training Population

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