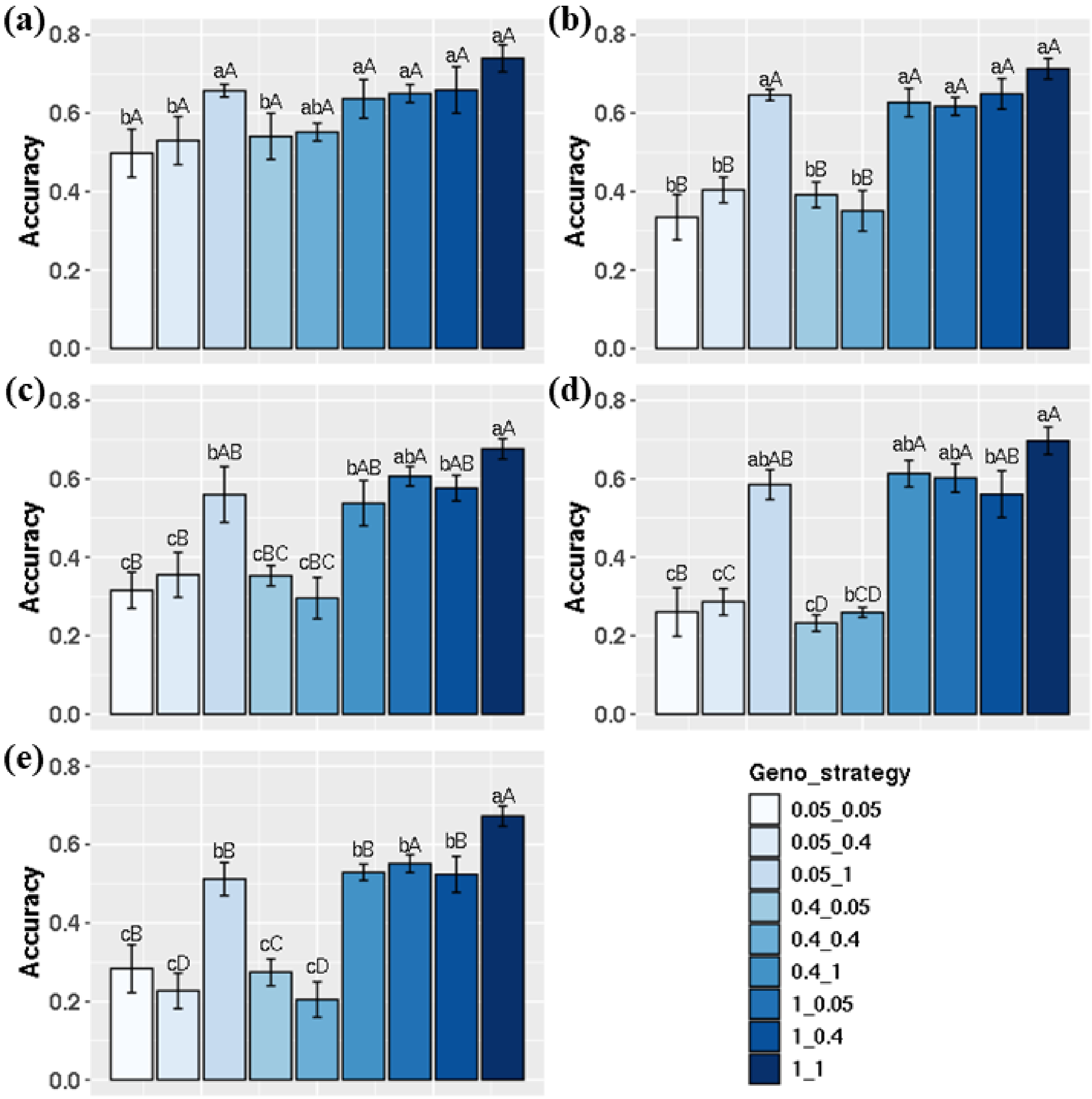
(a)
0.8
0.6
0.4
0.2
0.0
Accuracy
bA
bA
aA
bA
abA
aA
aA
aA
aA
(b)
0.8
0.6
0.4
0.2
0.0
Accuracy
bB
bB
aA
bB
bB
aA
aA
aA
aA
(c)
0.8
0.6
0.4
0.2
0.0
Accuracy
cB
cB
bAB
cBC
cBC
bAB
abA
bAB
aA
(d)
0.8
0.6
0.4
0.2
0.0
Accuracy
cB
cC
abAB
cD
bCD
abA
abA
bAB
aA
(e)
0.8
0.6
0.4
0.2
0.0
Accuracy
cB
cD
bB
cC
cD
bB
bA
bB
aA
Geno_strategy
0.05_0.05
0.05_0.4
0.05_1
0.4_0.05
0.4_0.4
0.4_1
1_0.05
1_0.4
1_1

Figure 1: Accuracies of genomic predictions for the simulations with 0 % of missing pedigree and 0 % of sire pedigree errors (a), 5 % of missing pedigree and 5% of sire pedigree errors (b), 5 % of missing pedigree and 20% of sire pedigree errors (c), 20 % of missing pedigree and 5% of sire pedigree errors (d), and 20 % of missing pedigree and 20 % of sire pedigree errors (e). 0.05_0.05: 5% of males and 5% of females genotyped; 0.05_0.4: 5% of males and 40% of females genotyped; 0.05_1: 5% of males and 100% of females genotyped; 0.4_0.05: 40% of males and 5% of females genotyped; 0.4_0.4: 40% of males and 40% of females genotyped; 0.4_1: 40% of males and 100% of females genotyped; 1_0.05: 100% of males and 5% of females genotyped; 1_0.4: 100% of males and 40% of females genotyped; 1_1: 100% of males and 100% of females genotyped. Based on Tukey's test, the same lower-case letters mean no statistical difference comparing genotyping strategies (Geno_strategy) within pedigree scenario at 5% significance level. The same Upper-case letters mean no statistical difference comparing the same genotyping strategy across pedigree scenarios at a 5% significance level based on Tukey's test.