**Impact of genotyping strategy on the accuracy of genomic prediction in simulated populations of purebred swine**

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**Table S1**. *Regression coefficients±standard errors of genomic prediction in S20D10N10 estimated from ssGBLUP with different reference populations which included different previous generations having genotypic records in the simulated populations of purebred swine*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genotype rate | Gen1 | Gen2 | Gen3 | Gen4 | Gen5 | Gen7 |
| Trait A ($h^{2}$=0.35) | 20% | 1.04±0.04 | 1.02±0.04 | 1.03±0.03 | 1.01±0.03 | 1.01±0.03 | 1.03±0.02 |
|  | 30% | 1.03±0.03 | 1.02±0.04 | 1.04±0.03 | 1.03±0.03 | 1.01±0.02 | 1.02±0.02 |
|  | 40% | 1.01±0.04 | 1.03±0.04 | 1.02±0.03 | 1.02±0.02 | 1.01±0.02 | 1.00±0.02 |
|  | 50% | 1.02±0.03 | 1.03±0.04 | 1.03±0.03 | 1.01±0.02 | 1.01±0.02 | 1.00±0.01 |
|  | 70% | 1.04±0.03 | 1.02±0.03 | 1.01±0.03 | 1.01±0.02 | 1.00±0.01 | 1.00±0.01 |
|  | 100% | 1.02±0.03 | 1.02±0.03 | 1.01±0.03 | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 |
|  |  |  |  |  |  |  |  |
| Trait B ($h^{2}$=0.10) | 20% | 1.11±0.14 | 0.97±0.04 | 1.03±0.04 | 1.08±0.04 | 1.11±0.07 | 1.06±0.04 |
|  | 30% | 1.12±0.15 | 0.98±0.06 | 1.04±0.05 | 1.09±0.06 | 1.08±0.06 | 1.04±0.05 |
|  | 40% | 1.12±0.12 | 1.00±0.05 | 1.03±0.04 | 1.10±0.06 | 1.09±0.05 | 1.06±0.05 |
|  | 50% | 1.16±0.15 | 1.02±0.05 | 1.06±0.04 | 1.08±0.06 | 1.10±0.06 | 1.05±0.05 |
|  | 70% | 1.15±0.15 | 1.02±0.06 | 1.06±0.05 | 1.10±0.06 | 1.09±0.06 | 1.07±0.05 |
|  | 100% | 1.17±0.16 | 1.03±0.05 | 1.06±0.04 | 1.09±0.05 | 1.09±0.05 | 1.07±0.05 |

Genotyping rate: 20%, 30%, 40%, 50%, 70% or 100% of animals in each litter in previous generations were genotyped, respectively.

Gen\*: last generations, i.e., generations 1–23 .

S20D10N10: 20 sires, 10 dams per sire and 10 offspring per dam in each generation.

ssGBLUP: Single-step genomic best linear unbiased prediction.

Trait A: A simulated trait with heritability 0.35; Trait B: A simulated trait with heritability 0.10.

**Table S2**. *Regression coefficients±standard errors of genomic prediction in S50D20N10 estimated from ssGBLUP with different reference populations which only included different previous generations having genotypic records in the simulated populations of purebred swine*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genotype rate | Gen1 | Gen2 | Gen3 | Gen4 | Gen5 | Gen7 |
| Trait A ($h^{2}$=0.35) | 20% | 0.97±0.01 | 0.99±0.01 | 1.01±0.010 | 1.00±0.01 | 1.00±0.01 | 1.01±0.01 |
|  | 30% | 0.99±0.01 | 0.99±0.01 | 0.99±0.01 | 1.01±0.01 | 1.00±0.01 | 1.00±0.01 |
|  | 40% | 0.99±0.01 | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | 1.01±0.01 | 1.01±0.00 |
|  | 50% | 0.99±0.01 | 0.99±0.01 | 1.00±0.01 | 1.01±0.01 | 1.00±0.01 | 1.00±0.01 |
|  | 70% | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | NA |
|  | 100% | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | 1.00±0.01 | NA | NA |
|  |  |  |  |  |  |  |  |
| Trait B ($h^{2}$=0.10) | 20% | 0.98±0.03 | 1.00±0.02 | 1.01±0.02 | 1.02±0.01 | 1.01±0.02 | 1.02±0.02 |
|  | 30% | 1.00±0.03 | 1.00±0.02 | 1.02±0.02 | 1.01±0.02 | 1.02±0.01 | 1.01±0.02 |
|  | 40% | 1.02±0.03 | 0.99±0.02 | 1.01±0.02 | 1.01±0.02 | 1.02±0.01 | 1.01±0.01 |
|  | 50% | 1.02±0.04 | 1.00±0.02 | 1.02±0.02 | 1.00±0.01 | 1.01±0.01 | 1.02±0.01 |
|  | 70% | 1.02±0.03 | 1.00±0.02 | 1.01±0.01 | 1.01±0.01 | 1.01±0.01 | NA |
|  | 100% | 1.02±0.02 | 1.01±0.02 | 1.02±0.02 | 1.01±0.01 | NA | NA |

Genotyping rate: 20%, 30%, 40%, 50%, 70% or 100% of animals in each litter in previous generations were genotyped, respectively.

Gen\*: last generations, i.e., generations 1–23 .

S50D20N10: 50 sires, 20 dams per sire and 10 offspring per dam in each generation.

ssGBLUP: Single-step genomic best linear unbiased prediction.

Trait A: A simulated trait with heritability 0.35; Trait B: A simulated trait with heritability 0.10.

**Table S3**. *The prediction accuracy±standard error in S20D10N10 estimated from ssGBLUP with different reference populations including different previous generations having genotypic records and validation populations including the same genotyping rate of each litter with reference populations in the simulated populations of purebred swine*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genotyping rate | Gen1 | Gen2 | Gen3 | Gen4 | Gen5 | Gen7 |
| Trait A ($h^{2}$=0.35) | 20% | 0.69±0.02a | 0.72±0.02ab | a0.77±0.02abc | a0.80±0.01bc | 0.81±0.01bc | 0.84±0.01c |
| 30% | 0.70±0.02a | 0.76±0.02ab | ab0.80±0.02b | ab0.81±0.02b | 0.83±0.02b | 0.84±0.02b |
|  | 40% | 0.71±0.02a | 0.77±0.02ab | ab0.81±0.02bc | ab0.83±0.02bc | 0.84±0.02bc | 0.86±0.02c |
|  | 50% | 0.73±0.01a | 0.79±0.02ab | ab0.82±0.01bc | ab0.84±0.02bc | 0.85±0.01bc | 0.87±0.02c |
|  | 70% | 0.77±0.01a | 0.82±0.01ab | b0.84±0.02bc | ab0.86±0.02bc | 0.87±0.02c | 0.88±0.01c |
|  | 100% | 0.78±0.01a | 0.83±0.01b | b0.86±0.01b | b0.88±0.01b | 0.89±0.01b | 0.90±0.01b |
|  |  |  |  |  |  |  |  |
| Trait B ($h^{2}$=0.10) | 20% | 0.52±0.01a | 0.58±0.01ab | a0.64±0.01bc | a0.68±0.02cd | 0.69±0.01d | 0.73±0.01d |
| 30% | 0.53±0.02a | 0.60±0.02ab | ab0.65±0.02bc | ab0.68±0.02bc | 0.71±0.01c | 0.73±0.01c |
|  | 40% | 0.57±0.01a | 0.63±0.02ab | abc0.68±0.01bc | abc0.72±0.01cd | 0.73±0.01cd | 0.75±0.02d |
|  | 50% | 0.58±0.01a | 0.64±0.02b | abc0.69±0.02bc | abc0.70±0.01bcd | 0.74±0.01cd | 0.77±0.01d |
|  | 70% | 0.62±0.02a | 0.68±0.01b | bc0.72±0.01bc | abc0.74±0.01cd | 0.77±0.01cd | 0.79±0.01d |
|  | 100% | 0.63±0.01a | 0.69±0.01b | c0.74±0.01bc | c0.77±0.01cd | 0.79±0.01d | 0.81±0.01d |

a-d the prediction accuracy of genomic estimated breeding value (GEBV) in a row within trait with no common superscript different significantly (P-value<0.01).

a-c the prediction accuracy of genomic estimated breeding value (GEBV) in a column within trait with no common subscript different significantly (P-value<0.01) in generation 3-4.

Genotyping rate: 20%, 30%, 40%, 50%, 70% or 100% of animals in each litter in previous generations were genotyped respectively;

Gen\*: last \* generations from 1-23 generation;

S20D10N10: 20 sires, 10 dams per sire and 10 individuals per dam in each generation.

ssGBLUP: Single-step genomic best linear unbiased prediction.

Trait A: A simulated trait with heritability 0.35; Trait B: A simulated trait with heritability 0.10.