**Evaluation of the potential use of a meta-population for genomic selection in autochthonous beef cattle populations**

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***Supplementary Table S1.*** *Accuracy from purebred genomic evaluation in testing populations (h2=0.4)*

|  |  |  |
| --- | --- | --- |
|  |  | Training sets |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Validation sets | AV | Gen1 | **0.580**(0.014) | 0.125(0.032) | 0.117(0.022) | 0.135(0.029) | 0.146(0.012) | 0.144(0.015) | 0.137(0.025) |
| Gen2 | **0.475**(0.026) | 0.158(0.021) | 0.112(0.019) | 0.111(0.021) | 0.144(0.018) | 0.112(0.028) | 0.137(0.021) |
| Gen3 | **0.437**(0.029) | 0.171(0.017) | 0.130(0.021) | 0.128(0.019) | 0.138(0.011) | 0.137(0.025) | 0.167(0.012) |
| ANI | Gen1 | 0.170(0.037) | **0.605**(0.012) | 0.167(0.022) | 0.166(0.022) | 0.106(0.016) | 0.136(0.016) | 0.126(0.019) |
| Gen2 | 0.160(0.035) | **0.495**(0.015) | 0.168(0.009) | 0.188(0.013) | 0.124(0.018) | 0.154(0.019) | 0.155(0.033) |
| Gen3 | 0.150(0.029) | **0.454**(0.020) | 0.151(0.011) | 0.203(0.016) | 0.121(0.014) | 0.192(0.022) | 0.139(0.015) |
| BP | Gen1 | 0.121(0.030) | 0.155(0.010) | **0.603**(0.013) | 0.137(0.017) | 0.131(0.017) | 0.128(0.025) | 0.160(0.022) |
| Gen2 | 0.152(0.028) | 0.108(0.012) | **0.475**(0.008) | 0.153(0.020) | 0.142(0.016) | 0.148(0.026) | 0.159(0.017) |
| Gen3 | 0.156(0.026) | 0.106(0.023) | **0.420**(0.011) | 0.140(0.023) | 0.121(0.012) | 0.107(0.022) | 0.145(0.025) |
| Mo | Gen1 | 0.132(0.018) | 0.164(0.015) | 0.132(0.022) | **0.591**(0.015) | 0.104(0.019) | 0.149(0.025) | 0.143(0.018) |
| Gen2 | 0.130(0.014) | 0.166(0.015) | 0.133(0.024) | **0.486**(0.023) | 0.141(0.010) | 0.155(0.007) | 0.161(0.006) |
| Gen3 | 0.082(0.018) | 0.139(0.011) | 0.143(0.006) | **0.442**(0.017) | 0.140(0.020) | 0.134(0.016) | 0.142(0.022) |
| Pi | Gen1 | 0.138(0.017) | 0.141(0.014) | 0.177(0.019) | 0.127(0.020) | **0.613**(0.017) | 0.128(0.026) | 0.101(0.013) |
| Gen2 | 0.125(0.026) | 0.149(0.019) | 0.198(0.023) | 0.105(0.012) | **0.525**(0.017) | 0.124(0.028) | 0.125(0.017) |
| Gen3 | 0.112(0.017) | 0.122(0.024) | 0.190(0.011) | 0.148(0.011) | **0.496**(0.012) | 0.124(0.032) | 0.098(0.022) |
| Re | Gen1 | 0.120(0.021) | 0.124(0.027) | 0.131(0.013) | 0.116(0.022) | 0.087(0.015) | **0.608**(0.015) | 0.132(0.018) |
| Gen2 | 0.124(0.021) | 0.128(0.018) | 0.149(0.026) | 0.143(0.023) | 0.101(0.027) | **0.543**(0.027) | 0.114(0.018) |
| Gen3 | 0.131(0.014) | 0.146(0.032) | 0.159(0.021) | 0.137(0.009) | 0.100(0.023) | **0.481**(0.015) | 0.107(0.011) |
| RG | Gen1 | 0.136(0.033) | 0.156(0.024) | 0.168(0.021) | 0.136(0.019) | 0.172(0.032) | 0.126(0.010) | **0.637**(0.005) |
| Gen2 | 0.133(0.025) | 0.158(0.014) | 0.184(0.012) | 0.159(0.022) | 0.163(0.025) | 0.147(0.024) | **0.545**(0.014) |
| Gen3 | 0.123(0.021) | 0.131(0.021) | 0.177(0.018) | 0.161(0.016) | 0.161(0.021) | 0.149(0.028) | **0.474**(0.024) |

***Supplementary Table S2.*** *Accuracy from purebred genomic evaluation in testing populations (h2=0.1)*

|  |  |  |
| --- | --- | --- |
|  |  | Training sets |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Validation sets | AV | Gen1 | **0.387**(0.013) | 0.077(0.014) | 0.091(0.031) | 0.054(0.018) | 0.079(0.031) | 0.080(0.025) | 0.063(0.016) |
| Gen2 | **0.307**(0.019) | 0.096(0.024) | 0.105(0.037) | 0.040(0.015) | 0.084(0.043) | 0.087(0.023) | 0.052(0.026) |
| Gen3 | **0.270**(0.021) | 0.091(0.054) | 0.099(0.034) | 0.099(0.013) | 0.073(0.017) | 0.085(0.022) | 0.058(0.022) |
| ANI | Gen1 | 0.076(0.018) | **0.419**(0.006) | 0.069(0.011) | 0.091(0.013) | 0.079(0.017) | 0.071(0.017) | 0.071(0.017) |
| Gen2 | 0.064(0.020) | **0.346**(0.013) | 0.079(0.014) | 0.094(0.031) | 0.067(0.011) | 0.083(0.023) | 0.091(0.016) |
| Gen3 | 0.096(0.006) | **0.284**(0.011) | 0.090(0.013) | 0.122(0.025) | 0.087(0.014) | 0.085(0.039) | 0.093(0.012) |
| BP | Gen1 | 0.106(0.033) | 0.059(0.018) | **0.385**(0.015) | 0.087(0.039) | 0.077(0.018) | 0.104(0.025) | 0.092(0.019) |
| Gen2 | 0.099(0.025) | 0.080(0.018) | **0.292**(0.013) | 0.086(0.022) | 0.080(0.017) | 0.108(0.014) | 0.082(0.013) |
| Gen3 | 0.103(0.021) | 0.084(0.014) | **0.244**(0.018) | 0.105(0.012) | 0.074(0.017) | 0.059(0.020) | 0.063(0.019) |
| Mo | Gen1 | 0.129(0.017) | 0.077(0.017) | 0.054(0.027) | **0.440**(0.025) | 0.070(0.031) | 0.067(0.018) | 0.090(0.016) |
| Gen2 | 0.119(0.019) | 0.063(0.017) | 0.068(0.011) | **0.377**(0.017) | 0.070(0.028) | 0.052(0.029) | 0.086(0.033) |
| Gen3 | 0.066(0.022) | 0.083(0.021) | 0.059(0.014) | **0.312**(0.009) | 0.073(0.019) | 0.033(0.017) | 0.081(0.033) |
| Pi | Gen1 | 0.063(0.017) | 0.033(0.020) | 0.076(0.016) | 0.101(0.027) | **0.419**(0.016) | 0.059(0.028) | 0.080(0.021) |
| Gen2 | 0.039(0.032) | 0.055(0.022) | 0.080(0.020) | 0.087(0.016) | **0.362**(0.015) | 0.057(0.028) | 0.087(0.019) |
| Gen3 | 0.050(0.016) | 0.059(0.018) | 0.063(0.033) | 0.095(0.022) | **0.294**(0.017) | 0.082(0.013) | 0.091(0.009) |
| Re | Gen1 | 0.087(0.023) | 0.095(0.009) | 0.030(0.018) | 0.120(0.013) | 0.055(0.017) | **0.380**(0.036) | 0.078(0.016) |
| Gen2 | 0.096(0.027) | 0.113(0.014) | 0.063(0.022) | 0.111(0.009) | 0.090(0.016) | **0.300**(0.013) | 0.077(0.021) |
| Gen3 | 0.091(0.017) | 0.085(0.013) | 0.063(0.033) | 0.123(0.014) | 0.071(0.016) | **0.285**(0.017) | 0.069(0.011) |
| RG | Gen1 | 0.053(0.027) | 0.057(0.025) | 0.103(0.029) | 0.034(0.019) | 0.049(0.021) | 0.045(0.025) | **0.398**(0.025) |
| Gen2 | 0.045(0.018) | 0.070(0.018) | 0.107(0.021) | 0.061(0.020) | 0.068(0.012) | 0.066(0.020) | **0.334**(0.022) |
| Gen3 | 0.051(0.022) | 0.060(0.019) | 0.097(0.039) | 0.073(0.020) | 0.090(0.028) | 0.080(0.022) | **0.291**(0.019) |

***Supplementary Table S3.*** *Accuracy from genomic evaluation in admixed ×2 populations in the generation 1 (h2=0.4).*

|  |  |  |
| --- | --- | --- |
|  |  | Validation sets |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Training sets | AV-ANI | **0.475**(0.013) | **0.498**(0.012) | 0.150(0.015) | 0.180(0.012) | 0.153(0.018) | 0.126(0.015) | 0.167(0.018) |
| AV-BP | **0.481**(0.020) | 0.179(0.032) | **0.500**(0.016) | 0.144(0.024) | 0.169(0.007) | 0.141(0.010) | 0.186(0.027) |
| AV-Mo | **0.480**(0.017) | 0.178(0.026) | 0.160(0.015) | **0.504**(0.018) | 0.136(0.013) | 0.126(0.023) | 0.163(0.027) |
| AV-Pi | **0.477**(0.016) | 0.164(0.028) | 0.140(0.025) | 0.126(0.021) | **0.525**(0.012) | 0.111(0.009) | 0.180(0.028) |
| AV-Re | **0.482**(0.016) | 0.174(0.028) | 0.146(0.019) | 0.150(0.024) | 0.120(0.024) | **0.518**(0.017) | 0.175(0.021) |
| AV-RG | **0.478**(0.013) | 0.150(0.020) | 0.150(0.024) | 0.154(0.014) | 0.111(0.020) | 0.140(0.017) | **0.545**(0.011) |
| ANI-BP | 0.121(0.018) | **0.495**(0.013) | **0.498**(0.016) | 0.176(0.018) | 0.185(0.009) | 0.140(0.015) | 0.167(0.022) |
| ANI-Mo | 0.126(0.023) | **0.497**(0.011) | 0.170(0.018) | **0.506**(0.015) | 0.158(0.007) | 0.126(0.028) | 0.139(0.016) |
| ANI-Pi | 0.120(0.024) | **0.491**(0.014) | 0.149(0.016) | 0.162(0.020) | **0.529**(0.010) | 0.117(0.017) | 0.164(0.016) |
| ANI-Re | 0.124(0.015) | **0.494**(0.013) | 0.149(0.013) | 0.181(0.023) | 0.151(0.024) | **0.518**(0.015) | 0.153(0.022) |
| ANI-RG | 0.114(0.024) | **0.490**(0.016) | 0.162(0.015) | 0.185(0.011) | 0.134(0.015) | 0.137(0.024) | **0.543**(0.011) |
| BP-Mo | 0.138(0.038) | 0.173(0.012) | **0.499**(0.019) | **0.501**(0.017) | 0.172(0.015) | 0.137(0.014) | 0.158(0.028) |
| BP-Pi | 0.134(0.016) | 0.159(0.033) | **0.498**(0.014) | 0.122(0.022) | **0.531**(0.011) | 0.124(0.013) | 0.181(0.015) |
| BP-Re | 0.135(0.020) | 0.165(0.025) | **0.499**(0.016) | 0.144(0.021) | 0.163(0.017) | **0.521**(0.016) | 0.172(0.021) |
| BP-RG | 0.133(0.028) | 0.144(0.023) | **0.497**(0.017) | 0.151(0.010) | 0.152(0.015) | 0.153(0.019) | **0.544**(0.012) |
| Mo-Pi | 0.138(0.023) | 0.154(0.012) | 0.151(0.010) | **0.499**(0.016) | **0.526**(0.012) | 0.110(0.014) | 0.152(0.024) |
| Mo-Re | 0.140(0.025) | 0.165(0.014) | 0.165(0.019) | **0.506**(0.016) | 0.132(0.016) | **0.517**(0.015) | 0.142(0.016) |
| Mo-RG | 0.134(0.031) | 0.143(0.015) | 0.165(0.023) | **0.505**(0.017) | 0.118(0.017) | 0.136(0.026) | **0.542**(0.011) |
| Pi-Re | 0.141(0.015) | 0.150(0.017) | 0.141(0.019) | 0.128(0.025) | **0.527**(0.013) | **0.514**(0.015) | 0.168(0.020) |
| Pi-RG | 0.130(0.020) | 0.125(0.012) | 0.145(0.011) | 0.131(0.008) | **0.523**(0.011) | 0.124(0.017) | **0.542**(0.009) |
| Re-RG | 0.134(0.022) | 0.133(0.016) | 0.153(0.012) | 0.151(0.009) | 0.103(0.016) | **0.521**(0.015) | **0.543**(0.011) |

***Supplementary Table S4.*** *Accuracy from genomic evaluation in admixed ×2 populations in the generation 1 (h2=0.1).*

|  |  |  |
| --- | --- | --- |
|  |  | Validation sets |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Training sets | AV-ANI | **0.303**(0.020) | **0.318**(0.011) | 0.094(0.027) | 0.101(0.014) | 0.045(0.019) | 0.078(0.016) | 0.071(0.022) |
| AV-BP | **0.299**(0.023) | 0.056(0.014) | **0.317**(0.023) | 0.122(0.023) | 0.086(0.018) | 0.064(0.012) | 0.113(0.028) |
| AV-Mo | **0.298**(0.020) | 0.066(0.021) | 0.090(0.019) | **0.334**(0.036) | 0.071(0.015) | 0.092(0.013) | 0.051(0.017) |
| AV-Pi | **0.299**(0.021) | 0.079(0.019) | 0.097(0.021) | 0.105(0.019) | **0.335**(0.021) | 0.051(0.015) | 0.069(0.033) |
| AV-Re | **0.301**(0.021) | 0.069(0.022) | 0.108(0.016) | 0.097(0.026) | 0.045(0.029) | **0.299**(0.025) | 0.058(0.018) |
| AV-RG | **0.295**(0.020) | 0.075(0.019) | 0.105(0.020) | 0.116(0.017) | 0.060(0.025) | 0.097(0.026) | **0.317**(0.039) |
| ANI-BP | 0.085(0.015) | **0.315**(0.013) | **0.313**(0.025) | 0.074(0.021) | 0.076(0.010) | 0.058(0.019) | 0.103(0.026) |
| ANI-Mo | 0.065(0.020) | **0.315**(0.010) | 0.072(0.019) | **0.327**(0.037) | 0.061(0.011) | 0.086(0.018) | 0.040(0.030) |
| ANI-Pi | 0.071(0.020) | **0.317**(0.017) | 0.081(0.013) | 0.060(0.013) | **0.331**(0.020) | 0.047(0.007) | 0.056(0.031) |
| ANI-Re | 0.085(0.014) | **0.318**(0.014) | 0.095(0.014) | 0.058(0.012) | 0.034(0.023) | **0.298**(0.026) | 0.047(0.015) |
| ANI-RG | 0.066(0.016) | **0.318**(0.014) | 0.089(0.012) | 0.070(0.017) | 0.048(0.032) | 0.086(0.028) | **0.311**(0.039) |
| BP-Mo | 0.060(0.024) | 0.054(0.019) | **0.312**(0.028) | **0.333**(0.035) | 0.099(0.020) | 0.073(0.017) | 0.085(0.018) |
| BP-Pi | 0.064(0.029) | 0.065(0.023) | **0.313**(0.026) | 0.077(0.015) | **0.338**(0.018) | 0.030(0.011) | 0.098(0.041) |
| BP-Re | 0.076(0.027) | 0.055(0.020) | **0.315**(0.028) | 0.073(0.019) | 0.073(0.018) | **0.293**(0.025) | 0.091(0.031) |
| BP-RG | 0.056(0.020) | 0.064(0.021) | **0.315**(0.026) | 0.092(0.014) | 0.086(0.025) | 0.075(0.029) | **0.320**(0.043) |
| Mo-Pi | 0.047(0.026) | 0.072(0.025) | 0.073(0.023) | **0.326**(0.039) | **0.336**(0.019) | 0.062(0.016) | 0.037(0.022) |
| Mo-Re | 0.057(0.023) | 0.067(0.028) | 0.086(0.023) | **0.327**(0.039) | 0.060(0.015) | **0.301**(0.026) | 0.029(0.012) |
| Mo-RG | 0.040(0.008) | 0.073(0.023) | 0.084(0.023) | **0.328**(0.037) | 0.072(0.027) | 0.106(0.021) | **0.308**(0.038) |
| Pi-Re | 0.065(0.028) | 0.079(0.021) | 0.091(0.011) | 0.058(0.022) | **0.331**(0.019) | **0.290**(0.026) | 0.044(0.031) |
| Pi-RG | 0.047(0.021) | 0.085(0.038) | 0.090(0.013) | 0.071(0.019) | **0.333**(0.019) | 0.063(0.021) | **0.311**(0.042) |
| Re-RG | 0.056(0.017) | 0.077(0.011) | 0.103(0.012) | 0.072(0.020) | 0.044(0.025) | **0.301**(0.024) | **0.312**(0.042) |

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***Supplementary Figure S1.*** *Accuracy from single-breed genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.



***Supplementary Figure S2.*** *Relationship between the linkage disequilibrium with a causal gene with an additive effect of 20.16 units and the estimated SNP effects for the 1000 closest markers in one case of the 4MG scenario.*

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***Supplementary Figure S3.*** *Accuracy from admixed ×2 genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.

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***Supplementary Figure S4.*** *Accuracy from admixed ×7 genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.