**Effects of common full-sib families on accuracy of genomic prediction for tagging weight in striped catfish *Pangasianodon hypophthalmus***

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Supplementary Table S1. Variances components, heritability estimates (h2) for tagging weight when the common full-sibs were included or excluded from the statistical models

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | omission of c2 | | | inclusion of c2 | | | | | |
| Method |  |  | h2 ± se |  |  |  | h2 ± se | c2 ± se |
| PBLUP | 52.1 | 19.8 | 0.72±0.01 | 22.0 | 105.2 | 20.8 | 0.15±0.01 | 0.71± 0.03 |
| ssGBLUP | 53.0 | 19.1 | 0.74±0.01 | 12.0 | 109.1 | 25.8 | 0.08±0.02 | 0.74± 0.03 |
| ssGWAS | 52.0 | 19.9 | 0.72±0.01 | 19.9 | 105.4 | 21.8 | 0.14±0.04 | 0.72±0.02 |

, are genetic , common environmental and residual variances

Supplementary Table S2. Prediction accuracy for tagging weight when the common full-sib families (*c2*) were included or excluded in univariate model of AIREMLf90 using original (un-imputed) and imputed genotypes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Original genotype | | | Imputed genotype | | |
| Method | Without *c2* | With *c2* | Difference (%) | Without *c2* | With *c2* | Difference (%) |
| PBLUP | 0.6232 ± 0.025 | 0.3172 ± 0.027 | 96.5 | n.a. | n.a. |  |
| ssGBLUP | 0.6359 ± 0.024 | 0.2761 ± 0.025 | 130.3 | 0.6359 ± 0.024 | 0.3114 ± 0.027 | 104.2 |
| ssGWAS | 0.6575 ± 0.022 | 0.3264 ± 0.026 | 101.4 | 0.6575 ± 0.022 | 0.3114 ± 0.034 | 111.1 |

n.a. = not available (PBLUP uses phenotype and pedigree information only)

Supplementary Table S3: Correlation of estimated breeding values for tag weight between the two statistical models (with and without c2).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Methods* | *BLUP\_ without* c2 | *ssGBLUP\_ without* c2 | *ssGWAS\_ without* c2 | *BLUPwith* c2 | *ssGBLUP with\_* c2 |
| ssGBLUP\_ *without* c2 | 0.793 |  |  |  |  |
| ssGWAS\_ *without* c2 | 0.776 | 0.827 |  |  |  |
| BLUPwith c2 | 0.615 | 0.318 | 0.454 |  |  |
| ssGBLUP with\_ c2 | 0.464 | 0.295 | 0.364 | 0.863 |  |
| ssGWAS with\_ c2 | 0.464 | 0.295 | 0.364 | 0.863 | 1.000 |