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

Nguyen Thanh Vua,b,c, Tran Huu Phucc,1, Nguyen Hong Nguyena,b\*, and Nguyen Van Sangc,1,\*

aSchool of Science, Technology and Engineering, University of the Sunshine Coast, 90 Sippy Downs drive, Sippy Downs, QLD 4556, Australia

bCenter for Bio-innovation, University of the Sunshine Coast, Australia

cResearch Institute for Aquaculture No.2, 116 Nguyen Dinh Chieu Street, District 1, Ho Chi Minh city, Vietnam

1Equal contribution

\*Correspondence to N.H. Nguyen nnguyen@usc.edu.au and N. V. Sang: sangnv.ria2@mard.gov.vn

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 | $$σ\_{a}^{2}$$ | $$σ\_{e}^{2}$$ | h2 ± se | $$σ\_{a}^{2}$$ | $$σ\_{c}^{2}$$ | $$σ\_{e}^{2}$$ | 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 |

$σ\_{a}^{2},$ $σ\_{c}^{2}$, $σ\_{e}^{2}$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  |