Additional file 4: Assumptions on the nature of non-additive genetic variance and the impact on estimates of additive genetic variance

Genomic dissection of maternal, additive and non-additive genetic effects for growth and carcass traits in Nile tilapia

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Joshi et al. (2018)[1] showed how the variance components of the basic factorial mating design used in this study were translated into estimates of maternal, dominance and additive variances related to a pedigree. The basic factorial mating design had 3 core components (V_{Sire}, V_{Dam}, and V_{Fsib}) which can be related to the covariances (C) between individuals, i and j, assuming a mean is fitted to the population.

i, j no common parent (U), $\quad\quad$ $C_U \quad = 0$ $\hfill$ (1)

i, j paternal half-sibs (PHS), $\quad\quad$ $C_{PHS} \quad = V_{Sire}$ $\hfill$ (2)

i, j maternal half-sibs (MHS), $\quad\quad$ $C_{MHS} \quad = V_{Dam}$ $\hfill$ (3)

i, j full-sibs (FS), $\quad\quad$ $C_{FS} \quad = V_{Sire} + V_{Dam} + V_{Fsib}$ $\hfill$ (4)

For this population i and j were in generation 22, and Joshi et al. (2018)[1] published the main results with a base set at generation 20.

Dominance. Assuming the non-additive genetic variation was primarily arising from dominance then Joshi et al. (2018)[1] showed:

$$C_U \quad = (4\sigma^2_A + \sigma^2_D)/16 \hfill (5)$$

$$C_{PHS} \quad = (6\sigma^2_A + 2\sigma^2_D)/16 \hfill (6)$$

$$C_{MHS} \quad = (6\sigma^2_A + 2\sigma^2_D)/16 + \sigma^2_M \hfill (7)$$

$$C_{FS} \quad = (8\sigma^2_A + 4\sigma^2_D)/16 + \sigma^2_M \hfill (8)$$

The fitted mean will account for the genotypic drift from the base generation, which is represented by C_U, and Equation 5 can be subtracted from the (6), (7) and (8).

$$C_{PHS} \quad = (2\sigma^2_A + \sigma^2_D)/16 \hfill (9)$$

$$C_{MHS} \quad = (2\sigma^2_A + \sigma^2_D)/16 + \sigma^2_M \hfill (10)$$

$$C_{FS} \quad = (4\sigma^2_A + 3\sigma^2_D)/16 + \sigma^2_M \hfill (11)$$

Solving these equations and equating them to (2) to (4) results in the following:

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[1] Joshi R, Woolliams JA, Meuwissen THE, Gjøen HM. Maternal, dominance and additive genetic effects in Nile tilapia; influence on growth, fillet yield and body size traits. Heredity (Edinb). 2018;120:452-62.

- σ^2_M is estimated as $C_{MHS} - C_{PHS}$.
- σ^2_D is estimated as $16(C_{FS}-C_{PHS}-C_{MHS}) = 16V_{Fsib}$
- σ^2_A is estimated as $16C_{PHS}-8(C_{FS}-C_{MHS}) = 8(V_{Sire} - V_{Fsib})$.

Epistasis[2]. Consider now an assumption that the non-additive genetic variation was primarily arising from A#A, denoted σ^2_I :

$$C_U = (16\sigma^2_A + 4\sigma^2_I)/64 \tag{5}$$

$$C_{PHS} = (24\sigma^2_A + 9\sigma^2_I)/64 \tag{6}$$

$$C_{MHS} = (24\sigma^2_A + 9\sigma^2_I)/64 + \sigma^2_M \tag{7}$$

$$C_{FS} = (32\sigma^2_A + 16\sigma^2_I)/64 + \sigma^2_M \tag{8}$$

As with dominance the fitted mean removes C_U and this is subtracted from remaining covariances.

$$C_{PHS} = (8\sigma^2_A + 5\sigma^2_I)/64 \tag{6}$$

$$C_{MHS} = (8\sigma^2_A + 5\sigma^2_I)/64 + \sigma^2_M \tag{7}$$

$$C_{FS} = (16\sigma^2_A + 12\sigma^2_I)/64 + \sigma^2_M \tag{8}$$

The solutions to these equations are:

- σ^2_M is estimated as $C_{MHS} - C_{PHS}$.
- σ^2_I is estimated as $32(C_{FS}-C_{PHS}-C_{MHS}) = 32V_{Fsib}$
- σ^2_A is estimated as $28C_{PHS}-20(C_{FS}-C_{MHS}) = 8V_{Sire} - 20V_{Fsib} = 8(V_{Sire} - V_{Fsib}) - 12V_{Fsib}$.

Therefore the estimate of σ^2_A from this design is reduced when the non-additive variation is assumed to be additive-by-additive epistasis rather than dominance, and this reduction is of the order of $3/8\ \sigma^2_I$.

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[2] Cockerham CC. An extension of the concept of partitioning hereditary variance for analysis of covariances among relatives when epistasis is present. *Genetics*. Genetics Society of America; 1954;39(6):859-82.