Additional file 3: Equivalence of contrasts used to construct $\mathbf{H}_a$ for HWE and NOIA genomic relationship matrices

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

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Let x_{ij} be the count of an arbitrarily chosen alternative allele for locus j (j = 1 … m) in individual i (i = 1 … n) so that x_{ij} = 0, 1 or 2. Following the notation of [1], the genomic relationship matrices for additive effects are constructed from contrasts h_a to give coefficients $h_a[i, j]$ for each locus for each individual and the $h_a[i, j]$ form an n x m matrix $\mathbf{H_a}$. $\mathbf{G}$ is then calculated as

$$\mathbf{G}_{\text{NOIA}} = [tr(\mathbf{H_a}\mathbf{H_a^T})/\text{n}]^{-1}\mathbf{H_a}\mathbf{H_a^T}$$

$$\mathbf{G}_{\text{HWE}} = [2\sum_{j=1}^{m} p_j(1-p_j)]^{-1}\mathbf{H_a}\mathbf{H_a^T}$$

For HWE the $h_a[i, j]$ coefficients are commonly used and are given in [1] (un-numbered equation on page number 1299) as:

Genotype	Coefficient	
AA	$2-2p_j$	
Aa	$1-2p_j$	[S2.1]
aa	$-2p_j$	

Note that in the text of [1], $p_j = p_A$ and for comparison we continue to use both subscript j and subscript A as in [1].

For NOIA the $h_a[i, j]$ coefficients are given in [1] in their Equation 1 as:

Genotype	Coefficient	
AA	$-(-p_{Aa}-2p_{aa})$	
Aa	$-(1-p_{Aa}-2p_{aa})$	[S2.2]
aa	$-(2-p_{Aa}-2p_{aa})$	

These are equivalent forms. The allele frequencies can also be calculated from the genotype frequencies by: $p_j = p_A = p_{AA} + \frac{1}{2}p_{Aa}$ and $p_a = 1-p_j = p_{aa} + \frac{1}{2}p_{Aa}$. Substituting these into S2.2 gives S2.1 as shown below.

Genotype	Coefficient

AA $\quad -(-p_{Aa}-2p_{aa})=p_{Aa}+2p_{aa} \quad =2p_a \quad =2(1-p_j) \quad =2-2p_j$

Aa $\quad -(1-p_{Aa}-2p_{aa})=p_{Aa}+2p_{aa}-1 =2p_a-1 =2(1-p_j)-1 =1-2p_j$

aa $\quad -(2-p_{Aa}-2p_{aa})=p_{Aa}+2p_{aa}-2=2p_a-2 =2(1-p_j)-2 =-2p_j$

Example. Let $p_{aa}=0.3$, $p_{Aa}=0.2$ and $p_{AA}=0.5$; so $p_A=p_j=0.6$ and $p_a=0.4$. The locus is not in HWE as $2p_Ap_a=0.48 \neq p_{Aa}$. Then the coefficients are as follows:

Genotype	From S2.1		From S2.2	
AA	2 − 2 x 0.6	= 0.8	-(-0.2 − 2 x 0.3)	= 0.8
Aa	1 − 2 x 0.6	= -0.2	-(1 − 0.2 − 2 x 0.3)	= -0.2
aa	− 2 x 0.6	= -1.2	-(2 − 0.2 − 2 x 0.3)	= -1.2

In conclusion the difference between $\mathbf{G}_{HWE}$ and $\mathbf{G}_{NOIA}$ lies only in their scaling and not in the contrasts used to calculate the elements of $\mathbf{H}_a$.

Literature Cited

1. Vitezica ZG, Legarra A, Toro MA, Varona L. Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. Genetics. 2017;206:1297–307.