**Hybrid Prediction**

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Genomic prediction of hybrid performance is based on the traditional idea of general and specific combining ability (GCA, SCA). The genotypic value of hybrid , created from inbreds *i* and *j*, is denoted . The linear model looks similar to the decomposition into additive and dominance effects introduced previously. One difference is that, to allow for differences between heterotic groups, the maternal and paternal additive effects are not necessarily drawn from the same distribution:

|  |  |
| --- | --- |
|  | [1] |

In Eq. 1, *i* is the GCA of parent from group 1, and is the GCA of parent from group 2. The residual is the SCA. If the inbreds are derived from populations in panmictic and linkage equilibrium, then genetic variance can be decomposed as

|  |  |
| --- | --- |
|  | [2] |

The covariance between the GCA effects for two inbreds (e.g., ) from the same group can be expressed in terms of their kinship or additive relationship:

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| --- | --- |
|  | [3] |

The rationale behind Eq. 3 is that the covariance between the GCA effects is nonzero only when the genes in the two inbreds are IBD. By the same logic, the covariance between the SCA effects depends on the product of the kinship coefficients for both pairs of inbreds:

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| --- | --- |
|  | [4] |

Eq. 4 represents another difference between the hybrid and standard one-locus model. In the latter, the covariance between the dominance effects has a different mathematical form. A better analogy for SCA is additive x additive epistasis.

**Estimation from Markers**

One approach to genomic prediction of hybrid performance is to use Eq. 3-4 but replace the pedigree relationship matrix with the genomic marker relationship matrix. The vector equation corresponding to Eq. 1 is

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|  | [5] |

The GCA and SCA effects are multivariate normal with the following covariance structure:

|  |  |
| --- | --- |
|  | [6] |

The symbol is called the Kronecker product and is a type of elementwise multiplication.A screenshot of a cell phone

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