Dominance in Stochastic Simulation of Animal Breeding Programs

Chris Gaynor, Gregor Gorjanc, and John Hickey
Why It Matters

• Stochastic simulation is a useful tool
  – Can evaluate new breeding schemes

• Dominance is an important genetic property
  – Relates to inbreeding depression and heterosis

• Simulations often ignore dominance
  – Or use arbitrary values
Maize Example

• Sold as hybrids
  – Fully inbred parents
  – ~100% heterosis

• Brute force tuning
  – Multiple possible solutions
Long-Term Gain for Maize Yield

How Much Dominance to Use

• Depends on the trait
  – Some suggestions in literature

• Pick values to achieve genetic properties
  – Inbreeding depression
  – Midparent heterosis
  – Purebred-crossbred correlation
Previous Work

- Wellmann and Bennewitz (2011)
  - Lower bound for number of QTN
  - Relatively few assumptions
  - Considered a single population
    - No crossbreeding

Simulation Design

Additive effect
\[ a \sim N(0, \sigma_a^2) \]

Dominance effect
\[ d = \delta |a| \]

Dominance coefficient
(degree of dominance)
\[ \delta \sim N(\mu_\delta, \sigma_\delta^2) \]

Additive effect variance
\[
E(\sigma_a^2) \approx \frac{\sigma_A^2}{2 \sum_{i=1}^{n_{QTN}} p_i q_i \left[1 + (\mu_\delta^2 + \sigma_\delta^2)(q_i - p_i)^2\right]}
\]

AlphaSimR: https://bitbucket.org/hickeyjohnteam/alphasimr
Inbreeding Depression (F=0 to F=1)

\[ I = 2 \sum_{i=1}^{n_{QTN}} d_i p_i q_i = 2 \sum_{i=1}^{n_{QTN}} \delta_i a_i p_i q_i \]

\[ E(I) \approx \frac{2\mu_\delta \sigma_A \sum_{i=1}^{n_{QTN}} p_i q_i}{\sqrt{\pi} \sum_{i=1}^{n_{QTN}} p_i q_i \left[ 1 + (\mu_\delta^2 + \sigma_\delta^2)(q_i - p_i)^2 \right]} \]
Inbreeding Trends

\[ E(I) \propto \sigma_A \]

\[ E(I) \propto \sqrt{n_{QTN}} \]

\[ E(I) \propto \frac{\mu_\delta}{\sqrt{c + \mu_\delta^2 + \sigma_\delta^2}} \]

Number of QTN

- 1000
- 4000

Genetic Variance

- 1
- 4
Midparent Heterosis

\[ y = p - p' \]

\[ H = \sum_{i=1}^{n_{QTN}} d_i y_i^2 = \sum_{i=1}^{n_{QTN}} \delta_i |a_i| y_i^2 \]

\[ E(H) \approx \frac{\mu_{\delta} \sigma_A \sum_{i=1}^{n_{QTN}} y_i^2}{\sqrt{\pi \sum_{i=1}^{n_{QTN}} p_i q_i \left[ 1 + (\mu_{\delta}^2 + \sigma_{\delta}^2)(q_i - p_i)^2 \right]}} \]
Heterosis Trends

\[ E(H) \propto \sigma_A \]

- Same as trends for inbreeding

\[ E(H) \propto \sqrt{n_{QTN}} \]

- Also depends on QTN frequency differences

\[ E(H) \propto \frac{\mu_\delta}{\sqrt{c + \mu_\delta^2 + \sigma_\delta^2}} \]
Purebred-Crossbred Correlation

• More QTN frequency difference, less correlation

• More dominance, less correlation

• Initial correlations are high
  – Selection on purebreds decreases correlation
  – Use Bulmer effect to predict change
Maize Results

• Number of QTN = 3,000
  – 10 chromosome pairs

• Mean dominance coefficient = 0.92
Conclusions

• Dominance should be included in more simulations

• Try to match trait specific values
  – i.e. inbreeding depression

• Consider the trade-off between number of QTN and magnitude of dominance coefficient
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