# Distribution and Location of Genetic Effects for Dairy Traits

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# Experimental Design

- Predict April 2008 daughter deviations from August 2003 PTAs
  - Similar to Interbull trend test 3
  - 3576 older Holstein bulls
  - 1759 younger bulls (total = 5335)
- Results computed for 27 traits: 5 yield, 5 health, 16 conformation, and Net Merit (NM$)

# Linear and Nonlinear Predictions

- **Linear model**
  - Infinitesimal alleles model in which all loci have non-zero effects
- **Nonlinear models**
  - **Model A:** infinitesimal alleles with a heavy-tailed prior
  - **Model B:** finite locus model with normally-distributed marker effects
  - **Model AB:** finite locus model with a heavy-tailed prior

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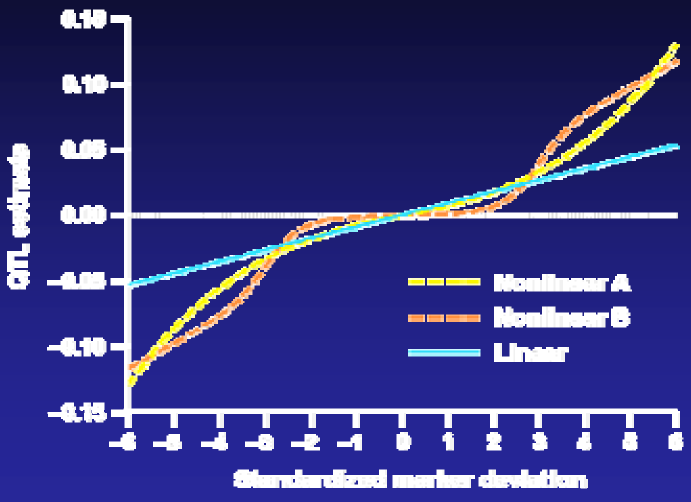
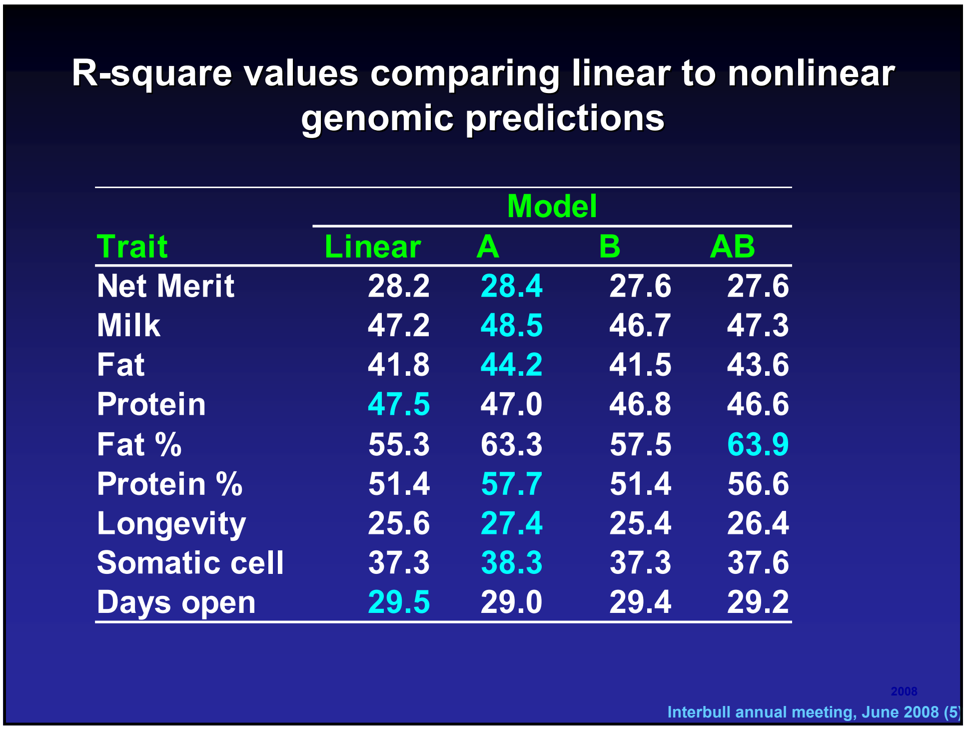
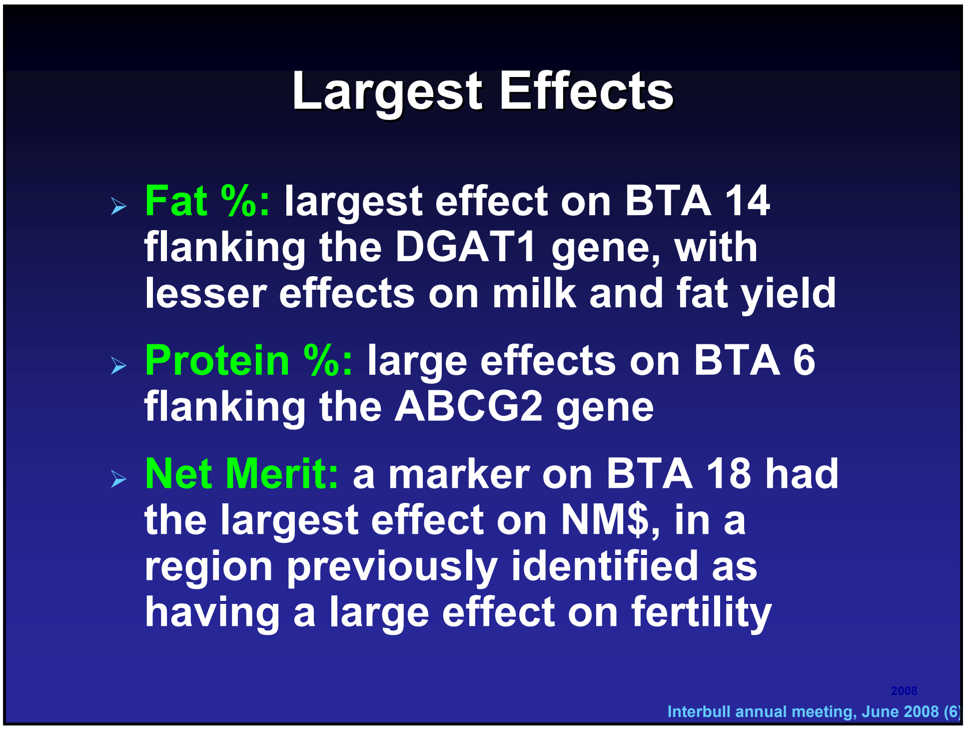
# Regressions for marker allele effects





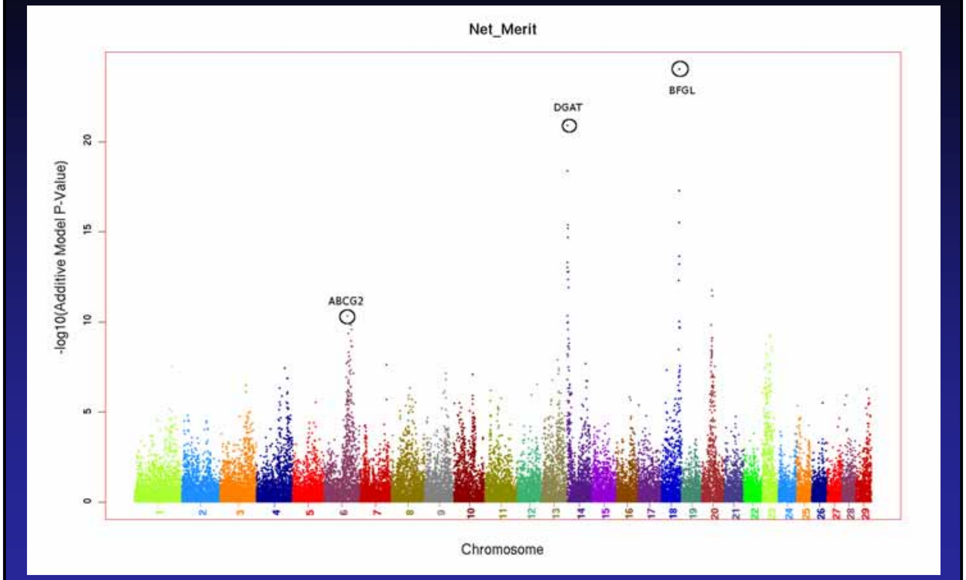
## R-square values comparing linear to nonlinear genomic predictions

| | Model | | | |
|---|---|---|---|---|
| **Trait** | **Linear** | **A** | **B** | **AB** |
| Net Merit | 28.2 | 28.4 | 27.6 | 27.6 |
| Milk | 47.2 | 48.5 | 46.7 | 47.3 |
| Fat | 41.8 | 44.2 | 41.5 | 43.6 |
| Protein | 47.5 | 47.0 | 46.8 | 46.6 |
| Fat % | 55.3 | 63.3 | 57.5 | 63.9 |
| Protein % | 51.4 | 57.7 | 51.4 | 56.6 |
| Longevity | 25.6 | 27.4 | 25.4 | 26.4 |
| Somatic cell | 37.3 | 38.3 | 37.3 | 37.6 |
| Days open | 29.5 | 29.0 | 29.4 | 29.2 |



## Largest Effects

- **Fat %:** largest effect on BTA 14 flanking the DGAT1 gene, with lesser effects on milk and fat yield
- **Protein %:** large effects on BTA 6 flanking the ABCG2 gene
- **Net Merit:** a marker on BTA 18 had the largest effect on NM$, in a region previously identified as having a large effect on fertility



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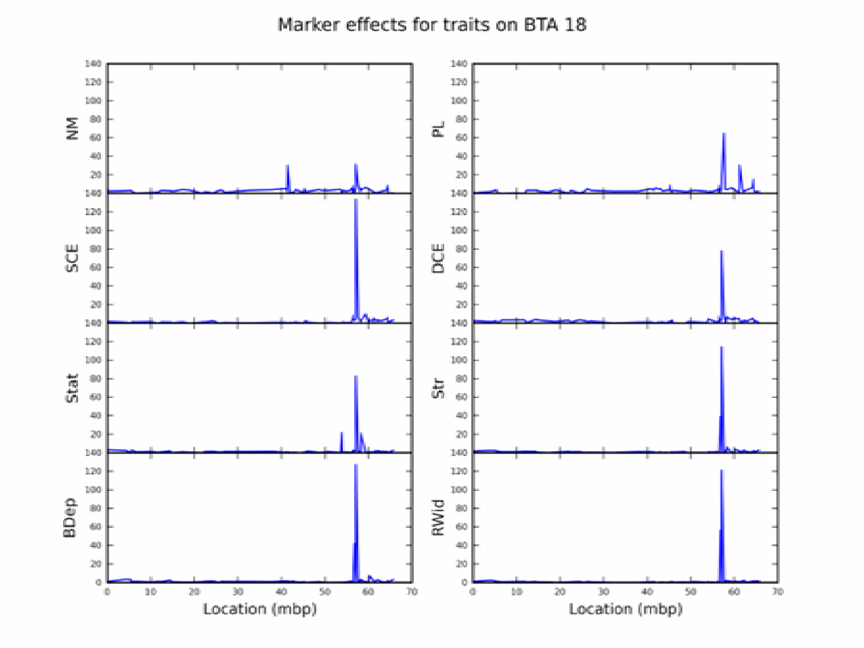
# Dystocia Complex

- Markers on **BTA 18** had the largest effects for several traits:
  - **Dystocia:** Sire and daughter calving ease
  - **Conformation:** rump width, stature, strength, and body depth
  - **Efficiency:** longevity and net merit
- Large calves contribute to shorter PL and decreased NM$



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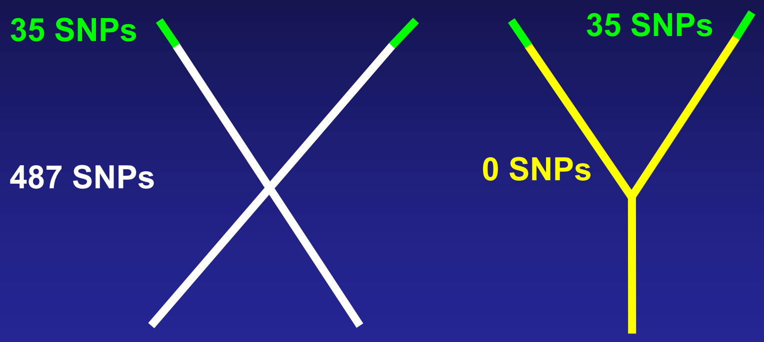
# SNP on X Chromosome

- Each animal has two evaluations
  - Expected genetic merit of daughters
  - Expected genetic merit of sons
  - Difference is sum of effects on X
  - SD = 0.1 $\sigma_G$, smaller than expected
- Correlation with sire's daughter vs. son PTA difference was significant ($P$ < 0.0001), regression close to 1.0

# X, Y, Pseudo-autosomal SNPs



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# Conclusions

- A heavy-tailed model provides better fits to the data than a linear or finite loci models.
- Markers on BTA 18 had large effects on net merit, longevity, calving ease, and conformation.
- Results validate quantitative genetic theory, most notably the infinitessimal model.

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# Net Merit by Chromosome for O Man