Improvement of insects with genomic tools: GBS-based genomic prediction in *Nasonia vitripennis*

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B I N G O

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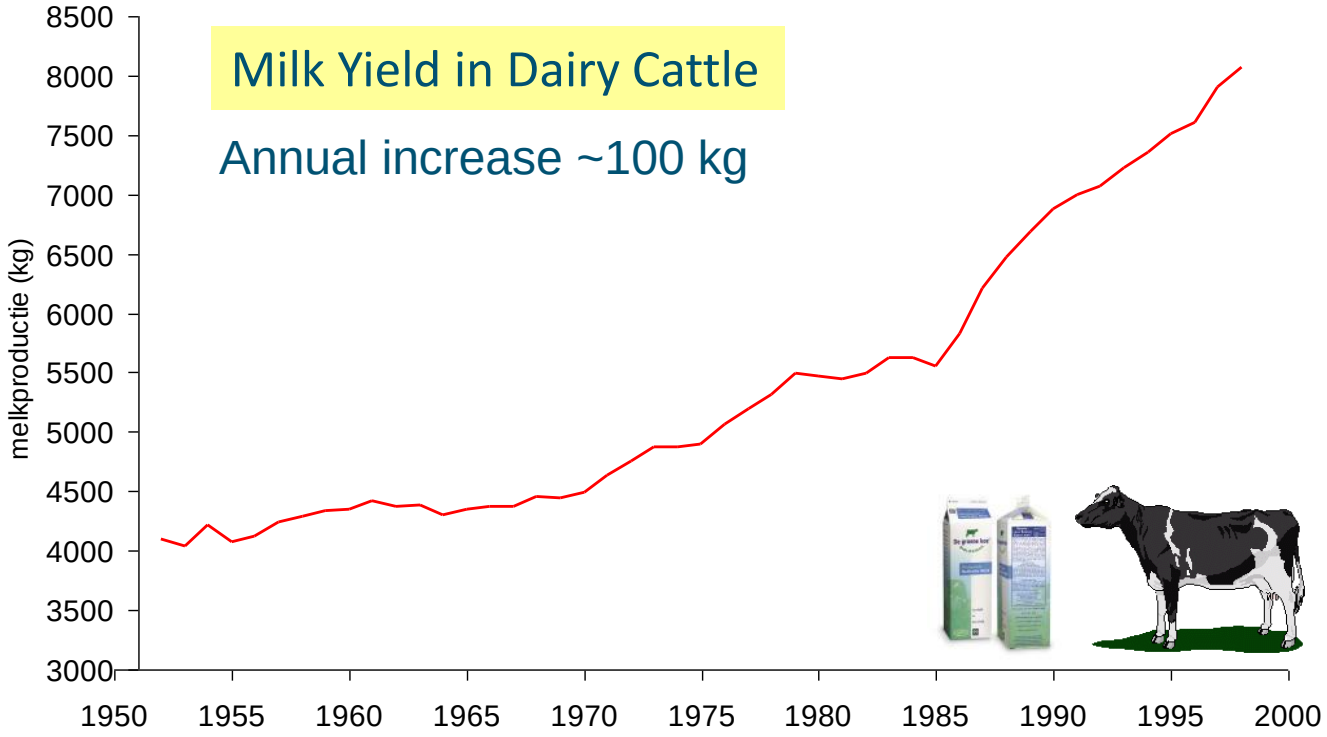
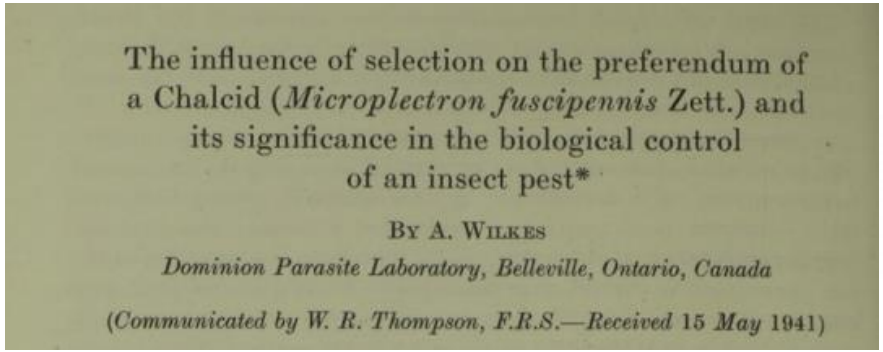
Genetic improvement



Genetic improvement

- Genetic improvement for insects is not new
  - artificial selection
- With the advent of sequencing, genomic prediction becomes possible

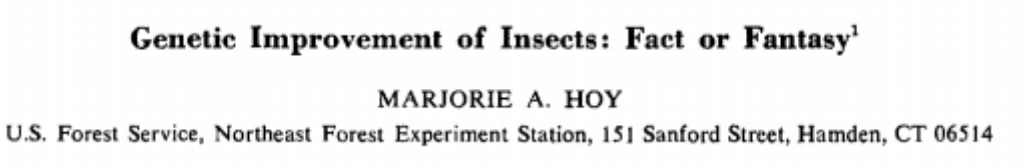


The influence of selection on the preferendum of a Chalcid (*Microplectron fuscipennis* Zett.) and its significance in the biological control of an insect pest*

By A. Wilkes

Dominion Parasite Laboratory, Belleville, Ontario, Canada

(*Communicated by W. R. Thompson, F.R.S.—Received* 15 *May* 1941)



Genetic Improvement of Insects: Fact or Fantasy[1]

MARJORIE A. HOY

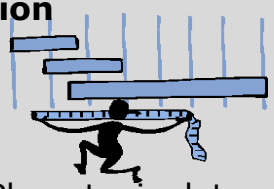
U.S. Forest Service, Northeast Forest Experiment Station, 151 Sanford Street, Hamden, CT 06514

Hoy, 1975

Genomic prediction

Reference Population

Genotyping data



Phenotypic data

Prediction equation to derive marker effects:

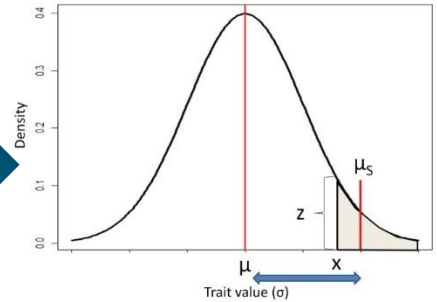
$$y = \mu + \sum_{i}^{n} x_i g_i + \mathrm{e}$$

Selection candidates

Genomic breeding values:

$$GEBVs = \sum_{i}^{n} x_i \hat{g}_i$$

Selection

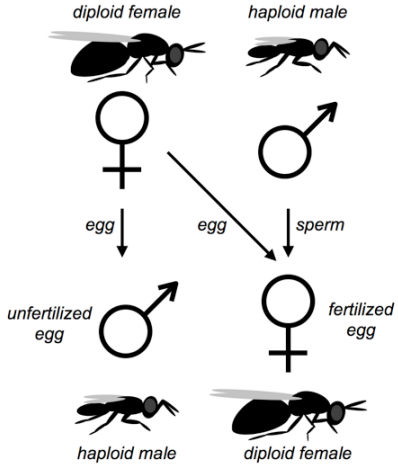


Aim

- To seek proof-of-principle for the use of genomic prediction in insects
  - how well does it work?
  - what are the obstacles?
- model parasitoid: Nasonia vitripennis

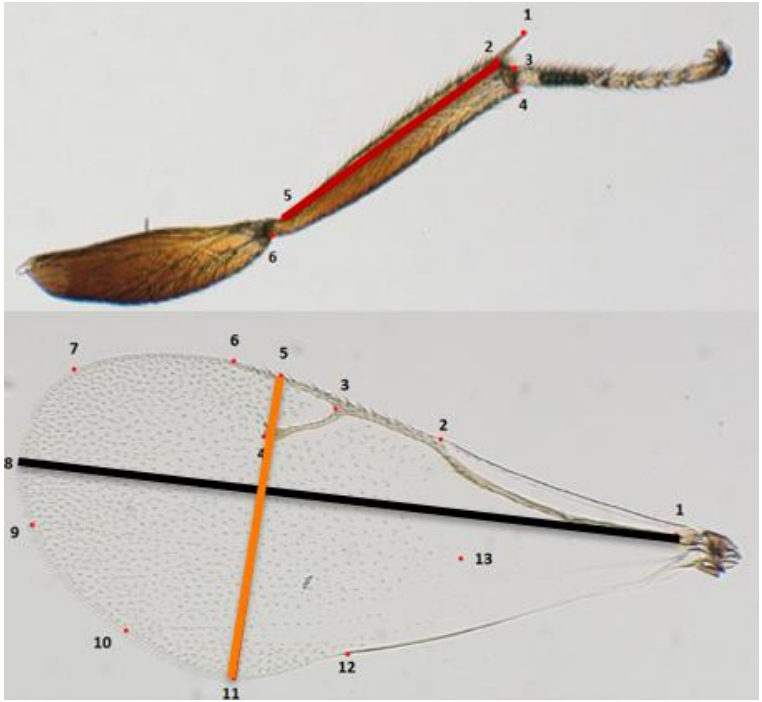
Nasonia vitripennis

- Parasitoid of blowfly pupa
- Short generation interval
- Large family size
- Haplo-diploid sex determination system:
  - haploid males
  - diploid females
- Genetic model system for developmental and evolutionary biology
- Genome has been released (Werren et al. 2010)



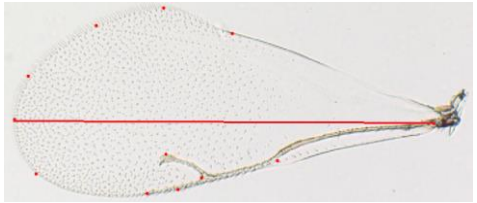
Wing morphology and body size traits

- Traits
  - tibia length
  - wing length
  - wing width
  - 2nd moment area
  - wing aspect ratio



Data analysis

- Phenotype = genotype + environment



1230 individuals

8639 DNA markers

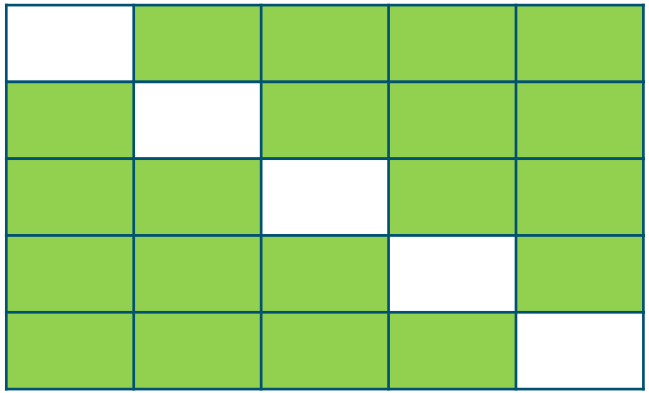
186 hosts

Accuracy: cross-validation

- **Accuracy** = Correlation between **true breeding value** and **predicted genomic breeding value**
- Randomly divided dataset into 5 groups

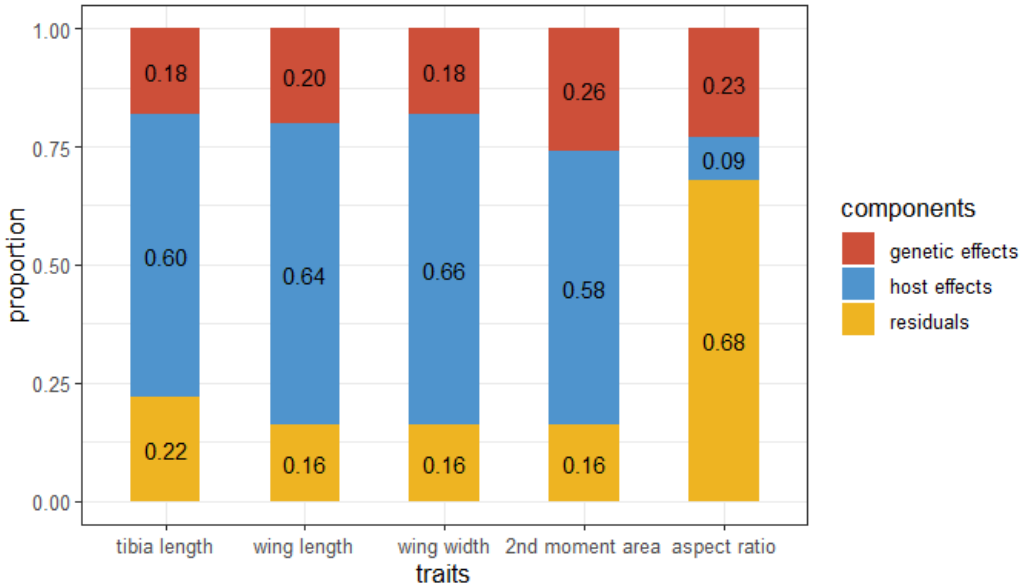
  - one group as validation group

  - four groups as training group
- Repeat 50 times



Genetic and host effects

- Sufficient genetic variation
- Apart from aspect ratio, hosts explain more than 50% of phenotypic variation



Accuracies of predicting breeding values

- Accuracy on average: ~0.6
- Bias: a value of 1 means no bias
- Genomic prediction is promising in insects: small genome sizes

Traits	accuracy	bias
Tibia length	0.52	0.96
Wing length	0.60	1.18
Wing width	0.68	1.19
2nd moment area	0.62	1.07
Aspect ratio	0.55	0.79

Challenges

- Small body size

  - cannot use the same individual for DNA isolation and selection

- Short life-span

  - need time for genotyping and GEBV estimation

Take home messages

- Genomic prediction in insects is **feasible**
  - sufficient genetic variation
  - promising prediction accuracies
- However**,** biology of some insects may **challenge** the use of genomic selection

Accuracy

- Accuracy also can be approximated by (Daetwyler *et al.* 2008):

$$r = \sqrt{\frac{Nh^2}{Nh^2 + M_e}}$$

  - r = accuracy of GEBV that can be obtained
  - N = size of the reference population
  - h^2 = heritability of the trait
  - M_e = number of independent chromosome segments

Generate data