

## 612. Impact of genetic selection in insect populations using different selection designs – a simulation study

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### Abstract

Insects are highly nutritious and rich in proteins and could help fulfil the worldwide increasing demand for proteins. Selection can provide lasting genetic improvements. Therefore, the aim of this study was to investigate the effect of genetic parameters in four different selection designs using a simulation study. Simulated were a mixed, half sib and full sib selection design and a combination of phenotypic selection and/or breeding values as selection method. The results show that in ten generations an improvement in body mass and development time is possible in all four selection designs and only minor differences between these designs were observed. Using estimated genetic parameters from literature, an improvement of 146-150% in biomass yield per year was observed. Thus, selection can provide lasting genetic improvements in insect populations, however inbreeding should be monitored and estimation of genetic parameters is necessary to prevent unfavourable correlated responses.

### Introduction

Insects are considered to be highly nutritious and rich in proteins (Rumpold and Schlüter, 2013a) and improving the production of insects could help fulfil the worldwide increasing demand for food and proteins in 2050 (FAO, 2012). Rumpold and Schlüter (2013b) concluded that in order to maximize protein production the appropriate species should be selected. These species must be suitable for mass production and should have characteristics like good health, efficient and high quality proteins. Genetic selection could improve these important characteristics within a species, however setting up an insect breeding program has some challenges. Insect populations are often kept in large groups and individual identification is not possible. Furthermore, insects often have multiple mates and the number of mates has an effect on the fecundity of females (Pai and Yan, 2005). Considering these factors the application of genetic selection in insect populations is challenging. To show the potential and impact of genetic selection in insect populations we have conducted a simulation study that mimic flour beetle (*Tribolium castaneum*) populations. Simulated traits were pupal body mass (BM), development time (DT) till first day of pupation and biomass per year (BY). The effect of genetic parameters (heritability and genetic correlation) was investigated using single trait selection on BM in four different selection designs. To show the impact of genetic parameters on response to selection.

### Materials & methods

To simulate BM and DT in flour beetle populations we used estimated genetic parameters from Ellen *et al.* (2016; Table 1). A simulation program (RStudio; R Core Team, 2019) was used to simulate four selection designs: a mixed parents design (MixedSel), a Half Sib (HS) family design (HSfam) and two versions of a Full Sib (FS) family design (FSfam and FSfamBV). Of the four selection designs, MixedSel would be the least expensive and FSfamBV would be the most expensive and labour intensive design for insect producers, since animals have to be kept individually to be able to identify them.

**Basic simulation program.** Phenotypes for BM and DT of the founder population were simulated as  $P = \mu + A + E$ , where A and E were randomly drawn from a multivariate normal distribution, where the covariance matrices of A and E were based on estimates by Ellen *et al.* (2016). Phenotypes for each

**Table 1.** Parameters for body mass (BM) in mg and development time (DT) in days.

Trait	Mean	$h^2$	$\sigma_a^2$	$\sigma_p^2$
BM	2.33	0.38	0.027	0.071
DT	27.05	0.41	2.526	6.114

consecutive generation were simulated similarly, however  $A = 0.5 A_{sire} + 0.5 A_{dam} + MS$  and MS (mendelian sampling) is drawn from a covariance matrix adjusted for inbreeding. The simulation program was applied for a given number of batches, generations and replicates. To reduce the amount of inbreeding a batch rotation scheme was simulated where males rotate over batches.

In the MixedSel design males and females were kept together and mated at random. Per batch, selection candidates to produce the next generation were phenotypically selected on highest BM. In the HSfam design, individual males were kept with multiple females, creating HS families where sire-pedigree information was available. For each sire the BM estimated breeding values (EBV) were calculated using a univariate model in ASReml (Gilmour, *et al.*, 2015) and HS families were ranked on sire EBV. Offspring from 50% of the best performing sires were ranked on BM phenotype and selection candidates were phenotypically selected from this ranking. In the FSfam design individual males were kept with one female, creating FS families. The selection families were ranked on the average BM EBV of the sire and dam. Offspring from 50% of the best performing families were ranked on BM phenotype and selection candidates were phenotypically selected from this ranking. The FSfamBV design was identical to the FSfam design, however before hatching the eggs were kept individually making it possible to identify each insect individually and know their associated pedigree. BM EBVs for each individual were estimated using a univariate animal model in ASReml. Individuals with the highest BM EBV were selected to produce the next generation. An overview and detailed information of the four selection designs is given in Table 2.

**Scenarios.** We have tested the effect of: (1) genetic correlation; and (2) heritability ( $h^2$ ) on response to selection in the four selection designs. In scenario 1 three genetic correlations between BM and DT were simulated, 0.15 as estimated by Ellen *et al.* (2016; Scenario 1A), a strongly positive (0.70; Scenario 1B) and a strongly negative (-0.70; Scenario 1C) genetic correlation. A high positive or high negative genetic correlation is unlikely in real life, however to study the effect of genetic parameters on the four selection designs a correlation estimated in literature and two extreme scenarios were chosen. In scenario 2 we replaced the estimated heritability for BM ( $h^2 = 0.38$ ) with a  $h^2$  of 0.10 to investigate the impact of a lower  $h^2$  when performing genetic selection. Results were presented as the biomass yield per year (BY) which was calculated as  $BY = (BM / DT) \times 365$ . The baseline BY based on Ellen *et al.* (2016; Table 1) is 31.44 mg BY  $((2.33 / 27.05) \times 365)$ .

**Table 2.** Detailed information per generation on batch level.

	MixedSel	HSfam	FSfam	FSfamBV
Mating	Random	1:2	1:1	1:1
# males	20	10	20	20
# females	20	20	20	20
Selected prop.	0.100	0.075	0.100	0.100
Selection	↑ BM	↑ BM within best families	↑ BM within best families	↑ EBV BM
Pedigree	-	6 generations	6 generations	6 generations

## Results

The highest BM improvement after ten generations was found in the FSfamBV design  $3.72 \pm 0.04$  mg, although FSfam and HSfam showed similar results, respectively  $3.67 \pm 0.05$  and  $3.70 \pm 0.04$  (Table 3). MixedSel (phenotypic selection) resulted in a total of 45.29 mg BY, while adding more pedigree information (HSfam, FSfam and FSfamBV) resulted in  $\sim 46.5$  mg BY. Inbreeding was lowest in the MixedBase design and highest in the FSfamBV design. Using more pedigree information in the breeding program increased inbreeding (Table 3), even though a rotational scheme was used to reduce inbreeding.

Scenario 1A (genetic parameters estimated by Ellen *et al.* (2016)) yielded a biomass between 45.29 (MixedSel) and 46.72 (FSfam) mg per year (Table 4). Scenario 1B (high positive genetic correlation) showed a lower BY after ten generations, whereas scenario 1C (high negative genetic correlation) showed a higher BY after ten generations in the four selection designs compared to scenario 1A and 1B. Furthermore, reducing the BM  $h^2$  (scenario 2) resulted in lower improvement of BY in all selection designs compared to scenario 1A.

## Discussion

We compared four different selection designs in simulated insect populations and the effect of genetic parameters on these four methods. As expected, the genetic parameters have an impact on the selection response (how fast you can improve your population). The favourable direction of breeders would likely be a higher BM and a shorter DT, as this gives the fastest increase in BY. A strong positive genetic correlation (scenario 1B) resulted in a lower BY, because DT becomes longer reducing the number of pupa grown per year. Furthermore a lower heritability (scenario 2) resulted in less improvement of BY after ten generations, compared to a higher heritability (scenario 1A). Ellen *et al.* (2016) estimated a genetic correlation between BM and DT of  $0.15 \pm 0.10$  and Mwenya *et al.* (1986) estimated genetic correlations of  $0.15 \pm 0.14$

**Table 3.** Genetic level after ten generations with genetic parameters from literature (scenario 1A).

	Mean $\pm$ SD BM <sup>1</sup>	Mean $\pm$ SD DT <sup>2</sup>	BY <sup>3</sup>		F <sup>5</sup>
	Mg	Days	Mg	% <sup>4</sup>	%
MixedSel	3.59 $\pm$ 0.04	28.93 $\pm$ 0.29	45.29	146	0.047 $\pm$ 0.007
HSfam	3.70 $\pm$ 0.04	29.13 $\pm$ 0.35	46.29	149	0.048 $\pm$ 0.005
FSfam	3.67 $\pm$ 0.04	28.71 $\pm$ 0.72	46.72	150	0.059 $\pm$ 0.004
FSfamBV	3.72 $\pm$ 0.04	29.10 $\pm$ 0.62	46.62	150	0.084 $\pm$ 0.008

<sup>1</sup> Body mass ( $h^2=0.38$ ).

<sup>2</sup> Development time.

<sup>3</sup> Biomass yield.

<sup>4</sup> Percentage of BY improvement relative to generation 0.

<sup>5</sup> Inbreeding level in generation 9.

**Table 4.** BY in mg after ten generations for each scenario and selection design.<sup>1</sup>

Scenario		MixedSel	HSfam	FSfam	FSfamBV
1A	$r_a$ 0.70	45.29 (146)	46.29 (149)	46.72 (150)	46.62 (150)
1B	$r_a$ 0.15	36.60 (118)	37.23 (120)	36.76 (118)	37.27 (120)
1C	$r_a$ -0.70	71.66 (230)	76.42 (246)	75.63 (243)	79.10 (254)
2	$h^2$ 0.15	34.81 (112)	35.01 (113)	36.07 (116)	35.97 (116)

<sup>1</sup> Percentage of improvement after 10 generations (relative to generation 0) in parentheses.

and  $0.45 \pm 0.10$  depending on the mating design. Our results show that selection on more than one trait (multi trait) and knowing the correct genetic parameters is important to prevent unfavourable correlated responses. In our simulation study inbreeding was relatively low. However, including pedigree information increased the inbreeding rate. So far, inbreeding has not been considered in insect production. However, Rhode *et al.* (2020) showed a black soldier fly population collapsing after five generations due to a lack of genetic diversity. Comparable to conventional livestock breeding programs, monitoring of inbreeding in insect populations is important.

Insect breeders face many challenges, conventional livestock breeders do not face, such as the difficulty to identify an individual insect. Remating, where females lay eggs from multiple males, affects identification and the number of mates has an effect on the fecundity of a female (Pai and Yan, 2003). In all scenarios the differences between the four selection designs were relatively small. Considering the costs and labour intensiveness of breeding programs where insects are kept individually (FSfamBV) and the responses observed in phenotypic selection (MixedSel) being similar, using pedigree information and/or breeding value estimation is not beneficial in the case of single trait selection.

To conclude, genetic selection could improve important characteristics in insect populations. Using single trait selection, a MixedSel or HS design, without individual identification, is favourable. However, breeding programs contain more than one trait and therefore, future research should focus on multi-trait selection. For insect populations, inbreeding should be monitored and estimation of genetic parameters is necessary to prevent unfavourable correlated responses.

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