A simple model of worm adaption to livestock bred for improved worm resistance

A Simple Model of Worm Adaptation to Livestock Bred for Improved Resistance to Worms

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Introduction

Domestic livestock can be bred for improved resistance to internal nematodes using the indicator trait faecal worm egg count (Bishop & Morris, 2007). Animals with improved worm resistance change the host environment for the worm population and the worm's capacity to reproduce is reduced. Co-evolutionary theory may suggest that worms should adapt to this new fitness constraint, although several experiments have found no evidence for differential adaptation of worms to hosts either resistant or susceptible worms (Saulai et al., 2001; Kemper et al., 2009). To explore this issue we developed a simple model to investigate the selection pressures acting on worm populations when livestock are selected for improved resistance to worms. The aim of this paper is to determine the factors which are important for worm adaptation to hosts selected for improved resistance to worms.

Material and methods

Overview. We model a (hypothetical) situation where animals in a population of animals vary in a single gene for resistance to worms, worms in a population of worms vary in a single gene for fitness, and these genes interact. This means the fitness of the worm genotypes is determined by the allele frequency in the animal population. Host populations vary in allele frequency (x) and hence in resistance to worms, but allele frequency is assumed to be constant within a host population. We examine the changes in allele frequency in the worms (p) as a consequence of resistance in the host population that they parasitize.

Interaction of animal and worm genotypes. Loci are bi-allelic and have only additive effects (Table 1). The wild-type worm genotype has frequency $(1-p)^2$. The difference in survival between wild-type and alternate worm genotypes in the host is determined by the value of s_h, which depends on animal genotype. However, as suggested by experimental results (Jørgensen et al. 1998), the worm genotypes may also differ in survival outside the host. This is determined by the parameter s_p, which is independent of animal genotype.

Table 1. The fitness of worm genotypes as a function of the host genotype

Worm genotype		**Host genotype**		
		susceptible	heterozygous	resistant
	frequency	$(1-x)^2$	$2x(1-x)$	x^2
wild-type (aa)	$(1-p)^2$	1	$1 - ¼s_h$	$1 - ½s_h$
heterozygous (Aa)	$2p(1-p)$	$1 - ½s_p$	$1 - ½s_p$	$1 - ½s_p$
alternate (AA)	p^2	$1 - s_p$	$(1 + ¼s_h)(1 - s_p)$	$(1 + ½s_h)(1 - s_p)$

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Generational change in allele frequency. The model predicts the change per generation in worm allele frequency for a given animal population. The generational fitness (Ω) is the average fitness from Table 1 weighted by the frequency of the three different host genotypes

$$\Omega_{aa} = (1-x)^2 + 2x(1-x)\,(1-\tfrac{1}{4}\,s_h) + x^2(1-\tfrac{1}{2}\,s_h)$$
$$\Omega_{Aa} = (1-\tfrac{1}{2}\,s_p)$$
$$\Omega_{AA} = (1-s_p)[(1-x)^2 + 2x(1-x)\,(1+\tfrac{1}{4}\,s_h) + x^2(1+\tfrac{1}{2}\,s_h)]$$

and thus the change in allele frequency, from Falconer and Mackay (1996), is:

$$p' = \left(\frac{p^2\Omega_{AA} + p\ (1-p)\ \Omega_{Aa}}{p^2\Omega_{AA} + 2p\ (1-p)\ \Omega_{Aa} + (1-p)^2\Omega_{aa}} \right)$$

where p' is the frequency of the alternate allele in the next generation.

Scenarios tested. Four animal populations were modeled over 80 worm generations when x = 1.0, s_h = 20% and s_p = 0, 10, 20, or 30%. Next, the final allele frequency following 80 worm generations was determined when the allele frequency in the host population was either 0.2, 0.5 or 0.8 and values of s_h and s_p ranged from 0 to 30%.

Results and discussion

The model assumes that the worm allele that is advantageous in a resistant host can be deleterious outside the host, so the relative values of s_h and s_p determined the direction and rate of allele frequency change. When x = 1.0 and $s_h > s_p$ (Figure 1, i & ii), the overall worm fitness was improved by the alternate allele and thus the frequency of p increased. Conversely, when $s_h < s_p$ the wild-type allele was favourable and the alternate allele was lost. The rate of change was determined by the magnitude of difference between s_h and s_p, where a large difference resulted in rapid change and a small difference a slower change. When $s_h = s_p$, then neither allele was obviously favoured and the locus remained polymorphic.

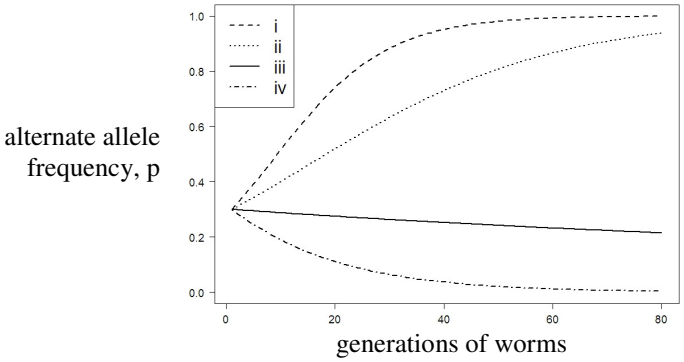

Figure 1. Change in worm allele frequency, over 80 generations, for an allele which increases worm survival in resistant hosts by 20% (s_h = 20%) but which may have a (i) zero, (ii) small, (iii) moderate or (iv) large disadvantage for survival in other life stages (i.e. s_p = 0, 10, 20, 30%).

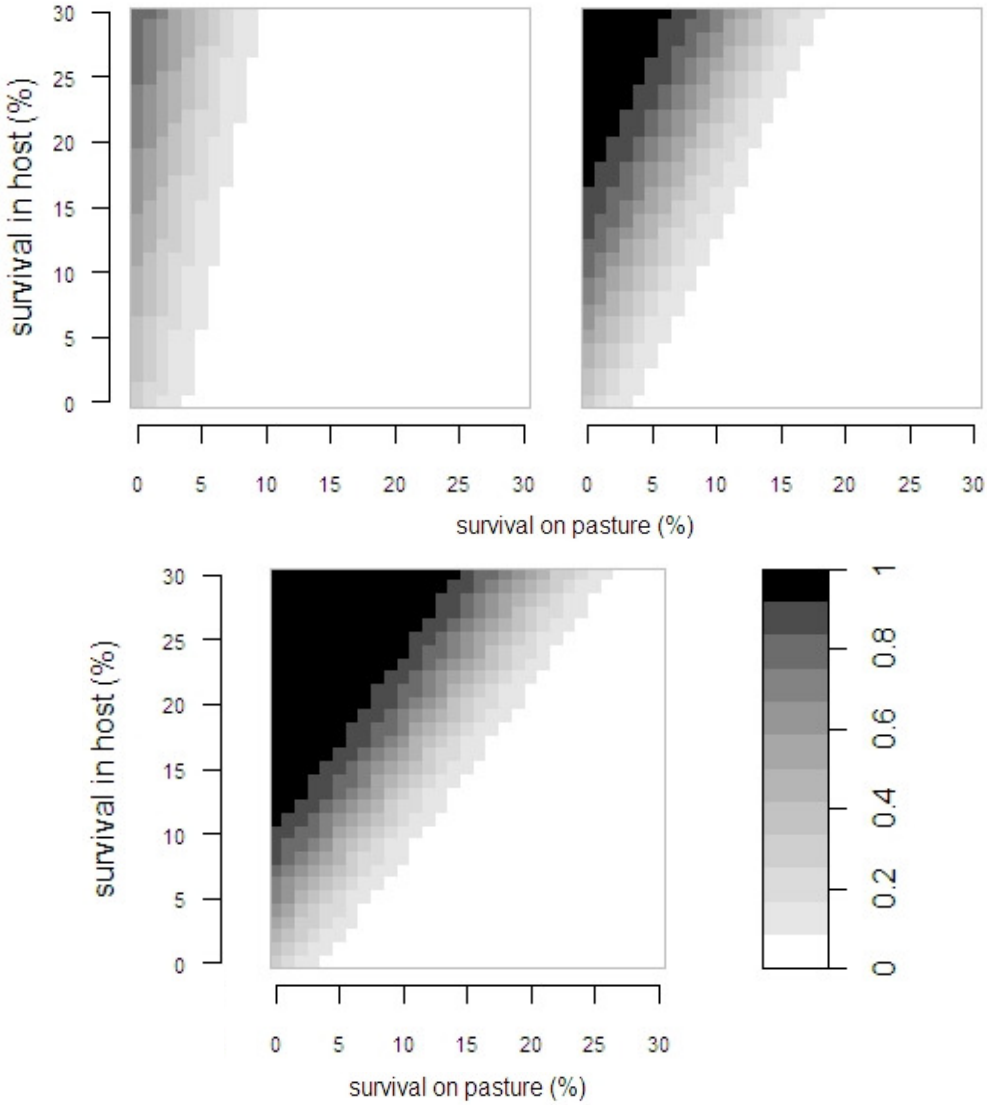

Figure 2. The final allele frequency of the alternate worm allele (p) after 80 worm generations when within-host worm survival (s_h, y-axis) and worm survival outside the host (s_p, x-axis) ranged from 0 to 30 %. Shown are cases when the resistance allele in the host population (x) is 0.2 (top left), 0.5 (top right) and 0.8 (bottom).

Many host and trade-off survival scenarios are summarised in Figure 2, where the color of each square corresponds to the alternate allele frequency in the worm population after 80 worm generations. The figure shows that, in most cases, the alternate allele is either lost (i.e.

p' < p, white) or fixed (p' > p, black); and that there were very few conditions where the locus remained with polymorphism (p' ≈ p, grey). Increasing the number of worm generation, to 1000 for example, would reduce the size of the polymorphic region further. The implication is that many of the loci which show polymorphism in current worm populations are likely to have either a zero or near zero net effect on worm fitness. This is because worms have been maximizing their fitness for millennia and beneficial alleles are likely to be readily fixed. Only worm alleles that would be deleterious in susceptible animals but beneficial in resistant animals lead to adaptation of worms to worm resistant animals. Even such alleles are unlikely to be segregating in a population of susceptible hosts and so their evolution would depend on suitable mutations occurring. Hence the heritable variation available for worm adaptation to worm resistant animals is probably low. Low heritabilities for traits closely associated with fitness are observed in other animal populations (Mousseau & Roff 1987).

The polymorphic regions in Figure 2 occur when survival in the host is balanced by the survival trade-off, and there is no overall net benefit from either allele. This means that if a worm population did show genetic variation in host survival, then the overall fitness of the polymorphic alleles would necessarily be neutral for the current (unselected) animal population. For adaptation to occur, the overall fitness of these alleles would need to change from neutral to favorable and the magnitude of the change would determine the new rate of adaptation. However, this new rate of adaptation is likely to be similar to the current rate of adaptation because the change to worm fitness will probably be small. This arises because complex traits, such as resistance to worms, commonly have many loci of relatively small effect (Hayes & Goddard, 2001). Genetic improvement in these traits is made by making small favourable changes to alleles at each of several loci. If small favourable changes are made to each locus in the host, then the difference in fitness for worm between worm resistant and susceptible animals is relatively minor and the change to the rate of adaptation slight. The small change to the rate of adaptation between worm resistant and susceptible animals is likely to be undetectable in experiments.

Conclusion

We postulate that worms will not adapt quickly to worm resistant hosts. Results from our model suggest that (i) there is likely to be low heritable variation for worm survival in the host and (ii) the partial difference to worm fitness between worm resistant and susceptible animals is most probably small. Hence we do not expect a noticeable change to the current rate of adaptation in worms as a result of breeding animals for improved resistance to worms.

References

Bishop, S. and Morris, C. (2007). *Small Rum. Res.,* 70:48-59.

Falconer, D. and Mackay, T. (1996). Introduction to Quantitative Genetics.

Hayes, B. and Goddard, M. (2001). *Genet. Sel. Evol.,* 33:209-229.

Jørgensen, L., Leathwick, D., Charleston, P. *et al.* (1998). *Int. J. Para.,* 28:1347-1352.

Kemper, K., Elwin, R., Bishop, S.C. *et al.* (2009). *Int. J. Para*., 39:607-614.

Mousseau, T. and Roff, D. (1987). *Heredity,* 59:181-197.

Saulai, M., Cabaret, J., Hostache, G. *et al.* (2001). *Genet. Sel. Evol*., 33:S25-S44.