

SYNTHESIS

Group selection and social evolution in domesticated animals

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Keywords

artificial breeding, group selection, hidden heritability, indirect genetic effects, kin selection.

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Received: 25 May 2010

Accepted: 4 June 2010

First published online: 3 August 2010

doi:10.1111/j.1752-4571.2010.00147.x

Abstract

Social interactions, especially those involving competition among individuals, are important in domesticated livestock and in natural populations. The heritability of traits affected by such interactions has two components, one originating in the individual like that of classical traits (direct effects) and the other originating in other group members (indirect effects). The latter type of trait represents a significant source of 'hidden heritability' and it requires population structure and knowledge from relatives in order to access it for selective breeding. When ignored, competitive interactions may increase as an indirect response to direct selection, resulting in diminished yields. We illustrate how population genetic structure affects the response to selection of traits with indirect genetic effects using population genetic and quantitative genetic theory. Population genetic theory permits us to connect our results to the existing body of theory on kin and group selection in natural populations. The quantitative genetic perspective allows us to see how breeders have used knowledge from relatives and family selection in the domestication of plants and animals to improve the welfare and production of livestock by incorporating social genetic effects in the breeding program. We illustrate the central features of these models by reviewing empirical studies from domesticated chickens.

Introduction

Group selection has long been a controversial subject in evolutionary biology, if not in the artificial breeding of plants and animals for economic improvement (Lush 1947). Darwin considered the existence of the sterile reproductive castes in the social insects as potentially 'annihilating' for his theory. Although caste in the social insects can be a highly specialized adaptation for defense, for food storage, or for brood care, its attendant sterility does not serve caste members well in leaving offspring of their own for the next generation. Darwin (1859, p. 238) argued that 'This difficulty ...disappears, when it is remembered that selection may be applied to the family as well as to the individual, and may thus gain the desired end.' Darwin (1859, p. 239) used the example of a breeder selecting fruit or meat for flavor, who must destroy a particular animal or fruit in order to taste it, but who 'goes with confidence to the same family.' Similarly, modern breeders of dairy cattle and laying hens use multi-level selection, a combination of individual and family

selection, in the improvement of desired traits. In the cases of dairy cattle and laying hens, they select sires on the basis of the performance of female relatives, thereby combining direct individual selection on females with among-family selection (or other genetic kin selection) on males. In animal breeding, such selection has also proven especially effective as a means for reducing antagonistic interactions between penned animals that would otherwise lower yield. Similarly, in plant breeding, selection among stands allows incorporation of competitive effects with neighbors into artificial breeding programs (Griffing 1967, 1976; Muir 2005). We will review results from an experiment designed to estimate such effects in order to increase the efficiency of selection to increase egg lay in hens. We will then discuss why multi-level selection can be so effective in artificial breeding and why it might be important in nonagricultural (i.e., natural) situations.

The group selection debate within evolutionary biology has also been concerned with multi-level selection and the genetic basis for heritability and response to selection (for recent discussion cf. Coyne et al. 1997, 2000; Wade

and Goodnight 1998; Goodnight and Wade 2000). Here, the argument is about individual selection as a sufficient explanation for adaptation and whether or not there is or could be a significant effect of random genetic drift or interdemic selection (Wright 1931) on adaptive evolution. The adaptations in question on both sides of this debate are for the improvement of the individual; it is not an argument about adaptation for the good of the group or the benefit of genetic relatives. This debate centers on whether natural selection acting among individuals is the primary way in which individual adaptations evolve and whether or not there are genetic and/or ecological circumstances in which multi-level selection can be or has been an important component of individual adaptation.

Those favoring an individual or gene-based 'inclusive fitness' approach to adaptation acknowledge a mathematical equivalence between the inclusive fitness and multi-level selection approaches (Wade 1980; Keller 1999; Wild et al. 2009; Wade et al. 2010). For simple genetic models, the equivalence extends to selection and the genetic response to selection when one uses the Price covariance formulation of selection as the covariance between genotype and relative fitness (Price 1970). Despite this equivalence, some inclusive fitness adherents argue that the group or multi-level selection perspective is irrelevant and useless for understanding adaptation in nature (e.g., Wild et al. 2009, 2010 and the response by Wade et al. 2010). To the extent that Darwinian natural selection is driven by competitive interactions between individuals within populations, we believe that the successful and growing use of multi-level selection in agricultural systems to reduce interference competition between penned animals or stand growing plants can inform our understanding of the process of multi-level selection in nature.

In many organisms, the family is the most important 'group context' affecting an individual's traits, including its size, viability and reproductive fitness. There are many empirical examples of among-family selection in the literature on artificial selection in the domestication of plants and animals and it arises in discussions of kin selection as well (Wade 1980, 1982; Cheverud 2003). Maternal genetic effects are an especially common example of among-family selection and, for that reason, their evolution shares much in common with the sib-social behavioral phenotypes influenced by kin selection (Cheverud 2003). Distinctive patterns of sequence polymorphism within species and divergence among taxa have been documented for maternal-effect genes (Cruickshank and Wade 2008). This theory and its predictions have recently been extended to genes with caste-limited expression in social insects (Linksvayer and Wade 2009) allowing one to distinguish adaptations based on what H. Robinson has called 'we genes' from those founded on 'me genes' in

terms of distinctive patterns of sequence polymorphism and divergence. It is the latent polymorphism in IGEs, genes with indirect effects (whether the effects are competitive, maternal or sib-social), that permits a rapid response to multi-level selection.

We will first review empirical data on the contribution of social interactions to the response to selection in animal breeding. Antagonistic interactions among penned individuals are a type of IGE that present both a worldwide economic problem because they reduce productivity and an animal welfare problem because such interactions greatly reduce animal well-being and increase mortality. These empirical results will illustrate the importance of IGEs in animal breeding as well as the methods used to measure them. We will then turn to simple one-gene population genetic models of antagonistic interactions to demonstrate how different population genetic structures affect the evolution of IGEs. In particular, we will focus on the difference between soft selection, where IGEs play no role, and hard selection, where IGEs play a substantial role. Soft selection is a breeding design often used in mutation accumulation experiments and long recommended for animal breeders (Moorad and Hall 2009). Importantly, *because of the absence of among-group selection*, this design allows the accumulation of IGEs, thereby worsening the economic and animal welfare problems associated with antagonistic competitive interactions. Lastly, we will turn to quantitative genetic models of IGEs of the sort being used to reduce the deleterious effects of IGEs in modern animal breeding and relate the parameters of these models to those developed in the evolutionary theory of social behaviors.

Empirical estimates of heritable social effects of trait values (IGEs)

There is theoretical and empirical evidence that social interactions contribute to the heritable variation in traits (Wade 1976, 1977; Moore 1990; Muir 1996, 2005; Brichette et al. 2001; Bijma et al. 2007b; Bergsma et al. 2008; Ellen et al. 2008). Several studies have shown that social interactions have a substantial effect on traits important in agriculture, e.g., growth rate and feed intake in pigs (Bergsma et al. 2008), mortality due to cannibalism in laying hens (Bijma et al. 2007b; Ellen et al. 2008), growth rate, feed intake and mortality in quail (Muir 2005), and growth rate in fish (Brichette et al. 2001). In laying hens, for instance, Bijma et al. (2007b) and Ellen et al. (2008) found that one-third to two-thirds of the heritable variation in survival days is due to social interactions. In domesticated pigs, Bergsma et al. (2008) found that social interactions contribute two-thirds of the heritable variation in growth rate and feed intake.

For agriculture, it is important to understand how to improve traits affected by social interactions, to enhance animal well-being and productivity in confined high intensity rearing conditions (Muir 2005). Determining the relevance of social interactions for breeding programs requires the knowledge of the genetic parameters underlying such interactions (Bijma et al. 2007b). Just as the estimation of genetic parameters of individuals requires controlled breeding and replication, estimation of the genetic parameters for social interactions requires variation and replication of the social context. As we will show below as well as in the theory sections to follow the contribution of social interactions to the response to artificial selection depends upon how the multi-level selection is imposed. In this section, we summarize evidence of IGEs on mortality due to cannibalism in laying hens, and on body weight in quail, described in Craig and Muir (1996), Muir (2005), Bijma et al. (2007b) and Ellen et al. (2008) and show how different selection methods result in different outcomes.

Social interactions and mortality due to cannibalism in laying hens and quail

Mortality due to cannibalism in laying hens is a worldwide economic and welfare problem occurring in most types of commercial poultry housing systems (Blokhuys and Wiepkema 1998). One of the possibilities to reduce mortality due to cannibalism is selective breeding. Mortality due to cannibalism is, however, caused by social interactions among group members (Ellen et al. 2008). Traditional selection methods, currently used in animal breeding, ignore an individual's IGE on its group members. To reduce mortality due to cannibalism, therefore, the classical model for a given genotype must be extended to consider not only the individuals' direct effect of its own genes, but also the indirect or associative effect of the individual on its group members (Griffing 1967). Moreover, a selection method is required that targets IGE, such as group selection and the use of related group members (see theory sections below).

In the first application of group selection to poultry, Muir (1996) selected for increased egg production based on half sib family means housed in 12 bird cages. In six generations, mortality was reduced from 67% to 8%, with most of the response occurring within the first few generations of selection (Craig and Muir 1996). Eggs per hen housed increased from 91 to 237 eggs, mainly as a result of increased survivability, but also the rate of lay per bird per day increased, primarily in the later generations. The realized heritability in terms of response per selection difference was greater than 1 in the first generation. While a realized heritability greater than 1 is not possible

in classical theory, when one considers the impact of group selection on IGEs, Bijma et al. (2007b) shows that such a response is theoretically possible.

Muir and Schinckel (2002) and Muir (2005) first proposed a linear animal model to simultaneously estimate genetic parameters for direct and indirect effects on trait values. Bijma et al. (2007a) expanded on those models to include environmental correlations due to shared group environment. Arango et al. (2005) showed that, if the environmental correlation among pen mates was positive, it could be accounted for as a random cage effect.

Applying the mixed linear model to separate direct from IGE on body weight in cannibalistic quail, Muir (2005) observed a negative correlation between direct and IGEs, and a large variance due to IGEs. The large indirect estimate is most likely an overestimate as the effect of cage was ignored which could bias the estimate (Bijma et al. 2007b). Nevertheless, Muir (2005) demonstrated that even with biased estimates, it was possible to increase body weight in quail at 6 weeks of age using an optimal index weighting direct and indirect effects according to their contribution to the group mean. In contrast, selection using classical methods based on performance of the individual resulted in a reduction in the weight. Furthermore, mortalities increased with individual selection but were reduced with optimal weighting of direct and indirect effects. These results confirm that selection on the individual can be in opposition to performance of the group, and that the linear animal model separating direct from IGE is somewhat robust to estimation errors.

In the study of Ellen et al. (2008), data on 16 780 laying hens of three purebred White Leghorn layer lines were used to estimate the variance due to direct and IGEs on mortality due to cannibalism in laying hens. Hens of the same line were housed at random in four-bird cages. For each hen, information was collected on survival (0,1) and number of survival days. Survival rate of the population was defined as the percentage of laying hens still alive at the end of the study. Survival day of an individual was defined as the number of days from the start of the laying period till either death or the end of the experiment. The three lines showed differences in survival rate, ranging from 53% through 74% (Table 1; Table 3 in Ellen et al. 2008).

When using the traditional linear animal model, the (direct) additive genetic standard deviation of survival days ranged from 16 through 44 days, and heritability ranged from 2 through 10%. When using the direct-IGE model, the standard deviation of the total additive genetic merit of survival days (the parameter, σ_G , in eqn 11 below) ranged from 30 through 55 days, and the parameter analogous to heritability, $T^2 = \sigma_G^2 + \sigma_Z^2$, ranged from

Table 1. Survival rate, average survival days, and estimates of genetic parameters* with standard errors on survival days using the traditional linear animal model and the IGE model of Bijma et al. (2007b), for three layer lines.

	Unit	W1	WB	WF
Survival	%	57.8 ± 0.6	52.9 ± 0.6	74.6 ± 0.7
Survival days	d	352 ± 1.5	326 ± 1.7	373 ± 2.0
<i>Traditional</i>				
σ_A	d	30 ± 4	44 ± 5	16 ± 5
σ_z^2	d ²	12 814 ± 239	20 066 ± 367	13 936 ± 333
h^2		0.07 ± 0.02	0.10 ± 0.02	0.02 ± 0.01
<i>Direct & IGE</i>				
σ_G	d	50 ± 8	55 ± 9	30 ± 21
σ_z^2	d ²	12 847 ± 245	20 111 ± 374	13 999 ± 343
T^2		0.19 ± 0.06	0.15 ± 0.05	0.06 ± 0.06
r_A		0.18 ± 0.21	-0.31 ± 0.18	0.11 ± 0.55

* σ_A is the additive genetic standard deviation. σ_z^2 is the phenotypic variance: $\sigma_z^2 = \sigma_A^2 + \sigma_e^2$ with the traditional model. h^2 is the heritability: $h^2 = \sigma_A^2 / \sigma_z^2$. σ_G is the standard deviation of the total additive genetic merit: $\sigma_G^2 = \sigma_{AD}^2 + 2(n-1)\sigma_{ADS}^2 + (n-1)^2\sigma_{AS}^2$. σ_z^2 is the phenotypic variance: $\sigma_z^2 = \sigma_{AD}^2 + (n-1)\sigma_{AS}^2 + \sigma_e^2$ using the IGE model. T^2 expresses the total heritable variance relative to the phenotypic variance: $T^2 = \sigma_G^2 / \sigma_z^2$. r_A is the additive genetic correlation between direct and IGE.

6% through 19%. These results indicate that heritable variation in survival days is substantially larger (two- or threefold larger) than suggested by the traditional linear animal model (Ellen et al. 2008). The genetic correlation between the direct and IGEs ranged from -0.31 through 0.18. A negative genetic correlation can lead to a negative response to selection, when using individual selection ($g = 0$ in eqns 14 and 15). This agrees with results of Craig and Muir (1996) discussed above, who found increased mortality when using individual selection.

Predicted response to selection against mortality due to cannibalism using different selection models

To quantify the possibilities to reduce cannibalism in laying hens by means of genetic selection, we predicted response to selection using genetic parameters in Table 1 for three selection methods: (i) individual selection when groups are full sibs; (ii) group selection when group members are full sibs; and (iii) selection based on relatives, when relatives are full sibs of the candidate and of each other.

With a selection intensity of unity ($i = 1$), predicted responses for the three populations range from 4.8 through 15.5 survival days for individual selection, from 7.7 through 22.0 days for group selection, and from 6.1 through 17.6 days for selection based on relatives (Table 2). Note that with group selection only one group

Table 2. Predicted response to selection (days) for three selection methods; individual selection, group selection, and selection based on relatives, for the three layer lines of Table 3.

	W1	WB	WF
Individual selection	15.5	14.9	4.8
Group selection	21.7	22.0	7.7
Selection based on relatives*	17.4	17.6	6.1

Group size equals $n = 4$, selection intensity equals $i = 1$. *Using a single group of four full sibs of the candidate.

with information is available, whereas with selection based on relatives information on multiple groups could be used, but here we used a single group (Ellen et al. 2007). Those results show that, even with moderate positive correlation ($r_g = +0.18$ in line W1), selection based on group selection or on information from relatives kept in family groups enables substantially greater response to selection than individual selection alone. Hence, kin and group selection are not only useful to avoid negative response when direct effects and IGEs are negatively correlated, but may also yield greater response in cases of a positive correlation between them.

These results show the very large contributions that IGEs can make and have made to increasing individual survivorship and increasing egg lay when standard breeding methods are extended to estimate their magnitude and to employ this 'hidden variation' in the improvement of domestic breeds using multi-level selection. Below, we turn first to population genetic models and then to quantitative genetic models to better understand how the role of IGEs in evolution and selection response changes with the genetic structure of populations, whether wild or domestic.

Selection within and among families

There are several selection methods that can be used to improve the population mean of the next generation.

Individual and family selection

In Fig. 1, we contrast individual and family selection for larger body size. In both schemes, larger individuals are favored while smaller individuals are discarded. Family selection (Fig. 1, lower panel) is different from individual selection (Fig. 1, upper panel) in that some small individuals are selected because their families have a high mean size and some large individuals are discarded because their families have a low mean size. Some of the same individuals are selected under either process. After selection, favored individuals are paired, randomly or otherwise, to begin the next generation. The two selection

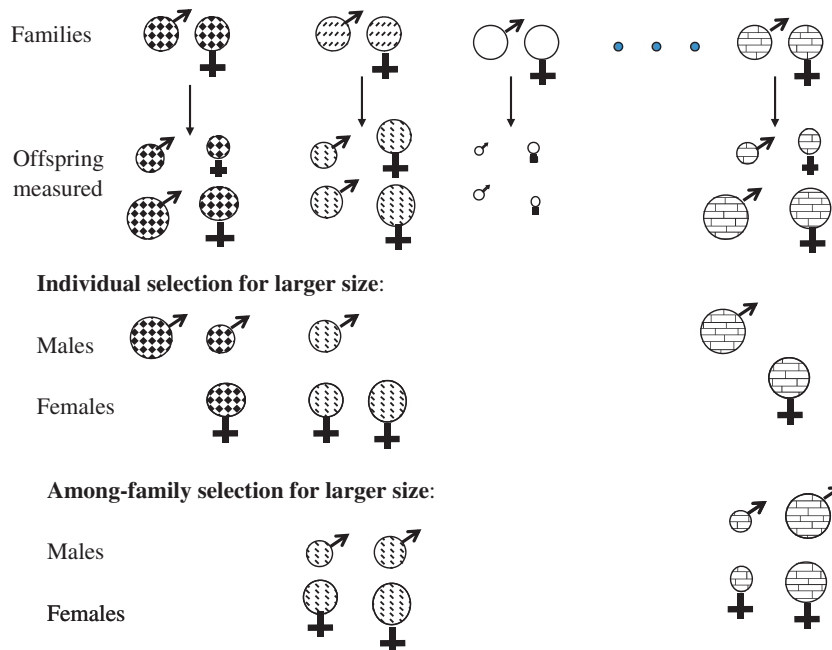


Figure 1 The contrast between individual and family selection of larger body size. Note that individuals and families differ from one another in body size. In this example, the experimenter causes individual and/or among family differences in viability by the way in which he/she selects individuals to found the next generation. With individual selection, the four largest males and the four largest females are selected, whereas with family selection, two males and two females are selected from each of the two families with the largest average body size.

methods can also differ at this stage, the response to selection, as we will show below in ways that depend upon the genetic basis for the trait (i.e., direct or indirect genetic effects) and the effects of environment.

Within-family or soft selection

There is a third type of selection, *within-family selection*, illustrated in Fig. 2. Breeders often use within-family selection as a means of mitigating the effects of inbreeding that result from selection. With individual selection, pairing selected individuals at random (Fig. 1, upper panel), results in many pairs being drawn from the same family with subsequent inbreeding. When the variation in fitness is large, so that some families contribute many more offspring than others to the next generation, it can be very difficult to avoid such inbreeding. As generations go by, the problem becomes more and more acute. Within-family selection reduces the among-family variance in fitness toward zero, because every family contributes the same number of pairs to the next generation. Thus, it maintains the largest number of maternal lineages and can be coupled with breeding schemes that minimize the longer term effects of inbreeding (such as mating the male from the last family in the row with the female from the first family). Notice that once one grasps

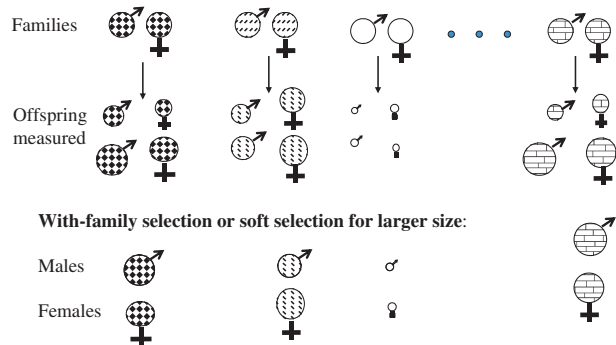


Figure 2 Within-family selection for larger body size: The largest individuals in each family are selected for breeding. Note that the largest individuals from the families of small mean size are selected even though they are smaller than some of the individuals discarded from families of larger mean size. Breeders use this type of selection to mitigate inbreeding by loss of lineages owing to selection. Importantly, it reduces the variance in fitness among families toward zero. When nature does this type of selection, it is called soft selection and the mechanism is the ecological regulation of density at the level of the family.

the distinction between among-family selection (Fig. 1, lower panel) and within-family selection (Fig. 2), individual selection (Fig. 1, upper panel) is clearly a combination of both types of selection. Once we have a better

Table 3. Direct effects on offspring fitness: large randomly mating population.

Mothers	Genotype frequencies	Offspring genotypes			Mean family fitness
		AA	Aa	aa	
AA	p^2	p $1 + 2s$	q $1 + s$	–	$1 + s(1 + p)$
Aa	$2pq$	$p/2$ $1 + 2s$	$1/2$ $1 + s$	$q/2$ 1	$1 + s(1/2 + p)$
aa	q^2	–	p $1 + s$	q 1	$1 + s(0 + p)$
Average fitness in population		$1 + 2s$	$1 + s$	1	$1 + 2sp$

understanding of the genetic basis for the apparent phenotypic differences in size in these figures in terms of direct and indirect effects, it will become clear why genes with indirect genetic effects (IGEs) respond differently to selection within and among groups.

In population genetic theory, this type of within-family selection has been called ‘soft selection’ (e.g., Wade 1985; Whitlock 2002) and it is known to prevent the operation of group selection on IGEs (Wade 1985) and to allow a higher equilibrium frequency of deleterious recessive alleles (i.e., direct effect genes) despite the increase in homozygosity caused by population genetic structure (Whitlock 2002; van Dyken 2010 in press). Following these earlier models, we combine the two existing theories, one for direct effect genes and one for indirect effect genes, to better illustrate our points about IGEs and multi-level selection in natural and artificial selection.

Simple genetics and ecology: combinations of hard and soft selection

Consider a large randomly mating population and a simple, additive genetic model with direct effects, where, for each additional *A* allele, the viability fitness of an individual is incremented by the direct fitness effect, *s* (Table 3). In Table 3, note that each female is randomly mating with a large number of males so that the frequency of AA offspring of AA mothers is *p* while the frequency of Aa offspring of AA mothers is *q*. Similarly, the frequency of Aa offspring of aa mothers is *p* while the frequency of aa offspring of aa mothers is *q*. That is, we assume that the frequency of alleles in the male sperm are representative of the frequencies in the population. Hence, male sperm bearing allele ‘A’ are in frequency *p* while sperm bearing the allele ‘a’ are in frequency *q*. The frequency of the *A* allele is *p*, that of the alternative *a* allele, is *q*, and average individual fitness in the population, *W*, is $(1 + 2sp)$. This average

can be calculated in two equivalent ways: (i) calculating the mean fitness of each family (row means in Table 3) and then taking average of these weighted by the respective family frequencies; or (ii) calculating the mean fitness of each genotype (column means in Table 3) and then taking the weighted average of these. The rate of change of gene frequency by natural selection in this population is

$$\Delta p = spq/W. \tag{1}$$

We now imagine that the population is genetically subdivided into groups, so that the genetic correlation or relatedness within groups is *f* (Whitlock 2002; van Dyken 2010 in press). If there is only among-group selection acting, then, from standard theory (e.g., Whitlock 2002; van Dyken 2010 in press), the change in allele frequency is reduced to

$$\Delta p = 2fspq/W, \tag{2}$$

because it depends on $2fspq$, the among-group genetic variance. If there is soft selection (i.e., selection is strictly within groups), then the change in allele frequency is reduced to

$$\Delta p = s(1 - f)pq/W, \tag{3}$$

because the response to selection depends on the average within-group variance, $(1 - f)pq$. Thus genetic subdivision leads to greater response in proportion to *f* from selection among groups (eqn 2) and a diminished response in proportion to $(1 - f)$ to selection within groups (eqn 3).

In ecological evolutionary genetics, hard selection is considered global density regulation in contrast with the local density regulation of soft selection (Whitlock 2002; van Dyken 2010 in press). It is the sum of the average within-group selection (3) and the among-group selection (2), so that the total change in allele frequency equals

$$\Delta p = s(1 + f)pq/W. \tag{4}$$

Genetically subdividing a population results in stronger selection in direct proportion to *f*, the degree of genetic subdivision (compare eqn 1 with 4).

Direct versus indirect genetic effects and population subdivision

Now imagine a different kind of gene, also with two alleles, which has a direct effect on fitness, *s*, and an indirect effect on fitness, *s_i*. The indirect effect of this gene causes an individual to have an effect, *s_i*, on the viability or reproductive fitness of other individuals in its family.

Individuals with genes of this sort are considered socially cooperative (when $s_s > 0$) or socially competitive or antagonistic (when $s_s < 0$). Like standard kin selection theory (e.g., Wade 1980, 1985), we further imagine an additive model for this social effect or IGE, so that the change in fitness from Aa heterozygous sibs is s_s times their frequency in the family, while that of AA sibs is $2s_s$ times their frequency. This is illustrated in Table 4. Notice that all individuals within a family have the same term in s_s (i.e., we assume for simplicity that groups are large) affecting their fitnesses; without variation in fitness among family members there can be no selection on the social effect or IGE within families!

For a gene with social effect, s_s , the equations for within- and among-family selection are these:

$$\text{Among – familyselection : } \Delta p = 2f(s_s + s)pq/W, \quad (5a)$$

$$\text{Within – familyselection : } \Delta p = s(1 - f)pq/W. \quad (5b)$$

$$\text{HardSelection : } \Delta p = (2fs_s + s[1 + f])pq/W. \quad (5c)$$

In the absence of genetic subdivision ($f = 0$), the indirect social effects of genes do not influence selection! They are present but ‘hidden’ from the response to selection. With strict local density regulation (i.e., soft or within-family selection; eqn 5b), the direct effect of an allele will determine its evolutionary trajectory. When $(s_s + s) < 0$, this means that mean fitness, $W = 1 + 2p(s_s + s)$, declines as the allele spreads to fixation. For animal breeders, where within-family selection is recommended for various breeds of cattle, sheep and chickens to avoid inbreeding depression by minimizing pedigree co-ancestry, this could well lead to an increase in competitive interactions ($s_s < 0$) which themselves can produce unwanted deleterious effects on mean fitness or yield, much like inbreeding depression itself.

Genetic considerations favorable to among-group or family selection

Breeders of domesticated plants and animals have identified circumstances in which family selection gives a better response than individual selection, especially: (i) when the environmental variation makes a larger contribution to the total phenotypic variation than the genetic variation; and (ii) when social interactions or IGEs contribute to the phenotypic variation among individuals.

In the first case, where the nonheritable phenotypic variation is high relative to genetic variation, the family-mean phenotype can be a better predictor of an individual’s genotype than the individual’s own phenotype. Differently put, the family-mean averages over the large and independent effects of environment on the phenotype and a breeder has more confidence that families differ genetically from one another in mean than individuals of different phenotype differ heritably. In the second case, the phenotype of an individual is ‘highly’ affected by the phenotype of its group members. Using individual selection, the effect of the individual on its group members is neglected, whereas, with family selection, the effect on group members is taken into account. We explore this aspect in the sections below.

The effect of social interactions

Social interactions among individuals can have a large effect on traits important in domesticated livestock and natural populations. The inheritance of traits affected by social interactions differs from that of classical traits, because trait values are determined in part by heritable effects that originate from group members (Wolf et al. 1999). In this way, response to selection consists of two components, the direct effect of a genotype on the phenotype of the individual itself and the effect of that genotype on phenotypes of group members (Willham 1963; Griffing 1967).

Table 4. Social effects on offspring fitness: large randomly mating population.

Mothers	Genotype frequencies	Offspring genotypes			Mean family fitness
		AA	Aa	aa	
AA	p^2	p $1 + 2s + (1 + p)s_s$	q $1 + s + (1 + p)s_s$	–	$1 + (1 + p)(s + s_s)$
Aa	$2pq$	$p/2$ $1 + +2s + (1/2 + p)s_s$	$1/2$ $1 + s + (1/2 + p)s_s$	$q/2$ $1 + (1/2 + p)s_s$	$1 + (1/2 + p)(s + s_s)$
aa	q^2	–	p $1 + s + (0 + p)s_s$	q $1 + (0 + p)s_s$	$1 + (0 + p)(s + s_s)$
Average fitness in population					$1 + 2p(s + s_s)$

Theory: inheritance and response to selection when individuals interact

Interactions among individuals can affect both the fitness and trait values of other individuals (as shown above). An IGE is a heritable effect of one individual on the trait value of another, the classical example being a genetic maternal effect (Dickerson 1947; Willham 1963; Cheverud 1984; Moore et al. 1998). Though social effects on trait values are commonly ignored in main stream kin and group selection theory, the increasing body of literature on IGEs clearly indicates the presence of such effects (e.g., Bleakly and Brodie 2009; and the work of Muir and Ellen and co-workers summarized below). Bergsma et al. (2008), for example, showed that IGEs contribute substantially to genetic variance in growth rate and feed intake in domestic pigs.

In a series of papers, Griffing (1967, 1976, 1981a,b) showed theoretically that social effects on trait values alter response to genetic selection, and demonstrated that response depends strongly on relatedness among interacting individuals and on the level of selection. Results of Griffing, however, do not fit easily in common theoretical frameworks for response to selection, and have largely been overlooked. Griffing (1977) summarized his results into a more common theoretical framework, but because it was published in a proceedings was also largely overlooked. Bijma et al. (2007a) rediscovered those results independently 30 years later, but more importantly addressed the importance of those finds.

In this section, we generalize Griffing's results and integrate IGEs into the general expression for response to artificial selection, building on the work of Bijma and Wade (2008). The following describes the inheritance of traits values and response to genetic selection when (i) trait values are affected by IGEs, (ii) the individuals that interact may be genetically related, and (iii) selection may take place at multiple levels, ranging from the individual to the kin and group level.

Response to selection

In livestock genetic improvement, response to genetic selection is commonly expressed as the product of the intensity of selection, i , the accuracy of selection, ρ , and the genetic standard deviation, σ_G (e.g., Bourdon 2000),

$$\Delta \bar{G} = i\rho\sigma_G. \quad (6)$$

The selection intensity expresses the selection differential, S , in standard deviation units, $t = S/\sigma$. The accuracy is the correlation between the value of the selection crite-

rium (SC) and the additive genetic merit for the trait value within individuals,

$$\rho = \text{corr}(G, SC) \quad (7)$$

When a measurement taken of an individual's phenotype is imprecise and subject to measurement error (replicated measurements on the same individual vary from one another), it reduces the correlation between the SC (the value of the trait that determines whether a breeder includes or excludes a specific individual) and genetic merit, the underlying genetic basis of the individual's phenotype. Furthermore, when environmental effects on the phenotype are large, information from an individual's relatives can be a better predictor of that individual's genetic merit than any measurement made on its own phenotype. (The terms 'accuracy' and 'genetic merit' are not found in standard population genetic theory because of the direct mapping of genotype onto phenotype. They are necessary in animal breeding where the mapping can be much more complicated and must be understood through measurement and experimentation.)

In classical quantitative genetic theory, σ_G is the additive genetic standard deviation in the trait value (Falconer and Mackay 1996). With IGEs, however, σ_G has a different interpretation, which will be discussed below. Equation 6 applies to any selection strategy and inheritance model. It equals the first term of Price's Theorem (Price 1970), and represents the change in trait value due to change in allele frequency, keeping average effects of alleles constant for all elements of the inheritance model as in eqn 1.

Equation 6 nicely separates response into three clearly distinct components; a scale-free measure of the strength of selection, i ; a scale-free measure of how accurately the SC resembles an individual's true genetic merit for the trait, ρ ; and a measure of the magnitude of the heritable differences in the population that can be utilized by genetic selection, σ_G .

In the following, we first consider the impact of social interactions on σ_G , and subsequently the effects of multi-level selection and information from kin on the accuracy of selection. (The intensity of selection depends on the ecology or on the breeding design, and will not be considered any further here.)

Trait model and heritable variance with IGE

The inheritance of traits affected by social interactions differs from that of classical traits, because trait values are determined in part by heritable effects originating from

other individuals (Willham 1963; Griffing 1967; Moore et al. 1997). As a model, consider a population where social interactions occur within groups, each consisting of n individuals (note that above, in the population genetic formulation, we assumed groups were large, unlike here where group size is explicit; see also Wade 1980). In this model, individual trait values are the sum of a direct effect due to the focal individual, and the indirect effects due to each of its $n-1$ group members. Both direct and indirect effects can be decomposed into an additive genetic (*i.e.*, heritable) component, A , and a remaining nonheritable component, E . The trait value of individual i , therefore, equals (Griffing 1967).

$$z_i = A_{D,i} + E_{D,i} + \sum_{j \neq i}^{n-1} A_{S,j} + \sum_{j \neq i}^{n-1} E_{S,j}, \quad (8)$$

where $A_{D,i}$ is the direct genetic effect (DGE) of focal individual i , $A_{S,j}$ the IGE of each of its group members j , and $E_{D,i}$ and $E_{S,j}$ are the corresponding nonheritable terms. From eqn 8, it follows that response to genetic selection equals the change in mean DGE plus group size minus one times the change in mean IGE (Griffing 1967),

$$\Delta \bar{z} = \Delta \bar{A}_D + (n-1)\Delta \bar{A}_S \quad (9)$$

Equation 9 indicates that an individual's total genetic merit, representing its heritable impact on the mean trait value of the population, may be defined as (Bijma et al. 2007a)

$$G_i = A_{D,i} + (n-1)A_{S,i}, \quad (10)$$

so that response to selection equals change in mean G -value, $\Delta \bar{z} = \Delta \bar{G}$. The G_i is the sum of all heritable effects of i on trait values of individuals, of which $A_{D,i}$ surfaces in the focal individual itself, and $(n-1)A_{S,i}$ in its group members.

From eqn 10, it follows that the genetic variance determining the potential response to selection in the population equals (Bijma et al. 2007a),

$$\sigma_G^2 = \sigma_{A_D}^2 + 2(n-1)\sigma_{A_{DS}} + (n-1)^2\sigma_{A_S}^2 \quad (11)$$

This result shows that IGEs alter the genetic variance that determines the potential response to selection in the population. In the absence of IGEs, eqn 11 reduces to $\sigma_G^2 = \sigma_{A_D}^2$, which is the classical result. Equation 11 can be generalized to account for other types of social interactions, such as the combination of social and maternal genetic effects (Bijma 2010; Bouwman et al. in press).

Note that eqn 11 defines genetic variance from a response-to-selection perspective. In other words, the

σ_G^2 as defined in eqn 11 is the genetic variance that is valid for use in eqn 6. It differs from the genetic component of phenotypic variance, $Var_G(z)$. For example, when interacting individuals are unrelated, it follows from eqn 8 that $Var_G(z) = \sigma_{A_D}^2 + (n-1)\sigma_{A_S}^2$, but eqn (9) implies that $\Delta \bar{G} \neq t\rho\sqrt{Var_G(z)}$. Because σ_G^2 is not a component of phenotypic variance, IGEs create a situation where the genetic variance available for response to selection may exceed the phenotypically observed variance, $\sigma_G^2 > \sigma_z^2$. Hence, part of the genetic variance is hidden. Thus, in theory, with IGEs a response expressed in phenotypic standard deviation units can be substantially greater than in classical quantitative genetic theory as we saw with heritability exceeding 1 in the first section on empirical results. Eaglen and Bijma (2009) discuss the distinction between σ_G^2 and $Var_G(z)$ in the context of maternal genetic effects.

The effect of information from kin and multilevel selection on accuracy

As shown above, the σ_G^2 follows directly from the inheritance model; it does not depend on the mode of selection. Rather, information from kin and multilevel selection affect the accuracy with which selection at the phenotypic level translates into a change in mean G -value. Hence, in terms of eqn 6, they affect the value of ρ .

First consider individual selection, where individual fitness is determined entirely by individual trait value, $SC_i = z_i$. In this case, accuracy equals the correlation between an individual's G -value and its trait value, $\rho = Corr(G, z)$. Substitution of eqns 8 and 10 shows that accuracy of individual selection equals

$$\rho(r) = \frac{r\sigma_G^2 + (1-r)[\sigma_{A_D}^2 + (n-1)\sigma_{A_{DS}}]}{\sigma_z\sigma_G}, \quad (12)$$

where r denotes relatedness between interacting individuals, which takes values between 0 and 1. (Note, r in eqn 12 is identical to f in eqns 2–5; the use of f is common in population genetics, whereas the use of r is common in quantitative genetics and kin selection theory.)

The numerator of this result shows that accuracy can be partitioned into two components. First, a component due to relatedness, $r\sigma_G^2$, which represents the proportion of selection acting directly on the G -values of individuals, and which is always positive. Second, a component due to the complement of relatedness, $(1-r)[\sigma_{A_D}^2 + (n-1)\sigma_{A_{DS}}]$, which may take negative values when direct effects and IGEs are negatively correlated. The second component explains why individual selection without kin information can yield a response opposite to the direction of selection, which was first shown theoretically by

Griffing (1967), and observed empirically by Craig and Muir (1996). When this component is negative, individual selection alone increases competition so much that the net response becomes negative as we discussed earlier. Equation 12 shows that relatedness among interacting individuals shifts selection away from a potentially negative term toward the genetic variance in trait value. In other words, relatedness causes utilization of the available genetic variance, thereby avoiding response in the ‘wrong’ direction.

Second, consider multilevel selection when group members are unrelated. Only individual and only group selection represent the extremes of a continuous scale of multi-level selection [see Bijma and Wade (2008) or van Dyken (2010) for a treatment of soft-selection in this context]. A selection model allowing for a continuous degree of multilevel selection is given by (Bijma et al. 2007a)

$$SC_i = z_i + g \sum_{j=1}^{n-1} z_j, \tag{13}$$

where the sum is taken over the $n-1$ group members of the focal individual, and g represents the degree of between-group selection. A $g = 0$ yields $SC_i = z_i$, indicating selection solely on individual trait value. A $g = 1$ yields $SC_i = \sum z_j$, the sum being taken over all n group members including the focal individual, so that all group member have the same SC-value and selection occurs fully between groups. Hence, g is a measure for the degree of between-group selection, and takes values in the same range as relatedness, $g \in [0..1]$

Substitution of eqns 10 and 13 into eqn 7 shows that the accuracy of multilevel selection in the absence of kin equals

$$\rho(g) = \frac{g\sigma_G^2 + (1-g)[\sigma_{AD}^2 + (n-1)\sigma_{A_{Ds}}]}{\sigma_{SC}\sigma_G} \tag{14}$$

Note that this result is strikingly similar to that for individual selection with related individuals (eqn 12); in the numerator, r is replaced by g . Hence, accuracy is partitioned into a proportion g acting directly on the G -values of individuals, and a remaining proportion $(1-g)$ acting on a potentially negative term. Hence, the effect of between-group selection on the sign of the accuracy is identical to the effect of relatedness. For example, to obtain positive accuracy while $[\sigma_{AD}^2 + (n-1)\sigma_{A_{Ds}}]$ is negative, either requires a certain degree of relatedness, or exactly the same degree of between-group selection.

Third, consider combined selection. Substitution of eqn 13 into eqn 7, and accounting for relatedness among individuals, shows that the accuracy of combined kin and multilevel selection equals

$$\rho(g, r) = \frac{[g + r + (n-2)gr]\sigma_G^2 + (1-g)(1-r)[\sigma_{AD}^2 + (n-1)\sigma_{A_{Ds}}]}{\sigma_{SC}\sigma_G} \tag{15}$$

The first term of the numerator demonstrates that both relatedness and multilevel selection act directly on the genetic variance in trait value, and thus contribute to a positive accuracy. Moreover, as indicated by the term $(n-2)gr$, the positive effects of relatedness and multilevel selection on accuracy amplify each other. Hence, if direct and IGE are negatively correlated, then the combination of kin and multilevel selection is a very powerful way to avoid negative response due to increased competition.

Figure 3 illustrates the relationship between ρ , g and r for a correlation of -0.6 between direct and IGE. In this example, a positive accuracy requires for example $r > 0.11$ with $g = 0$, or $g > 0.11$ with $r = 0$, or a combination of g and r such as $g = r = 0.05$. For $g, r > 0.11$, accuracy increases less with multilevel selection than with relatedness, because greater g yields greater σ_{SC} which limits the increase in accuracy (eqn 14).

Finally, consider selection based on relatives. In this case, the selection candidates are housed individually and they are selected based on the information of relatives kept in family groups (Ellen et al. 2007). Selection based on phenotypes recorded on relatives is very common in livestock genetic improvement, for example because recording the trait requires sacrificing the individual (e.g., carcass meat yield), or the trait is expressed only in

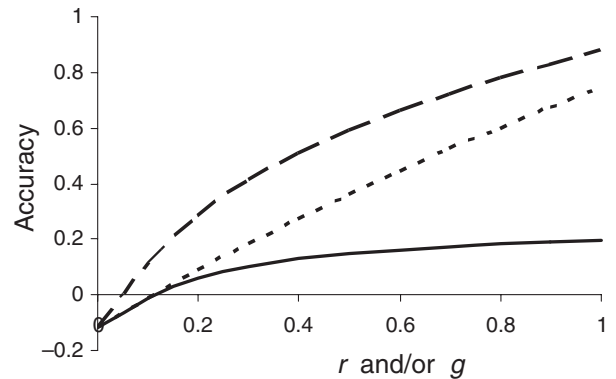


Figure 3 Example of the effect of kin and multilevel selection on accuracy of selection. Solid line represents multilevel selection, $r = 0$, g ranges from 0 to 1. Dotted line represents kin selection, $g = 0$, r ranges from 0 to 1. Dashed lines represents combined kin and multilevel selection, using $r = g$. Input values: $\sigma_{AD}^2 = 1$, $\sigma_{AS}^2 = 0.2$, $\sigma_{E_D}^2 = 2.33$, $\sigma_{A_S}^2 = 0.466$, $Corr(A_D, A_S) = Corr(E_D, E_S) = -0.6$, $n = 8$. Hence, IGE contribute slightly more to phenotypic variance than DGE, i.e., $(8 - 1) \times 0.2 = 1.4 > 1$, and ‘heritabilities’ of direct and social effects are 30%, i.e., $1/(1 + 2.33) = 0.3$ and $0.2/(0.2 + 0.466) = 0.3$.

females (e.g., egg number or litter size). In the absence of IGEs, the accuracy of selection based on relatives is commonly expressed in terms of relatedness between the candidate and its relatives, r , the square root of heritability, h , and the intraclass correlation t between the relatives. Also with IGEs, the accuracy of selection based on relatives can be expressed in that way, provided that the relatives are kept in family groups. With IGEs, the accuracy is given by (Ellen et al. 2007)

$$\rho_{rel} = \frac{r\eta}{\sqrt{\tau + (1 - \tau)/mn}} \quad (16)$$

where $\eta = \sigma_G/\sigma_{TPV}$ is an analogy of the square root of heritability, $h = \sigma_A/\sigma_P$, $\tau = r_{br}\eta^2$ is an analogy of the intraclass correlation between relatives $t = r_{br}h^2$, and mn is the number of relatives in m groups consisting of n individuals each. The r denotes relatedness between the candidate and its relatives, whereas r_{br} denotes mutual relatedness among the relatives. For example, when selection male candidates based on phenotypes recorded on their half-sib offspring, then $r = 0.5$ and $r_{br} = 0.25$. The η and τ account for interactions among individuals, and, therefore, depend on the genetic variance in the population and on the total phenotypic value (TPV) contributed by an individual. The TPV is the phenotypic analogy of the genetic merit of an individual (G , defined in eqn 10). The TPV represents an individual's total phenotypic effect on the population mean, which equals its direct phenotypic effect plus $n-1$ its indirect phenotypic effect. Hence, analogous to eqn 11, $\sigma_{TPV}^2 = \sigma_{P_d}^2 + 2(n-1)\sigma_{P_{ds}}^2 + (n-1)^2\sigma_{P_s}^2$. (Further details are in Ellen et al. 2007).

In conclusion, response to genetic selection can be partitioned into the strength of selection, the accuracy of selection, and the genetic variance available in the population (eqn 6). Social interactions alter the genetic variance available for response (eqn 11). Kin and multilevel selection shift the accuracy of selection in a positive direction, and therefore increase the utilization of genetic variance by selection. Finally, the effects of kin and multilevel selection on accuracy are strikingly similar (eqn 15).

Discussion

Darwin used the actions of human breeders and their 'artificial selection' as a model for his process of 'natural selection.' In his discussion of the evolution of social traits, like the sterile caste in the social insects, he made the analogy to breeders, who must destroy individual fruits or animals in order to determine their nutritional or gustatory quality, but return to the family of the sacrificed individual(s) for breeding. The formal theoretical underpinnings for this type of 'family' selection have been

developed in the fields of evolutionary and quantitative genetics and animal breeding over the past several decades, beginning with the works of Lush (1947) and Griffing (1967). Modern breeders have used these theoretical findings to alter selection methods to incorporate IGEs, significantly improving yield and animal welfare by antagonistic interactions between penned animals that are a primary source of mortality and lower yield. When the effects of IGEs are ignored in breeding programs in favor of classic individual selection, the direction of the response to selection is often negative. Yield may decline instead of increase when IGEs are present because the fastest growing and most robust individuals may also be those most effective in the competition for resources, achieving growth at the expense of the growth of their neighbors.

In applied quantitative genetics, the response to selection is expressed as the product of the intensity of selection, i , the accuracy of selection, ρ , and the genetic standard deviation, σ_G . In evolutionary genetics, this same 'breeder's equation' is the foundation of the theory of phenotypic selection developed by the so-called Chicago School of evolution (e.g., Lande 1980). In classic theory, it is the additive genetic standard deviation in individual trait value that determines the response to selection. With IGEs, the individual's total genetic merit includes the additive direct effects on its own phenotype as well as the individual's heritable impact on the mean trait value of the other members of its population (see eqn 11 above). When these effects are of opposite sign, the genetic variance available for response to selection may exceed the phenotypically observed variance among individuals. Hence, part of the genetic variance is hidden. Therefore, when breeding designs take account of IGEs, the response to selection expressed in phenotypic standard deviation units can be substantially greater than in classical quantitative genetic theory.

When IGEs affect the heritable phenotypic variance, multilevel selection and information from kin can be used to improve the accuracy of selection. Whenever direct effects and IGEs are negatively genetically correlated (as often happens with competitive social interactions), then the combination of kin and multilevel selection provides an efficient means for avoiding the negative response to selection that would otherwise attend selection on direct effects alone. The large gain in accuracy potentially available through the use of kin and multilevel selection is illustrated in Fig. 3. Conversely, when direct effects and IGEs are negatively genetically correlated and kin and multilevel selection are not used, the response to selection is diminished. In the absence of selection, over the long term, the amount of 'hidden genetic variance' owing to IGEs uncorrelated with direct effects will increase in the

population. This is the reason that adding kin and multi-level selection to the long-term breeding program focused solely on direct effects could so significantly increase the response to selection for egg lay in the work of Craig and Muir (1996).

The data from Muir (1996, 2005) and Ellen et al. (2008) illustrates that taking account of IGEs substantially increases the heritable variance in mortality due to cannibalism in laying hens. This highlights the importance of incorporating social effects into poultry breeding programs. Among-group selection or information from groups of relatives is important because it allows access to the additional or otherwise 'hidden' heritable variation. In addition to laying hens, social interactions are important in other livestock, like pigs and fish. Thus, among-group selection or selection on estimated IGE might be used more generally to improve the welfare and production of livestock by incorporating social genetic effects in the breeding program.

In summary, Griffing (1967) developed the theory of IGEs to avoid negative responses to individual selection. More than simply avoiding negative selection responses, we showed how the theory allows the breeder to access significant amounts of 'hidden heritability,' two to three fold greater than the 'classic' estimates in some empirical cases. However, breeders had to change both their methods of estimation and the nature of their selection regimes, away from individual selection and toward multi-level selection, in order to access the variation associated with IGEs.

In contrast to animal breeders, evolutionary biologists continue to dispute the value of the multi-level perspective (e.g., West et al. 2007; Wild et al. 2010) and resort to explanations based on among-group selection only when the evolution of a trait cannot be explained by individual selection. If the response to classic individual selection can be negative when IGEs are ignored in breeding programs, it seems reasonable to extrapolate that adaptive scenarios in evolutionary biology based solely on individual selection may also mistakenly identify the direction of selection (see also Wolf and Wade 2001, 2009). If breeders require information from genetic relatives and/or replicated social contexts to estimate the genetic parameters for a response to selection in the presence of IGEs, it is reasonable to extrapolate that experimental evolutionary biologists will also require such methods, particularly when the goal of laboratory studies is to understand evolution in species whose members live in genetically subdivided meta-populations. Indeed, to the extent that antagonistic competitive interactions lie at the heart of Darwin's theory of evolution by natural selection and to the extent that IGEs underlie these interactions, it does not seem possible to understand adaptive evolution in

genetically subdivided populations solely on the basis of individual selection. As we showed in eqn 15, the positive effects of relatedness and multilevel selection on accuracy amplify one another making multi-level selection particularly powerful whenever there is competition between individuals and direct and indirect effects are of opposite sign.

Acknowledgements

Both PB and EDE are financially supported by the Dutch science council (NWO) and the research was co-ordinated by the Netherlands Technology Foundation (STW). MJW is supported by NIH R01-GM065414-05A1.

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