Re: Hamilton's rule

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- *From*: Guy Hoelzer <hoelzer@xxxxxxx>
- *Date*: Thu, 17 Nov 2005 01:10:27 −0500 (EST)

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in article dlft8t$2fog$1@xxxxxxxxxxxxxxxxxxx, Perplexed in Peoria at
jimmenegay@xxxxxxxxxxxxx wrote on 11/16/05 10:20 AM:

> "Guy Hoelzer" <hoelzer@xxxxxxx> wrote in message
> news:dldgfc$1drk$1@xxxxxxxxxxxxxxxxxxxxxxx
>> in article dl58qa$p8l$1@xxxxxxxxxxxxxxxxxxx, Catherine Woodgold at
>> an588@xxxxxxxxxxxxxxxxxxx wrote on 11/12/05 9:29 AM:
>>
>>> Guy Hoelzer (hoelzer@xxxxxxx) writes:
>>>> My confusion is rearing its ugly head again. If the axes of the graph are
>>>> "frequency in focal individual (Y axis) vs frequency in population (X
>>>> axis)", then I don't see how dominance/recessiveness can influence the
>>>> lines
>>>> at all. What am I missing?
>>>
>>> One of the lines is labelled "donor". The only individuals
>>> who act out the "donor" phenotype are the ones which have
>>> the set of genes that code for altruism. If altruism is
>>> a recessive trait, then all of the "donors" must have
>>> two copies of the altruism gene. Therefore the frequency
>>> in the "donor" focal individual is always 1 if altruism
>>> is a recessive trait.
>>>
>>> But if the altruism gene
>>> is dominant, then the set of "donors" includes some
>>> individuals with one copy of the gene and some individuals
>>> with two copies of the gene. If an individual is
>>> observed to carry out an altruistic act, or if it
>>> finds itself experiencing an overwhelming urge to
>>> carry out an altruistic act, then an observer
>>> (or the organism itself) can conclude that the
>>> individual has one or two copies of the altruism gene.
>>> The expected frequency in this individual can thus be
>>> predicted to lie between 0.5 and 1 (closer to 1 if
>>> the altruism gene is very common in the population).
>>
>> Maybe I should have said more. All of this was apparent to me. In the
>> artificially restricted world of modeling perfect dominance/recessiveness
>> the starting point of the donor line would be 0.5 (pure recessiveness) or

>> 1.0 (pure dominance). In either case, however, there is a simple linear
>> relationship on the frequency/frequency graph that converges on the point
>> (1,1). The comment you quoted above came from a discussion where I thought
>> it was implied that the shape of the relationship (e.g., linearity) was said
>> to depend on dominance/recessiveness. I may have been reading too much into
>> Jim's comments, which I still think reached way outside the scope of the
>> simple frequency/frequency graph.
>
> Reached way outside how? My claims are fairly simple:
> − If the (single) altruism locus is purely recessive, the graph of allele
> frequency in donors is a constant 1.0. (Obviously).
> − If the altruism locus is purely dominant, the graph of allele frequency
> in donors rises linearly from 0.5 to 1.0 as the allele frequency in the
> population rises from 0.0 to 1.0. I am uninterested in a 'glitch' in
> this curve at allele frequency exactly 0.0 − there technically are no
> donors at exactly this frequency.

I'm with you so far.

> − Given other assumptions about gene expression besides pure dominance or
> recessiveness, it is possible that the donor line may be something other
> than linear. That doesn't matter as long as the donor D line never drops
> below the 45 degree population P line. Regardless of how the line runs,
> or of how many loci are involved, it remains the case that the recipient
> R line lies a fraction 'r' of the way up from the P line to the D line.
> This fact is a consequence of the definition of IBD 'r' and the assumption
> of random mating.

Ooooooh. I got lost in semantics here. Let me try to put some words in
your mouth and you tell me how they taste. The R line does not represent
the frequency of the allele among actual recipients. Instead, it represents
the tipping point of HR. If the recipients of altruism fall above the R
line relative to their donors, then HR predicts that kin selection will
favor the altruism allele. It would be optimal, from the viewpoint of the
allele, if actual recipients had the maximum number of altruism alleles
possible (2).

> This fact is all that is needed to establish Hamilton's rule.

I'm going to have to apologize again for being dense, but I don't see how
your graph justifies HR at all. It would be a nice graphical representation
of the HR claim, but how would it lead to the conclusion that the R line
ought to lie "a fraction 'r' of the way up from the P line to the D line."
This is essentially the claim of HR, but it seems to be something that you
have assumed here. As you said, "this fact is a consequence of the
definition of IBD 'r' and the assumption of random mating." Because it
relies so fundamentally on the definition of IBD 'r', how can it justify the
use of IBD 'r'?

> The rule does not depend on linearity. The frequency
> independence of the rule does not depend upon frequency.

OK.

> − What MAY depend on frequency is how fast the altruism allele spreads.
> That will depend upon just how separated the lines are, and the count
> of altruists (or of acts of altruism, depending on what b and c measure).
> It will also depend on the size of b and c. I offered my straight lines
> as an argument against YOUR claim that the impetus toward the spread of
> the altruism alleles pretty much peters out at gene frequencies of 30−40%.

Under your graphical model, which I accept as a representation of Hamilton's model, the strength of kin selection diminishes monotonically with the frequency of the allele. I guess you have swayed me to the position that under Hamilton's model, as opposed to a more realistic version of the same model, there is not a frequency threshold where kin selection becomes irrelevant. Instead, it becomes irrelevant monotonically.

> So, I have to ask, what exactly are your claims? Do you still believe that
> the spread of kin−selected altruism peters out at this level, and that only
> reciprocity can take things further?

Well, I still believe that the strength of kin selection peters out as the allele becomes more common. Your graphical model confirms that for me. I also still think that the kin selection model is entangled with the reciprocal altruism model, which I see as more general and a more plausible explanation for most altruism in nature.

> If so, what kind of D and R curves
> are you postulating? And why do you think the curves have that shape?

I accept your explanations of D and R curves. Thanks for your patience.
:−)

Guy

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- ***References***:
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    - ◊ *From:* Catherine Woodgold
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