

Re: Reviving group selection

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From: Tim Tyler (*tim_at_tt1lock.org*)

Date: 08/13/04

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Perplexed in Peoria <jimmenegay@sbcglobal.net> wrote or quoted:

>
> "Tim Tyler" <tim@tt1lock.org> wrote in message news:cfg2sf\$nc0\$1@darwin.ediacara.org...
>> Perplexed in Peoria <jimmenegay@sbcglobal.net> wrote or quoted:
>>>
>>> "Tim Tyler" <tim@tt1lock.org> wrote in message news:cf693l\$hb5\$1@darwin.ediacara.org...
>>>> I wrote an essay about group selection recently.
>>>> It can be found at:
>>>> http://alife.co.uk/essays/reviving_group_selection/
>>>> A brief summary here:
>>>> Many of the theoretical arguments against group selection deny that sexual
>>>> groups vary much from place to place – because the stirring effect of
>>>> sexual recombination is too great for this to happen – and partial group
>>>> isolation and population viscosity are normally not enough to prevent it.
>>>
>>> In the first place, sexual recombination has nothing to do with any
>>> "stirring". Perhaps you meant to refer to the stirring effects of
>>> intergroup migration and crossbreeding.
>>>
>> This is a mysterious comment. Genes *_do_* get stirred together in sexual
>> populations by sexual recombination.
>>
> Yes, in some sense. But that stirring is within groups, not between groups.
> No theoretical argument against group selection is based on within-group
> stirring.

I'm assuming the groups interbreed to some extent. Otherwise they would be likely to rapidly turn into new species.

>> Without such recombination, organisms would be asexual – and no
>> cross-breeding would occur.
>>
> I'm not sure I agree, but this disagreement has nothing to do with group
> selection.

I /suspect/ this may have something to do with you interpreting "sexual recombination" as referring to a process that happens between homologous chromosomes – whereas I intended it to refer to any process

sci.bio.evolution: Re: Reviving group selection

that produces new combinations of genes via sex.

That is a hypothesis which would explain your comment, anyway.

- > > > *But more importantly, "stirring" can only reduce variation between groups*
- > > > *if there was already significant variation to be "stirred". Your essay*
- > > > *says absolutely nothing about how such variation arises.*
- > >
- > > *Variation arises by mutation. My essay is not about mutation – I take*
- > > *the existence of mutations for granted.*
- >
- > *Mutation is a sufficiently strong force for creating variation within a*
- > *group, but it is very weak as a force for creating variation between groups.*
- > *For that, you need something like drift or sampling error during new group*
- > *formation.*

Mutation is pretty critical.

Without it, drift tends to rapidly run out of variation to magnify.

I tend to regard mutations as the "true" origin of all variation ;–)

- > > > *Furthermore, variation between groups for any trait subject to*
- > > > *individual selection must decrease even without "stirring".*
- > >
- > > *It is not clear what you mean. You are suggesting variation between*
- > > *groups for any trait subject to individual selection must decrease?!?*
- >
- > *Yes definitely! We discussed this recently. Any trait which has selectable*
- > *variation in two different groups must move to fixation in both groups.*
- > *Hence, the variation for this trait BETWEEN groups must diminish to zero.*

A confusing thing to say. IMO, you need to add the words "if selection is the only force acting" and you need to put that in IN CAPITAL LETTERS if that is your assumption here – since otherwise it is not at all obvious that that is what you mean. The words which you actually wrote are not correct without such a qualification.

- > > *That is not correct – the groups can diverge if they are subjected to*
- > > *mutations and insufficient gene flow between them.*
- >
- > *Yes. If, due to mutation, there is variation in only one of two groups,*
- > *then the group containing the variation will evolve, while the group without*
- > *the variation remains static. In this case, intergroup variation for this*
- > *trait can arise and increase. And, in the absence of gene flow, the*
- > *intergroup variation can persist. But, notice, this is not an example*
- > *of group selection as a positive force for evolution. It is an example*
- > *of gene-flow barriers as an impediment to evolution.*

I was trying to address the question of under what circumstances group differences can arise and persist – by identifying some

mechanisms responsible for generating between group differences.

Whether the resulting variation that could fuel group selection resulted in a "positive" or "negative" force (whatever that might mean) was not an issue I was trying to address.

- > > *A trip to Africa followed by a trip to Iceland illustrates clearly that*
- > > *the notion that gene flow homogenises interbreeding sexual populations*
- > > *is incorrect in practice.*
- >
- > *Very unconvincing, to me at least. Gene flow between Africa and Scandinavia*
- > *would have to pass through an enormous number of groups along the way.*
- > *You could have large gene flows between each and every neighboring group*
- > *along the way (sufficient to kill group selection as you see it) and still*
- > *not have enough mixing of Scandinavian and African genes to homogenize*
- > *skin/eye color and hair structure – particularly if there are mild selective*
- > *advantages to different traits in different climates.*

The significance of selection on the basis of climate was one of the points I was attempting to draw attention to.

Whether it is enough to "kill group selection as I see it" seems to me to depend on the details of the genetic model I presented at the end of my essay:

In the case where just one gene is being selected for, only that gene – and some genes it is closely linked to – are likely to be affected – and gene flow is free to homogenise the rest of the genome.

However, if selection favours not a single–gene trait – but rather a complex of genes spread across a number of chromosomes – then the genes being selectively favoured will be numerous – and they are likely to be spread across multiple chromosomes – and in that case, much of the genome might well be linked to them.

To illustrate the plausibility of this consider the example from my essay of an organism depending on slow moving sedentary creatures on one continent – but forced to chase fast–moving creatures on another one.

These organisms may be under selective pressure to develop different adaptations in the two environments do deal with the different problems they face.

However, the adaptations required may well be many and various – and may affect many genes at many loci.

Under such circumstances, gene flow between the populations may face powerful selective barriers at a wide range of loci – due to the linkage of those genes with numerous genes that /are/ directly

affected by the selection.

Another good example of geographic variation in sexual species springs to mind at this point: ring species.

Ring species are not common – but there /are/ sexual ring species – for example:

"Song variation in an avian ring species"

– <http://calorierestriction.org/pmid/?n=10937272>

Ring species are interesting in this context – since the issue of whether there is much variation or division between neighbouring groups is of reduced importance. There is a /lot/ of variation between neighbouring groups at at least one point – and there the groups may well be in competition with one another – and are in a good position to invade and displace one another from each other's territory.

This conjures up a picture of the "join" in the ring species rotating back and forth around the planet – as the two ends of the ring species take it in turns to drive local populations of their competitors extinct – changing the global frequency of genes in the population in the process.

I'd classify such a process as a form of group selection.

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