

# Re: The Cost of Substitution [possible REPOST]

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- *From:* "John Edser" <edser@xxxxxxxxxxxxxxxx>
  - *Date:* Thu, 30 Nov 2006 01:52:46 -0500 (EST)
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"Perplexed in Peoria" jimmenegay@xxxxxxxxxxxxxxxx wrote:-

Wilson basically supports ReMine on the 'misrepresentation' question, while remaining quite skeptical on whether the Dilemma constitutes a problem for 'evolutionists'.

JE:-

The following problems

- 1) What is the cost of substituting one gene for another in a single population?
- 2) What is significance of the many different answers to the cost of substitution to "Haldane's Dilemma"?

are related but remain separate propositions. In this thread we are only concerned with 1. If you wish to debate 2 (which depends entirely on a resolution of 1) please start another thread.

Here is a copy of that posting:

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In article <pan.2006.11.24.21.52.33.239921@xxxxxxxxxxxxxxxx> on November 24th  
in talk.origins Mark Isaak <eciton@xxxxxxxxxxxxxxxx> wrote:

On Thu, 23 Nov 2006 22:01:57 +0000, Perplexed in Peoria wrote:

snip<

1. "Since humans and apes differ in  $4.8 \times 10^7$  genes, ..."

This claim has already misled at least one talk.origins poster to  
ridicule

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ReMine for making such a silly blunder. But the blunder here is entirely the fault of whoever wrote CB121. ReMine does not make this claim in \_The Biotic Message\_ (or anywhere else as far as I know).

2. "Only 1,667 nucleotide substitutions in genes could have occurred if their divergence was ten million years ago."

JE:–

No, 1667 \_fitness dependent\_ gene sets (NOT separate single genes). Haldane employed Fisher's oversimplified gene centric assumption which disallowed heritable genetic epistasis. This preempted Haldane's false dilemma.

"The vast majority of differences would probably be due to genetic drift, not selection."

JE:–

Drift acts randomly so these genes were being randomly substituted long before humans and chips even evolved and continued to do so afterwards. The genes which have to be proven to evolve and substituted in 5–10 million years were NON neutral genes carried by a supposed common ancestor to both. This answer was provided by the human and chimp genome project: less than 1% of 20–25,000 polypeptide coding genes are different between man and chimp (which well within Haldane's 1667).

The only significant question to be answered is WHY did Haldane et al reason that 1667 was much too small a number for a significant selectable gene difference? The short answer is because they assumed genetic epistasis was inherited but remained non heritable and therefore non selectable (after Fisher's oversimplification). The number 1667 remains too little to code for just heritable (additive) differences between man and chimp but sufficient to code for any heritable NON ADDITIVE differences, IOW heritable epistatic traits. Key example: ANY gene fitness! Not one, single, additive gene fitness has ever been documented in nature, no matter how you define fitness.

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The criticisms which CB121 makes of Haldane's "Cost of Natural Selection" are

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also erroneous in my opinion:

1. "Haldane's "cost of natural selection" stemmed from an invalid simplifying assumption in his calculations. He divided by a fitness constant in a way that invalidated his assumption of constant population size, and his cost of selection is an artifact of the changed population size."

JE:–

The only valid constant (at least one constant algebraic term is always required to supply a necessary Galilean frame of reference allowing a proposition to remain rational and not just logical) is the proposed size of the original population to be substituted. This CANNOT be changed "ad hoc" (Felsenstein reduced it "ad hoc") so as provide a relative cost to just nothing defined by anybody. If you increase the size of the original population "ad hoc" the cost of substitution can NEVER be paid. If you can reduce it "ad hoc" you can substitute the population "for free" via an illegal concealed payment.

2. "He also assumed that two mutations would take twice as long to reach fixation as one, but because of sexual recombination, the two can be selected simultaneously and both reach fixation sooner."

This is nonsense. Haldane did not assume this. He derived it from his other assumptions. The derivation is given at the bottom of page 20 of The Cost of Selection". It does not assume that the mutations only become fixed one at a time, and it does take full account of the role of sexual recombination. Contrary to the specious conclusions which at least one talk.origins poster has tried to draw from a calculation given on ReMine's web-site, he does not assume this either. It would appear that he has read Haldane's paper a little more carefully than some of his critics, since he says explicitly on page 216 of The Biotic Message:

"This does not mean these substitutions occur sequentially, one by one. Several genes can undergo substitution simultaneously at various speeds. If you average all these speeds, then the total rate can be one per 300 generations."

And this is an accurate description of what Haldane showed (given his assumptions).

Haldane's arguments, and hence his conclusions, are, however, limited to sets of genes which have independent effects on fitness.

JE:–

The above constitutes the key as to why Haldane's gene centric dilemma was

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always just a gene centric \_misrepresentation\_. Not one, single, additive gene fitness has ever been documented within NATURE (including meiotic gene fitnesses). At least one is required to verify an independent fitness "effect" (no matter how you define fitness).

All genomic genes (please note: I include meiotic drive gene fitnesses here and remain happy to debate this point) were and remain fitness DEPENDENT on just the one, same, \_genome\_ fitness. The only refutable fitness that actually exists is TDF (Total Darwinian Fitness). This is defined as: the total number of \_fertile\_ forms reproduced per parent per population. It is this fitness constant per parent per population which represents a refutable Darwinian maximand allowing a refutable Galilean frame of reference to exist for ALL of evolutionary theory.

snip<

In the 1950s Haldane calculated the maximum rate at which genes could be replaced through differential reproduction and survival. He concluded that it posed a serious problem for evolution. His conclusion was that the long-term average rate at which beneficial alleles become fixed in a population can be no greater than one every 300 generations. This means that over 10 million years of alleged human evolution from an ape-like ancestor, with an average generation time of 20 years, at most 1,667 nucleotides could be selectively replaced in the population. This is insufficient to account for the difference between modern humans and any such alleged ancestor.

JE:–

The above assumption predicted on a misuse of Fisher's oversimplified assumption of what is and what is not heritable in nature was refuted empirically via the human and chimp genome projects.

What remains evaded via the (quiet) dumping of Haldane's false Dilemma is: why Haldane and Fisher predicated this false dilemma on empirically false premises and even more critically, have these false premises been corrected today? Shamefully, the short answer to is NO, they haven't been corrected. They remain the basis of today's population genetics.

snip<

Regards,

John Edser  
Independent Researcher

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