

Subject: Re: CDB On Line forum

From: Fred Gould <fgould@ncsu.edu>

Date: 7/30/2017 2:47 PM

To: Royden Saah <royden.saah@islandconservation.org>

CC: "Fred_gould@ncsu.edu" <fred_gould@ncsu.edu>, Todd Kuiken <tkuiken@ncsu.edu>

This post sounds accurate to me. I suggest a longer introduction such as....

Researchers are attempting to create a synthetic biology systems that could potentially benefit biodiversity, such as gene drives used to manage invasive animals known to cause extinctions.

However, there are important concerns about the robustness of these gene drives in face of genetic diversity in the populations of invasive species.

On Jul 30, 2017, at 10:29 AM, Royden Saah <royden.saah@islandconservation.org> wrote:

Hi Fred and Todd,

I have been monitoring the on-line forum and it appears to be well articulated from a position of information and material to support continued investigation into gene drives at least. I would like you to see if this posts makes sense. It is in response to the resistance alleles brought up by Lazaro (Post #8621). I believe I have 10.5 hours from now to submit. Any suggestions, especially critical and honing, would be much appreciated! Below is what I am suggesting:

Dear Dr. Regalado,

Thank you for your comments in Post#8621. Researchers have found it difficult to create a synthetic biology systems that could potentially benefit biodiversity, such as gene drives used to manage invasive animals known to cause extinctions (<https://doi.org/10.1016/j.ecolecon.2004.10.002>).

Because of this, I would like the AHTEG to also consider the recent publication on resistance which states,

“The variation in resistance rates among lines we observed in this study has important implications for the feasibility of gene drive strategies in the wild. The likelihood that resistance evolves against a drive should be determined primarily by those individuals that have a high rate of resistance allele formation, even when the average rate in the population is low. This will be particularly relevant for target populations that harbor high levels of genetic diversity, such as *A. gambiae* [53]. It also has important implications for the assessment of gene drive parameters in the laboratory, which should include cage experiments of large, genetically diverse populations followed over many generations, instead of focusing on crosses of isogenic lines. Finally, variation in drive parameters among individuals will need to be included in our theoretical models, which currently rely on rather simplistic assumptions such as constant resistance and conversion rates across the whole population [6–11, 30–32].”

<http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1006796>

Sincerely,

J. Royden Saah

