

Subject: RE: CDB On Line forum
From: Royden Saah <royden.saah@islandconservation.org>
Date: 7/30/2017 8:59 PM
To: Fred Gould <fgould@ncsu.edu>

Teamwork is much appreciated.

-rs

From: Fred Gould [mailto:fgould@ncsu.edu]
Sent: Monday, July 31, 2017 9:59 AM
To: Royden Saah <royden.saah@islandconservation.org>
Subject: Re: CDB On Line forum

I just posted your comments.

On Jul 30, 2017, at 7:39 PM, Royden Saah <royden.saah@islandconservation.org> wrote:

Hi Fred,

Thanks for your various discussions and emails. I just tried to post and found that although registered, I was not registered as an expert, so my registration only allows observation, not contribution. It is too late for me contributing to this topic area. I think only Todd, you, and Mark Tizard from CSIRO are registered from GBIRD. Here is a draft if you would like to post:

Dear Dr. Regalado,

Thank you for your comments in Post#8621. 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(<https://doi.org/10.1016/j.ecolecon.2004.10.002>). However, there are important concerns about the robustness of these gene drives considering genetic diversity in the populations of invasive species.

Because of this, I would like the AHTEG to also consider the recent publication (<http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1006796>) 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*. 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.”