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RESPONSE

Response to Chi, Mou, Lee and Smith

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In our article, 'Invariance of demographic parameters using total or viable eggs' by C. Hernandez-Suarez, P. Medone and J. E. Rabinovich (this issue), we provide three different mathematical proofs that R_o will yield the same result using total or viable eggs, as long as the participating stages are defined accordingly. Thus, R_o can be defined as the 'number of eggs that will replace each initial egg of a cohort in the period of one generation', the 'number of viable eggs that will replace each viable egg in the period of one generation', the 'number of adults that will replace each adult in the period of one generation' and so on.

Regrettably, Chi, Mou, Lee and Smith (CMLS)'s response to our article is merely tautological. In the last paragraph they mention: 'Based on the above mathematical proof...', however, there is no mathematical proof in their arguments, which even lacks of a single equation. They merely refer to equations in their original article (Mou et al. 2015), some of which have been criticized in our article, so no new formal mathematical evidence has been provided.

Additionally, CMLS mention: '...misinterpretation and errors in their proof', but again, there is no single exhibition of such errors in our work; in fact, there is no reference to any of our equations identifying them in our work, which discards any mathematical refutation to our proof.

In their response, the authors used hypothetical and simplified data (tables 1–5 in CMLS) to substantiate their arguments, and sound scientific procedures indicate that no data set can be valued against mathematical proofs as the ones we have provided.

Chi, Mou, Lee and Smith confirm our impression that there was a flaw in the experimental design, when they say 'When the egg hatch rate of a particular species varies with maternal age, it is impossible to collect eggs representative of the entire population unless a prohibitively large number of eggs are used'. So, if the sample of the original number of eggs for initiation of the cohort study was not statistically representative of the population as a whole (at least in terms of hatching rates, something that we have confirmed from the article on

H. dimidiata), then increasing the number of eggs should have been a methodological sound option, and the argument of excessive work should not override scientific procedures.

Furthermore, CMLS make an unsustainable statement that because the hatch rates of female daily fecundity were based on a much large sample size and thus are more representative than the parent cohort, then the l_x , m_x and h_x calculated using only viable eggs are more representative than those based on total eggs. There is no demonstration anywhere in the original CMLS article, nor in their rebuttal to our article, in the direction that the hatch rates of female daily fecundity can be considered more representative of the population as a whole. The sole fact that the number of eggs from the female's daily fecundity that was analysed to estimate the cohort's hatch rate was really high (23,309 eggs) cannot be used as an argument for representativeness; this would be so if all other conditions could be guaranteed as being identical. Furthermore, in the Discussion section of the original CMLS article, it was mentioned that Gillani et al. (2007) reported 96% hatching rate, even higher than the original batch of eggs used for the initiation of the cohort, and so further deviant from the average hatch rate of the female's daily fecundity that CMLS consider 'more representative'.

In relation to mean generation time, the authors have focused their critique on a simple semantic concern (i.e. stage versus age). Our argument still holds if we replace stage by age.

Chi, Mou, Lee and Smith also claim that as a theoretical proof must be inclusive and that our discussion regarding r and λ is based on the approximate (or simplified method) of Birch (1948) that this needs no more refutation. Our mathematical proofs involving r and λ are completely general and not restricted to any particular estimation method.

Many years ago, there was a discussion on whether to calculate R_o by considering only females (because these are the ones laying eggs) or all individuals. Biologists then had to count how many eggs gave birth to

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females, which required a huge amount of extra work. That discussion is over, and it is common knowledge now that one can use all individuals. CMLS's article put us back a few years and confuses the readers.

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