How do population cycle frequency and dispersal interact to shape population genetic structure?

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Introduction

- Population cycling is common across many taxa, including irruptive forest insect pests such as the mountain pine beetle.

- However, the influence of population cycling on the spatio-temporal dynamics of population genetic structure remains unknown.

- Due to successive population bottlenecks during cycling, successive outbreaking populations are expected to become genetically differentiated[1].

- Such differentiation might depend on dispersal[2] and cycle frequency, although the nature of their interactions have not been explored.

Objective: Using the mountain pine beetle as motivation, we examine how outbreak cycle frequency and dispersal capacity affect genetic differentiation between successive outbreaks using a spatially explicit individual based demo-genetic simulation model.

Methods

Individual based simulation

- Mountain pine beetle demographic and genetic dynamics were simulated using CDMetaPop[3].

- We simulated 3 levels of dispersal and 3 outbreak frequencies (9 scenarios total) each replicated 10x.

- Initial conditions: 270 individuals placed in a 3*3 centre refuge.

- Total grid size varied with cycle length and dispersal.

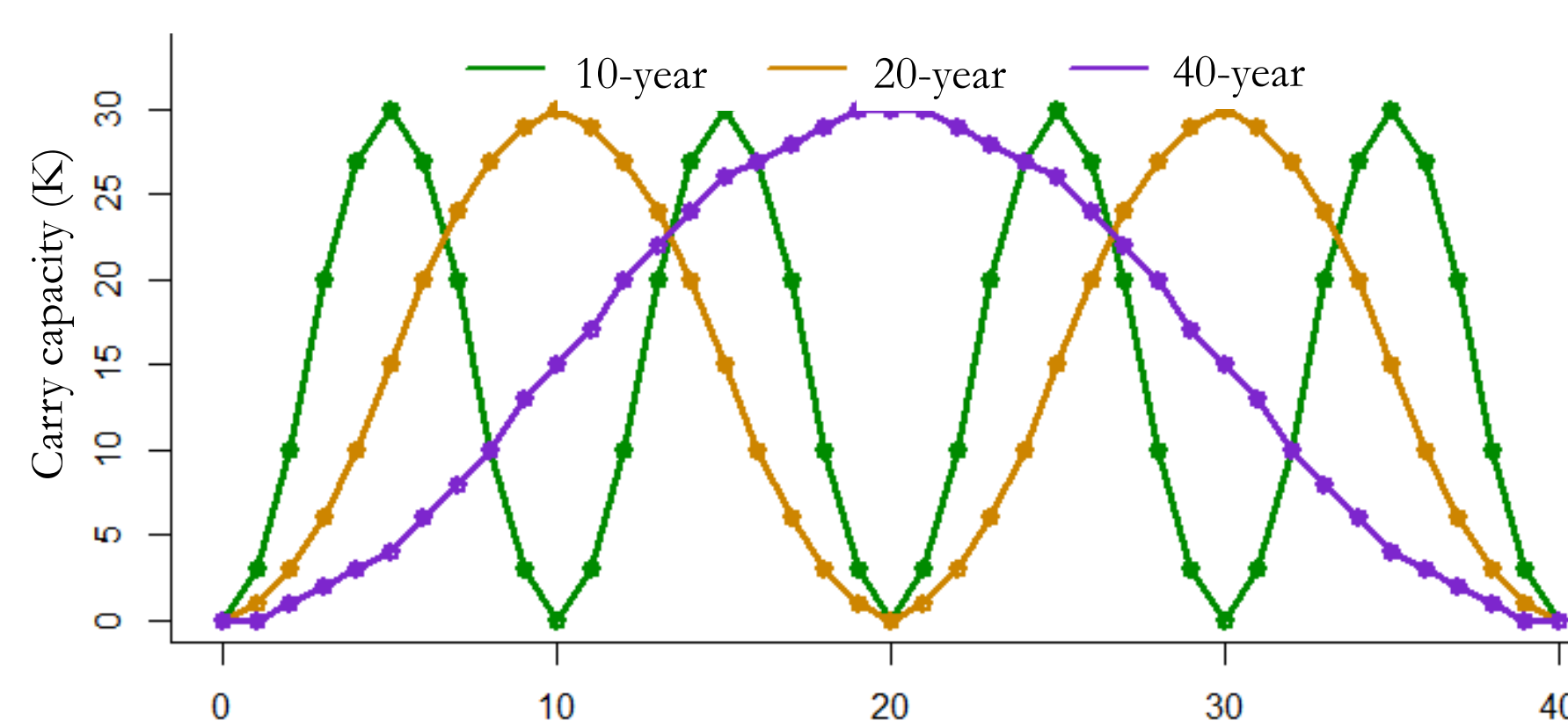- Time horizon for each scenario was 10 outbreak cycles.

Frequencies

Fig.1- Outbreak cycles were forced through the use of a sinusoidal variation in carrying capacity (K) of each lattice cell (Krefuge=30, Kcell=0~30). Three outbreak frequencies were examined: 10-year, 20-year and 40-year.
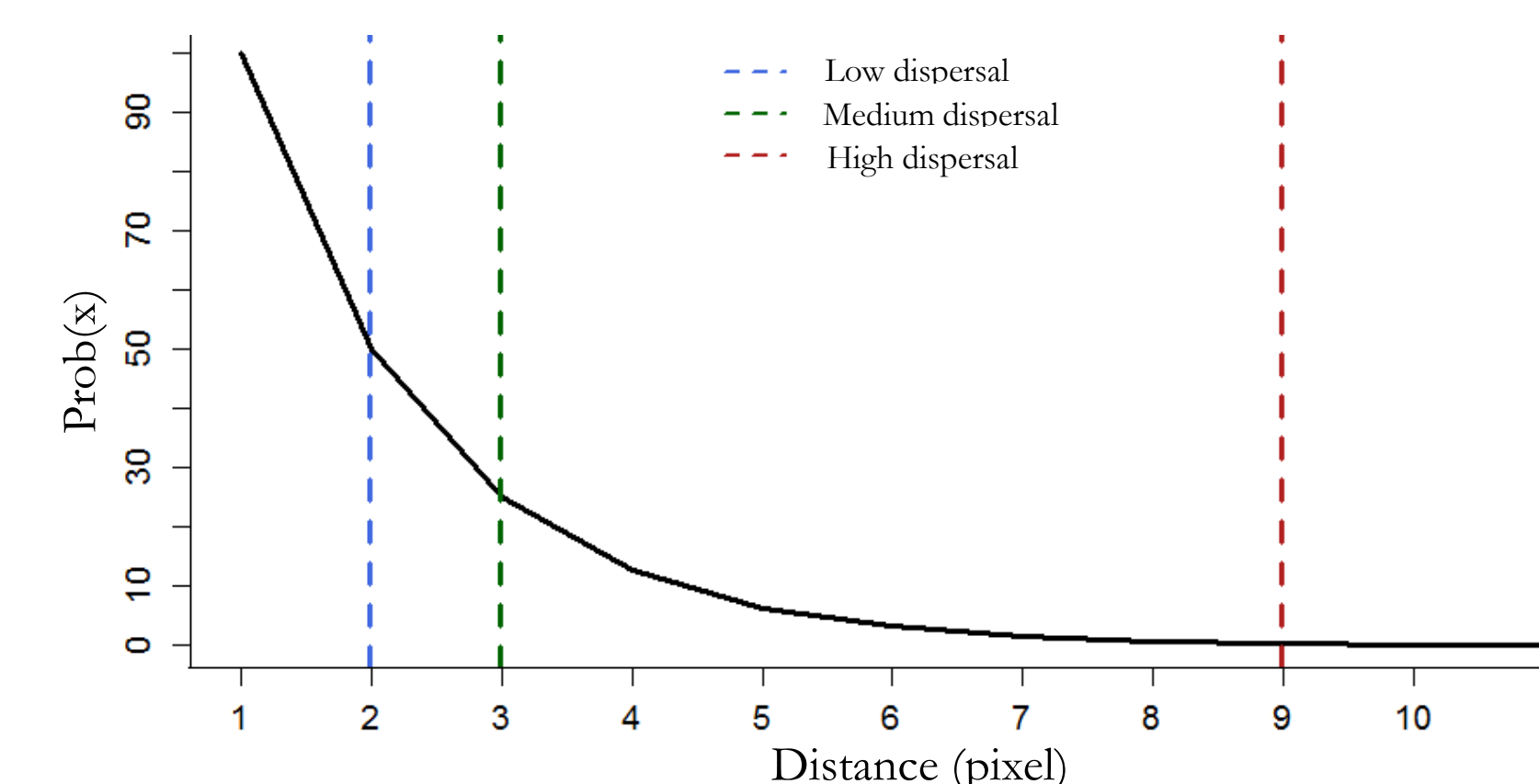
Dispersal

Fig.2- Dispersal was simulated using a fixed negative exponential dispersal kernel. Dispersal capacity was varied by limiting the maximal possible dispersal distance. Low=2 cells, Medium=3 cells and High=9 cells.

Results & Discussion

1. Population dynamics

- Trough: K=0, except for refuge (Krefuge=30).
  → Bottleneck

- Growing phase: population expands from the refuge.
  → Allee effect caused by low population size

- Decreasing phase: population density decreases synchronously in all the cells outside the refuge (e).
  → Allee effect caused by low density

- Asymmetry[4]:
  → The actual population peaks slightly later than the peak of the forced cycle in K.

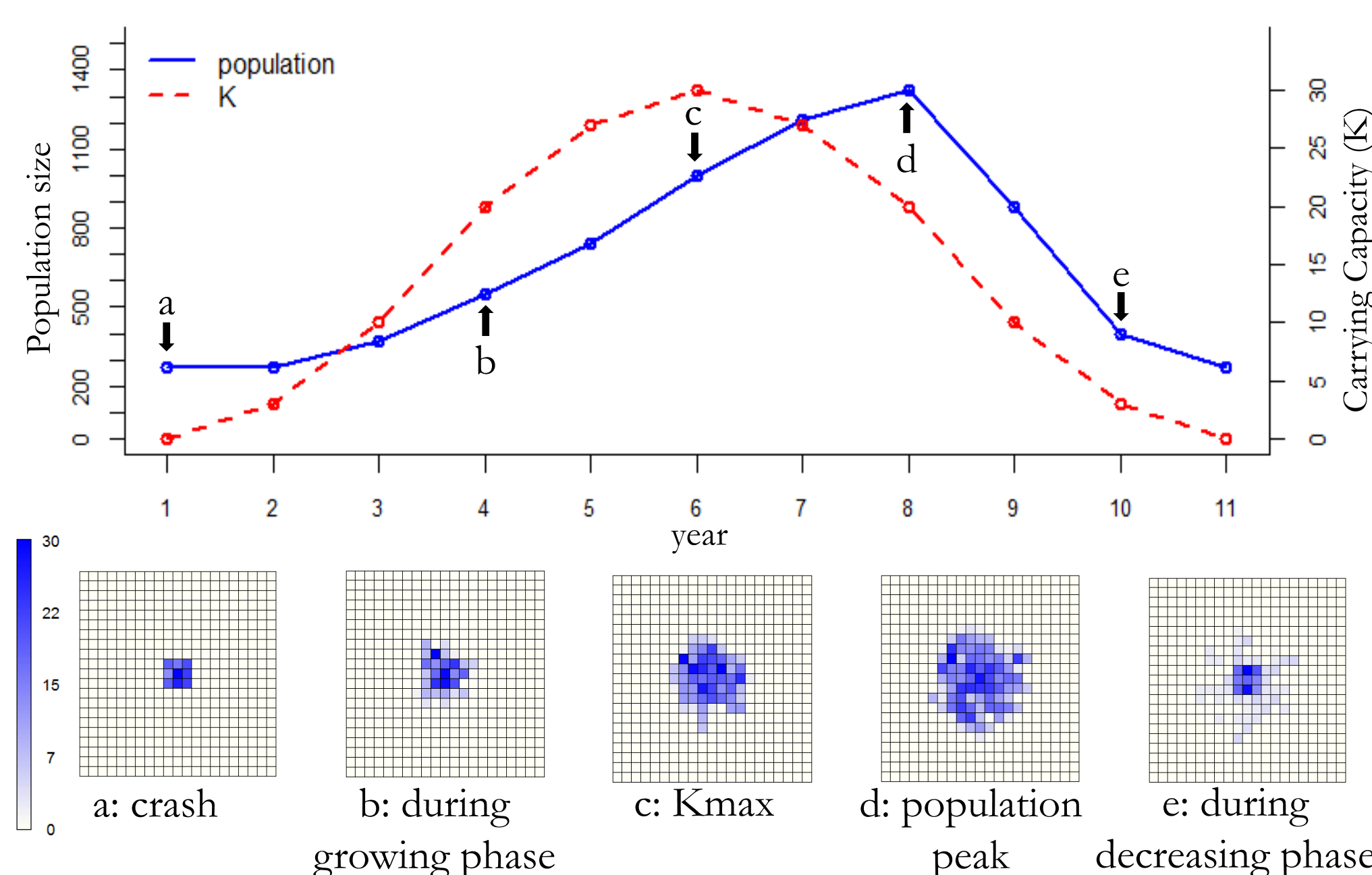a: crash   b: during growing phase   c: Kmax   d: population peak   e: during decreasing phase

Fig.3-Simulated population dynamics and spatial patterns for a 10-year cycle. At peaks, cells contain a maximum of K=30 individuals. During population crashes all cells go to K=0, except a centre refuge cell that remains at K=30.

2. Genetic diversity (He) vs. Outbreak Frequency

- Genetic diversity decreases as the number of outbreak cycles increases.

- With the same dispersal capacity, lower outbreak frequency favours greater diversity loss during each cycle.

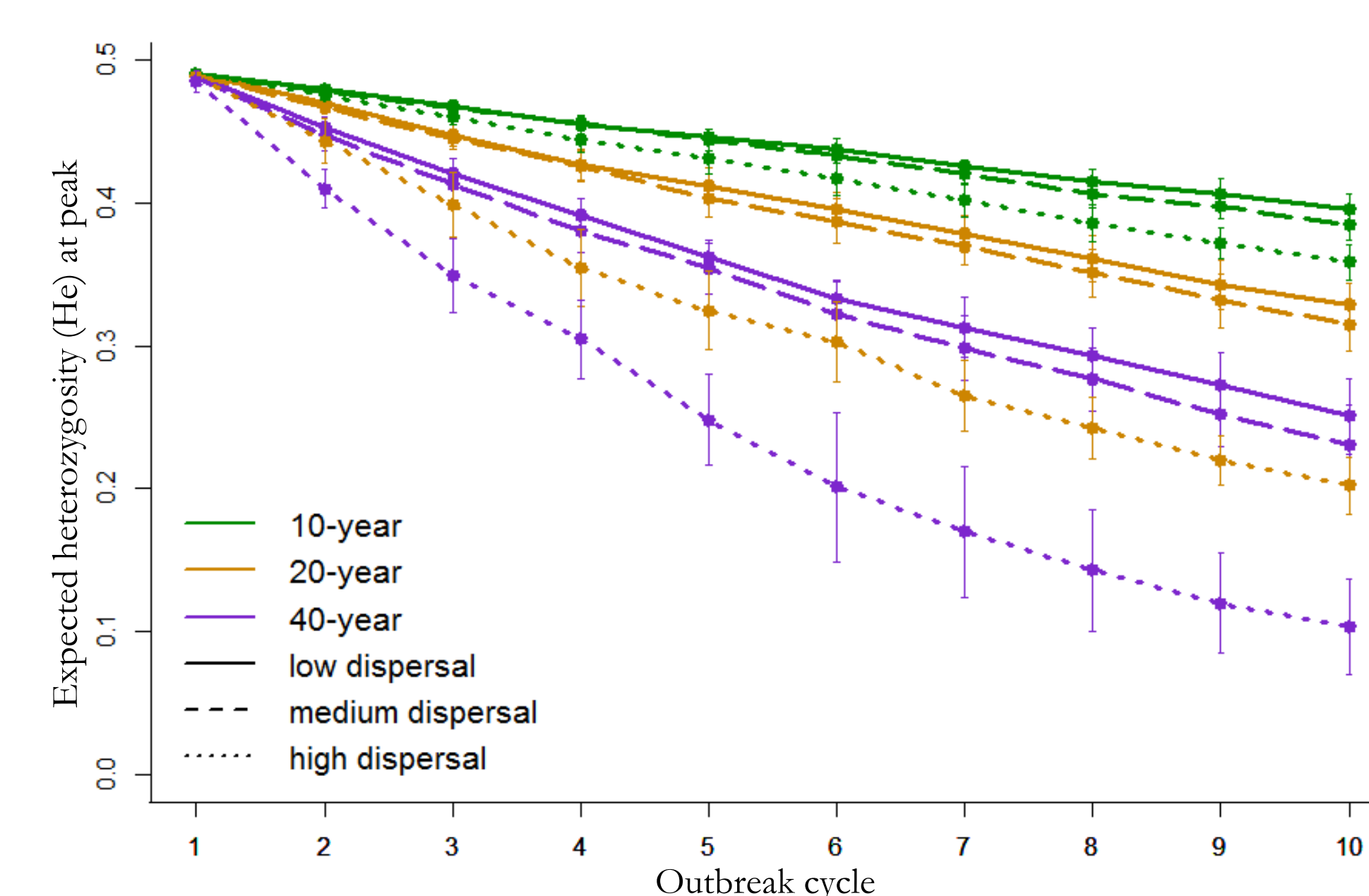- Genetic diversity is affected by both dispersal and outbreak frequency.

Fig.4- Expected heterozygosity at each population peak. Please notice that for different frequencies, time between peaks is different.

3. Genetic diversity (He) vs. Dispersal

- Greater dispersal produces an Allee effect that reduces reproductive success during low-density phases of the outbreak cycle (Fig.5).

- Genetic diversity decreases as dispersal capacity increases (Fig.6).

- Higher frequency cycles shorten the duration of dispersal-induced Allee effects, but create more bottlenecks through time.
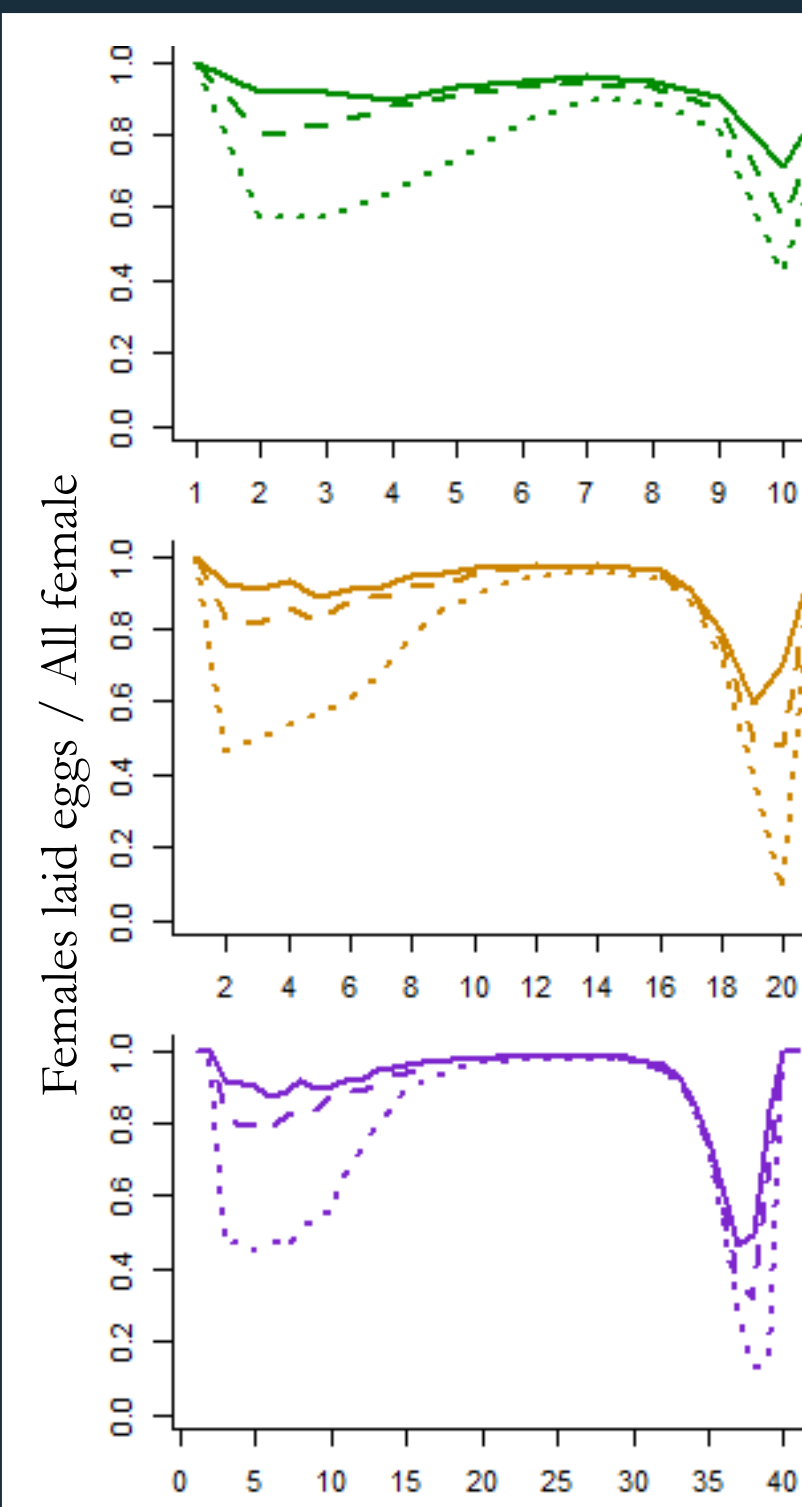
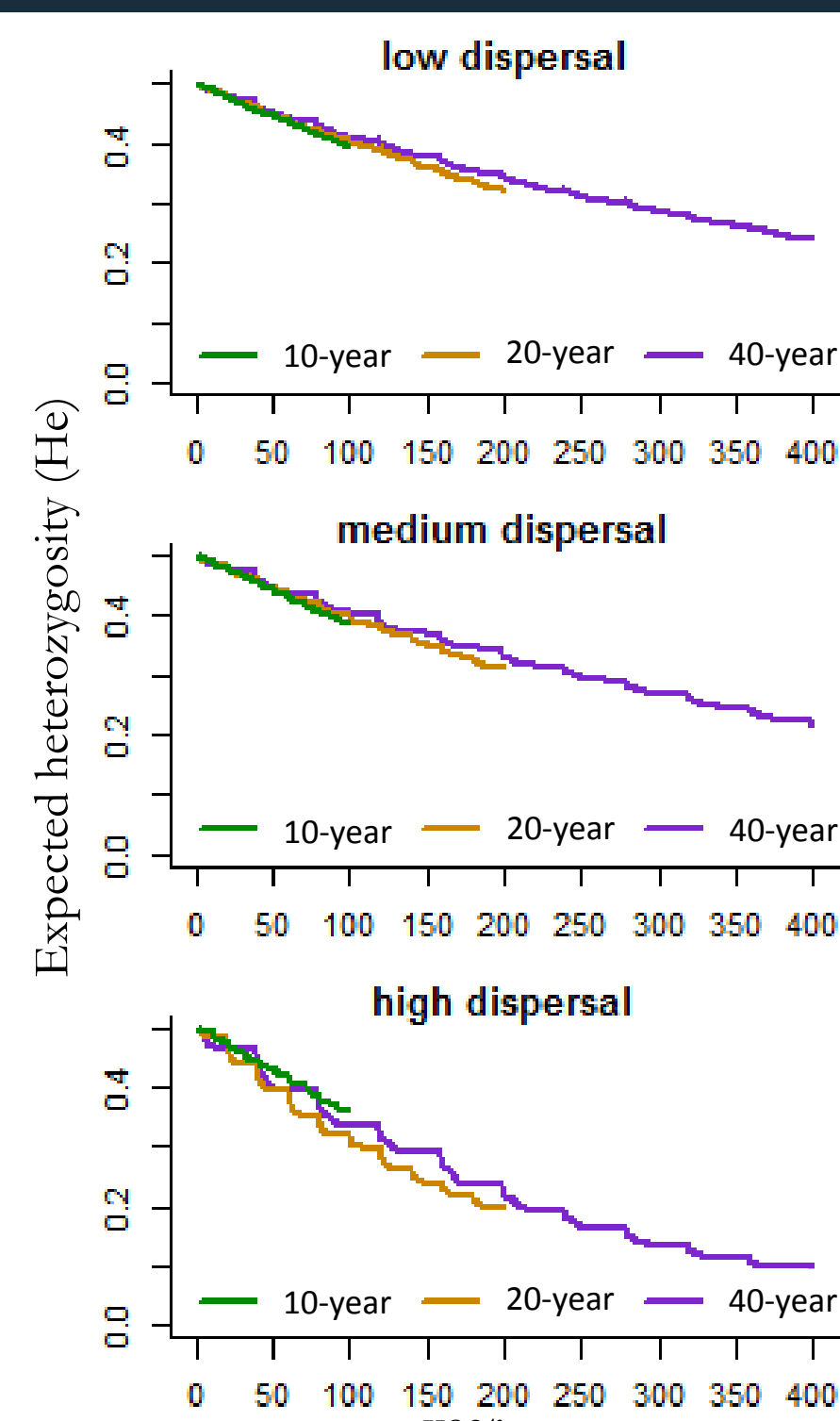Fig.5- The change of female reproducing rate in one outbreak cycle.

Fig.6- Expected heterozygosity over time.

4. Genetic differentiation

- Mean genetic differentiation (i.e., *Fst*) between outbreak peaks increases with the number of cycles (i.e., isolation by time; IBT) (all $r > 0.9$ & all *pvalue* > 0.05).

- Differentiation is affected by both dispersal and outbreak frequency.

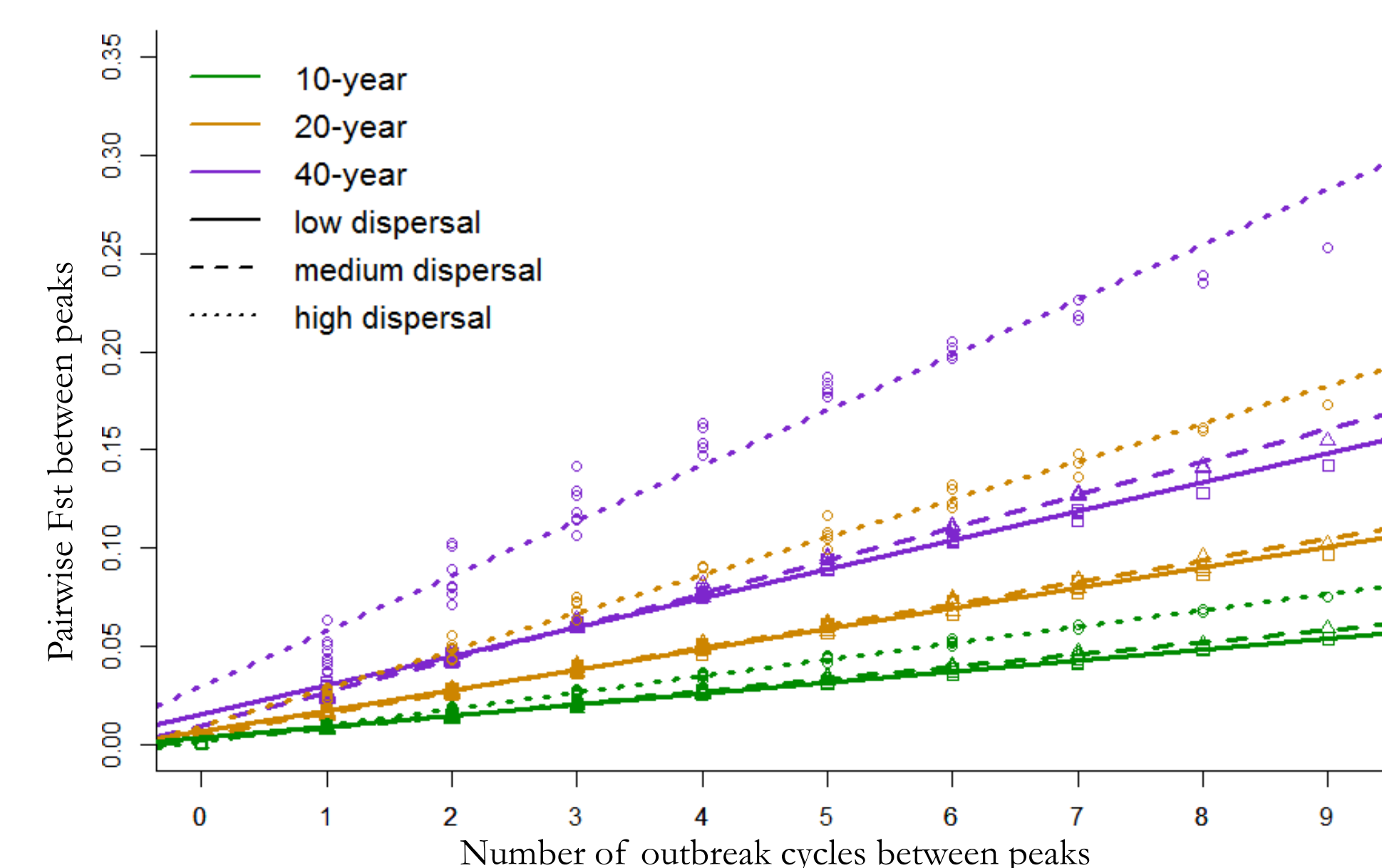- Higher dispersal and lower outbreak cycle frequency favours genetic differentiation between peaks.

Fig.7- Genetic differentiation by numbers of outbreak cycles. Please notice that for different frequencies, time between peaks is different.

Conclusions

- Both outbreak frequency and dispersal can affect genetic differentiation and genetic diversity through time in irruptive populations.

- Frequency determines the number of bottlenecks and the length of time that a population remains at low density, both of which reduce genetic diversity and increases differentiation.

- High dispersal can induce a spatial Allee effect that reduces reproduction during endemic periods and increases genetic differentiation through time.

- Genetic differentiation that arises due to spatio-temporal processes (i.e., population cycling) have the potential to confound efforts to characterize population genetic structure at a single point in time.

References: [1] Row, Jeffrey R., Paul J. Wilson, and Dennis L. Murray. 2016, Oikos 125 (11): 1617–26. [2]Franklin, Myers, and Cory 2014, PLoS ONE 9 (5). [3] Landguth, Erin L., Andrew Bearlin, Casey C. Day, and Jason Dunham. 2017, Methods in Ecology and Evolution 8 (1): 4–11. [4] Myers JH. 2018 Population cycles: generalities, exceptions and remaining mysteries. Proc. R. Soc. B 285: 20172841.