



Supporting Online Material for  
**Stability via Asynchrony in *Drosophila* Metapopulations With Low  
Migration Rates**

Sutirth Dey and Amitabh Joshi\*

\*To whom correspondence should be addressed. E-mail: [ajoshi@jncasr.ac.in](mailto:ajoshi@jncasr.ac.in)

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## Supporting Online Material

### Materials and Methods

#### Experiments

One hundred and eight subpopulations, each represented by a single vial culture, were derived from a long-standing, outbreeding laboratory population (JB-1) of *Drosophila melanogaster*, maintained on a three-week discrete generation cycle. Details of the ancestry and regular maintenance regime of this population have been presented previously (S1). Each subpopulation was initiated by placing exactly 20 eggs in a 30 ml glass vial containing ~ 1 ml of banana-jaggery medium. The flies resulting from these eggs were labeled as generation 0, and from that point onwards, no direct control was exercised on the density of eggs in a vial. Once the adults started eclosing around day 8-9 after egg-lay, they were collected daily in corresponding holding vials. The adults were transferred to fresh holding vials every alternate day, until day 18 after egg-lay. Extreme care was taken to ensure one-to-one correspondence between egg vials and adult collection vials. On day 18, the flies were supplied with excess live-yeast paste for three days, to enhance their fecundity. On day 21 after egg-lay, the adult flies were sexed, censused, subjected to migration, and allowed to lay eggs for 24 hours in vials containing ~ 1 ml banana-jaggery medium. After oviposition, the adults were discarded while the eggs formed the next generation. This maintenance regime (low larval and high adult food levels) has been extensively studied and is known to induce large amplitude periodic oscillations in population numbers (S2-S6).

Twelve metapopulations, each consisting of nine subpopulations, were set up and sets of four metapopulations each were subjected to one of three different migration rates – control (no migration; CMs), low (10%; LMMs) and high (30%; HMMs). The nine subpopulations (single vial *Drosophila* cultures) were arranged on the periphery of a circle, with each vial exchanging migrants only with its two nearest neighbors, i.e. a one-dimensional array with periodic boundary conditions. In nature, such metapopulations might exist, for example, on the shorelines of lakes or along the edges of ecosystems. Migration was manually imposed by removing the required number of flies from a subpopulation and distributing them equally to the two neighboring vials, just prior to reproduction in every generation. Desired levels of migration were imposed by moving mated females, as the population dynamics of a sexual species is governed largely by the number of females. In order to calculate the number of females to be moved, the total count in a vial was halved (i.e. we assume an equal sex ratio) and rounded upwards in case of fractions. This number was multiplied by the desired fraction (0.1 or 0.3) and rounded off in both directions to the nearest even integer, to give the total number of female migrants. All analyses were performed on total population size (i.e. number of males + females) after migration.

#### Simulations

We modeled subpopulation dynamics with the discrete version of the Ricker map [ $n_{t+1} = n_t \exp(r(1 - n_t / K))$ ] (S7), where  $n_t$  represents the subpopulation size at time  $t$ , and  $r$  and

$K$  refer to the intrinsic per capita growth rate of the subpopulation and carrying capacity of the patch, respectively. A metapopulation consisted of nine linearly arranged subpopulations, with nearest neighbor migration under periodic boundary condition (S8). The migration rates in the simulations were restricted to those used in the experiments, *viz.* no migration (CMs), 10% (LMMs) and 30% (HMMs). All the subpopulations in a given run had the same value of  $r$  with a noise term  $\varepsilon$  ( $0 < \varepsilon < 0.2$ ; uniform random distribution) added to  $r$  for each subpopulation at every generation, to simulate stochastic variation in population growth rates. We estimated the value of  $r$  in *Drosophila* cultures, by fitting the Ricker map to the experimental time series derived from the subpopulations of the CMs. Based on these estimates, we simulated the experimental system for  $r$  values of the subpopulations ranging from 2.7 to 3.0 in increments of 0.02. Since a Ricker map does not take zero values, we stipulated a 50% probability of extinction when the population size fell below four. Further, all extinctions in the controls were reset to a value of eight while there was no such resetting in the LMMs and HMMs. Each migration rate  $\times r$  combination of metapopulation was simulated 10 times, and all statistics were calculated on the first 100 time steps of the simulated populations. This means that we explicitly looked at the transient behaviour of the model, rather than the equilibrium conditions. We consider this more ecologically meaningful (S9) as often very large number of iterations are needed for a coupled map lattice to reach equilibrium (supertransients) (S10); numbers that are much larger than the lifetime of any natural population, let alone the duration of our experiment.

## Supporting Online Text

### Measures of synchrony and statistical analysis

Presence of long-term trends and temporal autocorrelations in the data complicate the quantification of synchrony across multiple time series (*S11*). Correlations arising due to long-term trends in population size can potentially mask the synchrony on shorter time scales. On the other hand, presence of temporal autocorrelation within the series leads to the violation of the among-sample independence assumption for any parametric test of significance (*S12*). Several statistics, each with its own strengths and weaknesses, have been proposed to measure synchrony across two or more time series (*S11,12*). In the present study, we have determined synchrony using cross-correlation at lag zero of first differenced natural log-transformed data (*S13*). Log-transformation of data makes the variance independent of the mean (*S14*), while first differencing the series leads to the study of the rates of change, which obviates the need for any further detrending (*S11*). The problem of temporal autocorrelation is taken care of as we have multiple time series and a single test for synchrony can be performed using the pairwise correlations between nearest neighbors (*S11*). This leads to the new complication that the correlations between the various series (subpopulations) are not independent due to migration. However, we used four independent replicate metapopulations (random factors), nested within the migration treatments (fixed factor) for the analysis of variance (ANOVA). The conclusions drawn are based on the observed significance levels of the factor 'migration' which is tested over a denominator term reflecting the average variation among replicate metapopulations within migration regime. Since the metapopulations themselves are independent of each other, the among-sample independence assumption of ANOVA is not violated in our analysis. We use the same analytical framework for all statistical analysis in this study.

In order to check the robustness of our conclusions, we also measured synchrony amongst nearest neighbors using two other statistics:

1. Cross-correlation of untransformed series values: The Pearson correlation coefficient is a very commonly used statistic that provides a direct measure of the synchrony in population sizes (*S12*). The average cross-correlation coefficient across the nearest neighbors was found to be significantly different amongst the three migration treatments ( $F_{2,9} = 10.02, p < 0.005$ ). The average for the LMMs was found to be negative and significantly different (Tukey's MSD,  $p < 0.01$ ) from CMs and HMMs, both of which were positive in sign. Thus, this bolsters the conclusion that in the LMMs, the nearest neighbors are out of phase with each other.

2. Measure based on number of times two series change in the same direction: The number of times two series increase or decrease together, can be used as a measure of synchrony between them. In case of multiple series, the average of these values is also the proportion of times that pairs of series change in the same direction (*S12*). ANOVA on this statistic suggested that there was a significant effect of migration ( $F_{2,9} = 11.08, p < 0.004$ ) with the LMM subpopulations having the lowest average value for number of times the neighboring subpopulations increased or decreased together. This again shows that low level of migration pushes the neighboring populations out of phase, thus leading to stability at the metapopulation level.

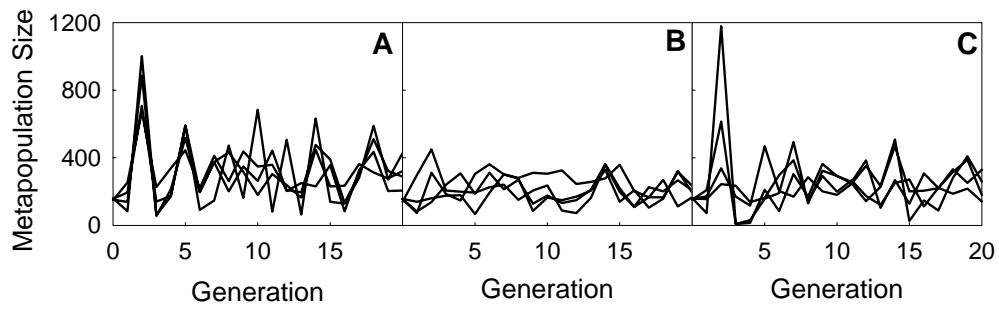


Figure S1. Time series of replicate metapopulations at the three different migration rates. **A)** No migration (CM), **B)** 10% migration (LMM), **C)** 30% migration (HMM). Each line in a panel represents the time series of one replicate metapopulation. The metapopulations in LMM underwent less fluctuation than the CM or HMM. The scale on Y-axis is the same for all three panels.

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