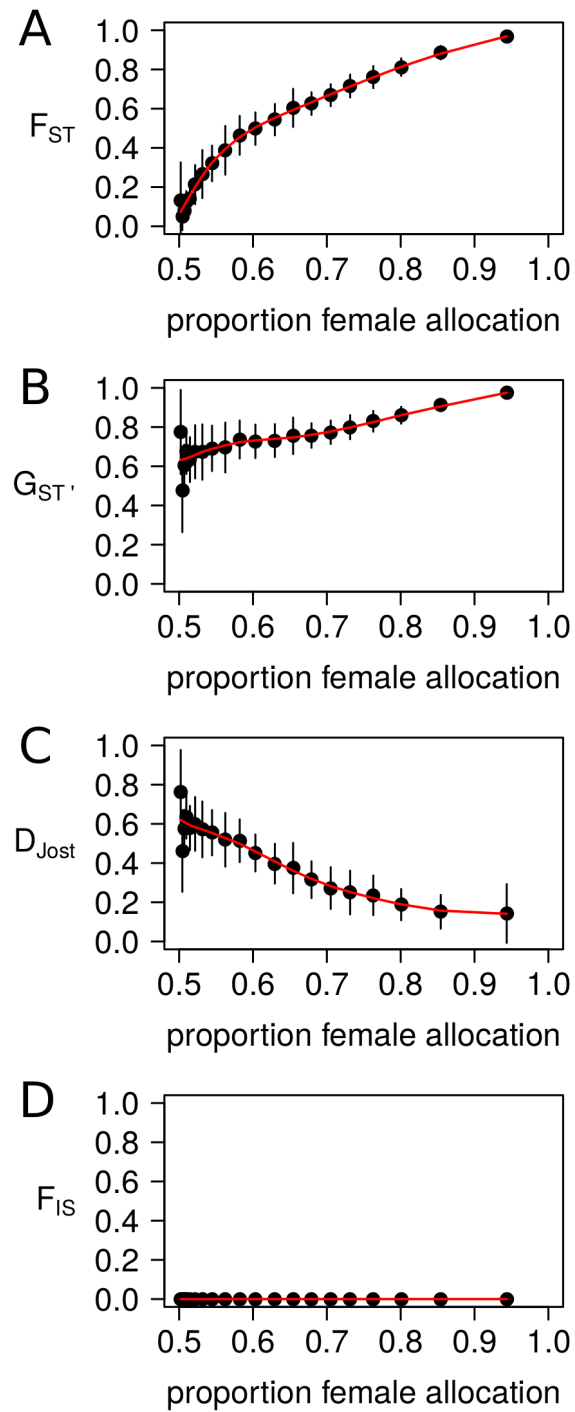


**Figure 1: effect of migration and extinction rates on female allocation**

Colours show the average female allocation measured over the metapopulation at the end of simulations, in a scale lying from 0.5 (white: 50% of female allocation) to 1 (black: 100% of female allocation).

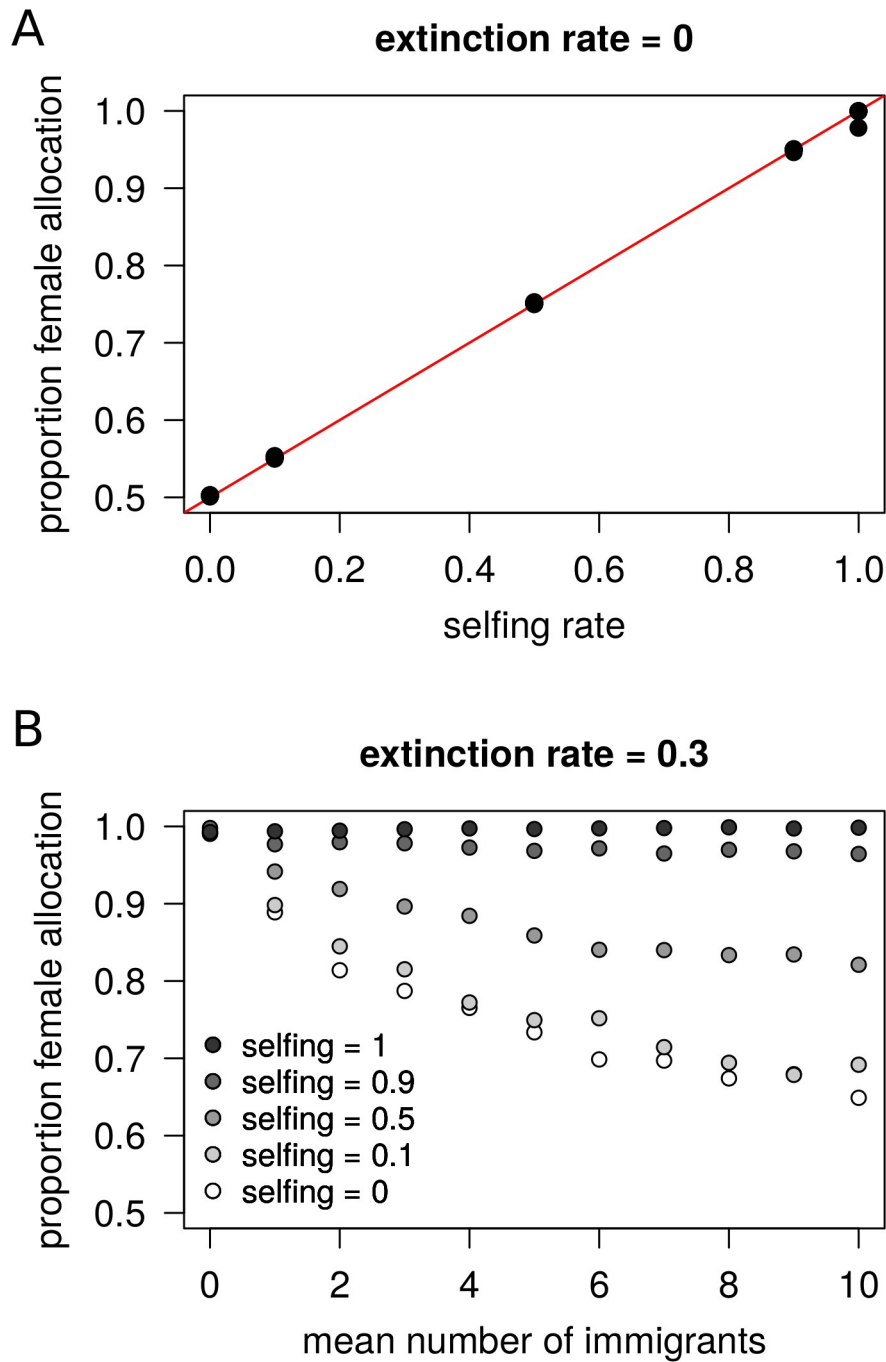


**Figure 2: relations between female allocation and descriptive statistics in population genetics at neutral markers.**

The x-axis shows the measured female allocation at the end of simulations described in figure 1-A. The y-axis show;  $F_{ST}$  (A),  $G_{ST'}$  (B), Jost's  $D$  (C) and  $F_{IS}$  (D).

Each points represent a 5% quantile of the female allocation along the x-axis, and the mean descriptive statistics within each 5% quantile along the y-axis. Vertical bars represent the standard deviation of the descriptive statistics within each 5% quantile.

The red line represents the loess regression between female allocation and descriptive statistics.



**Figure 3: female allocation in a metapopulation as a function of the migration rate and the base selfing rate of individuals**

A) Simulations with an extinction rate of zero.

The x-axis represent the base selfing rates fixed during simulations. The y-axis represent the measured female allocation at the end of simulations. The red line shows the expected female allocation as a function of selfing rate (from the equation 3 in Charlesworth and Charlesworth, 1981).

B) Simulations with an extinction rate of 0.3.

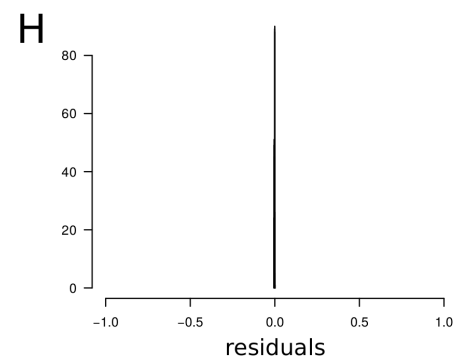
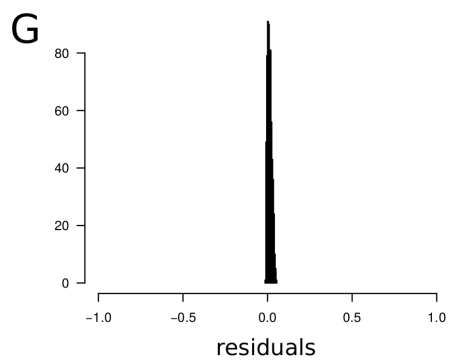
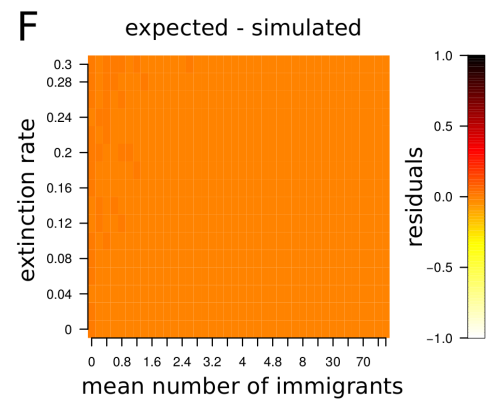
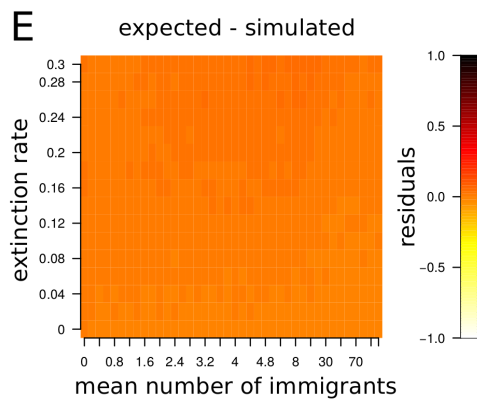
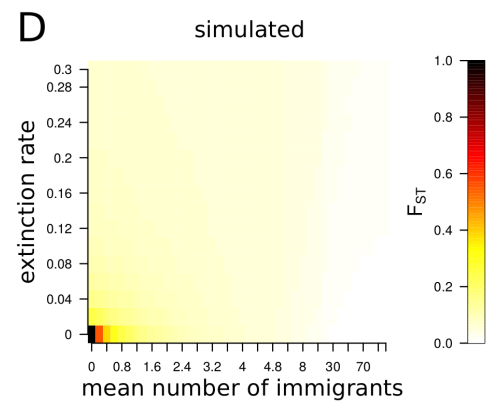
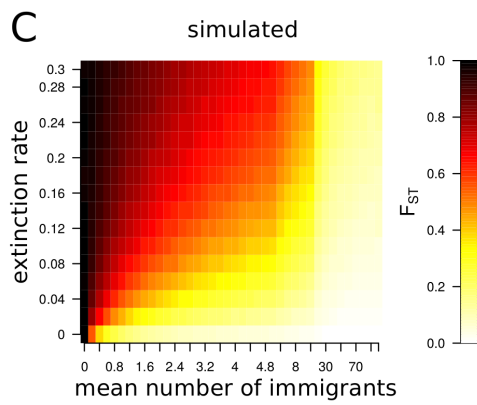
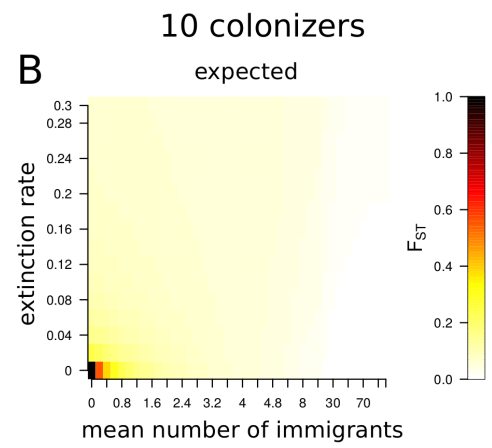
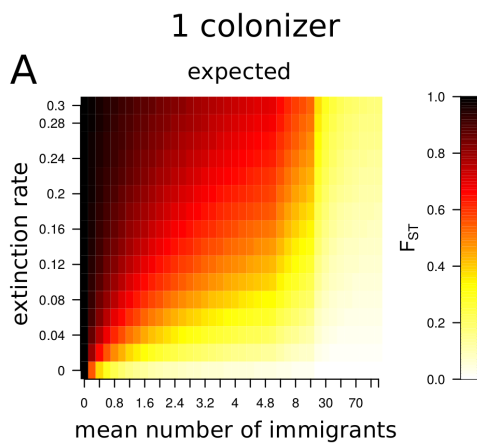
The x-axis represent the immigration rates expressed as the mean percentage of individuals coming

from random demes in the metapopulation per generation.

The y-axis represent the measured female allocation at the end of simulations.

Dots are represent the average over three independent replicates. Variation over replicates was very small, so that error bars are not shown.

The selfing rate here is the probability for an ovule to be fertilized by a male gamete coming from the same hermaphroditic individual prior to random mating; the realised selfing rate could thus be higher, depending on the population size. Four values of selfing were explored from 0 (white) to 1 (black).



**Figure S1: ability of simulations to produce expected  $F_{ST}$  values.**

The migration rate is expressed as the mean percentage of individuals coming from random demes in the metapopulation per generation.

The extinction rate is expressed as the mean probability for a deme to become extinct and recolonized per generation.

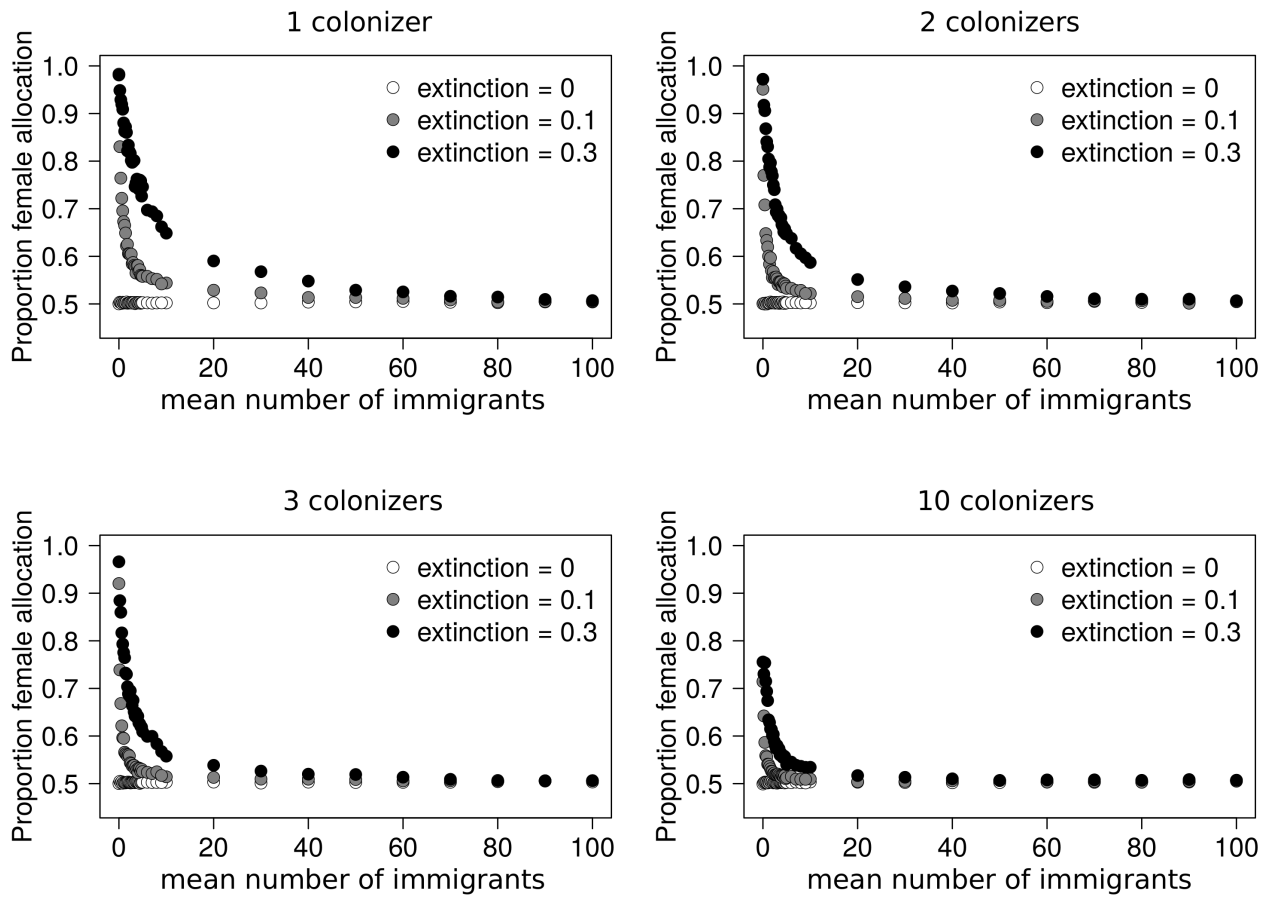
Here, the number of colonizers is fixed to 1 (**A**, **C**, **E**, and **G**) or 10 (**B**, **D**, **F** and **H**).

**A, B.** Analytical expectations following Rousset (2003) for  $F_{ST}$  as a function migration and extinction. Colours represent  $F_{ST}$  values lying from 0 (white) to 1 (black).

**C, D.**  $F_{ST}$  measured at 20 simulated neutral markers after 3,000 generations. 640 grid points were explored with combination of parameters similar to Fig. S1-A. Colours represent  $F_{ST}$  values lying from 0 (white) to 1 (black).

**E, F.** Residuals are the differences between expected (Fig. S1-A) and simulated (Fig. S1-B) values of  $F_{ST}$  for all combination extinction and migration rates. Colours represent possible values of residuals ( $= F_{ST-Expected} - F_{ST-Simulated}$ ), putatively lying from -1 (white) to 1 (black).

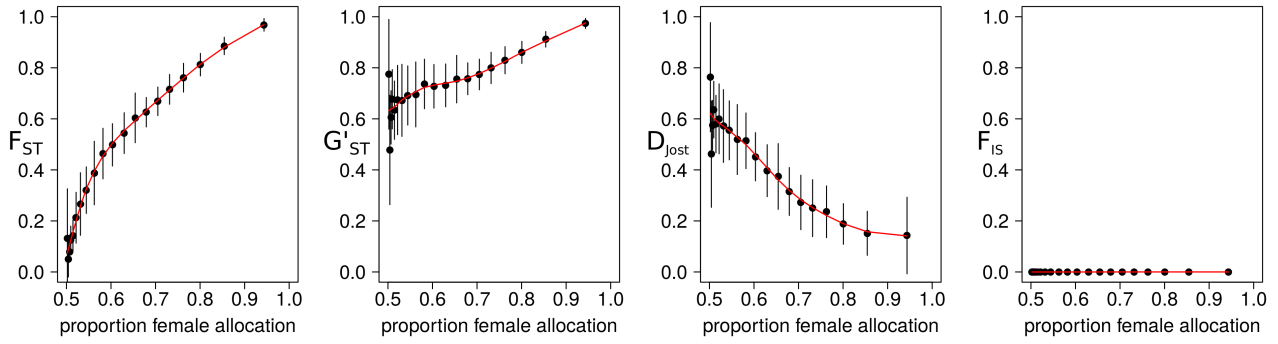
**G, H.** Distributions of residuals over 1,920 simulations (640 combinations of parameters replicated three times).



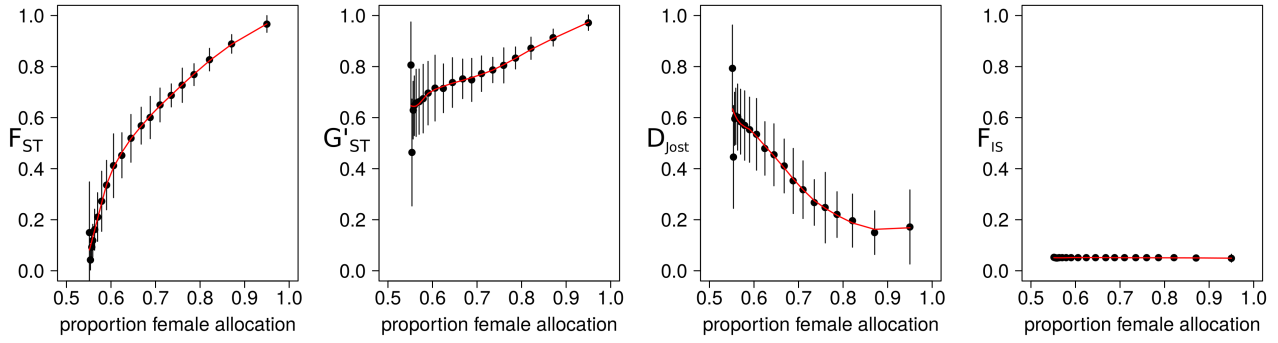
**Figure S2: effect of migration rate and extinction rate on female allocation.**

Results are shown when the number of colonizers making the propagule pool is equal to 1, 2, 3 and 10.

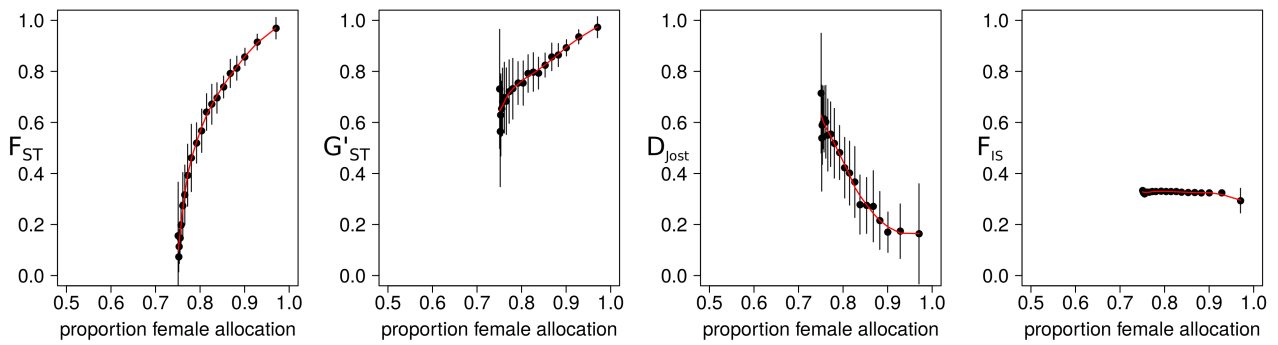
selfing rate = 0



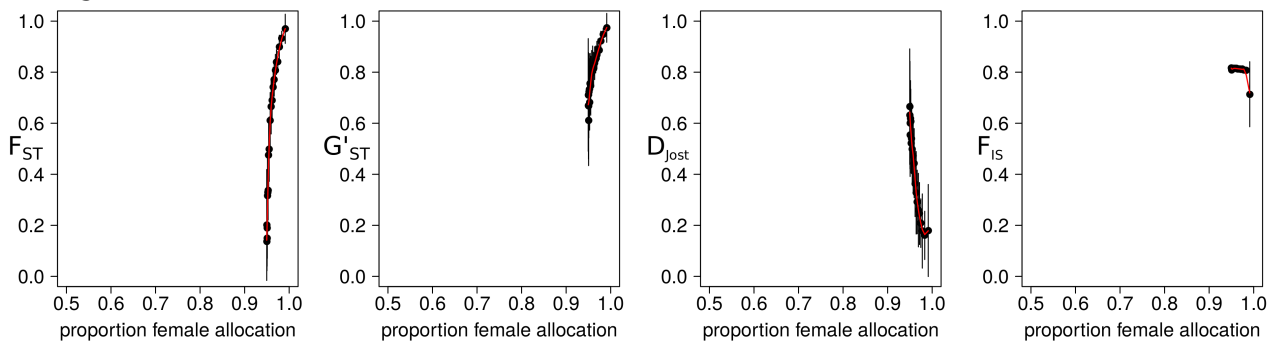
selfing rate = 0.1



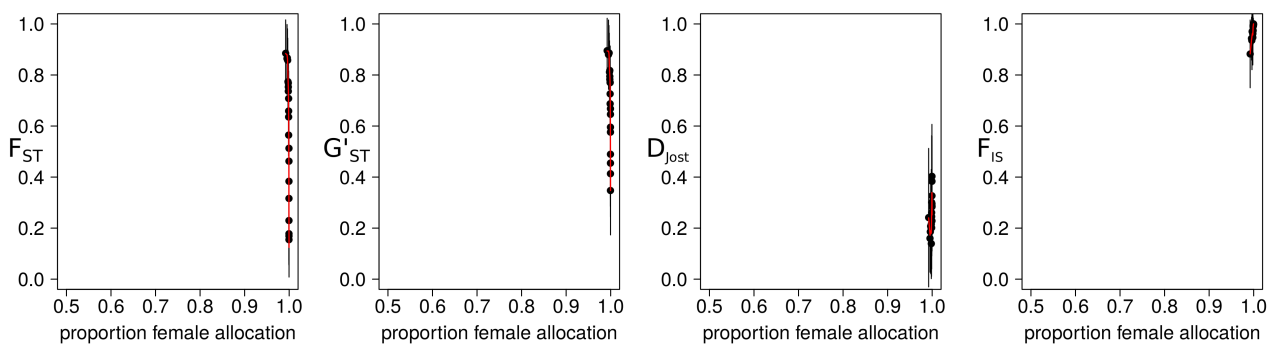
selfing rate = 0.5



selfing rate = 0.9



selfing rate = 1





**Figure S3: relations between statistics in population genetics at neutral markers and female allocation for different selfing rates.**

For each individual graphic window, the x-axis shows the measured female allocation at the end of simulations.

The y-axis show the measured  $F_{ST}$ ,  $G_{ST}'$ , Jost's  $D$  and  $F_{IS}$ .

Five different selfing rates were explored:

First row of plots: selfing = 0.

Second row of plots: selfing = 0.1

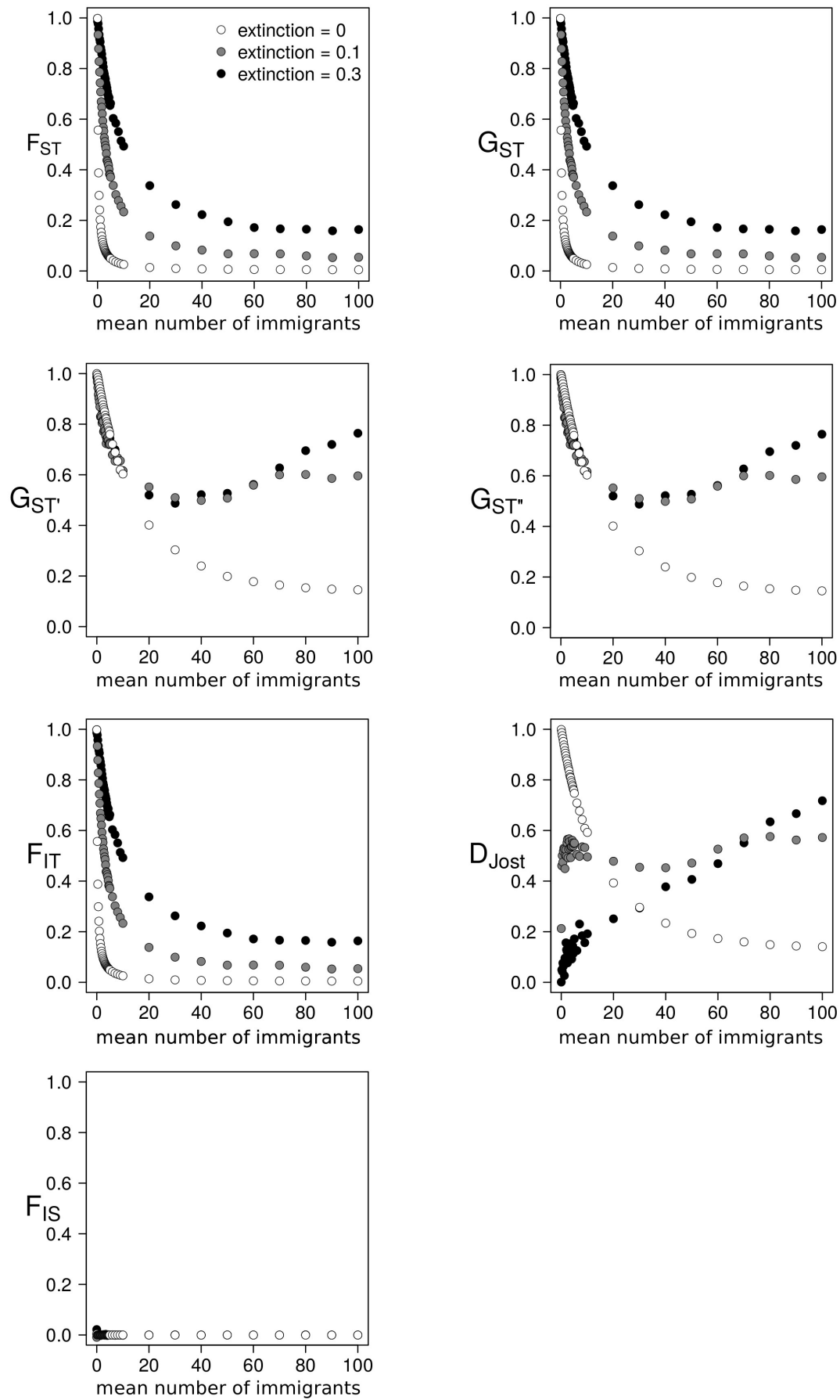
Third row of plots: selfing = 0.5

Fourth row of plots: selfing = 0.9

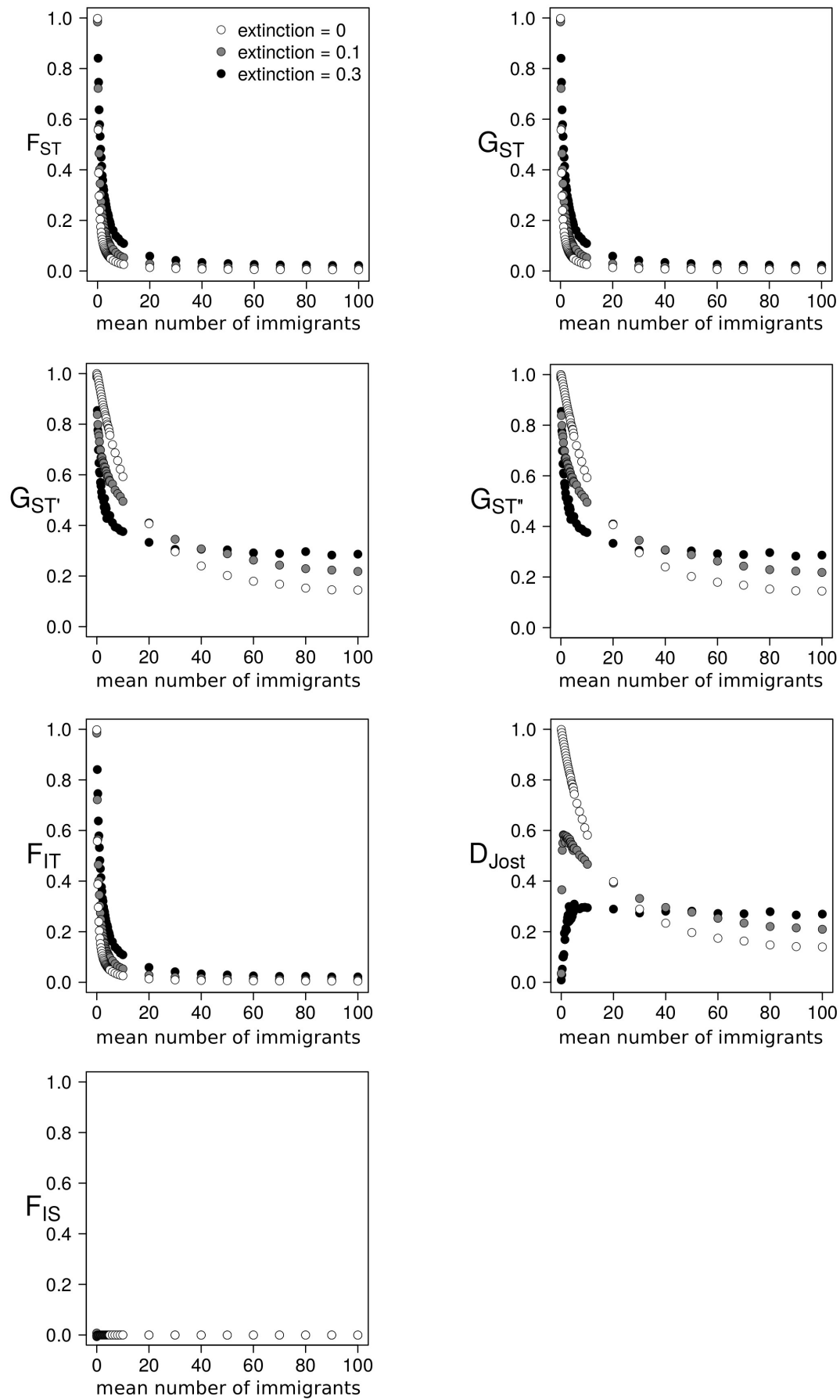
Fifth row of plots: selfing = 1

Each points represent a 5% quantile of the female allocation along the x-axis, and the averaged descriptive statistics within each 5% quantile along the y-axis. Vertical bars represent the standard deviation of the descriptive statistics within each 5% quantile.

The red line represents the loess regression between female allocation and descriptive statistics.



**Figure S4: relation between migration rate and 7 statistics in population genetics at neutral markers when the number of colonizer is fixed to 1.**



**Figure S5: relation between migration rate and 7 statistics in population genetics at neutral markers when the number of colonizers is fixed to 10.**