## Predicting Wolbachia invasion dynamics in Aedes aegypti populations using models of density-dependent demographic traits

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BMC Biology 2016

**Additional file 1: Table S1.1.** Definitions and values of model parameters.

Symbol	Definition	Value		Source
$T_P$	Duration of the pupal stage	2 days		This study
$T_G$	Minimum time for females to become gravid following emergence	4 days		This study
$T_H$	Time between oviposition and hatching of eggs	6 days		This study
ω	The proportion of uninfected offspring produced by <i>Wolbachia</i> -infected females	0.01		(Walker <i>et al.</i> 2011)
Sh	The proportion of unviable offspring from an incompatible mating	0.99		(Walker <i>et al.</i> 2011)
		Semi-field cage population	Field release simulations	
$(lpha_U,eta_U,\gamma_U); \ (lpha_W,eta_W,\gamma_W)$	Parameters of functions describing mean larval development time	(0.68, 0.16, 0.68) <sup>a</sup> ; (2.2, 0.013, 0.98) <sup>a</sup> ; (1.8, 0.54, 0.53) <sup>b</sup> ; (4.5, 0.22, 0.64) <sup>b</sup> ;	(1.8, 0.54, 0.53); (1.8, 0.54, 0.53);	This study
$( u_U, \eta_U, \psi_U);$ $( u_W, \eta_W, \psi_W)$	Parameters of functions describing the standard deviation of larval development time	(8.3, 0.81, 0.33) <sup>a</sup> ; (4.1, 1.7, 0.27) <sup>a</sup> ; (0.22, 0.017, 0.87) <sup>b</sup> ; (4.8, 0.029, 0.80) <sup>b</sup> ;	(0.22, 0.017, 0.87); (0.22, 0.017, 0.87)	This study
$a_{U}$ , $b_{U}$ ; $a_{W}$ , $b_{W}$	Parameters of functions describing per-capita female fecundity	(29.5, -3.36) <sup>a</sup> ; (28.5, -3.25) <sup>b</sup> ; (29.1, -3.35) <sup>b</sup> ;	(28.5, -3.25); (28.5, -3.25);	This study
$\mu_L^c$	Daily larval mortality	0.25-0.01	0.05	This study
$\mu_A^c$	Daily pupal and adult mortality	0.03	0.03	(Walker <i>et al.</i> 2011)
$\lambda_{ ext{min}}, \mu_{ ext{max}}, \ \sigma_{ ext{max}}$	Lower limit on per-capita female fecundity, and upper limits on larval development time means and standard deviations	0.5, 60 days, 40 days	0.5, 60 days, 40 days	This study

a,b Value corresponding to the MCMC iteration with the highest posterior probability when observations from Population A (a) and Population B (b) are used to inform the Bayesian MCMC model (see text)