



**Fig. S3.** Posterior probability distributions of the number of migrant per generation ( $M$ ; in one direction) and the symmetrical migration rate ( $m$ ) for ten datasets simulated without gene flow. The settings used in the MIMARfor2 analysis were the same as for the *L. alabamica* – *L. crassa* analyses, except that parameter  $M$  was given a uniform prior from ( $e^{-30}$  –  $e^2$ ).