Supporting Information

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SI Materials and Methods

Controlled Pollination Study. For 30 trees (15 in the forest habitat and 15 in the shade coffee habitat), we performed six pollination treatments (three flowers per treatment) on inflorescences bagged before the flowering period. Bags were opened only during the 3-d flowering period for the pollination treatment. The treatments included flowers with no pollination, self-pollinated flowers, self–buzz-pollinated flowers, cross-pollinated flowers, cross–buzz-pollinated flowers, and open pollinated flowers. Pollination treatments were conducted using a tuning fork, as done in previous studies (1). Non-buzz treatments were conducted by touching the donor anthers with a nonvibrating tuning fork six times and then contacting the tuning fork to a receptive stigma six times. Buzz pollination was simulated by vibrating the tuning fork before touching the donor anthers and then contacting the stigma once.

Pollen Dispersal. Seeds from the 60 "fruit trees" were removed from the fruit pulp, dried, and sorted. Fertilized *M. affinis* seeds are yellow, pyramidal, and three to four times larger than the dark, crescent-shaped, unfertilized ovules. Unfertilized ovules produce an observable but unviable seed that can be added to the number of fertilized seeds to calculate the total number of ovules per fruit (mean = 50.01 ± 0.37 ovules per fruit). Proportion seed set was calculated by dividing the number of fertilized seeds by the total number of ovules per fruit. The program CERVUS 3.0 (2) conducts paternity analysis by generating paternity assignment criteria (Δ) derived from the likelihood ratios of the two most likely sires based on multilocus segregation probabilities. Confidence levels were calculated by comparing the distribution of Δ scores, given that the most likely sire is the true sire with the distribution of Δ scores, given that the most likely sire is not the true sire. The exponential power dispersal function, which best fit the genetic data in both forest and coffee habitats, is represented by $p(a,b;x,y) = \frac{b}{2\pi a^2\Gamma(2/b)} \exp\left(-\left|\frac{r}{a}\right|^b\right)$, where $r = \sqrt{x^2 + y^2}$ describes the pollination distance. In the equation, Γ is the classically defined gamma function, a is the scale parameter, and b is the shape parameter, which indicates the "fatness" of the tail of the dispersal distribution (3). For pollen dispersal distance and proportion seed set reported, the ± values represent SEs.

1. Buchmann S (1983) Buzz pollination in angiosperms. *Little Handbook of Experimental Pollination Biology*, ed Jones CER (Van Nostrand, New York), pp 73–113.
2. Marshall TC, Slate J, Kruuk LEB, Pemberton JM (1998) Statistical confidence for likelihood-based paternity inference in natural populations. *Mol Ecol* 7:639–655.
3. Austerlitz F, et al. (2004) Using genetic markers to estimate the pollen dispersal curve. *Mol Ecol* 13:937–954.