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From horticultural plantings into wild populations: movement of pollen and genes in *Lobelia cardinalis*

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Abstract Understanding the potential movement of genes from horticultural plantings into conspecific wild populations requires fundamental knowledge of pollen flow distances and of the siring abilities of genetically differentiated pollen types on local plants. We addressed these issues using *Lobelia cardinalis*, a native, hummingbird-pollinated species, which is available horticulturally both as wild types and cultivated varieties. Potential pollen and gene flow between relatively isolated populations were measured in an artificial array experiment. Potted plants were placed at discrete distances (50, 100, 500, and 1000 m) from either a local or one of three non-local potted pollen sources and scored for pollen and gene flow. Pollen movement was assessed with a dye analogue. The pollen source population did not significantly influence the results, but dye movement, fruit set, and to a lesser degree fruit volume declined with distance from the pollen source. Even at 1 km away from the pollen source, 20–50% of flowers set fruit, indicating substantial gene movement. Siring ability of four non-local pollen types on local plants was assessed by comparing paternity success when each type comprised 75, 50, and 25% of the pollen in controlled mixed load pollinations. Pollen type affected the percentage of non-local offspring. A cultivated variety of *L. cardinalis* showed poor siring success on the Virginia maternal plants at all mix ratios. Mating was random in mixes with Virginia pollen and pollen from geographically distant wild-type varieties. Finally, pollen from a neighboring county was significantly favored over local sires. These results demonstrate that pollen movement from horticultural plantings into native populations and the production of hybrid seed on native plants is possible in *L. cardinalis*.

Keywords Crop-to-wild gene flow · Gene flow · Pollen competition · Pollen flow · Siring ability

Introduction

The study of gene dispersal from cultivated and engineered crop plants into related wild populations has been vigorously pursued in recent years due to concerns about the escape of advantageous and weedy traits into the wild (Ellstrand et al. 1999). Hybrids resulting from escaped cultivated genes are documented for maize (Doebley 1990), squash (Kirkpatrick and Wilson 1988), radish (Klinger et al.

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