

[LI, JIANHUA](#)^{1,2,3*}, JOHN H. ALEXANDER III¹, and DONGLIN ZHANG². ¹Arnold Arboretum of Harvard University, 125 Arborway, Jamaica Plain, MA 02130; ²Department of Biosystems Science and Engineering, 5722 Deering Hall, Orono, ME 04469; ³Department of Plant Biology, University of New Hampshire, Durham, NH 03824. - The genus *Syringa* (Oleaceae) is paraphyletic: evidence from sequences of nuclear ribosomal DNA ITS and ETS regions.

Sequences of nuclear ribosomal DNA ITS and ETS regions were used to examine phylogenetic relationships of *Syringa* and *Ligustrum*. Thirty samples were included in parsimony analyses, representing all major groups of these two genera. Two species of *Fraxinus* and one species of *Jasminum* were also included in analyses for rooting purposes. Species of series *Vulgares* (*Syringa*) and the monotypic series *Pinnatifoliae* (*Syringa*) are basal clades followed by a clade containing *Ligustrum* species and the remaining *Syringa* species. Species of *Ligustrum* form a well-supported clade, which is sister to a clade containing the rest of species of *Syringa*, including subgenus *Ligustrina*, and series *Pubescentes* and *Villosae*. All these groups are monophyletic. *Parasyringa sempervirens* is phylogenetically embedded within the *Ligustrum* clade, supporting its placement in *Ligustrum*. Our results indicate that *Ligustrum* is derived from within *Syringa*, suggesting that *Syringa* as traditionally circumscribed is paraphyletic. Berries are a synapomorphy of *Ligustrum* species, and the dehiscent berry of *Parasyringa sempervirens* is an evolutionary reversal to a capsule, which is characteristic of *Syringa*. The evolution of berries might have resulted in an accelerated speciation in *Ligustrum*.

Key words: ETS, ITS, *Ligustrum*, Oleaceae, paraphyly, phylogeny, *Syringa*