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Ploidy Level and Genome Size of *Vincetoxicum nigrum* and *V. rossicum* (Apocynaceae), Two Invasive Vines in North America

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Abstract

Vincetoxicum nigrum (L.) Moench (black swallow-wort) and *V. rossicum* (Kleopow) Barbarich (pale swallow-wort) (Apocynaceae) are perennial vines that are targeted for classical biological control as a result of their massive invasion in natural areas and horticultural nurseries in the U.S. and Canada. Native ranges of *V. nigrum* and *V. rossicum* are limited to southwestern Europe and to Ukraine-southwestern Russia, respectively. The evolutionary mechanisms that have facilitated the range expansion since their introduction 150 years ago into North America have yet to be understood. In this study we examine two characteristics of the genome organization, i) the most frequently assessed ploidy level and ii) the variation in genome size, i.e., variation in the amount of DNA per monoploid set of chromosomes through loss or gain of repeated DNA sequences. Both can allow rapid changes in key phenotypic traits that enhance invasive ability. Flow cytometry using propidium iodide for the analysis of genome size variation and chromosome counting using DAPI were conducted on plants sampled from the introduced and native ranges of both species. In *V. nigrum*, accessions from Southern France and North America were all tetraploid ($2n = 4x = 44$). In *V. rossicum*, accessions from Russia and North America were all diploid ($2n = 2x = 22$). The mean 2C value (\pm STD) of *V. nigrum* and *V. rossicum* is 1.44 ± 0.03 pg and 0.71 ± 0.02 pg, respectively. This is the first report of genome size for the genus. At the species level, no evidence for genome size variation was found between the two ranges. Our data indicate that the invasive spread of both species was not triggered by differences in ploidy level or genome size between native and introduced populations. Alternative explanations should be sought.