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# A large-scale survey of genetic variation and genome evolution within the invasive *Reynoutria* complex

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The taxa from the genus *Reynoutria*: *R. japonica*, *R. sachalinensis*, originating from Asia, and their hybrid *R. ×bohemica* are some of the most troublesome alien invasive species in Europe and North America, particularly dangerous to riparian ecosystems. Simultaneously, these taxa constitute a unique model system for the creation of hybrids and the initiation of evolutionary processes in an invaded range. The aim of the study was: (i) to examine the level of genetic diversity using *Amplified Fragment Length Polymorphism* (AFLP) markers in selected populations of three *Reynoutria* taxa from Poland, Hungary, Ukraine and Slovakia in comparison with Japan, (ii) to identify marked chromosomes in all taxa using fluorescence *in situ* hybridization (FISH) with rDNA sequences, and (iii) to establish genome size and ploidy level in the knotweed species using flow cytometry (FCM).

The results showed presence of genetic diversity within all taxa, including genetic diversity between individuals of *R. japonica*, from selected Polish populations which were considered to be genetically uniform in entire Europe, because they were introduced as a single female clone. The variation in ploidy among individuals of *R. japonica* and within hybrids was confirmed.

Among *R. japonica*, individuals octoploids ( $2n=88$ ;  $2C=8.48pg$ ) were the ones which dominated, while hexaploids ( $2n=66$ ;  $2C=6.51pg$ ) dominated within *R. ×bohemica* plants. All individuals of *R. sachalinensis* were hexaploids ( $2n=66$ ;  $2C=6.01pg$ ). Chromosome identification and dynamics of chromosome re-arrangements was necessary to understand the evolution of a genome in the *Reynoutria* complex. Within the chromosome complement of *R. japonica*, *R. sachalinensis* and *R. ×bohemica*, physical mapping of 5S and 18S–5.8S–26S rDNA (35S rDNA) loci provided markers for 16 out of 88 chromosomes, 13 out of 66 chromosomes and 10 out of 66 chromosomes, respectively. Assignment of known chromosomal markers to corresponding parental genomes in their hybrid *R. ×bohemica* is in progress. To date, genetic variation, ploidy level and genome size, and the chromosome complement of the *Reynoutria* complex in Poland in comparison with European population and population from native range have been worked out.

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