Forest Invasions: The Brutal Paradigm of the Bradford Pear

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Pyrus calleryana Decne. (Callery pear) includes popular ornamental cultivars in commercial and residential landscapes. The species has increasingly naturalized across portions of the eastern and southern US, yet the mechanisms behind its spread are not well understood. The relationship of genetics among present-day *P. calleryana* cultivars and escaped Callery Pear populations, to the genetics presented by their Asian counterparts (native trees from China, Japan, and Korea), are largely unknown. We developed and used 18 microsatellite markers to analyze DNA samples from populations of these groups and to articulate the status of genetic diversity within Asian *P. calleryana* and US cultivars. Analyses encompassed 36 specimens of Asian *P. calleryana* and 21 samples of 7 USA commercial cultivars of *P. calleryana*, as well as 6 escaped populations of 30 tree specimens each from across the southeastern US occurring within a ~177 km radius. We hypothesized that Asian *P. calleryana* specimens and US cultivars and escaped populations would be genetically diverse but would show genetic relatedness. Our data revealed high genetic diversity, high gene flow, and presence of population structure in *P. calleryana* both in native range and in the invaded areas, potentially relating to the highly invasive capability of this species. Our results revealed that *P. calleryana* populations had differentiated shortly after the introduction to the US, most likely from specimens imported from Asia, consistent with historical records and our prior findings. Evidence of pervasive cultivar mislabeling assessed using the microsatellite markers, S-locus genotyping, and Sanger sequencing data highlighted one of the possible invasion mechanisms for non-native plants. Our data argues for more broad-scale assessment of genetic diversity in the invasive areas, to uncover molecular mechanisms underlying such behavior.