USING SIMPLE SEQUENCE REPEAT MARKERS TO IDENTIFY CHESTNUT SPECIES AND HYBRIDS

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In the past, the American chestnut (*Castanea dentata*) was considered one of the most important forest tree species of the eastern North America, having a native range that extended from Mississippi to Maine and in to Canada. The once dominant species is primarily only found today as coppice-regenerated stump sprouts. The introduction of chestnut blight, an overwhelming stem canker disease caused by the fungal pathogen *Cryphonectria parasitica*, is the primary reason for the rapid decline in American chestnut across its natural range. American chestnut did not coevolve with chestnut blight, and thus little to no resistance to the pathogen exists in the native species. Resistance to chestnut blight exists in the Asian chestnut species, including Chinese chestnut, *C. mollissima*, as this species co-evolved with the fungal pathogen. Fortunately, the fungus does not spread to the root system of chestnut and this coupled with chestnut's ability to sprout from adventitious buds below the root collar has resulted in millions of sprouts of American chestnut still living across the native range. Young sprouts typically become infected after a few years and die back and are replaced by new sprouts that repeat the cycle. After many years the older stumps fail to thrive and eventually die thus decreasing the overall supply of sprouts. Numerous research groups are applying various techniques to develop resistant American chestnut that retain the native species characteristics while also providing resistance to the pathogen. Since the introduction of the pathogen, Asian chestnut species and selected hybrids have been introduced and widely planted. In addition, chinquapin chestnut, *C. pumilla*, shares a similar range with American chestnut and is also very susceptible to the disease. Unfortunately, due to the introduction of non-native species and inter-species hybrids, it is often difficult to determine if a sprout is an American chestnut, another related native species (chinquapin) or a natural hybrid with chinquapin or one of several introduced chestnut species based on leaf and stem morphology alone. For this reason, a set of simple sequence repeat (SSR) markers are being developed that would allow for chestnut species separation using statistical analyses. We will report on our progress in developing such a set of markers and discuss their application in chestnut breeding and restoration programs

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