

(285) Genetic Variability Among Eastern Black Walnut Cultivars

Michele R. Warmund*

University of Missouri, Columbia, MO; warmundm@missouri.edu

Mark Coggeshall

University of Missouri, Columbia, MO; coggeshallm@missouri.edu

Black walnuts (*Juglans nigra* L.) are valued for their uniquely fruity flavor and are often used as an ingredient in baked goods and ice cream, or are eaten as a snack food. Although black walnuts can be harvested from wild trees, several cultivars have been selected for such characteristics as ease of cracking, size of kernel, and thickness of husks and shells. Other characteristics, such as date of budbreak, time of flowering, length of season and date of harvest, are also important adaptive traits as there is considerable variation within the species. The University of Missouri Horticulture and Agroforestry Research Center (HARC) maintains a repository of more than 65 named cultivars of black walnut valued for their kernels. The identities of each of these cultivars have been confirmed by "fingerprinting", using a series of ten single sequence repeat microsatellite markers. A subset of cultivars maintained in the repository is used in an applied breeding program focusing on nut improvement. Average date of budbreak, flower type, bloom period, pollination date, nut season length, and harvest date of cultivars were collected from 2002 to 2006 at HARC in central Missouri. Photographic images of black walnut fruits were also obtained in 2007 as a visual aid for identification of confirmed cultivars and can be accessed on a web site.

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(286) Pollen Tube Growth in Compatible and Incompatible Pear Genotypes

Lin Zhang*

Central South University of Forestry and Technology, Huann 410004; triwoodtim918@163.com

Xiaofeng Tan

Central South University of Forestry and Technology, Hunan 410004; tanxiaofengcn@126.com

Donglin Zhang

University of Maine, Orono, ME; donglin@maine.edu

Deyi Yuan

Central South University of Forestry and Technology, Changsha; yuandeyi@126.com

Pollination compatibility between cultivars is essential for pear cultivation, production and breeding programs. In recent years, many new elite pear cultivars, such as 'Cuiguan', 'Xizilv', and 'Lvbaoshi', were bred in China. To provide functional data for further breeding work, we studied pollen tube growth in styles with fluorescence microscopy in two cross combinations 'Cuiguan' (S_3S_3) \times 'Lvbaoshi' (S_1S_4) and 'Xizilv' (S_1S_4) \times 'Lvbaoshi' (S_1S_4) in this work. The results showed that 'Cuiguan' \times 'Lvbaoshi' was compatible and the other one was incompatible via observation on pollen tube growth in styles. Pollen grains in both cross combinations could germinate on the stigma, while germination of pollen grains in incompatible pollination was slower than that of compatible pollination. Pollen grains in incompatible pollination germinated on the surface of stigma in two hours after pollination, whereas pollen tube stopped growth at the 1/3 location away from stigma after eight hours and the tip of which expanded into sphericity. In contrast, pollen grains in compatible pollination germinated in one hour after pollination, and the pollen tube elongated to the middle parts of style after eight hours, entered ovary after 24 hours, reached into embryo sac after 48 hours, and double fertilization was finally completed after 72 hours. Growers could plant different

pear genotypes in their orchard based on our findings.

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(287) Pawpaw Cultivar Fingerprinting and Progeny Determination Using Simple Sequence Repeat Markers

Jeremiah Lowe*

Kentucky State University, Frankfort, KY; jeremy.lowe@kysu.edu

Shandeep Dutta

Kentucky State University, Frankfort, KY; shandeep.dutta@kysu.edu

Li Lu

Kentucky State University, Frankfort, KY; li.lu@kysu.edu

Kirk Pomper

Kentucky State University, Frankfort, KY; kirk.pomper@kysu.edu

Sheri Crabtree

Kentucky State University, Frankfort, KY; sheri.crabtree@kysu.edu

Kyle Schneider

Kentucky State University, Frankfort, KY; kyle.schneider@kysu.edu

The North American pawpaw [*Asimina triloba* (L.) Dunal] is a tree fruit native to areas in the eastern United States and is in the early stages of commercial production. Since 1994, Kentucky State University (KSU) has served as the USDA National Clonal Germplasm Repository, or gene bank, for pawpaw; therefore, germplasm collection and assessment are research priorities. Not only would DNA fingerprinting methods for pawpaw cultivars allow the authentication of clones currently being sold at nurseries, it would also allow the determination of the parentage of a number of advanced selections that are potentially the result of crosses attempted by the PawPaw foundation breeding effort. The objectives of this study were to develop simple sequence repeat (SSR) fingerprinting techniques with pawpaw cultivars and to determine if three advanced selections were truly progeny from a cross between the pawpaw selections 11-13 \times 1-23. Leaf samples were collected from the pawpaw selections Taytwo, Sweet Alice, NC-1, 11-13, 1-23, and three progeny of 11-13 \times 1-23. Leaf samples were also collected from a cherimoya (*Annona cherimola*) tree in the KSU greenhouse; cherimoya is in the same family as pawpaw. DNA was extracted from the leaves using the DNAMITE Plant Kit. Primers B3, B103, B118, B129, and G119 were labeled with 6-FAM and used to amplify SSR products. These products were then separated using a 3130 Applied Biosystems capillary electrophoresis system. All primers failed to amplify products in cherimoya; however, products were amplified by the SSR primers in the pawpaw selections examined and fingerprint patterns were useful in separating the genotypes. Unique allelic combinations using the primer set B103 indicated that two advanced selections thought to be progeny of a cross between the selections 11-13 \times 1-23 are not actually the progeny from two parents. Pollen contamination during hand pollination or pollinator activity either before or after hand pollination resulted in seedlings that were not the result of a cross between 11-13 \times 1-23.

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(288) Assessment of Genetic Diversity of Pawpaw (*Asimina triloba*) Cultivars with Simple Sequence Repeat Markers

Kirk Pomper*

Kentucky State University, Frankfort, KY; kirk.pomper@kysu.edu