

Overview of Elite Apple Rootstocks from USDA-ARS/Cornell University

William C. Johnson^{1,2}, James N. Cummins¹,
H. Todd Holleran¹, Stephen A. Hoying³,
Terence L. Robinson¹

¹United States Department of Agriculture-Agricultural Research Service, Plant Genetic Resources Unit, Geneva, NY, USA; ²Department of Horticultural Sciences, Cornell University, New York State Agricultural Experiment Station, Geneva, NY, USA; ³Cornell Cooperative Extension, Newark, NY, USA.

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The Geneva, New York, based Apple Rootstock Breeding and Evaluation Program has released five new rootstock genotypes in recent years, and eleven additional genotypes are presently under consideration for possible release. Orchard performance of these rootstocks has been evaluated through numerous trials in New York and through recently initiated trials in Michigan and Washington. Some of these elite genotypes have also been evaluated at sites across North America as a part of the NC-140 regional project. The genotypes Novole, G.65, G.16, G.11, and G.30 have been patented and released for commercial production. Geneva 16 and G.11 are fire blight tolerant competitors for M.9 and M.26, respectively. The earlier expectations

of G.65 and G.30, possible competitors for M.27 and M.7, respectively, have been muted by horticultural problems in the nursery and by poor anchorage. Ten additional CG series genotypes are presently under evaluation in commercial nursery stoolbeds, and these represent the next possible releases from the program. CG.4202 and CG.6210 (formerly known as CG.202 and CG.210) merit particular attention for Southern Hemisphere growers because they appear to have resistance to the woolly apple aphid (*Eriosoma lanigerans*).

The apple rootstock breeding and evaluation program, a joint effort of the United States Department of Agriculture-Agricultural Research Service (USDA-ARS) and Cornell University, has been a leader in the development of new rootstock genotypes of apple. In comparison to rootstock development programs in other parts of the world, a greater emphasis has been placed on disease resistance, pest resistance and orchard tree performance, at the expense of a stronger focus on propagability through stoolbeds. Geneva series rootstocks undergo rigorous screening procedures to verify tolerance to fire blight (*Erwinia amylovora*), crown/collar rot (*Phytophthora* spp.), and woolly apple aphid. In addition, these genotypes are selected for high levels of productivity in replicated orchard trials. Finally, new rootstock genotypes are evaluated in highly replicated, extensive orchard trials as part of the NC-140 project, a joint evaluation protocol that includes observations from 30 states and provinces in the USA, Canada and Mexico.

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In addition to the five rootstock genotypes that have been released for commercial use, there are many additional genotypes in various stages of evaluation. Six genotypes, G.30, G.16, G.11, CG.3041, CG.5935 and CG.4202, warrant particular attention due to their promising performance in orchard trials and recent (G) or potential (CG) commercial release.

TABLE 1

Yield efficiency (yield/trunk cross-sectional area) of G.30 in relation to M.26 in first 4 years of the 1994 NC-140 planting, Gala scion.

State/Province	Yield efficiency (% of M.26)
British Columbia	136
Indiana	194
Iowa	122
Kentucky	69
Michigan	242
New Jersey	467
New York	146
North Carolina	156
Ontario	83
Utah	121
Virginia	103
Washington	102

ROOTSTOCKS

G.30

G.30 is a progeny from the 1974 *Malus* X Robusta 5 X Malling 9 population. G.30 has been evaluated extensively through the NC-140 system and was included in the 1992, 1993, 1994 and 1999 plantings. In addition, G.30 has been planted commercially in the US on a limited scale. The primary characteristic that has generated grower interest in G.30 is the extremely high, though somewhat variable, yield efficiency induced by this rootstock (Table 1). Out of 23 sites observed in the 1994 NC-140 trial, 14 showed a significant rootstock effect on yield. Thirteen of these sites reported that G.30 was the most productive rootstock, though some sites reported high mortality of trees on G.30. Clearly, G.30 exhibits strong genotype X location interactions. G.30 is highly resistant to fire blight. This rootstock produces a tree that is usually similar in size to M.7, about 60 to 65% the size of trees on standard seedling, and usually induces very heavy cropping. However, perhaps due to the extremely heavy crop loads carried by many trees on

G.30, the tree size has been variable, sometimes closer in size to M.26 (45 to 50% of standard seedling).

G.30 is susceptible to colonization by woolly apple aphids and is difficult to produce through traditional stoolbed propagation. In addition, G.30 appears to have brittle wood, and the graft unions have been found to be significantly weaker than other rootstock genotypes. Consequently, we recommend that this rootstock be used only where sturdy, multi-wire trellis support systems are available. Particular attention to support is necessary when using brittlewooded scion cultivars, such as Gala.

G.16

G.16 is a progeny from the 1981 Ottawa 3 X *Malus floribunda* population that was released for commercial production in the USA. Due to the recent origin of this rootstock, very little trial data are available. In the initial orchard trial G.16 was observed in New York for 10 years with 4 trees budded with each of 3 scion cultivars (Red Delicious, Mutsu, and McIntosh, Table 2). G.16 was observed to be similar to M.9 in

size, approximately 35 to 40% the size of a tree on standard seedling rootstock, based on these 12 trees. This genotype was not included in NC-140 trials until 1998, though it has been planted on a limited commercial scale in the USA. G.16 shows strong resistance to fire blight, good propagability in stoolbeds, and very strong early growth characters in stoolbeds, nurseries, and early orchard plantings. G.16 is susceptible to woolly apple aphids and is hypersensitive to at least one common latent virus. Nursery propagation requires virus-free scion wood to ensure success. G.16 was released prior to adequate testing, but in response to strong grower demand for a fire blight resistant rootstock in a vigor category similar to M.9.

G.11

G.11 is a progeny from the 1978 Malling 26 X *Malus* X Robusta 5 population. G.11 is now approaching commercialization in the USA, following a setback caused by misidentification of the genotype in the early 1990s. As a result of this setback, G.11 has not yet been planted in the NC-140 trials, but will be included in upcoming trials. According to early trial data, use of G.11 results in highly productive trees intermediate in size to M.9 and M.26, about 40 to 45% the size of trees on standard seedling. G.11 exhibits moderate levels of fire blight resistance in trials based on both direct inoculation and through systemic infection of young orchard trees (M.9 and M.26 exhibit, by comparison, extreme sensitivity). G.11 is susceptible to colonization by woolly apple aphid. G.11 has adequate stoolbed and nursery characters and should be commercially available in the USA and Europe in approximately 2005. Yield efficiency of G.11 trees in orchard trials has been impressively high (Table 3), and fruit size has been similar to M.26.

CG.3041

CG.3041 is a progeny from the 1975 Malling 27 X *Malus* X Robusta 5 population. CG.3041 has been observed in orchard trials in New York (Table 4), as well as in the NC-140 plantings of 1993, 1998, and 1999. CG.3041 is a likely competitor for M.9 and G.16 and produces trees similar in size to M.9 EMLA. CG.3041 has exhibited strong resistance to fire blight but is susceptible to colonization by woolly apple aphid. CG.3041 probably has adequate stoolbed and nursery characters for commercial nursery production but may suffer from problems with burrknots in the orchard if not managed properly.

TABLE 2

Performance of G.16 during first 10 years of observation at Geneva, NY, as compared to M.9 and M.26 controls (controls equal 100).

Rootstock	Trunk cross-sectional area	Yield efficiency
Spur Red Delicious at Geneva, NY, measurements as % of M.9		
M.9	100 a ^z	100 ab ^z
G.16	151 ab	125 a
M.26	228 b	81 b
Mutsu at Geneva, NY, measurements as % of M.9		
M.9	100 a	100 a
G.16	94 a	114 a
McIntosh at Geneva, NY, measurements as % of M.26		
G.16	59 b	129 a
M.26	100 a	100 a

^zLetters following numbers represent Duncan groupings, cells containing the same letter do not show significant difference. Results based on four trees per rootstock/scion combination. Data analysis using SAS (1988).

TABLE 3

Performance of G.11 during the first 6 years with Liberty or 10 years with McIntosh at Geneva, NY, as compared to M.26 controls.

Rootstock	Trunk cross-sectional area	Yield efficiency
Performance of G.11 at Geneva, NY, Liberty scion, 6 years trial data, measured as % of M.26		
M.26	100 a ^z	100 a ^z
G.11	97 a	131 b
Performance of G.11 at Geneva, NY, McIntosh scion, 10 years trial data, measured as % of M.26		
M.26	100 a	100 a
G.11	97 a	131 b

^zLetters following numbers represent Duncan groupings, cells containing the same letter do not show significant difference. Data analysis using SAS (1988).

CG.3041 might be commercially released soon and could be available for purchase in North America and Europe by 2006.

CG.5935

CG.5935 is a progeny genotype from the 1976 Ottawa 3 X *Malus* X Robusta 5 population. CG.5935 has been observed in orchard trials in New York (Table 4), as well as in the NC-140 planting in 1999. CG.5935 is a likely competitor for G.11 and M.26 and produces trees similar in size to M.26. CG.5935 has shown strong resistance to fire blight in direct inoculation studies but is susceptible to woolly apple aphid. CG.5935 probably has adequate stoolbed and nursery characters; a final evaluation of propagability characteristics will be completed in 2000. CG.5935 might be commercially released soon and could be available for purchase in North America and Europe by 2006.

CG.4202

CG.4202 is a Geneva series rootstock of unknown pedigree that has been observed in orchard trials in New York (Table 4) as well as in the NC-140 plantings in 1992, 1993 and 1999. CG.4202 will be a competitor for G.11, CG.5935, and M.26 and produces trees similar in size to M.26. Trial data for CG.4202 from the US are still somewhat suspect, pending verification that the trees are of the same genotype as those observed in New Zealand. Trial data generated in the US have been lackluster. This genotype typically has not shown statistically significant increases in yield efficiency compared to M.26 (Table 4), but New Zealand trials have been very promising. CG.4202 shows resistance to colonization by woolly apple aphid and has shown strong resistance to fire blight in trials based on both direct inoculation and through systemic infection of young orchard trees.

CG.4202 has adequate stoolbed and nursery characters. CG.4202 is scheduled for commercial release in New Zealand in 2002, with commercialization scheduled to follow in Australia. This genotype is under consideration for possible commercialization in North America, South America, South Africa and Europe as well.

CG.6210

CG.6210 (formerly known as CG.210) is a progeny from the 1975 Ottawa 3 X *Malus* X Robusta 5 population. CG.6210 has been tested in orchard trials in New York (Table 4) as well as in NC-140 trials in 1992, 1993, and 1999. CG.6210 has produced trees similar in size to M.7 in US trials, but trees in New

Zealand trials appear similar to M.26 in size. CG.6210 has shown resistance to colonization by woolly apple aphid and has shown strong resistance to fire blight. CG.6210 is not presently approaching commercialization due to propagation concerns; this genotype experiences a high mortality rate (20 to 50%) upon transplanting.

CG.7707

CG.7707 is a progeny from the 1975 *Malus* X Robusta 5 X Malling 9 population. CG.7707 has been tested in orchard trials in New York (Table 4) as well as in the 1992, 1993, and 1999 NC-140 trials. Trees on CG.7707 are characterized by highly vigorous early growth, very high crop loads, and moderate growth on mature trees that are similar in size to Malling 7. CG.7707 is resistant to colonization by woolly apple aphid and appears to be highly resistant to fire blight. CG.7707 appears to be tolerant of *Phytophthora* spp. induced root rots, making it an interesting alternative for growers of M.7 and MM.106. CG.7707 is difficult to propagate by traditional layerbed techniques and shows problems with anchorage that suggest support may be required if planted commercially.

CONCLUSION

Several promising new Geneva series rootstocks have recently become available or may become available soon to growers

worldwide. These genotypes offer improved disease and insect resistance characters over their competitors and will often provide improved yield efficiency. Further information about Geneva series rootstocks as well as non-Geneva series rootstocks is available on the internet at:

http://www.nysaes.cornell.edu/hort/br_eeders/appleroots/appleroostocks.html

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TABLE 4

Performance of controls and Geneva series rootstocks during first 10 years of observation in grower-cooperator orchard trials in Crown Point (Champlain Valley) and Marlborough (Hudson Valley), New York, with Empire as the scion variety. All trait value averages are expressed as a percentage of M.7.

Genotype	Average tree size ^z	Cumulative yield (kg/tree)	Cumulative yield efficiency ^y	Average fruit weight ^x	Cropload adjusted fruit size (CAFS) ^w
M.7	100 av	100 def	100 i	100 a	100
CG.7707	83 ab	183 a	233 ef	94 abcde	96
CG.6210	69 bcde	168 ab	251 cdef	95 abcde	97
G.30	62 cdef	160 ab	269 bcde	93 abcde	96
M.26	55 def	95 ef	190 fgh	96 abcd	98
CG.4202	54 def	119 cde	231 ef	98 ab	100
M.9/MM.111	52 efg	72 fgh	153 ghi	100 a	101
CG.5935	49 fg	146 abc	300 abcd	91 bcdef	95
CG.3041	34 gh	103 def	312 abc	96 abcde	100
M.9	34 gh	82 fg	246 def	96 abcde	98
Mark	25 hi	79 fg	323 ab	98 ab	102

^zTree size measured as trunk cross-sectional area following the 1998 growing season.

^yCumulative yield efficiency measured as the total fruit weight produced (1990-1999) divided by tree size.

^xAverage fruit size measured as the total weight of fruit produced divided by the total number of fruit produced.

^wCropload adjusted fruit size (CAFS) is calculated by regressing cropload vs. mean fruit size for all trees in each year, generating the residual value for variation of each tree from the pooled correlation and adding the residual for each tree to the overall mean fruit weight. No significant differences were observed for CAFS among the rootstocks described here.

^vLetters following numbers represent Duncan groupings, cells containing the same letter do not show significant difference. Results are based on an average of 12 trees per rootstock.