

OH × F Paternity Perplexes Pear Producers

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Abstract

Early in the 20th century, a collection of fire blight resistant pears from around the world was assembled in southern Oregon in an effort to develop improved rootstocks. ‘Old Home’ and ‘Farmingdale’ are two cultivars from Illinois that exhibited strong fire blight resistance and useful horticultural traits. Both became important as interstem stocks and as parents in the development of new rootstocks. In the 1950s, an Oregon nurseryman collected seed from an ‘Old Home’ tree in British Columbia purportedly pollinated by ‘Farmingdale’ and hundreds of numbered selections of this cross of ‘Old Home’ × ‘Farmingdale’ (OH×F) were evaluated. Several OH×F selections are now valued as rootstocks worldwide, and 45 unique OH×F selections are maintained at the USDA-ARS National Clonal Germplasm Repository (NCGR), in Corvallis, Oregon. Simple Sequence Repeat (SSR) or microsatellite-based profiles were generated for ‘Old Home’, ‘Farmingdale’, 8 OH×F selections, and several reference pear cultivars at NCGR using a standard fingerprinting set developed by the European Cooperative Programme for Plant Genetic Resources. ‘Farmingdale’ is thought to be a seedling of ‘Beurré d’Anjou’. Our study showed that ‘Farmingdale’ shared at least one SSR allele with ‘Anjou’ at each locus tested, confirming this parental relationship. Our studies showed that all OH×F selections shared an allele with ‘Old Home’ at each locus, with one allele carrying a suspected pair of base deletions. However, based on our SSR results, it is impossible for ‘Farmingdale’ to be the pollen parent for any of the OH×F selections examined. Evaluation of the world pear collection at NCGR with this fingerprinting set established the cultivar ‘Bartlett’ as the actual pollen parent of these rootstock clones. Fruit and leaf morphology is also consistent with ‘Bartlett’ and not ‘Farmingdale’ as a parent of OH×F rootstock selections. The highly fire blight resistant ‘Farmingdale’ is apparently very under-represented in the pedigrees of current pear rootstocks, and deserves renewed consideration.

Early in the 20th century, Oregon State University (OSU) professor Frank Reimer began scouring the world for *Pyrus* germplasm with resistance to the important bacterial disease fire blight (*Erwinia amylovora* (Burrill) Winslow et al.), which made its first appearance in the Rogue River Valley in 1906 (Reimer, 1925). Reimer was the first superintendent of the OSU Southern Oregon Experiment Station near Medford. From 1917 to 1919 his travels took him to China, Korea, Manchuria, and Japan where he collected scions from many local pear cultivars and seed from pear wild relative species (Reimer, 1919; Fig. 1). He also collected seed from wild and hedgerow perry pears in France, and clones of hundreds of the leading pear cultivars of Western Europe and North America. Seedling populations were generated and clones were grafted and established at the OSU

station in Talent, Oregon, where the diverse germplasm collections were evaluated for fruit quality, disease resistance and as potential rootstocks (Reimer, 1919; Reimer, 1925;

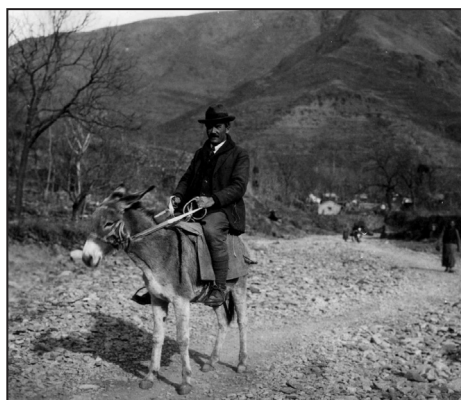


Fig. 1. Frank C. Reimer traveling while investigating pears in northern China in 1919.

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Hartmann, 1957). Two of Professor Reimer's most valuable discoveries came from a 1915 trip to visit fruit grower Benjamin Buckman in Farmingdale, Illinois. One was the cultivar 'Farmingdale', an open pollinated seedling Buckman had found near a 'Beurré d'Anjou' tree on his farm, and the other was 'Old Home', a seedling that had come from a nursery in Paris, Illinois some years earlier. Reimer observed both of these trees to be completely free of fire blight and he brought scions from 'Old Home' back to Oregon when he returned. 'Farmingdale' scions were sent to him several years later (Hummer, 1998; Westwood and Brooks, 1963; Westwood, 1967). After more than a decade of observing natural infections, and performing artificial inoculations in southern Oregon with *E. amylovora*, Reimer found many pear species selections and Asian cultivars with strong fire blight resistance, but only three European cultivars: 'Farmingdale', 'Longworth', and 'Old Home' had excellent blight resistance as trunk stocks (Reimer, 1925). The many valuable pear selections identified or developed by Reimer and his successors were later transferred to the National Clonal Germplasm Repository at Corvallis, Oregon when the USDA Agricultural Research Service established this genebank in 1981 (Postman et al., 2006; Westwood, 1982).

'Farmingdale'. The origin and characteristics of 'Farmingdale' are discussed in considerable detail by Reimer (Reimer, 1925; Reimer, 1950). It is apparently a pure form of *P. communis* which originated as a chance seedling in the orchard of Benjamin Buckman, at Farmingdale, Illinois. The fruit size is medium to large, and it resembles 'Anjou' in form and coloration. Flesh is white, fairly fine, buttery, moderately juicy, and quite free of grit. It is reasonably sweet but somewhat lacking in desirable flavor characteristics, and ripens in midseason. The original seedling was discovered close to an 'Anjou' tree, which was presumed to be the parent. Hartmann (1957) noted "while this pear is of little value for its fruit, it is quite remarkable in

other characteristics. Its tree is vigorous, well formed, fairly productive, and is the most blight resistant of all the *P. communis* cultivars tested at the Southern Oregon Branch Experiment Station."

'Old Home'. 'Old Home' is also apparently a pure form of *P. communis* that originated as a chance seedling with B.O. Curtiss, at Paris, Illinois (Hartmann, 1957) and was growing in Benjamin Buckman's trial orchard in Farmingdale prior to 1907 (Ragan, 1908). The fruit of 'Old Home' is small, round, slightly truncate, with no neck. Skin is yellow-green, becoming yellow when ripe. Flesh is white to yellow, fine textured, becoming soft and tender when ripe with few stone cells, medium dry, subacid and with poor flavor (Howlett, 1957). While its fruit is of no consequence, the variety was widely used as a blight resistant trunk and framework stock, and as a very good source of blight resistant seedlings. When crossed with 'Farmingdale', a high percentage of the seedlings were very blight resistant as well as vigorous and uniform in growth (Hartmann, 1957). Reimer (1925) found 'Old Home' to have very good graft compatibility with quince and it has since been used as an interstem bridge for incompatible pear cultivars. Westwood (1967) showed that 'Old Home' is also graft compatible on hawthorn (*Crataegus sp.*) rootstock. When the disease Pear Decline spread through the pear growing areas of British Columbia in the 1940s and through Washington, Oregon and California in the 1950s and 1960s, it was found that trees with 'Old Home' root or trunk stocks were much more resistant to pear decline as well as to fire blight. 'Old Home' was extremely difficult to propagate as a clonal rootstock, however, while many OH×F selections rooted much easier from hardwood cuttings (Westwood and Brooks, 1963).

'Old Home' and 'Farmingdale' in breeding. In the mid 1920s, following the death of Benjamin Buckman, the original 'Farmingdale' and 'Old Home' trees in Illinois were destroyed, and the trees established at South-

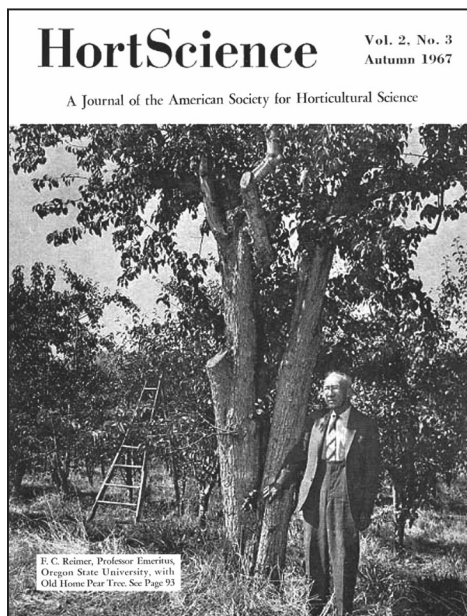


Fig. 2. HortScience cover in 1967 showing F. Reimer by original Old Home tree recently transplanted to Talent, Oregon.

ern Oregon Experiment Station became the primary source of nursery stock (Fig. 2; Brooks, 1984; Hummer, 1998; Westwood, 1967). Reimer (1950) found in the 1930s that when ‘Farmingdale’ was used as a pollen parent in crosses with other blight resistant selections, a high percentage of the resulting seedlings exhibited a high resistance to blight. This was especially true when ‘Old Home’ was the seed parent. Although a number of crosses between other blight resistant parents resulted in >90% seedlings that were resistant to blight following inoculation, many of those resistant seedlings became infected when a susceptible cultivar such as ‘Bartlett’ or ‘Beurré Bosc’ was grafted onto them. In those cases, fire blight could spread from an infected cultivar across the graft union into the rootstock. However, the OH×F seedlings were resistant even to the spread of fire blight from infection of a grafted cultivar (Reimer, 1950). Based on Reimer’s work, ‘Old Home’ and ‘Farmingdale’ became important parent

stocks for the development of both rootstock and edible pear cultivars. Several important Canadian cultivars obtained their fire blight resistance from ‘Old Home’, and at least two US fruit cultivars have ‘Farmingdale’ in their pedigrees (Table 1). By far, the most important use of ‘Farmingdale’ and especially ‘Old Home’ has been in the development of pear rootstocks. ‘Old Home’ in particular has been a valuable parent in rootstock breeding programs in France, UK, Germany, and elsewhere (Table 1; Elkins et al., 2012).

OH×F selections. One of Reimer’s goals was to establish a mother block of ‘Old Home’ and ‘Farmingdale’ at the Southern Oregon Experiment Station to generate seed for producing blight resistant seedling rootstocks. Oregon nurseryman Lyle Brooks was concerned about the variability of pear cultivars grafted onto OH×F seedling rootstocks, and he set out to develop clonal rootstocks from this cross. In 1952, he obtained half a kilogram of seed from an isolated block of ‘Old Home’ trees planted with ‘Farmingdale’ pollenizers at the Canada Research Station in Summerland, British Columbia. Of the thousands of resulting seedlings, he planted 516 in a nursery block and evaluated them for ease of propagation from cuttings and other traits (Brooks, 1984; Westwood and Brooks, 1963). Propagation by hardwood cuttings was successful, and thirteen of the more easily propagated OH×F numbered selections (OH×F 18, 34, 51, 69, 87, 97, 112, 198, 217, 230, 267, 333, and 361) were extensively evaluated at OSU for disease and insect resistance, environmental tolerance, anchorage, dwarfing and fruit production of grafted cultivars (Lombard and Westwood, 1987). More than 40 OH×F selections, including the 13 above, are preserved at the USDA genebank in Corvallis (Table 2). Some continue to be propagated worldwide and are in high demand for new plantings even though they lack the size control and precocity demanded for high density orchards (Elkins et al., 2012). OH×F 333 was selected for its resistance to multiple diseases and moderate size control

Table 1. Pear selections reported to have either ‘Old Home’ or ‘Farmingdale’ in the pedigree, and USDA genebank accession numbers.

Plant name	Pedigree	Accession no.	Origin
Farmingdale in Pedigree			
P. betulifolia-2 x Farmingdale	P. betulifolia-2 x Farmingdale	PI 541785	United States
Rogue Red	Comice x (Seckel x Farmingdale sdlg. 122)	PI 541252	United States
Vistica Nectar	Farmingdale x Burkett	none	United States
Old Home in Pedigree			
AC Harrow Gold (HW 616)	Harvest Queen x Harrow Delight	none	Canada
BU 2/33 (Pyro II)	Old Home x Bonne Louise d’Avranches	PI 617679	Germany
Harrow Delight (HW 603)	Bartlett x (Early Sweet x Old Home)	PI 541431	Canada
Harrow Sweet (HW 609)	Bartlett x (Old Home x Early Sweet)	PI 617562	Canada
Harrow selection HW 623	Harrow Sweet (Old Home x Early Sweet) x HW 605	none	Canada
Harrow selection HW 624	Harrow Sweet x NY10353	none	Canada
Nijisseiki x Old Home	Nijisseiki x Old Home	PI 541767	United States
OH 11 (Pyram)	Seedling of Old Home	CPYR 2700	France
OH 20 fire blight resistant rootstock	Old Home seedling selection	PI 541237	United States
OH 50 fire blight resistant rootstock	Old Home seedling selection	PI 541238	United States
Old Home x P. betulifolia-1	Old Home x P. betulifolia-1	PI 541787	United States
Old Home x P. betulifolia-1	Old Home x P. betulifolia-1	PI 541788	United States
Pyrodwarf	Old Home x Bonne Louise d’Avranches	PI 617654	Germany
QR 708-02	BP-1 x Old Home	PI 617680	United Kingdom
QR 708-12	BP-1 x Old Home	CPYR 2704	United Kingdom
QR 708-36	BP-1 x Old Home	CPYR 2705	United Kingdom
Nijisseiki x Old Home (seedlot)	Nijisseiki x Old Home W-6	PI 541753	United States
Old Home x Bartlett (seedlot)	Old Home x Bartlett	PI 541380	United States

to be the standard clonal rootstock for the thousands of pear clones maintained at the USDA genebank (Postman, 2008a; 2008b). A new generation of seedlings generated from open pollinated (OP) seed collected from an isolated group of select OH×F clones (OH×F 40, 51, 87, 333 and 339) resulted in the Horner rootstock series (Table 2; Mielke and Smith, 2002; Mielke and Sugar, 2004). Horner 4 is under evaluation in the 2005 NC-140 collaborative pear rootstock trial (Elkins et al., 2011), and a trial comparing Horner 4, Horner 10 and OH×F 87 was established in 2009 in the states of Oregon and Washington (Einhorn, personal communication).

DNA fingerprints. Bassil and Postman (2009) developed expressed sequence tag

(EST)-simple sequence repeat (SSR) markers and evaluated them for usefulness in a diverse collection of individuals from the three most commonly cultivated pear species: *P. communis*, *P. pyrifolia* and *P. ussuriensis* at the USDA genebank. They found that ‘Farmingdale’ shared one SSR allele with ‘Anjou’ at each of 10 loci, suggesting that ‘Anjou’ was very likely the maternal parent of ‘Farmingdale’, as Buckman and Reimer had suspected nearly a century earlier (Bassil and Postman, 2009; Hartmann, 1957; Reimer, 1925). OH×F 333 was the only selection included in that study and appeared to share one allele with either ‘Old Home’ or ‘Farmingdale’, thus confirming its reported parentage. This paper reports on the pheno-

Table 2. Pear selections reported to have both ‘Old Home’ and ‘Farmingdale’ in pedigree, and USDA genebank accession numbers.

Plant name	Pedigree	Accession no.	Origin
Harrow selection HW 621	(Anjou x Farmingdale) x Harrow Delight	none	Canada
Horner 4	O.P. from population of OHxF 40, 51, 87, 333 & 339	CPYR 2955	United States
Horner 10	O.P. from population of OHxF 40, 51, 87, 333 & 339	CPYR 2956	United States
Horner 51	O.P. from population of OHxF 40, 51, 87, 333 & 339	PI 657931	United States
OHxF 1	Old Home x Farmingdale seedling selection	PI 541408	United States
OHxF 2	Old Home x Farmingdale seedling selection	PI 541413	United States
OHxF 4	Old Home x Farmingdale seedling selection	PI 541409	United States
OHxF 5	Old Home x Farmingdale seedling selection	PI 541410	United States
OHxF 7	Old Home x Farmingdale seedling selection	PI 541399	United States
OHxF 9	Old Home x Farmingdale seedling selection	PI 541421	United States
OHxF 18	Old Home x Farmingdale seedling selection	PI 541397	United States
OHxF 23	Old Home x Farmingdale seedling selection	PI 541411	United States
OHxF 29	Old Home x Farmingdale seedling selection	PI 541398	United States
OHxF 34	Old Home x Farmingdale seedling selection	PI 541412	United States
OHxF 40	Old Home x Farmingdale seedling selection	PI 541402	United States
OHxF 51	Old Home x Farmingdale seedling selection	PI 541369	United States
OHxF 58	Old Home x Farmingdale seedling selection	PI 541454	United States
OHxF 69	Old Home x Farmingdale seedling selection	PI 665738	United States
OHxF 87	Old Home x Farmingdale seedling selection	PI 541415	United States
OHxF 97	Old Home x Farmingdale seedling selection	PI 541370	United States
OHxF 101	Old Home x Farmingdale seedling selection	PI 541416	United States
OHxF 109	Old Home x Farmingdale seedling selection	PI 541417	United States
OHxF 112	Old Home x Farmingdale seedling selection	PI 541418	United States
OHxF 130	Old Home x Farmingdale seedling selection	PI 541406	United States
OHxF 132	Old Home x Farmingdale seedling selection	PI 541404	United States
OHxF 198	Old Home x Farmingdale seedling selection	PI 541419	United States
OHxF 217	Old Home x Farmingdale seedling selection	PI 541371	United States
OHxF 226	Old Home x Farmingdale seedling selection	PI 541372	United States
OHxF 230	Old Home x Farmingdale seedling selection	PI 541420	United States
OHxF 247	Old Home x Farmingdale seedling selection	PI 541422	United States
OHxF 257	Old Home x Farmingdale seedling selection	PI 541396	United States
OHxF 259	Old Home x Farmingdale seedling selection	PI 541423	United States
OHxF 261	Old Home x Farmingdale seedling selection	PI 541401	United States
OHxF 266	Old Home x Farmingdale seedling selection	PI 541424	United States
OHxF 267	Old Home x Farmingdale seedling selection	PI 541400	United States
OHxF 280	Old Home x Farmingdale seedling selection	PI 541425	United States
OHxF 282	Old Home x Farmingdale seedling selection	PI 541426	United States
OHxF 288	Old Home x Farmingdale seedling selection	PI 541373	United States
OHxF 319	Old Home x Farmingdale seedling selection	PI 541427	United States
OHxF 333	Old Home x Farmingdale seedling selection	PI 541405	United States
OHxF 340	Old Home x Farmingdale seedling selection	PI 541403	United States
OHxF 361	Old Home x Farmingdale seedling selection	PI 541374	United States
OHxF 377	Old Home x Farmingdale seedling selection	PI 541428	United States
OHxF 501	Old Home x Farmingdale seedling selection	PI 541407	United States
OHxF 512	Old Home x Farmingdale seedling selection	PI 541414	United States
OPR-005 OHxF C-44	Bartlett x (Old Home x Farmingdale)	PI 617519	United States
OPR-013 OHxF C-34	Old Home x Farmingdale	PI 541368	United States

typic verification of the 'Farmingdale' and 'Old Home' clones growing at the USDA genebank, and the expanded SSR fingerprinting of these cultivars and several OH×F rootstock selections using a universal fingerprinting set previously described by Evans et al. (2009) that is made up of more polymorphic genomic SSR loci.

Materials and Methods

Plant material. Young, actively growing leaves were collected in the spring of 2007 from the clonal genebank accessions of 'Anjou', 'Old Home', 'Farmingdale', OH×F 51, OH×F 69 (3 sources), OH×F 87, OH×F 97, OH×F 230, OH×F 333 and several standard cultivars in the NCGR orchard collection in Corvallis, Oregon (44.554° lat., -123.222° long.). The OH×F 69 clone in the genebank collection had come from OSU with a note in its inventory record about a possible identity question. In 2008, additional clones of OH×F 69 that trace back to the original Daybreak Nursery tree were obtained from Fowler Nurseries (Newcastle, CA) and North American Plants (McMinnville, Oregon) for comparison.

DNA extraction. Thirty to 50 mg of leaf tissue was placed in a cluster tube (Corning, Tewksbury, MA) containing a 4 mm stainless steel bead (McGuire Bearing Company, Salem, OR). The samples were frozen in liquid nitrogen and stored at -80°C, until extraction. Grinding was performed in the Retsch MM301 Mixer Mill, (Retsch, Inc., Hann, Germany) rapidly at a frequency of 30 cycles·s⁻¹ using three 30 s bursts. DNA was extracted with the Qiagen protocol described in detail by Gilmore et al. (2011).

SSR genotyping. Twelve microsatellite primers that make up a standard primer set proposed by the European Cooperative Program for Plant Genetic Resources (ECPGR) (Evans et al., 2009) were used. A standard set of six reference cultivars (Table 3) was included to allow harmonization of genetic data when comparing results generated in different laboratories and using different sep-

aration platforms. The Type-it Microsatellite Multiplex PCR Kit (Qiagen Inc., Valencia, CA) was used to amplify SSRs in two reactions of 15 µL total volume. The 15 µL PCR reaction mix contained: 8.3 µL of 2x Type-it Multiplex PCR Master Mix (Qiagen), 1.7 µL of a 10x multiplex primer mix containing 2 µM of each primer, 1.7 µL Q solution, and 3.3 µL of 3ng·µL⁻¹ template DNA. Touch-down amplification was performed with a Tetrad thermocycler (MJ Research, Inc., Woburn, MA) using an initial step of 95°C for 5 min, followed by 10 cycles of 95°C for 30 s, annealing temperatures starting at 62°C for 90 s (decreasing by 1°C/cycle), and 72°C for 30 s for extension. This step was followed by 28 cycles of 95°C for 30 s, 52°C for 90 s, and 72°C for 30 s, with a final extension step of 60°C for 30 min. Success of the PCR was confirmed by 2% agarose gel electrophoresis. Fragment analysis followed separation on a Beckman CEQ 8000 capillary genetic analyzer (Beckman Coulter, Fullerton, CA). Allele sizing and visualization were performed using the fragment analysis module of the CEQ 8000 software. Alleles were scored by fitting the peaks into bins less than one nucleotide. For unweighted pair group method with arithmetic mean (UPGMA) cluster analysis, individuals were scored for the presence or absence of each allele and PowerMarker (Liu and Muse, 2005) was used for cluster analysis.

Paternity testing. Paternity analysis for the six OH×F selections included in this study (Table 3) was carried out using a likelihood approach with the CERVUS 3.0 software (Kalinowski et al., 2007). Using the genotype file at the 12 loci, CERVUS was used to determine allele frequency, to simulate paternity analysis and calculate critical values of likelihood ratios. The paternity analysis module (unknown sexes) used the twelve cultivars included in the study as candidate parents. Other parameters set for CERVUS were 0.99 for the proportion of loci typed and 0.022 for rate of genotyping error.

Phenotype verification. Fresh fruits and

Table 3. Genotypic information at 12 SSR loci for 'Old Home', 'Farmingdale', '6 OH×F selections, and 10 pear cultivars available at USDA-ARS, NCGR. Alleles present in Farmingdale but not observed in any of the OH×F selections are highlighted. Allele mismatches are underlined.

	CH05c06	EMPe117	GD147	EMPe11	CH04e04	CH01f07a	CH03g08	CH01d09	CH03d13	CH02b11	CH01d10	GD97
Abbe Fetel ^a	97/115	117/119	125/125	146/152	181/199	182/192	246/250	289/297	111/115	128/128	155/157	145/153
Anjou	97/115	117/121	125/125	142/152	181/181	182/196	252/260	283/285	113/127	132/138	155/157	159/175
Bartlett ^a	91/95	89/117	125/125	152/152	181/207	178/186	230/246	243/279	111/127	122/128	153/161	159/175
Comice ^a	91/91	117/117	125/131	152/156	181/199	184/186	232/236	279/285	111/115	134/138	155/161	145/153
Conference ^a	91/101	119/121	125/125	142/152	181/207	182/194	230/260	279/285	111/127	124/128	161/161	171/199
Farmingdale	91/115	99/121	125/125	142/142	181/181	182/190	230/260	283/285	111/113	138/138	157/161	159/175
Harrow Sweet	91/97	113/117	125/125	152/156	181/181	186/192	246/260	243/285	111/127	122/122	153/157	153/159
Hosui ^a	87/109	95/107	135/137	148/148	189/189	182/204	256/262	283/283	101/101	124/134	159/159	175/175
OH×F 51	95/95	89/119	125/125	152/152	181/181	178/182	230/246	279/279	111/127	122/132	135/153	159/167
OH×F 69	91/91	89/119	125/127	152/156	181/181	186/192	230/260	279/281	115/127	128/128	135/161	159/167
OH×F 87	91/91	117/117	125/127	152/152	181/207	186/192	230/246	243/281	111/115	122/132	135/153	159/173
OH×F 97	91/91	117/119	125/125	152/156	181/207	186/192	230/246	279/281	111/115	128/132	135/153	159/167
OH×F 230	95/95	89/119	125/127	152/156	181/181	178/192	230/246	279/279	111/127	128/132	135/153	159/173
OH×F 333	91/95	117/119	125/127	152/152	181/181	182/186	230/230	279/279	115/127	122/132	153/157	159/173
Old Home	91/95	119/119	125/127	152/156	181/181	182/192	230/260	279/281	111/115	128/132	135/159	167/173
Passe Crassane ^a	91/111	101/117	125/129	152/152	181/181	182/182	230/246	279/285	127/127	132/132	157/161	159/175
Pyrodwarf ^a	91/91	119/121	125/125	152/156	181/181	182/192	260/260	279/285	111/115	124/128	135/161	167/199
Rogue Red	91/95	117/121	125/127	146/152	181/181	186/210	236/260	279/279	111/111	138/138	161/161	145/159

^a Reference accessions recommended by Evans et al. (2009) to allow data comparison across collections.

leaves were photographed, or photos were examined from the genebank photo archives for ‘Anjou’, ‘Farmingdale’, ‘Old Home’, and several OH×F selections. Source histories of the genebank cultivars were reviewed and fruit characteristics were compared to published descriptions.

Results and Discussion

DNA fingerprints. Each of the 12 cultivars and OH×F selections were uniquely identified except for the three OH×F 69 selections obtained from different sources which had identical fingerprints (Fig. 3). All OH×F selections shared an allele with ‘Old Home’ at each of the 12 loci with two exceptions: OH×F 87 was homozygous for 117 at EMPc117 and did not have the 119 allele from ‘Old Home’; and OH×F 333 did not have the 135 or 159 alleles present in ‘Old Home’ at CH01d09 (Table 3). Neither of the two alleles at four SSR loci (EMPc117, EMPc11, CH01d08 and CH02b10) in ‘Farmingdale’ was found

in any of the OH×F selections indicating that ‘Farmingdale’ is highly unlikely to be the pollen parent for these selections (Table 3). ‘Farmingdale’ shared an allele with ‘Anjou’ at each locus (Table 3) confirming the latter as one of the likely parents as previously reported (Bassil and Postman, 2009).

Six of the cultivars selected as references (Evans et al., 2009) were included in this study to standardize microsatellite allele scoring and allow data comparison across collections and separation platforms in the future (Table 3). ‘Bartlett’ appeared to share one allele at each locus with the OH×F selections (Table 3). Paternity analysis using CERVUS (Kalinowski et al., 2007) was conducted to confirm this possibility. It confirmed ‘Old Home’ and ‘Bartlett’ as the most likely parent pair with the highest likelihood at the relaxed confidence level (80%) for OH×F 69, 87 and 333 and at the strict confidence level (95%) for OH×F 51, 97 and 230. No allele mismatches were observed for

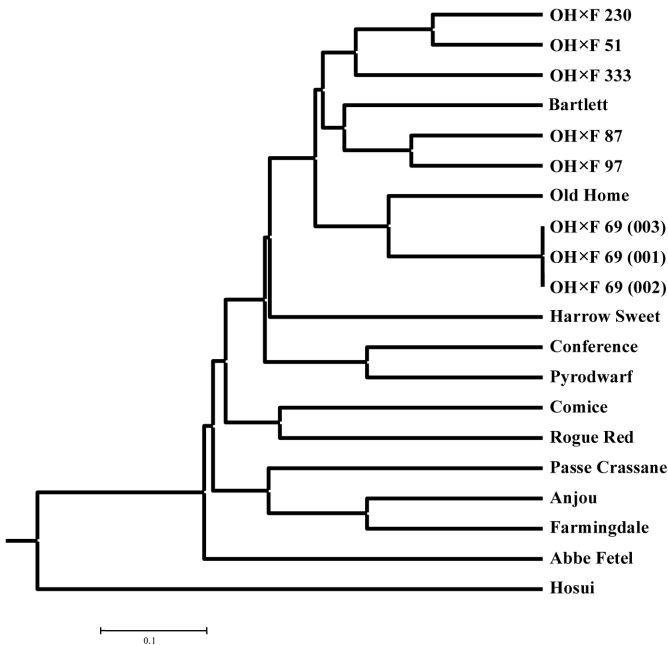


Fig. 3. Unweighted pair group method with arithmetic mean (UPGMA) cluster analysis of the evaluated pear cultivars and selection based on 12 SSR loci.

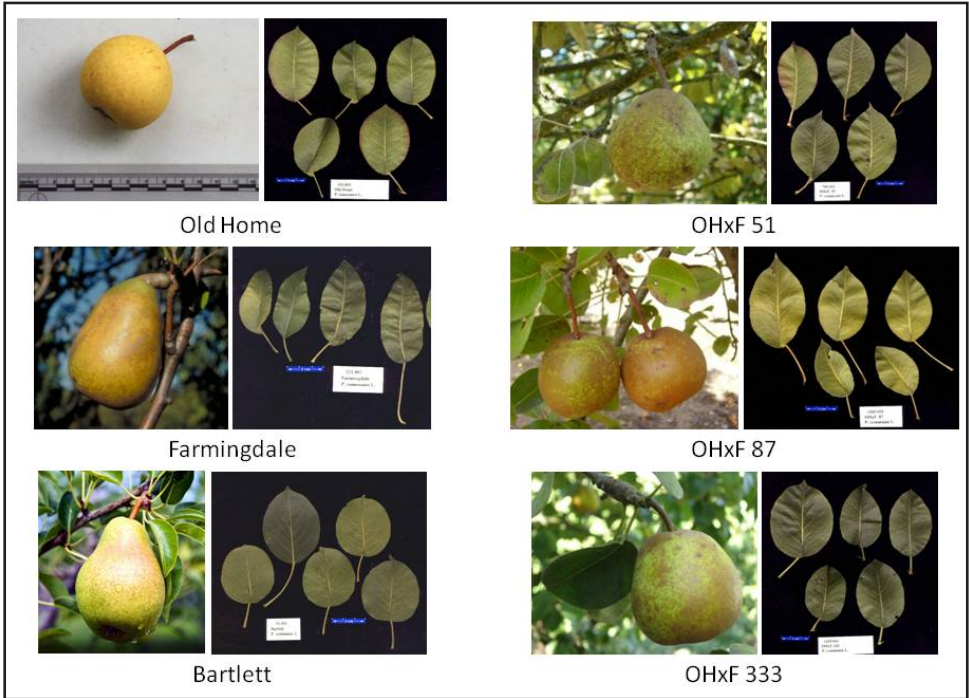


Fig. 4. Fruit and leaves of 'Old Home', 'Farmingdale', 'Bartlett' and 3 OH×F selections.

all but OH×F 87 and OH×F 333 which had a single mismatch. The mismatch of one allele at one locus (described above) for these two selections is most likely due to mutation, common at microsatellite sites. This result reveals 'Bartlett' as the original pollen parent for the OH×F clones included in this study. Based on the phenotypes of the 41 OH×F clones in the genebank collection, it is probable that 'Bartlett' was the pollen parent for all of them.

Cultivar source histories and phenotypes. Genebank records show that the 'Farmingdale' and 'Old Home' clones were obtained as scions from the original trees that Reimer had established at the Southern Oregon Experiment Station (USDA-ARS, 2012) and identity verification notes indicate that previous visual examination of these cultivars match those of the original trees as described by Hartmann (1957). 'Farmingdale' fruit has a very distinctive shape, not unlike a swollen

and slightly elongated 'Anjou' (Fig. 4) with a similar fine texture and good fruit quality. The peduncle is unusually short, thick and swollen where connected to the fruit. 'Old Home' is distinctively and unusually round for a European pear, with a slender peduncle of medium length (Fig. 4). The eating quality of 'Old Home' fruit is remarkably poor. The fruit as grown at NCGR clearly matches the photograph from the variety collection in Ohio taken in the mid 20th century (Howlett, 1957). The various 'Bartlett' and 'Anjou' clones in the genebank collection produce fruit that exactly matches those cultivars in fruit quality, ripening times, and disease susceptibility as they are known from U.S. commercial orchards. We are confident that the 'Farmingdale', 'Old Home', 'Anjou', 'Bartlett' and other five standard reference clones represented at the USDA genebank and used in this study are correctly identified based on their phenotypes. DNA fingerprints of 'Farmingdale' and the six

reference cultivars (Table 3) obtained from the National Fruit Collections (Brogdale Collections) in the UK also exactly match those from the NCGR collection (Evans, personal communication).

All OH×F clones produce fruit that is somewhat similar in size, shape and color (Fig. 4) with crisp, juicy texture and sweet sprightly flavor; although, they differ in maturity dates. All of the OH×F selections resemble 'Old Home', but not 'Farmingdale', in fruit shape and especially in peduncle size. The foliage of the various OH×F selections is similar in leaf length/width ratio, pedicel length and thickness, and pubescence, the latter of which is quite distinct. They all bear some resemblance to the foliage of 'Old Home', but not to 'Farmingdale' which has characteristically lanceolate leaves and less pubescence (Fig. 4).

While 'Bartlett', rather than the more blight resistant 'Farmingdale', may be the pollen parent of the OH×F selections now being used commercially, these OH×F selections have exhibited excellent blight resistance, as well as resistance to pear decline and good fruit production when used as rootstocks for our most important European pear cultivars (Elkins et al., 2012; Lombard and Westwood, 1987). The highly fire blight resistant 'Farmingdale' is apparently very under-represented in the pedigrees of present day pear rootstocks as well as in the parent clones currently being used in rootstock breeding programs. 'Farmingdale' as a parent is not likely to instill dwarfing or precocity traits in a rootstock, however if fire blight resistance is to be an important genetic component of future pear cultivars and rootstocks, the results of Frank Reimer (1925, 1950) should inspire the reconsideration of 'Farmingdale' germplasm in breeding.

Genetic testing of fruit varieties has become increasingly important in improving the efficiency of breeding new varieties (Iezzoni et al., 2010) and has the additional benefit of clarifying pedigrees of existing varieties (Sittther et al., 2012). Kimura et al. (2003)

used SSR markers to confirm and revise the paternity of several Japanese pear cultivars. Discovering the paternity of important or historic varieties like the OH×F rootstocks or 'Bing' cherry (*Prunus avium* L.) not only makes interesting news (Warner, 2013), but helps to avoid inbreeding and aids in the identification of sources of useful horticultural and adaptive traits. Future completion of DNA fingerprinting in the USDA pear genebank will help eliminate redundancy in the collection, streamline the introduction and conservation of unique and valuable germplasm accessions, and help breeders better understand the paternity of parents when making crosses to develop improved varieties.

Acknowledgements

We wish to thank David Hunter and Richard Bell for providing pedigree information for pear selections developed from 'Old Home' or 'Farmingdale'. We also thank Kate Evans and Todd Einhorn for their critical reviews of this manuscript and April Nyberg for her laboratory expertise in fingerprinting these accessions.

Literature cited

- Bassil, N.V. and J.D. Postman. 2009. Identification of European and Asian pears using EST-SSRs from *Pyrus*. *Genetic Resources and Crop Evol.* 57:357-370.
- Brooks, L.A. 1984. History of the Old Home × Farmingdale pear rootstocks. *Fruit Var. J.* 38:126-128.
- Elkins, R., R. Bell, and T. Einhorn. 2012. Needs assessment for future US pear rootstock research directions based on the current state of pear production and rootstock research. *J. Amer. Pomol. Soc.* 66(3):153-163.
- Elkins, R., S. Castagnoli, C. Embree, R. Parra-Quezada, T. Robinson, T. Smith, and C. Ingels. 2011. Evaluation of potential rootstocks to improve tree precocity and productivity. *Acta Hort.* 909:184-194.
- Evans, K.M., F. Fernandez-Fernandez, and C.L. Govan. 2009. Harmonizing fingerprinting protocols to allow comparisons between germplasm collections – *Pyrus*. *Acta Hort.* 814:103-106.
- Gilmore, B., K. Hummer, and N. Bassil. 2011. DNA Extraction protocols from dormant buds of twelve woody plant genera. *J. Amer. Pomol. Soc.* 65(4):201-207.

- Hartmann, H. 1957. Catalog and evaluation of the pear collection at the Oregon Agricultural Experiment Station. Technical Bulletin 41. 80 pp.
- Howlett, F.S. 1957. Preliminary evaluation of new and uncommon pear varieties. North Central Regional Bulletin 75 and Ohio Agricultural Experiment Station Research Bulletin 790. 131 pp.
- Hummer, K. 1998. 'Old Home' and 'Farmingdale,' the Romeo and Juliet of pear rootstocks: an historical perspective. *Fruit Var. J.* 52:38-40.
- Iezzoni, A., C. Weebadde, J. Luby, C. Yue, E. van de Weg, G. Fazio, D. Main, C.P. Peace, N.V. Bassil, and J. McFerson. 2010. RosBREED: Enabling marker-assisted breeding in Rosaceae. *Acta Hort.* 859:389-394.
- Kalinowski, S.T., M.L. Taper, and T.C. Marshall. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Mol. Ecol.* 16:1099-1006.
- Kimura, T., Y. Sawamura, K. Kotobuki, N. Matsuta, T. Hayashi, Y. Ban, and T. Yamamoto. 2003. Parentage analysis in pear cultivars characterized by SSR markers. *J. Jap. Soc. Hort. Sci.* 72:182-189.
- Liu, K. and S.V. Muse. 2005. Powermarker: integrated analysis environment for genetic marker data. *Bioinformatics* 21:2128-2129.
- Lombard, P.B. and M.N. Westwood. 1987. Pear rootstocks pp. 145-183 in R.C. Rom and R.F. Carlson (eds.). *Rootstocks for Fruit Crops*. John Wiley & Sons.
- Mielke, E.A. and L. Smith. 2002. Evaluation of the Horner rootstocks. *Acta Hort.* 596:325-330.
- Mielke, E.A. and D. Sugar. 2004. Initial seven-year evaluation of thirteen Horner pear rootstocks. *Acta Hort.* 658:513-517.
- Postman, J., K. Hummer, E. Stover, R. Krueger, P. Forsline, L.J. Grauke, F. Zee, T. Ayala-Silva, and B. Irish. 2006. Fruit and nut genebanks in the US National Plant Germplasm System. *HortScience* 41(5):1188-1194.
- Postman, J.D. 2008a. The USDA quince and pear genebank in Oregon, A world source of fire blight resistance. *Acta Hort.* 793:357-362.
- Postman, J.D. 2008b. World *Pyrus* collection at USDA genebank in Corvallis, Oregon. *Acta Hort.* 800:527-534.
- Ragan, W.H. 1908. Nomenclature of the pear; a catalog-index of the known varieties referred to in American publications from 1804 to 1907. USDA Bureau of Plant Industry Bulletin No. 126.
- Reimer, F.C. 1919. Report of a trip to the Orient to collect and study Oriental pears. Station report for the Southern Oregon Experiment Station and the USDA Office of Foreign Seed and Plant Introduction.
- Reimer, F.C. 1925. Blight Resistance in Pears and Characteristics of Pear Species and Stocks. Oregon Agricultural College, Experiment Station Bulletin 214, Corvallis, Oregon.
- Reimer, F.C. 1950. Development of blight resistant pear stocks. Oregon Agricultural Exp. Sta. Bulletin 485.
- Sitther, V., D. Zhang, D. Harris, W.R. Okie, S. Dhekney, and A. Yadav. 2012. Cultivar identification, pedigree verification, and diversity analysis among peach (*Prunus persica* L. Batsch) cultivars based on Simple Sequence Repeat markers. *J. Amer. Soc. Hort. Sci.* 137:114-121.
- USDA-ARS. 2012. Germplasm Resources Information Network - (GRIN). <http://www.ars-grin.gov/cgi-bin/npgs/acc/search.pl?accid=PI+541188> (Farmingdale); <http://www.ars-grin.gov/cgi-bin/npgs/acc/search.pl?accid=PI+541456> (Old Home) (December 6, 2012).
- Warner, G. 2013. Paternity test implicates Napoleon: scientists used genetic markers to identify Bing's parents. *Good Fruit Grower* (Jan. 1) 64(1):17-19.
- Westwood, M. N. 1967. About our cover: the quest for fire blight resistance in pear. *HortScience* 2(3):93.
- Westwood, M.N. 1982. Pear germplasm of the new National Clonal Repository: its evaluation and uses. *Acta Hort.* 124:57-66.
- Westwood, M.N. and L.A. Brooks. 1963. Propagation of hardwood pear cuttings. *Proc. Int. Plant. Prop. Soc.* 13:261-268.