

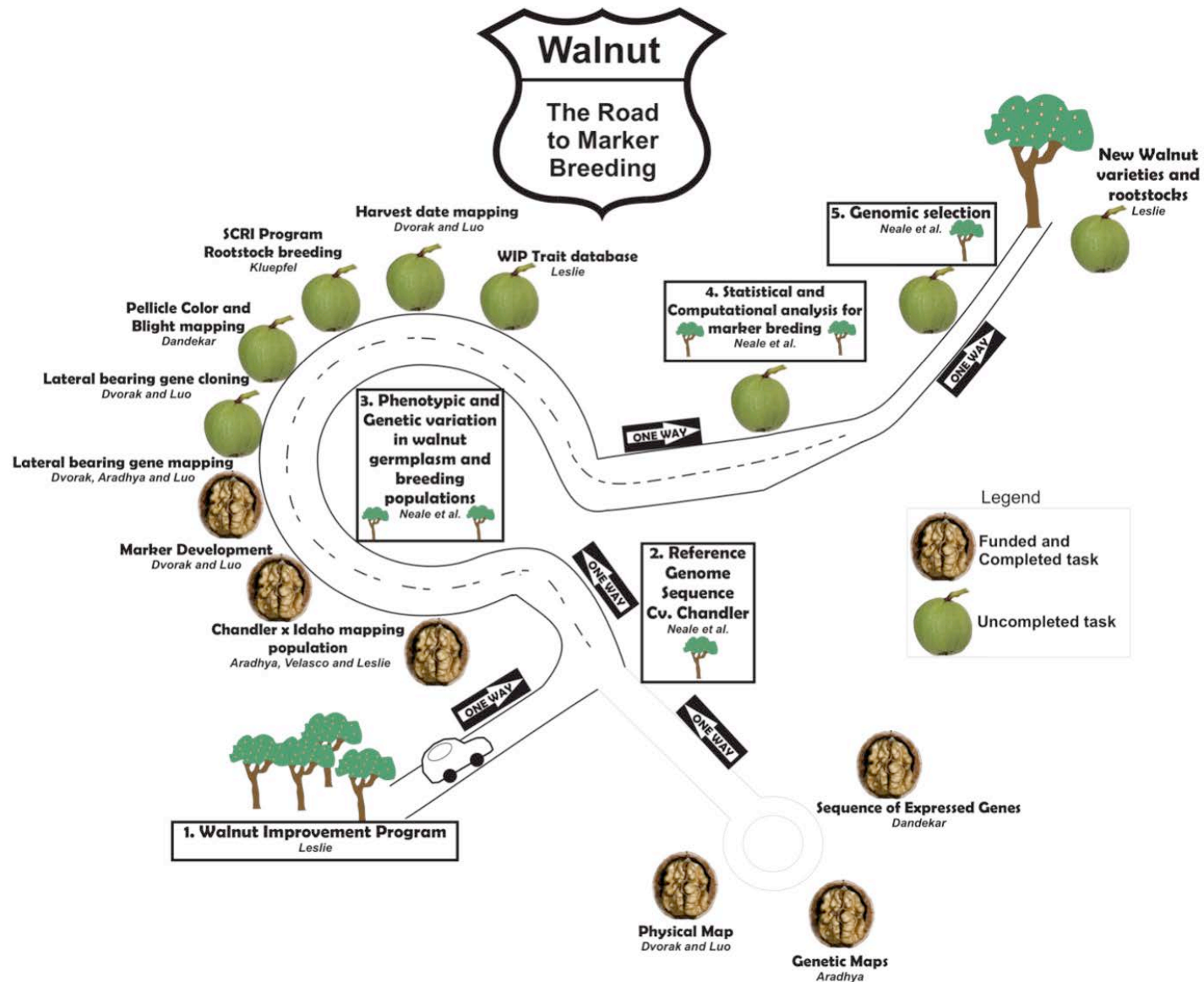


# Application of Marker Breeding in Pear Scion and Rootstock Improvement

David Neale

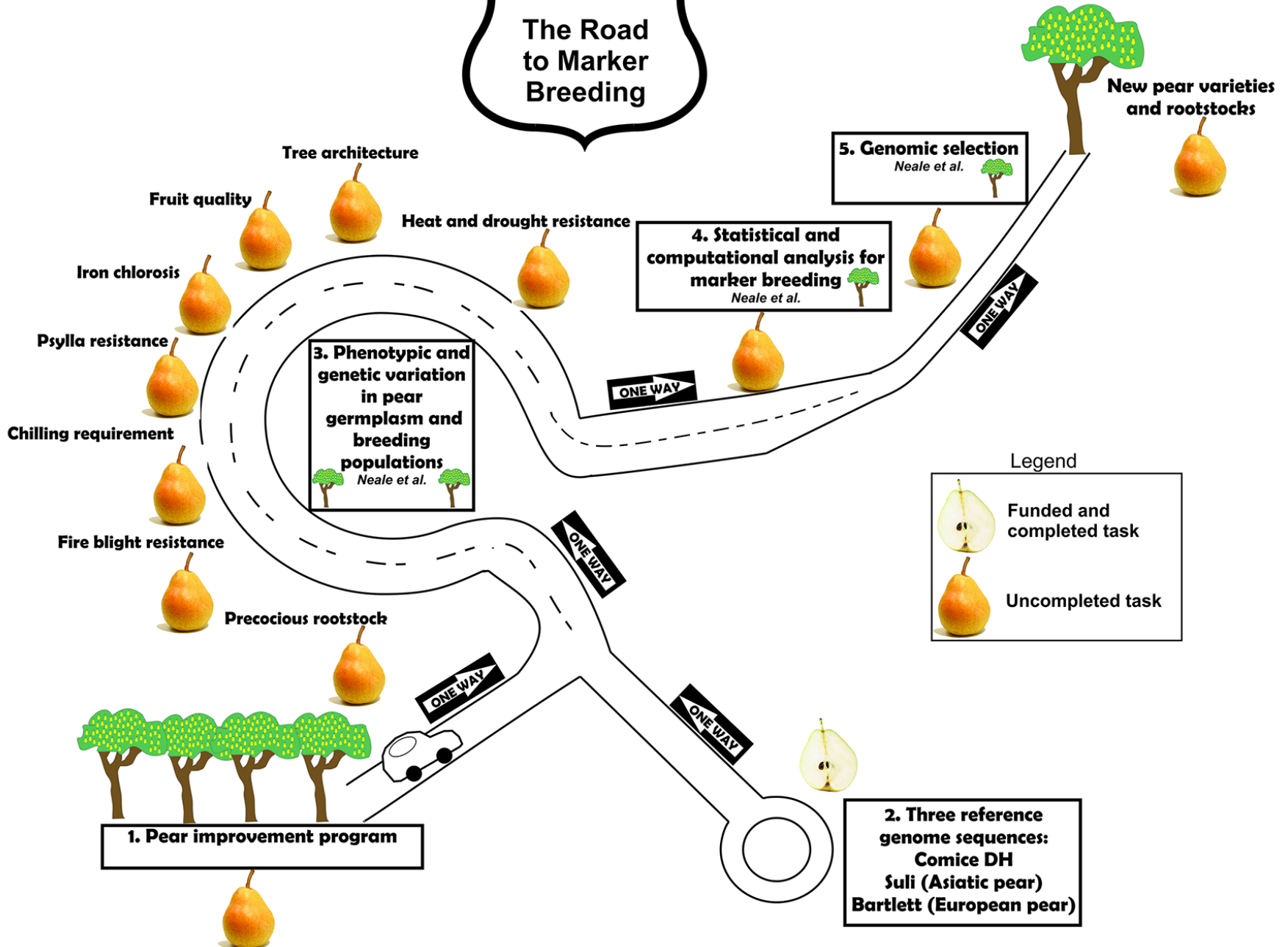


# Application of Marker Breeding



# Pear

## The Road to Marker Breeding





# Reference Pear Genome Sequences



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## The genome of pear (*Pyrus bretschneideri* Rehd.)

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### Abstract

The draft genome of pear (*Pyrus bretschneideri*) using a combination of BAC-by-BAC and next generation sequencing is reported. A 512.0 Mb sequence corresponding to 97.1% of the estimated genome size of this highly heterozygous species is assembled with 194x coverage. High-density genetic maps comprising of 2,005 SNP markers anchored 75.5% of the sequence to all 17 chromosomes. The pear genome encodes 42,812 protein-coding genes, and of these, ~28.5% encode multiple isoforms. High quality of the assembly and annotation is assessed and confirmed using Sanger-derived BAC sequences along with transcriptome sequences of different tissues. Repetitive sequences of 271.9 Mb in length, accounting for 53.1% of the pear genome, are identified. Simulation of eudicots to the ancestor of Rosaceae has re-constructed nine ancestral chromosomes. Pear and apple have diverged from each other ~5.4 to 21.5 MYA, and a recent whole-genome duplication (WGD) event must have occurred 30–45 MYA prior to their divergence, but following divergence from strawberry. When compared with the apple genome sequence, size differences between apple and pear genomes are confirmed mainly due to presence of repetitive sequences predominantly contributed by transposable elements (TEs), while genic regions are similar in both species. Genes critical for self-incompatibility, lignified stone cells (a unique feature of pear fruit), sorbitol metabolism and volatile compounds of fruit have also been identified. Multiple candidate SFB genes appear as tandem repeats in the S-locus region of pear; while, lignin synthesis-related gene family expansion and highly expressed gene families of HCT, C3H, and CCOMT contribute to high accumulation of both G-lignin and S-lignin. Expansion of S6PDH, SDH, and SOT along with evolutionary relationships of pear and apple have demonstrated their divergence from a common ancestor. Moreover,  $\alpha$ -linolenic acid metabolism is a key pathway for aroma in pear fruit.

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PLOS ONE

## The Draft Genome Sequence of European Pear (*Pyrus communis* L. 'Bartlett')

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### Abstract

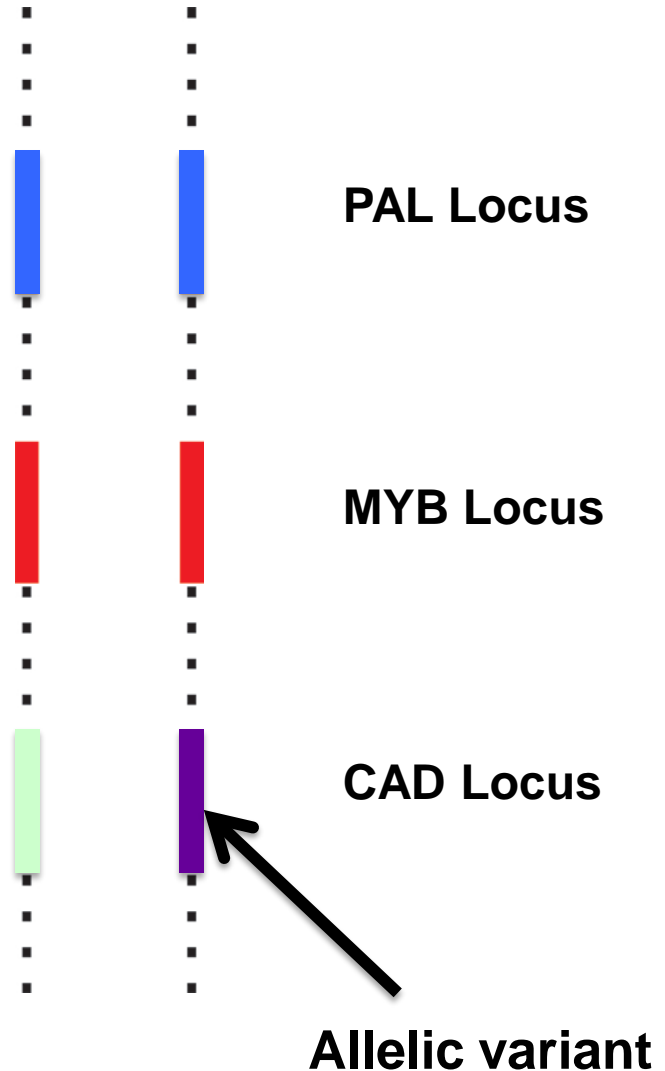
We present a draft assembly of the genome of European pear (*Pyrus communis*) 'Bartlett'. Our assembly was developed employing second generation sequencing technology (Roche 454), from single-end, 2 kb, and 7 kb insert paired-end reads using Newbler (version 2.7). It contains 142,083 scaffolds greater than 499 bases (maximum scaffold length of 1.2 Mb) and covers a total of 577.3 Mb, representing most of the expected 600 Mb *Pyrus* genome. A total of 829,823 putative single nucleotide polymorphisms (SNPs) were detected using re-sequencing of 'Louise Bonne de Jersey' and 'Old Home'. A total of 2,279 genetically mapped SNP markers anchor 171 Mb of the assembled genome. *Ab initio* gene prediction combined with prediction based on homology searching detected 43,419 putative gene models. Of these, 1219 proteins (556 clusters) are unique to European pear compared to 12 other sequenced plant genomes. Analysis of the expansin gene family provided an example of the quality of the gene prediction and an insight into the relationships among one class of cell wall related genes that control fruit softening in both European pear and apple (*Malus domestica*). The 'Bartlett' genome assembly v1.0 ([http://www.rosaceae.org/species/pyrus/pyrus\\_communis/genome\\_v1.0](http://www.rosaceae.org/species/pyrus/pyrus_communis/genome_v1.0)) is an invaluable tool for identifying the genetic control of key horticultural traits in pear and will enable the wide application of marker-assisted and genomic selection that will enhance the speed and efficiency of pear cultivar development.



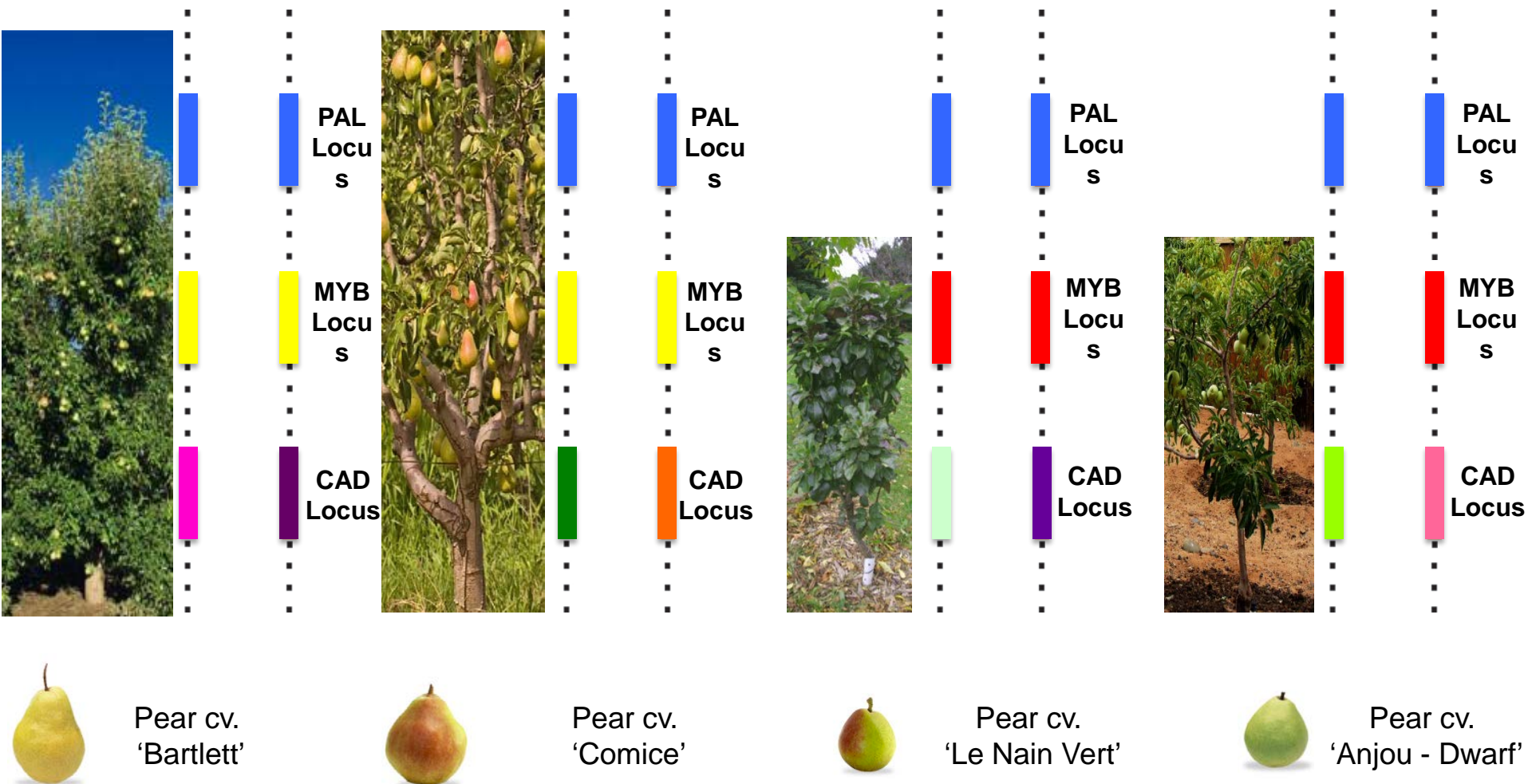
# Phase 1. Reference genomes sequencing in *Pyrus* (WSU and NZ/Italy).



Pears cv. "Doyenne du Comice" and  
'Barlett'



## Phase 2. Resequencing and discovery of genetic variation in *Pyrus* (UC Davis and ARS/Corvallis).





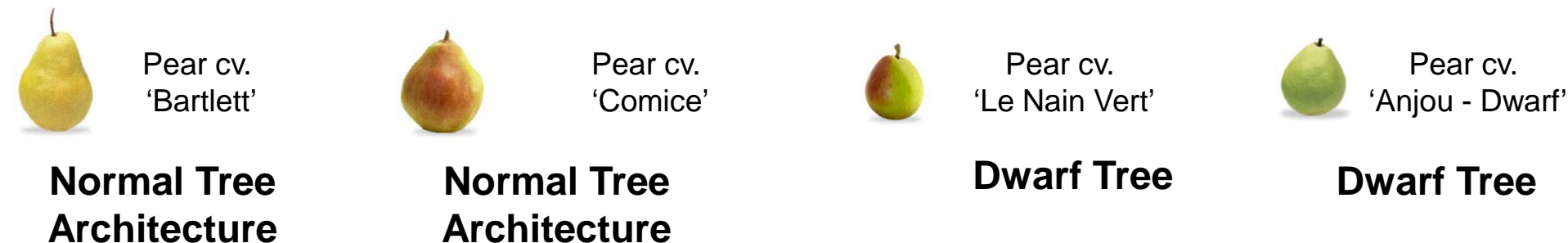
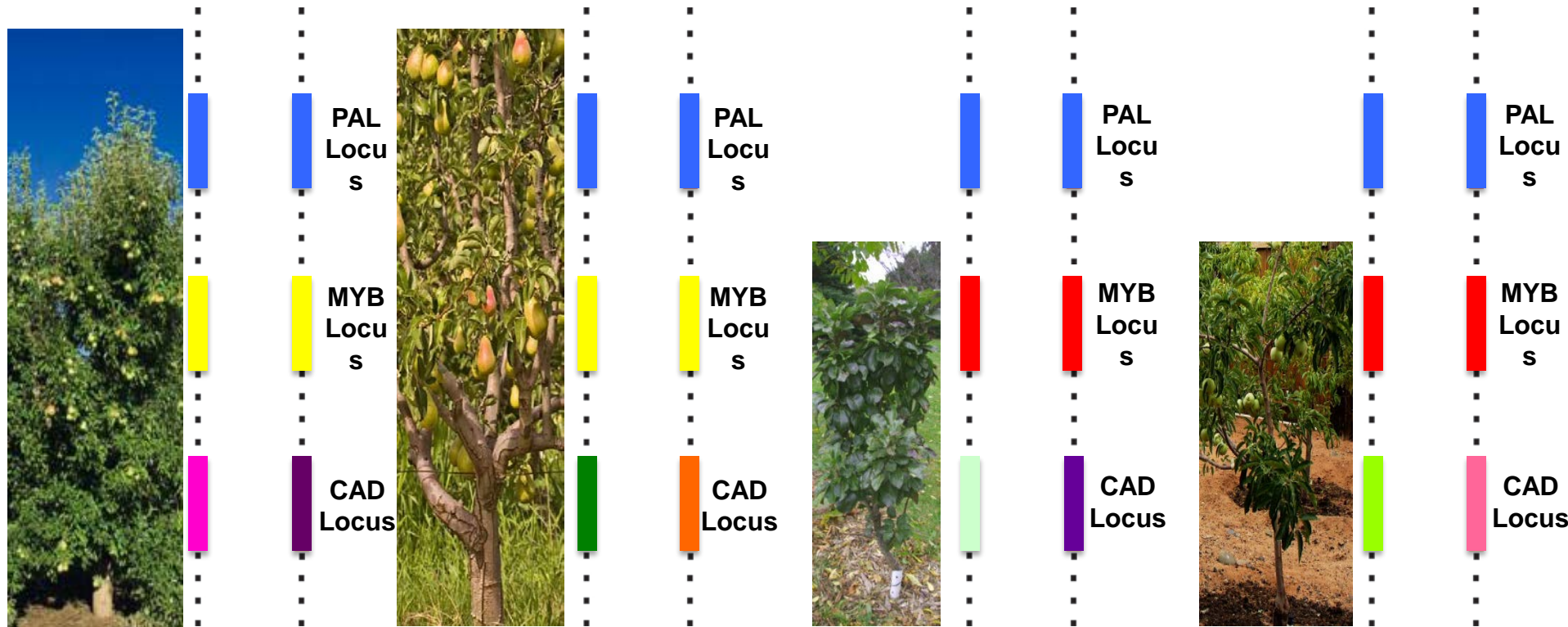
# Pyrus Germplasm Collection



	Clade	Name	Cpyr	Species	Comment
1	Xviii	P. betulifolia shaanxi	2291.001	betulifolia	
2	Xxv	P. calleryana 96107	2588.001	Calleryana	
3	Vi	Beurre d'Anjou	63.001	Communis	
4	Vii	Coscia tardive	159.002	Communis	
5	X	Seckel	519.001	Communis	Fire blight resistant
6	Xii	Gin	246.001	Communis	
7	Xxiii	Zao su li	2594.001	Pyrifolia	
8		P. salicifolia GE-2004-141	2849.001	Salicifolia	
9	Xix	Xiang shui li	2640.002	Ussuriensis	
10		Xuehua li	2681.002	X bretschneideri	Q27647
11	Xxiv	P. ussuriensis Korea	1202.001	Ussuriensis	
12	Xvi	P. syriaca Armenia	920.001	Syriaca	
13	Xiv	Para de zahar de bihor	1663.001	Communis	
14	Xv	Mednik	1549.001	Communis	Psylla resistant
15		Roi Charles de Wurtemberg	489.002	Communis	Fire blight resistant
16		US 309		Communis	Fire blight resistant, dwarf
17	Xvii	Erabasma	1524.002	Communis hybrid	Psylla resistant
18	Xvi	P. communis ssp caucasica	680.001	Communis ssp caucasica	
19		P. communis ssp pyrastrer alb-2011-024	2965.001	Communis ssp pyrastrer	
20	V	NY 10353	1660.001	Communis x ussuriensis	Psylla resistant
21		NJ B9 R1 T117		Communis x ussuriensis	Psylla resistant
22	Xv	P. cordata Turkey	1589.001	Cordata	
23	Xviii	P. cossonii	828.001	Cossonii	
24	Xviii	P. elaeagnifolia	765.001	Elaeagnifolia	
25		P. fauriei	772.004	fauriei	
26	Xvi	P. gharbiana 1	787.001	Gharbiana	
27		P. glabra	1205.001	Glabra	
28	Xxi	P. hondoensis Japan	2117.001	Hondoensis	
29	Xx	P. koehnei	825.001	Koehnei	
30	Xx	P. mamorensis	835.001	Mamorensis	
31	Xvi	P. nivalis	256.002	Nivalis	
32	Xx	Naspati	411.001	Pashia	
33		P. pseudopashia	875.001	Pseudopashia	
34	I	Beurre bosc	1165.001	Communis	
35	Ix	Takisha	1675.003	Communis	
36		Dan bae	2623	Pyrifolia	
37		Nijisseiki	413.001	Pyrifolia	
38	Xviii	P. regelii	890.001	Regelii	
39		P. sachokiana GE-2006-115	2882.001	Sachokiana	
40	Vi	Ho mon	2723.001	Sinkiangensis	
41	Xix	P. amygdaliformis Turkey	634.001	Spinosa	
42	Xviii	P. cordata pure	745.001	Cordata	
43		Illinois 76		Ussuriensis (x pyrifolia?)	Fire blight resistant
44		Ya li	1678.001	X bretschneideri	



# Phase 3. Association of genotype to phenotype (UC Davis and ARS/Corvallis).



**Normal Tree Architecture**

**Normal Tree Architecture**

**Dwarf Tree**

**Dwarf Tree**



# Pear

## The Road to Marker Breeding

