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Overview

Fresh and processed products derived from the Rosaceae plant family (almonds, apples, apricots, blackberries, peaches, pears, plums, sweet cherries, tart cherries, strawberries, raspberries, roses and other ornamentals) make vital contributions to human nutrition, health and well-being, and collectively constitute the economic backbone of many rural economies across the U.S. Currently the domestic production value of rosaceous crops is over \$7 billion and global per-capita production and consumption of these crops is expanding in both domestic and export markets. However, these industries face numerous urgent and escalating challenges, including competition from lower-cost foreign producers, cost, quality, and availability of labor, water, and power, continual pest and disease pressures, and loss of effective agricultural inputs. These direct threats to our agricultural economy and national food security have reverberated within industry, government, and research communities. Grassroots efforts have culminated in regional and national meetings of industries, scientists, and government agencies to define strategic means to mitigate these increasing threats. These national initiatives, supported by Congress and coordinated by the USDA, have unanimously identified genomics, genetics and breeding as critical research priorities for the community. This document outlines the U.S. genomics, genetics and breeding initiative for rosaceous crops. Coordinated research in these areas will sustain the profitable, safe, and quality production of rosaceous crops in the U.S.

Key Issues for the U.S. Rosaceae Industry

Improve fresh and processed fruit quality, shelf life, and safety

Crop producers must fulfill the product and quality demands of the marketplace to be economically sustainable. Producers of rosaceous fruit, nut, and ornamental crops must not only obtain high yields, but simultaneously meet ever more rigorous quality standards: taste and sensory attributes like firmness, sweetness, juiciness, and aroma, flower, fruit, and nut size, internal and external color, and freedom from defects, pests, and pathogens. Achieving this difficult goal is frequently the difference between a profitable and a non-profitable harvest. A further challenge is to maintain quality following harvest while avoiding excessive aging or ripening, chilling injury disorders, decay, and chemical contamination. Increased consumption of rosaceous fruit and nut crops can contribute directly to improved public health. Rosaceous fruits and nuts are rich sources of vitamins, minerals, dietary fiber, antioxidants, and other nutrients that are important to human health. To compete in the marketplace and encourage more consumption, research must focus on maximizing and maintaining quality, and guaranteeing the consumer a safe product. Addressing these challenges requires an

expansion of the genomics, genetics, and germplasm knowledge base of rosaceous flower, fruit, and nut development, ripening, senescence, and microbial contamination and the translation of such knowledge to the improvement of these traits.

Reduce chemical pesticide use

Pests and diseases cause significant losses to U.S. growers of rosaceous crops and are commonly controlled with chemical pesticides. However, severe economic pressures, environmental regulations, and chemical resistance in pest organisms are forcing growers and researchers to identify new tactics to meet these challenges. Natural sources of resistance to major pests and diseases can be found within the largely untapped genetic resources of each crop. Exploitation of resistance genes introduced from crop relatives is a cost effective tactic that will reduce environmental and human health risks while safeguarding fruit yield and quality. A long-term commitment is necessary to characterize, maintain, and increase availability of these beneficial genetic resources. Concomitantly, new genomics approaches hold great promise to accelerate the pace and increase the efficiency of achieving this goal.

Decrease labor and energy costs of crop production

Labor is the largest cost category in the production of high quality fruit, nuts and ornamentals. Likewise, the rising cost of energy is increasing costs in all aspects of the fruit industry. These increases directly translate into higher consumer prices, present roadblocks to domestic and international shipment and export, and make the U.S. fruit industry vulnerable to competition from countries with relatively inexpensive production costs. To maintain global competitiveness, the U.S. industry must improve production efficiency. This can be achieved by employing improved varieties with growth and development characteristics suitable for mechanization in combination with the implementation of new technologies and production practices.

Develop stress tolerant plants

Rosaceous crops require resources (e.g. water, fertile land, freeze-free planting sites) that are becoming increasingly scarce or unavailable because of urban sprawl and environmental regulations. With the exception of some berries, fruit crop agriculture typically requires long-term investments in durable infrastructure such as orchards and irrigation systems. Similarly, the ornamental industry is heavily reliant on expensive greenhouse-based propagation systems. For the industry to improve its profitability, it must reduce losses due to environmental stresses on current sites and utilize marginal resources more efficiently. Improving plant cold and heat tolerance, salt tolerance, and water- and nutrient-efficiencies are critical to a profitable and sustainable future for the U.S. rosaceae industries.

Priorities to Address Key Issues

Define and exploit the Rosaceae genome

Comprehensive analyses of Rosaceae genomes combined with comparative and functional genomics will provide the basis for understanding the complex biological processes underlying the array of diverse and unique traits seen in this family. This initiative will maximize knowledge transferability among the breadth of rosaceous crops, while concurrently developing key crop-specific resources. Sequencing peach (*Prunus*) as a ‘reference’ species while concurrently obtaining skim sequence of strawberry (*Fragaria*) and apple (*Malus*) are high priorities. Sequencing will be followed by the development of resources and tools optimized for gene and regulatory element discovery, transcriptome analysis, and characterization of epigenetic influences. High-density genotyping and polymorphism discovery will accelerate forward genetic approaches and provide insight into genome evolution. Functional genomic approaches will exploit tractable systems and target physiological and developmental pathways contributing to key crop attributes. Collectively this approach will streamline discovery of beneficial genes, leading to sustained improvements in fruit quality and plant productivity throughout the range of rosaceous crops.

Enhance Rosaceae genomics database resources

A centralized and curated community database is critical to facilitate comparative research into Rosaceae genomics and genetics data. The current database, Genomics Database for the Rosaceae (GDR), serves as a communications hub for the community and incorporates much of the family’s publicly available structural and functional genomics knowledge. Although widely used, the database requires further improvements to enhance its utility to researchers. This will include expansion of its gene, allele, trait, map, marker, and segregation data sets as well as the addition of genome sequence and gene expression data. Improvement of integrated sequence analysis services and tools is necessary, together with significant expansion of the database’s educational and outreach roles. Long term enhancement and maintenance of this database is essential to translate the investment in genomics and genetics into rosaceous crop improvements.

Revitalize U.S. Rosaceae breeding programs

The goal of U.S. breeding programs for rosaceous crops is to increase industry profitability by providing new variety-based opportunities. For example, breeding programs are developing new varieties that mitigate critical pest and pathogen threats, meet marketplace fruit quality demands, and reduce the risk of floral freeze damage. Improving rosaceous crops, many of which take several years after crop establishment to initiate sustained production of flowers, fruit, and nuts, requires long-term investments, diverse genetic resources, and modern breeding technologies. However, due to limited resources, the U.S. breeding programs often operate inefficiently, below desired capacity, and are unable to adopt routine marker-assisted selection strategies that genomics and genetics research can provide. To meet the critical need for the accelerated development of improved varieties, Rosaceae breeding programs will require substantial resource increases, including the hiring of new Rosaceae plant breeders trained in modern technologies.

Strategic Planning Document

The United State Rosaceae Genomics, Genetics, and Breeding Initiative

Overview:

Fresh and processed products derived from the Rosaceae plant family (almonds, apples, apricots, blackberries, peaches, pears, plums, sweet cherries, tart cherries, strawberries, raspberries, roses and other ornamentals) make vital contributions to human nutrition, health and well-being, and collectively constitute the economic backbone of many rural economies across the U.S. Currently, the domestic production value of rosaceous crops is over \$7 billion and global per-capita production and consumption of these crops is expanding in both domestic and export markets. However, these industries face numerous urgent and escalating challenges, including competition from lower-cost foreign producers, cost, quality, and availability of labor, water, and power, continual pest and disease pressures, and loss of effective agricultural inputs. These direct threats to our agricultural economy and national food security have reverberated within industry, government, and research communities. Grassroots efforts have culminated in regional and national meetings of industries, scientists, and government agencies to define strategic means to mitigate these increasing threats. These national initiatives, supported by Congress and coordinated by the USDA, have unanimously identified genomics, genetics and breeding as critical research priorities for the community. This document outlines the U.S. genomics, genetics and breeding initiative for rosaceous crops. Coordinated research in these areas will sustain the profitable, safe, and quality production of Rosaceae crops in the U.S.

Key Issues for the U.S. Rosaceae Industry

- Improve fresh and processed fruit quality, shelf life, and safety
- Reduce chemical pesticide use
- Decrease labor and energy costs of crop production
- Develop stress tolerant plants

Priorities to Address Key Issues

- Define and exploit the Rosaceae genome
- Enhance Rosaceae genomics database resources
- Revitalize U.S. Rosaceae breeding programs

Introduction

Rosaceous crops are among America's most important food crops. These crops include almonds, apples, apricots, blackberries, peaches, pears, plums, sweet cherries, tart cherries, strawberries, raspberries, and roses. The aggregate wholesale value of food produced from these crops in the United States exceeded \$7 billion last year (NASS 2005). Additional value came from the nursery sales of these plants used for either food or ornamental purposes.

Many of these rosaceous crops contribute significantly to a healthy, diverse diet, and can help deter obesity and other health risks facing Americans. Consumption of fruits is associated with reduced risk of chronic diseases (WHO 2003; Casto et al. 2002; Ding et al. 2004), as well as the ability to reverse age-related disorders (Joseph et al. 1999). A recent international conference summarized the health role of the dietary polyphenols found in these crops (Scalbert et al. 2005).

The history of improved varieties and production practices for these crops is in large part American. Many of the varieties and much of the technology used to grow these crops worldwide has come from publicly and privately funded efforts in the U.S. Initially, American farmers played a major role in the development of this industry by discovering and developing many of the early important varieties. Examples are Jesse Hiatt's discovery of the 'Delicious' apple in 1868 in Iowa, Seth Lewelling's introduction of the 'Bing' cherry in 1865, and James Wilson's development of the 'Wilson' strawberry in New York State in the 1840's. In the twentieth century, public institutions developed many of the varieties now in use worldwide. Examples include thornless and trailing blackberries developed by the USDA-ARS, the 'Haven' series of peaches released by the Michigan Agricultural Experiment Station, the 'Jonagold' apple developed at the New York Agricultural Experiment Station, and an important series of strawberry varieties released by the University of California.

In contrast, the regions of natural origin of a majority of these crop species is outside the U.S. For example, the center of origin and diversity for *Malus* (apple), *Pyrus* (pear), and *Prunus* (peach and nectarine, apricot, sweet cherry, tart cherry, some plums and almond) species is in Europe and Asia. Exceptions include the cultivated strawberry, raspberry, blackberry, and some native plums.

The improvement of rosaceous crops in the U.S. is a joint effort between public institutions such as the USDA and the Land Grant Universities, and privately funded organizations such as commodity commissions and for-profit corporations. The public institutions have invested heavily in the past thirty years in new technologies such as molecular genetics, and in the preservation of America's valuable germplasm resources. Today the community has the opportunity to accelerate the pace of biological discovery and translate these advances into crop improvement.

The purpose of the U.S. Rosaceae Genomics, Genetics and Breeding Initiative is to chart a collective research strategy targeting the key issues critical for the sustainability and profitability of the U.S. Rosaceae industries. The ultimate goal is optimization of the integrated gene activities that direct plant and fruit growth and development. This understanding will allow us to select for desirable gene variants through breeding, manipulate gene expression using external stimuli, and monitor gene expression changes using sensor technology.

Key Issues for the U.S. Rosaceae Industry

Improve fresh and processed fruit quality, shelf life, and safety

Rosaceae fruit, nut, and flower quality has a major effect on public health, quality of life, and the viability of multi-billion dollar agricultural industries across the United States. Fruits and nuts are rich sources of vitamins, minerals, dietary fiber, antioxidants (such as carotenoids, anthocyanins, phenolic compounds, and ascorbic acid), and other phytonutrients that can lower the risk of heart disease, cancer, and a host of other illnesses. However, there is significant room for improvement in fruit and nut intake as a dietary component. Consumers demand a consistently high quality and safe product at a reasonable price, while industry profitability relies on high production volume for cost efficiency. Unfortunately, high quality and large quantity are generally not positively correlated. A viable, sustained Rosaceae industry therefore depends on two contrasting requirements: fruits, nuts and flowers must be efficiently produced in tremendous volume while simultaneously satisfying rigorous consumer expectations. Unlike for most field crops, fruit quality is often the single most important trait for breeders of fruit crops.

The Rosaceae industry and consumers are deprived of the full benefits of this plant family because of quality problems. The industry commonly falls short of providing consistently high quality products to the consumer. Quality can be divided into three main categories: sensory, nutritional, and processing. Sensory quality includes such attributes as appearance (e.g. skin, flesh, and petal color, size, shape, and soundness – incidence of physiological disorders), flavor (e.g. characteristic taste, sweetness, acidity, sugar-to-acid ratio, and aroma and scent), and texture (e.g. firmness, crunchiness, juiciness, lack of seediness, and fibrousness). Nutritional quality describes the content of various nutrients within fruit and nuts. Processing quality is the set of traits that determines amenability to postharvest handling (e.g. size and shape, thorniness, pubescence, bruising and browning potential, skin firmness, and presence of stem), processing (e.g. ease of skin, seed, or shell removal, and proportion of extractable juice to pulp), and suitability for adding value. Quality can be compromised if varieties with fruit quality flaws are grown, or when the genetic potential of varieties is not maximally expressed prior to or at harvest (e.g. when fruit are picked before full development). Growers face the challenge of ensuring the sensory, nutritional, and processing quality of their products is maximized for harvest. However, even under the best of growing conditions, most varieties do not possess the optimum combination of all necessary qualities.

Quality can also be lost after harvest before reaching the consumer, and after sale but before consumption (which reduces consumer satisfaction and future demand). Fresh market fruit in particular are highly perishable, and it is often difficult and costly to maintain sensory and nutritional quality until the product is consumed while avoiding excessive aging or ripening, chilling injury disorders, decay by pathogens, and chemical contamination. Shelf life of fruit, nuts, and flowers is prolonged to meet transport and market requirements, using techniques such as cold storage, modified atmosphere, and chemicals that disrupt the ripening process. However, these efforts may induce or

exacerbate many devastating physiological disorders in Rosaceae fruit, such as internal breakdown in stone fruits, surface pitting in cherries, fast deterioration in strawberries, and scald and watercore in pome fruits. Pests and diseases also attack rosaceous products, causing problems such as surface blemishes, internal defects, decay, and aflatoxin contamination. Fresh produce is becoming recognized in the U.S. as an important source of foodborne illness. The Rosaceae industry must ensure that fruit and nut products remain safe for human consumption, uncontaminated with toxins of applied or microbial origin. For example, the vast majority of fruit juices sold in the U.S. are pasteurized to kill potentially harmful bacteria during the manufacturing process.

Some progress has been made in understanding the biological and non-biological factors that affect various sensory, nutritional, and processing qualities of fruits, nuts and flowers. Cultural practices for ameliorating these problems have been extensively researched. However, these methods often add further costs to production, limiting industry profitability and/or increasing costs for the consumer.

Attempts to seek long-term solutions through understanding the genetic control of fruit, nut, and flower quality have so far produced promising results. In peach, apple, cherry, almond, strawberry, pear, rose, and raspberry, genetic linkage maps have been constructed with the goal to identify the genomic regions controlling fruit size, sugar and acid production, pubescence, firmness, resistance to cold storage disorders, resistance to microbial attack, fruit flesh and skin color, and thorniness,. Plans for studying the genes controlling other quality traits, such as flavor and antioxidant capacity, are underway. Extensive databases of expressed genes in Rosaceae fruit and nuts have been developed with the primary purpose of identifying important quality trait genes. From efforts such as these, a few genes have already been identified and isolated that affect certain important quality traits in apple, peach, and strawberry. However, little of the information gained from these studies has yet to be extensively applied in breeding programs that influence the industry. This is in contrast to tomato, where revolutionary genomics and genetics research of the past several decades of this model fruit species has helped shape the varieties used in the industry grown today. Large genetic variation for almost every quality trait in available Rosaceae fruit germplasm signifies enormous potential for further genetic improvement. The overwhelming majority of useful genes that could be manipulated for improving and maintaining quality in Rosaceae remain uncharacterized.

Long-term improvement and maintenance of quality, shelf life, and safety requires an expansion of the genomics and genetics knowledge base of Rosaceae, and the translation of such knowledge to developing new varieties and new treatments. Understanding the genetic control of biochemical pathways underlying fruit development, ripening, and senescence, can greatly expedite the breeding of new varieties or developing cultural practice innovations that will increase quality when products are harvested and that will maintain that quality after harvest until consumption. Such targeted genetic improvement can improve the potential of varieties to reach superior quality standards, with better appearance, flavor, texture, and ease of processing and handling, or with novel and unique quality attributes. For better quality maintenance, varieties with an increased window of maximal quality are required, achievable through the ability to withstand cold storage, with resistance to physiological disorders, and with delayed and inducible ripening. For avoiding pest and disease problems and improving

safety, understanding the molecular genetics of plant-pathogen interactions will enable the design of safe pathogen elimination practices or development of resistant varieties.

Reduce dependence on chemical control

Rosaceous crops are susceptible to a myriad of diseases and insects that are commonly controlled with chemical pesticides. Diseases include those caused by groups of pathogenic fungi, bacteria, viruses, and phytoplasmas. Some of these diseases attack various groups of crops causing devastating economic losses. Examples include established diseases such as fire blight, caused by the bacterium *Erwinia amylovora*, that attacks pears, apples, quince, mountain ash, spirea, hawthorn, pyracantha, cotoneaster, and many other Rosaceae species, and emerging diseases such as Sharka, caused by an insect transmitted virus (*Plum pox virus* [PPV]) and whose hosts include all of the most important *Prunus* species. Control measures for such diseases are costly, laborious, and quite often remain ineffective. The development of disease resistance varieties has to date been limited due to various intrinsic factors of rosaceous crop species such as long generation times and complex polyploid genomes.

Insects attacking crops, such as apple, pear, and peach, include codling moth, pear psylla, and peach tree borer, respectively, cause extensive economic damage to these crops if they are not controlled through various measures including pesticide sprays. However, government mandated and anticipated restrictions on broad-spectrum pesticides are forcing growers to find new cost-effective tactics that pose reduced risk to both the environment and human health, but safeguard fruit yield and quality (Cooley and Autio 1997; Warner 2000).

The loss of chemical control measures and the increasing demand for cultivation practices that reduce risks to human health and the environment are putting pressure on the industry to develop alternative management strategies that will increasingly rely on the utilization of genetically resistant materials. At present, for most rosaceous crops, sources of resistance to the worst pests and diseases are underutilized.

Integrated genomics-genetics research offers new opportunities to enhance and characterize germplasm and streamline the incorporation of resistance genes into commercial cultivars and identifying new sources of resistance. In addition, transgenic technologies augmenting natural plant protection systems have shown promise as seen in the case of coat protein mediated resistance to PPV in C5 plum (Scorza et al. 2001) and coat and protein mediated resistance to *Raspberry bushy dwarf virus* in 'Meeker' red raspberry. The development of fruit, nut, and ornamental cultivars that are resistant to established and emerging diseases and pests is an important part of ensuring the future sustainability and security of U.S. Rosaceae industries.

Decrease labor and energy costs of crop production

Labor is the major cost in producing high quality fruit in rosaceous crops, primarily due to the necessity of hand harvesting and pruning for many of these crops. In addition, rising energy prices are rapidly elevating production costs. The rising costs of labor and energy are also the elements that make the U.S. fruit industry more vulnerable to competition posed by countries where these costs are comparatively low. The U.S. fruit

industry needs to improve the efficiencies of labor and energy use to maintain global competitiveness. Research and development of new technologies for fruit production are needed. These labor and energy efficiencies can be achieved in part through the development of improved cultivars adapted to mechanized harvesting and requiring less cultural inputs such as pruning. In addition, new cultural practices based on knowledge of genetic mechanisms underlying important physiological plant processes (e.g. sprays for uniform maturation of berries for single harvest) would also dramatically reduce labor and energy costs. An integrated genomics-mechanization research approach is needed for rosaceous crops to develop new fruit and rootstock cultivars that will be amenable to efficient production strategies that reduce labor and energy costs, thus enabling U.S. growers to remain competitive on global markets.

Some of the most important characters for optimizing fruit production efficiency are governed by genes that control the growth and development of the plant. For example, traits affecting plant architecture and size strongly influence the suitability of varieties for mechanization and high-density plantings. The genetic factors that influence uniform ripening and removal from the plant (abscission) are also of importance. Synchronized flowering of all plants within a field brings fruit to maturation in a single time frame, requiring only a single harvest. Thus, a fundamental understanding of the genes controlling such traits and effective technologies to manipulate them is tantamount to the sustainability and expansion of fruit crop plantings and the adoption of new planting strategies designed to promote or enhance productivity on limited space.

Develop stress tolerant plants

Rosaceous crops are an important part of regional economies throughout the U.S. and are dependent on several resources, some of which are increasingly scarce or unavailable (fertile land, water, fumigants, etc.) because of urban sprawl and environmental regulations. For the associated industries to maintain (if not improve) profitability, they must exploit marginal resources more efficiently. Research into developing drought tolerant, cold tolerant, and water- and nutrient-efficient varieties is critical.

Many environmental factors have an impact on yield and fruit quality for various members of the Rosaceae. Drought, heat, cold, and soil salinity are widely recognized as having the biggest effect, although flooding, sunburn, and air pollution are also problems for fruit growers. Fruit trees or perennial plants such as strawberries, raspberries and blackberries may be more or less susceptible to drought, temperature, and soil salinity at different stages in their developmental cycles. In certain crops, elevated temperatures can be particularly detrimental during flowering or the final stages of fruit ripening.

Drought tolerant varieties would allow for more efficient land and water usage, thus enabling the cultivation of marginal lands. In addition, more efficient plants would require less fertilizer or planting treatments and less land to maintain production volume. With the exception of strawberries and some ornamentals, the water, nutrient and space requirements along with physical characters of some rosaceous crops necessitate long-term investments in permanent infrastructures (e.g. orchards and irrigation systems). The development of varieties that require fewer infrastructures for their cultivation would ultimately decrease dependence on large initial investments and increase industry profitability. Increased concerted research in genomics of plant nutrition and tolerance to

water deficiency is required for the development of these superior genotypes and systems.

Additionally, as most rosaceous plants are perennial, characters such as winter dormancy, chilling requirement, flower bud cold hardiness, and bloom characteristics affect greatly the environmental ranges where many commercial flower, fruit, and nuts varieties can be productively grown, and so these characters are targets for genetic manipulation and gene discovery. The ability to expand production of superior varieties to new environments represents one of the major challenges of breeding programs and an important focus for genomic investigation.

Through the identification and isolation of genes controlling important growth traits, direct manipulation of these genes could be used to enhance or modulate the growth characteristics of the plants, to optimize productivity under particular growth conditions in various environments.

Priorities to Address Key Issues

Define and exploit the Rosaceae genome

Rosaceous crops represent species from multiple diverse lineages: Amygdaloideae (*Prunus*), Rosoideae (*Fragaria*, *Rosa*, *Rubus*), and Maloideae (*Malus*, *Pyrus*). This initiative will provide maximal knowledge transferability among the breadth of rosaceous crops, while concurrently developing key crop-specific resources. Sequencing peach (*Prunus*) as a ‘reference’ species while concurrently obtaining skim sequences of strawberry (*Fragaria*) and apple (*Malus*) are high priorities. Sequencing will be followed by the development of resources and tools optimized for gene and *cis*-element discovery, transcriptome analysis, and characterization of epigenetic influences. High-density genotyping and polymorphism discovery will accelerate forward genetic approaches and provide insight into genome evolution. Functional genomics approaches will exploit tractable systems and target physiological and developmental pathways contributing to key crop attributes. Collectively this approach will streamline discovery of beneficial genes, leading to sustained improvements in fruit quality and plant productivity throughout the range of rosaceous crops.

Evolutionary relationships

Rosaceae are traditionally divided into four subfamilies based on fruit type (e.g., Schulze-Menz 1964). In this classification, members of Rosoideae, which includes roses, strawberries, blackberries and raspberries, produce indehiscent one-seeded fruits; members of Spiraeoideae, which includes a number of ornamental shrubs generally bear dry dehiscent fruits; members of Amygdaloideae, which include cherries, almonds, peaches, plums, and apricots, produce fleshy one-seeded fruits with a hard inner layer around the seed (and so are commonly called stone fruit); and members of Maloideae bear a specialized fleshy fruit type known as a pome, of which apples and pears are familiar examples. Other morphological, chemical, and ecological features are largely, but not perfectly correlated with traditional subfamilial circumscriptions. Recent

phylogenetic analyses (Morgan et al. 1994; Evans et al. 2000; Potter et al. 2002) based on DNA sequences, however, suggest that this classification does not adequately reflect evolutionary relationships in the family (Fig. 1) and, as a result, a new phylogenetically based classification has been developed (Potter et al. submitted), in which only three subfamilies, with further divisions into supertribes, tribes, and subtribes, will be recognized.

Although the four subfamily system has not been supported by recent molecular phylogenetic analyses, it remains true that important crop plant species are found throughout the family in several distinct evolutionary lineages (Fig. 1). The results of molecular phylogenetic analyses, combined with traditional taxonomy, suggest that a selection of species that represent the evolutionary diversity of Rosaceae would include at least one member of each of the following groups (Fig. 1): (1) *Rosoideae sensu stricto*: *Fragaria*, *Rosa*, and *Rubus* are all possibilities; including *Rubus* plus one of the other two would ensure sampling of broad diversity within this group (Eriksson et al. 1998); (2) *Prunus*: sampling a cherry and/or a laurel-cherry species as well as peach, almond, apricot, or plum would ensure sampling of broad diversity here (Bortiri et al. 2001); (3) the former *Maloideae*: e.g., *Malus* or *Pyrus*; (4) one or more of the “Spiraeoid” lineages: each of the following genera belongs to a different lineage and includes one or more important ornamental species: *Spiraea*, *Kerria*, *Neillia*, *Exochorda*, *Sorbaria*; (5) the actinorhizal clade, whose members form symbiotic relationships with nitrogen-fixing actinomycete bacteria of the genus *Frankia*: inclusion of a representative from this group would be of great interest, given the ecological significance of symbiotic nitrogen fixation.

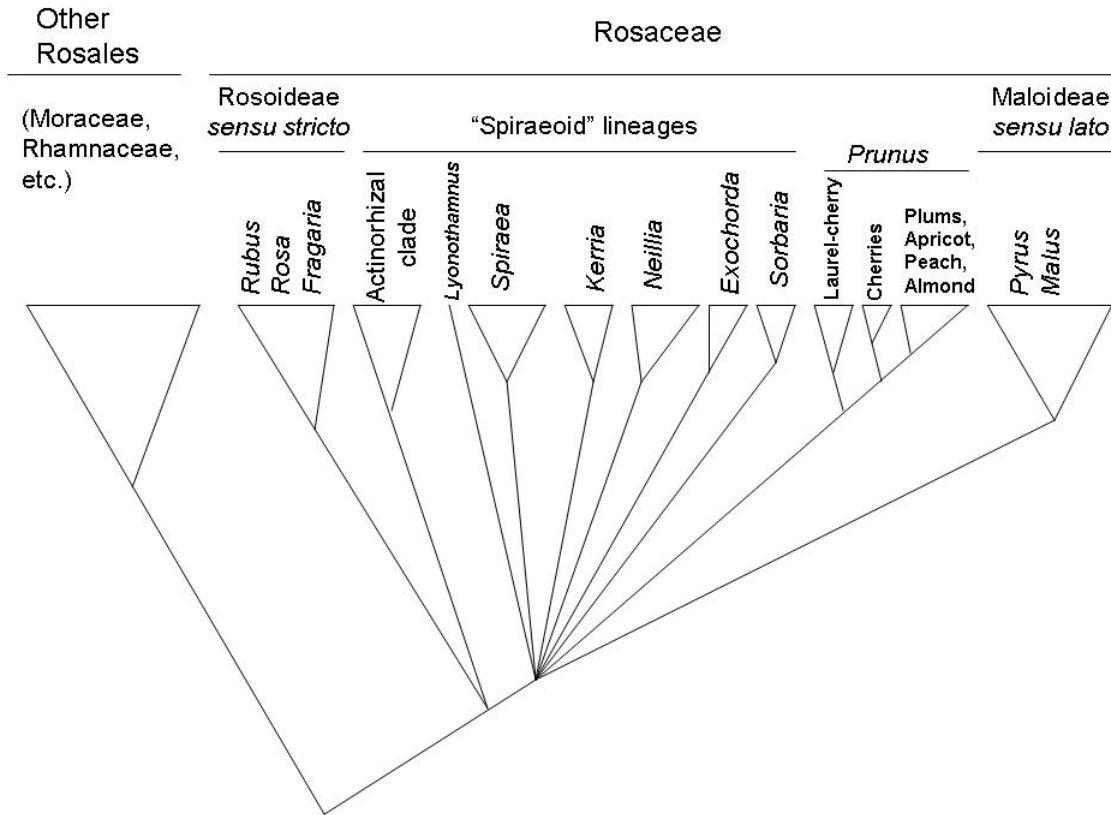


Figure 1. The Rosaceae lineages (courtesy of Dan Potter)

Structural Genomics

Structural genomics addresses the physical structure and organization of the genome describing absolute and relative locations of genes and other functional elements within the DNA, identifying polymorphic molecular features, and ultimately defining the complete DNA sequence of an organism. The most basic structural description of a genome is the haploid chromosome number. Among the rosaceous crop species, the number of chromosomes in a basic genomic set is either $x = 7$ (strawberry, blackberry, raspberry, rose), $x = 8$ (peach, plum, almond, apricot, cherry), or $x = 17$ (pear, apple). Some of these genera contain polyploid members with elevated chromosome numbers due to the presence of multiple (more than two) chromosome sets. The octoploid ($2n = 8x = 56$) genome composition of the cultivated strawberry (*Fragaria × ananassa*) accounts for the choice of diploid ($2n = 2x = 14$) *F. vesca* as a model species for strawberry genomics.

One of the next levels of complexity is the genetic linkage map. Genetic linkage map construction is a prerequisite and complement to genomics, and constitutes the indispensable channel through which genomic information is translated into molecular tools for marker-assisted selection in plant breeding. Genetic linkage maps, with varying degrees of resolution, have been constructed for many rosaceous crops. A priority for the Rosaceae community is to assess the extent of synteny among species and genera. A high

level of co-linearity will enhance the opportunity for transfer of genetic linkage information from one species to another. Therefore, it is of utmost importance to develop well-conserved, gene-based markers that can serve as transferable anchor loci for comparative mapping purposes in all the Rosaceae genera.

Unlike a linkage map where distance is measured in cM, the unit of measurement in a physical map is base pairs. Peach is the only Rosaceae species for which a physical map is currently available. The existing peach physical map which is projected to be complete by fall 2006, currently covers over 65% of the peach genome in ~1,200 contigs. This physical map is anchored on the *Prunus* general genetic linkage map (the current standard for the international community) and has over 3,000 EST locations, and locations for most of the *Prunus* genetically mapped anchor markers.

The ultimate structural genomic description of an organism is its completely assembled DNA sequence, supplemented by thorough sequence annotation to specify the locations and functions of its myriad features. For purposes of genomic research, small genome size is a highly favorable feature of the Rosaceae family. Genome size (C value) is expressed in units of Mb (millions of bases pairs, or megabase pairs, where 1 million bases pairs = 1 Mb). Genome sizes for representative members of the family include the diploid strawberry, *Fragaria vesca* (200 Mb), peach (270 Mb), raspberry (294 Mb), pear (539 Mb), and apple (750 Mb). For comparison, C values for other crop and model plant species that have been sequenced or selected for sequencing include *Arabidopsis thaliana* (164 Mb), rice (430 Mb), *Medicago truncatula* (466 Mb), poplar (480 Mb), and soybean (1,100 Mb). Illustrating the advantage of small genome size, the complete sequencing of the strawberry, peach, and apple genomes *combined* (a total of 1,220 Mb) would require a resource allocation only 10% greater than that committed to soybean alone, the second species of the legume family to be chosen by the DOE Community Sequencing Project for sequencing.

The initial sequencing and annotation of a Rosaceae "reference genome" is a top priority of the Rosaceae genomics community. Initial sequencing will be of peach as (1) it represents Prunoidae and as such plays a very important comparative genomics role for the genus, (2) it has the most highly characterized genome of the family with an extensive highly saturated marker map (less than 1 centimorgan (cM) per marker and a largest gap of 7cM) comprised of RFLPs, SSRs, ESTs, and STSs, positioned on eight linkage groups, and (3) a physical map is projected to be complete in fall 2006. The availability of the linkage and physical maps is critical as these can be used to position sequence contigs during final assembly. Unfortunately, the state of the art for other species in the Rosaceae family lags well behind that of the peach, and the community is currently addressing this for apple and strawberry, as these genomes are equally important targets for sequencing.

Understanding the structural similarities and differences among genomes of Rosaceae species will allow the knowledge gained in one species to advance discovery in other Rosaceae species. Low-resolution comparisons of gene order and distance achieved by linkage mapping using common marker loci allows the identification of highly or poorly conserved genomic regions. Molecular dissection of conserved regions will likely uncover genetic associations involving important traits; thereby identifying genomic regions important for molecular breeding. This information will significantly accelerate progress in less characterized Rosaceae species by facilitating linkage mapping and gene

identification and isolation. Rosaceae species with well-characterized small genomes will have a central role as reference genomes in comparative analyses.

Short Term Objectives

1. Facilitate comparative mapping with the placement of common ESTs, SSRs and other portable sequences on high-density linkage maps and physical maps of multiple Rosaceae species.
2. Continue the development of physical maps for key family members as tools for gene identification, candidate gene analyses, gene tagging, and as a starting point for genome sequencing.
3. Sequence the peach genome as an initial reference species for comparative genomic analyses and to facilitate sequence assembly in future Rosaceae genome sequencing projects. Concurrently obtain skim sequence coverage for both *Fragaria* and *Malus*. This will give sufficient information to identify specific regions of the *Fragaria* and *Malus* genomes for targeted complete sequencing, and to prioritize future whole genome sequencing efforts.
4. Perform high-resolution comparative sequence analyses in targeted regions of key species from different genera to determine the level of genome preservation and provide a blueprint for strategic planning of genome wide sequencing efforts.

Long term objective

Using the initial reference genome as a basis for comparison, sequence and annotate at least one genome representing each of the other two species groups. As noted under the systematics section, the three species groups are Amygdaloideae (*Prunus*), Rosoideae (*Fragaria*, *Rosa*, *Rubus*), and Maloideae (*Malus*, *Pyrus*).

Gene function determination

Functional genomics is the development and application of global (genome-wide or system-wide) experimental approaches to assess gene function by making use of the information and physical resources provided by structural genomics efforts. It is characterized by high throughput or large-scale experimental methodologies combined with statistical and computational analysis of the results. This expands the scope of biological investigations from studying single genes or proteins to studying large groups of genes or proteins at once in a systematic fashion. Functional genomics narrows the gap between sequence and function and yields new insights into the behavior of biological systems.

In many respects, the advent of functional genomics approaches has changed the way we do biology. Traditional disciplines may now adopt a genome-scale viewpoint when it comes to approaching research problems. This does not replace genetics, biochemistry, cell biology, and structural studies in gaining a detailed understanding of

biological mechanisms, but functional genomics can provide a framework for such analyses. Functional genomics tools speed gene discovery and provide methodologies to decipher the complex regulation of interactive gene networks linking genes and phenotypes.

In most organisms, even those with fully sequenced genomes, up to 40% of the genes (open reading frames), may have no known function at the biochemical level and are unrelated to any known gene. And, in terms of their effects on phenotype (appearance and function), the proportion of genes with known properties is much less. Given that plant genomes contain between twenty and forty thousand genes or more, functional genomic approaches offer significant advantages. Functional genomics technologies depend on both experimental and computational methods. These technologies generate data on global gene and protein expression, protein structure, protein-protein interactions, global metabolic status, etc., and these in turn require powerful information systems to manage the data, compile and integrate the information and establish new 'computer assisted experimental strategies'.

Other functional genomics procedures directly assess the phenotypic effects associated with individual or groups of genes. Many of these are high throughput or scaled up adaptations of older technology and include analysis of phenotypic changes resulting from mutagenesis and gene disruption. Gene disruption is a key tool in gene/trait validation where a loss-of-function mutant is used to validate the function of a gene. The production of specific gene knockouts using gene silencing approaches will be particularly helpful involving the full range of approaches, including sense induced co-suppression and virus induced gene silencing [VIGS or post transcriptional gene silencing (PTGS)] mediated by self-complementary RNA. Another approach to validation is expression in a heterologous system using plant transformation, where a gain-of-function can be used to validate the function of a gene of interest. To take full advantage of these approaches, transformation protocols will need to be developed or made more efficient for a range of Rosaceae species.

Functional genomics approaches have been developed and are in use for model plant systems such as *Arabidopsis*, rice, and tomato. The data being generated from these studies are rapidly expanding our knowledge of basic plant functions. Moreover, hundreds if not thousands of genes with potential applications to genetic improvement of diverse crop species have been identified. To take full advantage of the work conducted in model plant systems, the Rosaceae community must develop similar high-throughput approaches to test and confirm the functions of target genes (such as model species homologues) in their respective species.

The foundation of functional genomics is built on gene sequence repositories, thus a central goal of the consortium is to develop and utilize gene sequence repositories for the Rosaceae crops. We are promoting the creation of unigene sets of ESTs from a variety of important tissues in a number of important representative species. These ESTs serve as the substrate for genome wide gene expression analyses, gene candidates, and SNP mapping resources. In addition, having a highly characterized genetically mapped EST database for important species provides a framework for linking genes to important traits. This framework consists of mapping probes for use in other Rosaceae species mapping efforts, robust marker map development, and enabling comparative mapping approaches for gene identification studies.

Proteomics is a part of functional genomics (Hector and Boguski, 1997), specifically the effort to establish the identities, quantities, structures, and biochemical and cellular functions of all proteins in an organism, organ, or organelle, and how these properties vary in space, time, or physiological state. Just as the genome describes the genetic content of an organism, a proteome defines the protein complement of the genome. Proteomics includes the identification of proteins in biological tissues, the characterization of their physiochemical properties (complete sequence, post-translational modifications), and the description of their behavior (function, expression level). Proteomics is a combination of genetics, bioinformatics, biochemistry, and separation science.

A large-scale proteomics effort has been described as orders of magnitude more complicated and difficult than the sequencing of the human genome, because the proteome is far more complex than the genome. After processing and modifications, a single gene may express between one and a few dozen different protein products; by extrapolation, the approximately 50,000 human genes could produce over 500,000 different proteins, and similar numbers are likely for other organisms. Another complication is that a combination of technologies is required to characterize a proteome fully. A standard procedure, following protein extraction, is two-dimensional gel electrophoresis (2-DE) as the separation method, followed by mass spectrometry (MS) analysis of the separated and enzymatically digested and fragmented proteins. The results, peptide mass fingerprints, typically obtained using highly specialized mass spectrometers, are matched against sequence databases using dedicated bioinformatics tools. The whole procedure can be automated for high throughput purposes, but a huge amount of data results and even with the best bioinformatic computer tools, the techniques are at present only really applicable to fractions of cells, e.g., organelles and membranes, or similar partially purified preparations. At this time, whole tissues and organs are far too complex. Even so, the huge amounts of data generated have to be stored in specific databases, which can then be searched for pattern-matching recognition, characterization or functional relevance studies.

Despite the difficulties, several types of experiments are now possible. Minute quantities of proteins can be identified (from gels or from purified solutions). Protein mining involves identifying as many proteins as possible in a sample rather than making inferences from gene expression (arrays and chips). Protein profiling can assess differences in protein expression between two or more samples, with or without relative quantitation. Post-translational protein modifications and post-translational regulation can be analyzed, providing direct knowledge of proteins and their higher-order associations in contrast to less direct inferences about proteome composition drawn from RNA measurements (as in microarrays). In cells, proteins do not act in isolation, but usually form transitory or stable complexes in order to participate in pathways and act in networks. Protein interaction analyses allow insight into these essential aspects of the normal workings of the cell.

Longer term, but even in the near term, these technologies will allow more efficient breeding for improvements in rosaceous crop quality and yields. There will be better understanding of disease and pest resistance and environmental stress tolerance mechanisms, and as a consequence, development of new varieties that require fewer chemical inputs and controls. All of these will ultimately improve grower returns.

Short Term Objectives

1. Increase the range of tissue types used for EST discovery.
2. Within rosaceous crop species, use diverse genotypes to expand EST allelic diversity to accelerate SNP discovery.
3. Develop microarray platforms to study global gene expression utilizing the EST resources.
4. Improve regeneration and transformation for Rosaceae species, including the identification of efficient vectors and methods for enhancing and silencing gene expression.

Long term objective

Determine the function of genes controlling horticulturally important traits with the ultimate goal of optimizing the integrated gene activities that direct plant and fruit growth and development. This understanding will allow us to select for desirable gene variants through breeding, and ultimately manipulate gene expression using external stimuli, and monitor gene expression and protein changes using sensor technology.

Enhance Rosaceae genomics database resources

The NSF Plant Genome Program funded the Rosaceae Genome Database (GDR) in September 2003, recognizing the fundamental contribution of community databases to successful plant comparative genomics efforts as evidenced through projects such as Gramene, (<http://www.gramene.org>) for the grasses, the Solanaceae Genomics Network (<http://www.sgn.cornell.edu>), The Legume Information System (<http://www.comparative-legumes.org/>), and the Arabidopsis Information Resource (<http://www.arabidopsis.org/>). Initiated at Clemson University in response to the development of structural and functional genomic resources for peach, GDR has since grown to encompass all published structural and functional genomics data for the family.

The GDR database (<http://www.rosaceae.org>) contains comprehensive data for the genetically anchored peach physical map, Rosaceae maps, and markers and annotated databases of all publicly available Rosaceae ESTs. An integrated map viewer developed in-house, provides a graphical interface to the genetic, transcriptome, and physical mapping data. Mapped ESTs, BACs, and markers can be queried by multiple categories and the search result sites are linked to the integrated map viewer or the WebFPC physical map sites. Nineteen genetic maps (3 *Prunus*, 4 peach, 2 almond, 1 strawberry, 7 apple, and 2 sour cherry) are available in CMap for cross species comparisons, and the major genes affecting agronomic traits are now anchored to the *Prunus* general map TxE, and can be viewed in CMap. Other available web tools provide standalone batch analysis functionality for users. These include a BLAST and FASTA server, a CAP3 assembly server, a combined SSR and Primer3 server, and web service access to InterProScan for

sequence comparison with protein families, domains and functional sites. In addition, GDR provides access to Rosaceae publications and all community-based news including conferences, meetings, White papers, and executive committee reports.

As part of the tool development component, GDR provides researchers with access to a gene fragment analysis pipeline providing a suite of services ranging from trace file processing to full unigene development. Genus-specific unigene datasets for *Malus*, *Prunus*, *Rosa* and *Fragaria*, as well as a family-wide unigene set, have been generated by assembling all the publicly available gene fragments. Researchers can search these data sets for genes of interest by taxonomy, tissue type, homology, match organism, or match description.

The GDR team also provides free EST processing services to the community, and to date have processed datasets for individual researchers working on peach, almond, rose, strawberry, and blackberry. When investigators wish to make their data publicly available, the files are made live on the website and the new data is publicized on the website home page and through quarterly newsletters to the GDR community.

Since its inception, the use of GDR by the community has been phenomenal and in 2005 it received 24,124 visits, which represents just over half the number received by Gramene over the same time period (48,187 visits, <http://www.gramene.org/wusage/annual/2005/01/01/index.html>). This is a substantial figure for GDR given the disparate sizes of our audiences. This success may be partially attributed to GDR's role as communication hub for a close-knit community, who not only share and download data but also use the website as an information portal for executive committees, conferences, White papers, funding news, contact information and publications. Registered members of the GDR listserv also receive quarterly newsletters highlighting new data, information, and tools.

With continued funding, this information and data mining resource will be expanded to accommodate newly-generated data and develop sequence analysis pipelines and services in anticipation of the next round of data acquisition, namely microarray analysis and genomic sequence annotation. Extending the role of GDR as data curators and facilitators to another level, we propose to develop and test a standardized but flexible microarray platform for Rosaceae. If we do this as a community, we should be able to overcome many of the problems that other plant groups faced with lack of interoperability between arrays, and therefore, will significantly reduce the time for gene discovery to crop improvement. The final component of this phased expansion will be the significant extension of GDR's role as an information portal for all levels of users with an interest in rosaceous crops, including the public, producers/growers, government personnel and scientists.

Objectives

1. Develop additional database modules (protein, genomic sequence, ontology, gene, polymorphism/allele, QTL, microarray) to facilitate the comprehensive collection and integration of Rosaceae genetics and genomics data.
2. Develop comprehensive microarray and sequence analysis services resources for rosaceous researchers.

3. Add advanced species specific and integrated query and report tools to facilitate improved access to component datasets.
4. Develop a rosaceous genome annotation pipeline and implement genome and synteny browsers.
5. Integrate GDR with other web resources and databases using web services technology.
6. Significantly expand GDR's educational and outreach role.

Revitalize U.S. Rosaceae breeding programs

The goal of U.S. breeding programs for rosaceous crops is to increase industry profitability by providing new variety-based opportunities. Towards this goal, breeders are addressing the vast majority of useful traits identified in the section 'Key Issues'. However, breeders of rosaceous crops face numerous challenges that are not present in agronomic and vegetable crops. Many of these challenges could be mitigated if breeders had improved genetic and genomic knowledge of their crop.

Many of the rosaceous crops such as apple, pear, and sweet cherry, have a long generation time with three to as many as eight years required before a seedling starts to fruit. One approach to reducing the juvenility time is to bud each seedling on a rootstock that induces early flowering. However, this approach is almost always prohibitively expensive to screen a typical breeding population. If the breeder were able to implement marker-assisted selection to significantly narrow down the number of seedlings that need to be evaluated, the breeder would more likely be able to afford the remaining propagation cost. For example, in apple, using precocious rootstocks, this approach would double the number of generations possible within a ten year time frame.

Breeding populations for rosaceous tree crops require extensive field space and the associated cultural inputs. Implementation of marker-assisted selection at the seedling stage would minimize that challenge by significantly reducing the number of individuals for field testing. The large amount of field space required to maintain tree populations also negatively impacts genetic discovery. Often, tree breeders do not have the resources required to grow and maintain the large seedling populations needed for genetic studies. As a result, there are relatively few segregating populations of sufficient size (over 300 individuals) for QTL analyses.

Many rosaceous crop plants have a genomic complexity that makes it difficult to determine the genetic control of traits of interest and identify useful allelic variants. Most notably, cultivated strawberry is an octoploid with four heterozygous genomes. Although diploid strawberry species such as *Fragaria vesca* provide useful model systems for strawberry genetics and genomics, cultivated octoploid plant material must ultimately be elucidated. Blackberries represent another complex ploidy series, with the ploidy of interspecific varieties ranging from 4x, 6x, 7x, 8x, 9x, 10x to 12x and even some aneuploid varieties. Within *Prunus*, tart cherry is an example of a segmental allotetraploid where both disomic and tetrasomic segregation patterns in the same individual make determining the inheritance of even simple traits challenging. High

resolution linkage maps, constructed from diploid relatives of these complex polyploids, would provide critical linkage information that would dramatically increase the efficiency of identifying QTL and associated markers in higher ploidy populations.

For many of the rosaceous tree crops, the commercial variety is a “compound system” of a scion grafted onto a rootstock. Interactions may occur between these system components. For example, certain apple and cherry rootstocks positively affect scion phenotype by reducing the number of years to bearing and increasing the density of flowering spurs. However, this compound system further increases the complexity of predicting a variety-rootstock phenotype, as little is known about how rootstock-scion “cross-talk” changes scion performance. A functional understanding of this “cross-talk” would allow for more directed rootstock breeding efforts and scion-rootstock pairings.

All of the plant populations used in linkage and QTL studies in rosaceous crops are segregating populations of F₁, F₂, F₃ or BC generations. Unlike other crop species, where recombinant inbred lines (RILs) provide powerful statistical advantages to QTL studies and map-based cloning, no RIL populations are currently available in rosaceous crops. Many factors contribute to this. The long generation time required to advance at least six generations could take as long as 25 years in some crops. Most of the Rosaceae species suffer at least some degree of inbreeding depression. Many of these crops are also obligate outcrossers and self-pollination is not possible due to gametophytic self-incompatibility. The lack of homozygous genetic stocks means that all plant populations used for genetic analyses must be maintained as vegetatively propagated clonal individuals, often in vulnerable field plots. There is a need for breeders and geneticists to work together to overcome these obstacles and develop genetic populations that will accelerate scientific discovery and be available for evaluation by others.

Fruit from Rosaceae species must meet rigorous quality standards to assure profitable production and a high per capita consumption. Therefore any fruit variety will be unsuccessful if there is a flaw in product quality. One of the most damaging flaws is reduced fruit size, which results in an automatic reduction in grower price. Therefore, to broaden the germplasm base and ultimately introgress desirable traits such as disease or insect resistance, fruit breeders are reluctant to use wild species that almost exclusively have small fruit size. Using conventional breeding methods with wild species would require too many years to recover a marketable fruit type for rosaceous crops. As a result, the variety profile and germplasm base of many rosaceous crop plants is extremely narrow, and only a limited number of varieties with disease resistance introgressed from wild species have been released. In pear, approximately 50% of commercial production in the U.S. is accounted for by a single cultivar. The 100 year-old sweet cherry cultivar ‘Bing’ dominates sweet cherry production in the Pacific Northwest. The tart cherry industry in the U.S. is almost exclusively a monoculture of the 400-year-old variety ‘Montmorency’. Unfortunately the vulnerability of the ‘Montmorency’ monoculture was dramatically realized in 2002. Spring freeze damage reduced tart cherry production to the lowest level recorded since 1945 (2% of a normal crop) with a devastating effect on the industry and economies of the fruit-growing regions.

Natural sources of resistance to major pest, disease, and abiotic stresses can be found within largely untapped genetic resources. The USDA-ARS National Plant Germplasm System (NPGS) clonal repositories maintain extensive diverse germplasm that includes historic varieties, relatively undomesticated plants, landrace varieties, and

wild species (Appendix 2). These collections include individuals with desirable traits that are important for crop improvement. For example, the apple collection has individuals with resistance to fireblight and applescab and the pear collection has individuals with resistance to fireblight, pear psylla, *Fabraea* leaf spot, and pear scab. The *Prunus* collection has desirable individuals that include high sugar content apricots, dark fleshed peaches, low chill peaches, and stoneless plums. The *Fragaria* collection includes individuals valued for day neutrality and resistance to anthracnose and verticillium wilt diseases. The *Rubus* collection has sources of phytophthora root rot resistance.

Genomic analyses of plant material within the NPGS collections have great potential for fueling genetic advances in Rosaceae breeding programs. For example, mining for useful alleles can be facilitated by using panels of individuals genetically determined to represent the diversity of lineages within a larger collection. Additionally, a genetic description of population structure can provide the pedigree and genetic differentiation values critical in associative genetic studies. Making use of this recombinant diversity will aid in the discovery of desirable gene variants.

It is recognized that many landraces and wild individuals exhibit desirable traits along with undesirable characteristics. Inclusion of wild individuals in breeding populations becomes significantly more efficient with the use of marker-assisted backcrossing, where desirable traits can be teased apart from undesirable ones. If molecular markers were available for desirable fruit size and quality alleles, it would be possible to screen progeny individuals for the desired wild trait(s) targeted for introgression, concurrently select for the superior fruit quality traits of the cultivated germplasm, and regain the desirable fruit type in fewer backcross generations. Due to their long generation times, tree species are much closer genetically to their wild progenitors than other agriculturally important crops. Huge, rather than small incremental genetic gains are still possible in such crops.

The above discussion highlights the importance of genetics and genomics knowledge to increase the efficiency and effectiveness of rosaceous crop breeding. Unfortunately many rosaceous crops do not have even low-density linkage maps. Additionally, despite the growing number of molecular markers available, many of the markers are not polymorphic in breeding populations. Therefore, the generation of linkage maps and suitable markers is a high community priority.

Due to limited resources, U.S. Rosaceae breeding programs often operate inefficiently, below desired capacity, and are unable to adopt routine marker-assisted selection strategies. To meet the critical need for the accelerated development of improved varieties and adoption of genomics technologies, Rosaceae breeding programs will require substantial resource increases. In addition, due to the long-term commitment necessary, breeding of rosaceous crops is almost exclusively done by USDA-ARS and Land Grant University scientists. Over the last twenty years, the number of fruit breeders in these sectors has dramatically declined. New Rosaceae plant breeders trained in genomics and genetics technologies are required. Therefore, maintaining and enhancing current breeding capacity to ensure the translation of genomic discovery to the producer and consumer is a high community priority.

Short Term Objectives

1. Identify and develop an appropriate infrastructure to ensure that linkage maps are constructed from key rosaceous genomes and the resulting information is properly preserved and disseminated.
2. For all the commercially important Rosaceae species, continue and augment the development of genetic maps using up-to-the-minute technologies, emphasizing the identification of markers closely linked to commercially important traits such as disease and pest resistance, fruit quality, flowering control, and plant architecture.
3. Discover and characterize useful genetic diversity such as alleles conferring disease and pest resistance, fruit quality, flowering control, and plant architecture.
4. Support the acquisition, characterization, and preservation of additional plant genetic resources.

Long term objective

Build an infrastructure to ensure access to marker-assisted selection in rosaceous breeding programs.

Contributors

Abhaya Dandekar
Amy Iezzoni
Bert Abbott
Bryon Sosinski
Cameron Peace
Carlos Cristosto
Chad Finn
Chris Dardick
Chuck Simon
Dan Potter
Darek Swietlik
David Byrne

Dick Okie
Dorrie Main
Ed Stover
Ebenezer Ogundiwin
Gayle Volk
Gennaro Fazio
Herb Aldwinckle
Janet Slovin
Jay Norelli
Jim Hancock
Jim McFerson
Jim Olmstead
Joe Goffreda
Joeseeph Postman
Kevin Folta
Kim Hummer
Kim Lewers
Marvin Pritts
Phil Forsline
Ralph Scorza
Richard Bell
Schuylar Korban
Steve van Nocker
Susan Brown
Tom Davis
Tom Gradziel
Tom Sjulín
Vladimir Shulaev
Wayne Loescher

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Appendix 1. Evolutionary relationships within the Rosaceae

Current taxonomy based on recent phylogenetic analyses (Angiosperm Phylogeny Group 2003) places the family Rosaceae within the order Rosales along with eight other families, including Rhamnaceae (the buckthorn family), Moraceae (the fig family), and Ulmaceae (the elm family). The order Rosales, in turn, is classified within a larger group known as the eurosid I clade of flowering plants, a diverse group that includes all families in which symbiotic nitrogen fixation occurs in at least some of the members (Soltis et al. 1995), of which the legume family is the most familiar example.

Rosaceae are traditionally (e.g., Schulze-Menz 1964) divided into four subfamilies based on fruit type. In this classification, members of Rosoideae, which includes roses, strawberries, and raspberries, produce indehiscent one-seeded fruits; members of Spiraeoideae, which includes a number of ornamental shrubs generally bear dry dehiscent fruits; members of Amygdaloideae, which include cherries, almonds, peaches, plums, and apricots, produce fleshy one-seeded fruits with a hard inner layer around the seed (stone fruits); and members of Maloideae bear a specialized fleshy fruit type known as a pome, of which apples and pears are familiar examples. Other morphological, chemical, and ecological features are largely, but not perfectly, correlated with traditional subfamilial circumscriptions. Recent phylogenetic analyses (Morgan et al. 1994, Evans et al. 2000, Potter et al. 2002) based on DNA sequences, however, have suggested that this classification does not adequately reflect evolutionary relationships in the family. As a result, a new phylogenetically based classification has been developed (Potter et al., submitted), in which only three subfamilies, with further divisions into supertribes, tribes, and subtribes, will be recognized (Fig. 1)

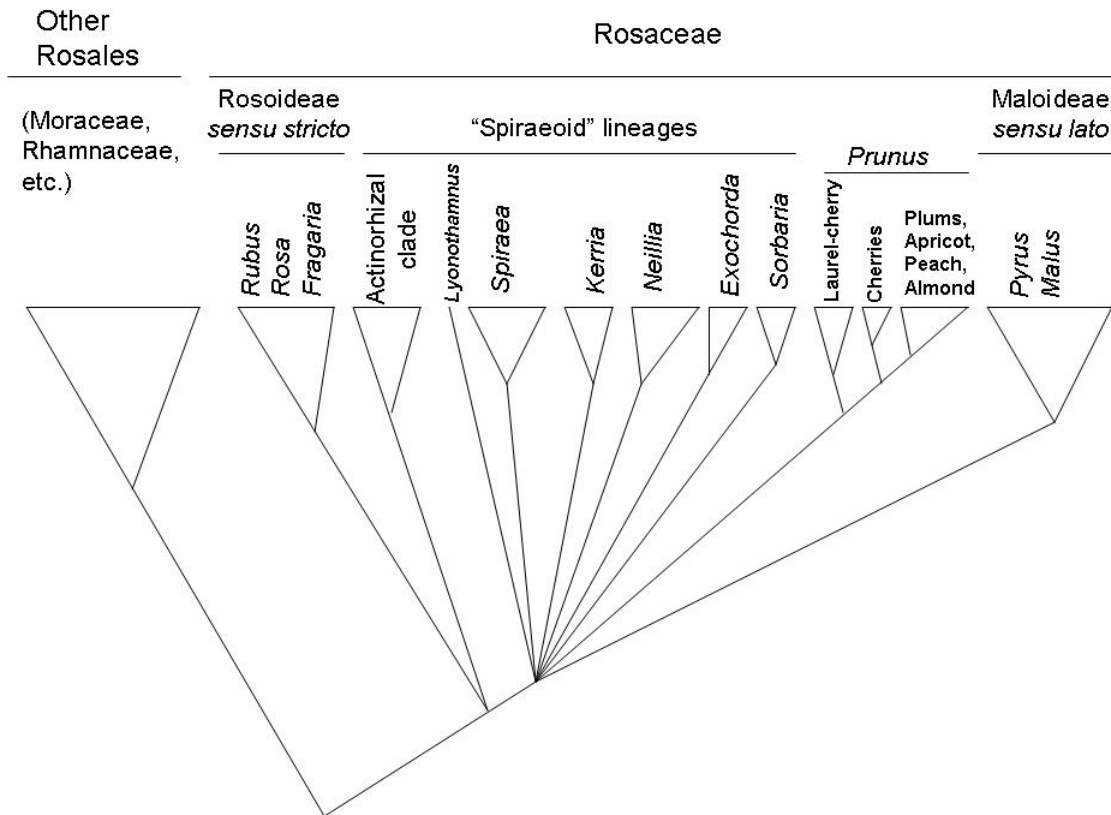


Figure 1. Rosaceaea lineages (courtesy of Dan Potter)

Although the four subfamily system has not been supported by molecular phylogenetic analyses, it remains true that important crop plant species are found throughout the family in several distinct evolutionary lineages (Figure 1). The results of molecular phylogenetic analyses combined with traditional taxonomy suggest that, if we wish to select index species that represent the evolutionary diversity of Rosaceae, we would be wise to select at least one member of each of the following groups: (1) Rosoideae *sensu stricto* (Eriksson et al. 1998): a focus on *Fragaria* and *Rubus* would ensure sampling of broad diversity within this group; (2) *Prunus*: sampling a cherry and peach, almond, apricot or plum would ensure sampling of broad diversity here (Bortiri et al. 2001); (3) the former Maloideae: e.g., *Malus* or *Pyrus*; (4) one or more of the "Spiraeoid" lineages that include important ornamental species: *Spiraea*, *Kerria*, *Neillia*, *Exochorda*, *Sorbaria*; (5) the actinorhizal clade, whose members form symbiotic relationships with nitrogen-fixing actinomycete bacteria of the genus *Frankia*: inclusion of a representative from this group would be of great interest, given the ecological significance of symbiotic nitrogen fixation.

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Appendix 2. Rosaceae germplasm in the U.S. National Plant Germplasm System

Species		# Cultivars & Improved Clones	# Unimproved individuals (wilds, landraces)	# Accns. maintained as seeds	Major center of diversity	Site
<i>Amelanchier</i>	serviceberry	5	3	50		Corvallis
<i>Cydonia</i>	quince (1 species)	75	35	13	Western Asia, Eastern Europe	Corvallis
<i>Fragaria</i> (strawberry)	multiple species (20+ species)	537	756	376	Americas	Corvallis
<i>Malus</i> (apple)	<i>domestica</i>	1405	0	0		Geneva
	hybrids (crabapples, 2 species)	320	0	0		Geneva
	<i>sieversii</i>	85	1592	903	Central Asia	Geneva
	<i>orientalis</i>	16	623	111	Western Asia	Geneva
	<i>sylvestris</i>	19	47	10	Europe	Geneva
	Chinese species (7 species)	72	574	130	China	Geneva
	other <i>Malus</i> species (45 species)	453	0	550	Europe, Asia, North America	Geneva
	<i>Mespilis</i>	medlar (2 species)	22	7	13	Western Asia, Eastern Europe China, Central Western Asia,
<i>Prunus</i>	<i>dulcis</i> - almond (+12 species)	48	108	0	Europe	Davis
	<i>armeniaca</i> - apricot (+4 species)	118	109	0	China, central Asia	Davis
	<i>avium</i> -sweet cherry	105	0	0	Europe, Asia	Davis
	<i>cerasus</i> - sour cherry	59	0	0	Central Asia	Geneva
	other cherry species (30 species)	0	149	0	Asia	Davis, Geneva
	<i>persica</i> - peach (+4 species)	233	112	0	China, central Western Asia	Davis
	<i>domestica</i> - European plum	143	5	0	Asia, Europe, North America	Davis
	<i>salicina</i> - Japanese plum	44	7	0	Eastern Asia	Davis
	<i>cerasifera</i> - Myrobalan plum	26	13	0		Davis
	other plum species (19 species)	0	243	0		Davis
<i>Pyrus</i>	<i>communis</i> - European pear	860	149	89	Western Asia	Corvallis
	<i>pyrifolia/ussuriensis</i> - Asian pear	149	72	30	Asia	Corvallis
	other pear species (25+ species)	0	699	199	Europe, Asia	Corvallis
<i>Rubus</i>	raspberry cultivars	221	0	0		Corvallis
	blackberry cultivars	257	0	0		Corvallis
	black raspberry cultivars	48	0	0		Corvallis

Appendix 2. Rosaceae germplasm in the U.S. National Plant Germplasm System con't

Species		# Cultivars & Improved Clones	# Unimproved individuals (wilds, landraces)	# Accns. maintained as seeds	Major center of diversity	Site
<i>Rubus con't</i>	hybridberry cultivars	24	0	0		Corvallis
	other <i>Rubus</i> species (700 species)	0	354	1122		Corvallis
<i>Sorbus</i>	mountain ash	17	53	161		Corvallis

Appendix 3. Crop reports

Maloideae

Apple

Domesticated apple (*Malus domestica* Borkh) is one of the worlds most important fruit crop. According to FAOSTAT (2004), world apple production exceeded 57,000,000 metric tons (MT) in 2003. Leading producing nations include (in descending order) China, USA, France, Poland, Turkey, Italy, and Russia. While there are well over 6,000 documented apple cultivars, commercial production still relies on fewer than twenty major cultivars, with 'Delicious', 'Golden Delicious', 'Granny Smith', 'Fuji' and 'Gala' accounting for 61% of the total production. Apples are processed into many products including juice, applesauce, slices (dried, frozen and canned), and cider (sweet and hard). Many *Malus* species are also important in the landscape market and in breeding for better ornamental types. In the past, the most important commercial cultivars arose as chance seedlings (Red Delicious, Golden Delicious, Granny Smith, Rome, McIntosh, etc.) from the North American gene pool, and such seedlings continue to be commercialized today, for example, 'Ginger Gold' and 'Cameo'. However, increasingly popular new cultivars such as 'Fuji', 'Gala', 'Jonagold', 'Empire', and 'Honeycrisp' are derived from breeding programs. One quarter of the total U.S. production of apples in 2004 was from 'bred' varieties whereas 70% was from 'chance seedling' apples. A downward trend for the two leading apple varieties (Red Delicious and Golden Delicious) is making space for newly bred apple varieties. To study genetic diversity, [Noiton and Alspach \(1996\)](#) analyzed pedigrees of 50 apple cultivars being used in breeding. 'Cox's Orange Pippin', 'Golden Delicious', 'Jonathan', and 'McIntosh' were the most frequent progenitors. Few of the cultivars sampled were substantially inbred, but continued inbreeding is a concern. Breeders currently are working with reduced genetic diversity and must attempt to expand the genetic base. Several breeding programs are tapping into wild species to harness disease resistance genes present in those species with conventional breeding and/or genetic engineering.

Fire blight disease, caused by the bacterium *Erwinia amylovora*, remains to this day as the most serious bacterial disease of pears, apples, quince, mountain ash, spirea, hawthorn, pyracantha, and cotoneaster, among many other Rosaceae species. Fire blight control measures are costly, laborious, and quite often remain ineffective. Breeding efforts to introduce genetic resistance to fire blight have been difficult as sources of genetic resistance to fire blight are small-fruited *Malus* species, and resistance is not under simple genetic control. Recently, transgenic approaches have been used to improve the genetic resistance to fire blight; e.g., the attacin E gene from the giant silk moth (*Hyalophora cecropia*) was transferred into the Gala variety and the M.26 rootstock, and some attacin-transgenic lines showed increased resistance to fire blight ([Ko et al., 2000](#)). However, due to the insect origin of the transgene, fruiting cultivars expressing the attacin gene may not be acceptable to some consumers and growers. Therefore, efforts are now emphasizing over-expression of genes involved in resistance, or silencing of genes involved in disease development.

Apple rootstocks

Apple rootstocks in the U.S. are almost exclusively propagated asexually from layering mother plants in stool beds. Production of apple rootstocks is highly centralized with 12 nurseries producing 90% of clonal rootstocks in the U.S. Dwarfing apple rootstocks account for roughly 98 % of new plantings in the U.S., while the remaining are standard seedling rootstocks. The germplasm diversity of dwarfing apple rootstocks in cultivation is highly restricted. Recent figures estimate that 85% percent of dwarfing apple rootstocks being planted originated from one breeding program (East Malling, UK). Roughly 12% originated from a Russian (Budagovsky) breeding program and 2% from a U.S. breeding program (Geneva). The leading genotype being planted today in the U.S. is Malling 9 (M.9, *Malus × domestica* Borkh.), with roughly 45% of new plantings. Second is Malling 26 (M.26, *Malus × domestica* Borkh., 25%) and third is Budagovsky 9 (B.9, *Malus × domestica* Borkh., 10%). Therefore three genotypes and their clones represent 80% of the diversity of apple rootstocks in new cultivation. This lack of diversity is compounded by the fact that the three rootstocks are closely related. The same genotypes are highly susceptible to fire blight (*Erwinia amylovora*) and components of the apple replant disease. The only successful attempts to increase genetic diversity of the U.S. apple rootstock market come from the Geneva breeding program that has used interspecific crosses (involving *Malus floribunda*, *M. prunifolia*, *M. robusta*, and *M. sieversii*) to introduce resistance to fire blight and other diseases in the cultivated germplasm. Several of these new rootstocks are beginning to be planted commercially.

Pear

Pears are tree fruit belonging to the genus *Pyrus*, native to temperate Europe and to temperate and sub-tropical Asia. There are 22 to 26 species, depending on the authority. Pears are grown in all temperate regions of the world. The major species producing edible fruit are *P. communis* L. for the European group, and *P. pyrifolia* (Burm.) Nak., *P. ussuriensis* Max., *P. × bretschneideri* Redh., and to a lesser extent, *P. pashia* D. Don. and *P. sinkiangensis* Yu for the East Asian group. World pear production in 2005 was estimated at 19.5 million MT produced in 84 countries (United Nations Food and Agriculture Organization, 2005). China is the world's leading producer of pears (United Nations Food and Agriculture Organization, 2005), but only a small percentage of these are European pears. Annual pear fruit production in the United States from 2001 through 2003 was estimated at approximately 836,000 MT, or 4.9% of the world production, ranking 3rd after Italy (O'Rourke, 2004). Spain, Argentina, Japan, South Korea, and Turkey are also major producers of pears.

All of the major cultivars grown in the USA and other countries outside of Asia belong to a single species, *Pyrus communis* L., the west European pear. Approximately 50% of commercial production is accounted for by a single cultivar, 'Bartlett' (syn. 'William's Bon Chretien'). An additional three cultivars, 'Beurre d'Anjou' (34%), 'Beurre Bosc' (10%), and 'Doyenne du Comice' (1%) account for the majority of the remaining production. Production from states and small orchards that are not included in the official USDA statistics is more `diverse. The Asian cultivars, such as 'Nijisseki' (syn. 'Twentieth Century'), 'Hosui', 'Shinseiki', and 'Kosui' belong to the species *Pyrus pyrifolia*. Together, their production amounts to less than 1% of the reported national

total. It is unlikely that major changes in production or diversity will occur within the next decade, but there is growing interest in evaluation of new cultivars. All of the major and most minor cultivars are chance, some over two hundred years old. Only 'Butirra Precoce Morettini', 'Concorde', and 'Kosui' came from breeding programs. Over two hundred cultivars of European pear and European \times Asian hybrids and almost forty Asian cultivars are listed in nursery catalogues selling to the general public ([Seed Savers Exchange, 2001](#)).

There are many fruit and tree characteristics amenable to improvement through traditional breeding and biotechnology. Fruit traits of major importance to the industry include fresh and processed fruit quality, freedom from physiological fruit disorders, storage and shelf life, and ease of ripening. Both green- and red-skinned 'Beurre d'Anjou' and other "winter" pears require a long period of cold storage to soften properly, and the red-skinned mutants suffer from inconsistent and slow ripening. Early maturing pears such as 'Starkrimson' and 'Bartlett' are limited in their storage life by susceptibility to core breakdown. Decay of fruit in storage due to post-harvest pathogens is a major source of economic loss and fruit resistance has not been extensively investigated. The major bacterial disease problems are fire blight (*Erwinia amylovora* [Burr.] Winslow et al.) and bacterial blossom blight (*Pseudomonas syringae* pv. *syringae* Van Hall), and the major fungal diseases are pear scab (*Venturia pirina* Aderh.) and, in the Midwest and eastern U.S., *Fabraea* leaf and fruit spot (*Fabraea maculata* Atk.). The key arthropod pests are codling moth (*Laspeyresia pomonella* L.) and pear psylla (*Cacopsylla pyricola* Föerster), although several other insect and mite pests require chemical or biological control. Pears are notorious for a long non-bearing period and therefore, precocious, consistent, and high fruit yields are needed.

The only major pear breeding program in the U.S. is conducted by the U. S. Department of Agriculture at Kearneysville, West Virginia. One private breeding program has produced limited numbers of selections for red-skinned fruit, and two small private breeding efforts have produced Asian-type pears. State university programs have either been terminated or are no longer actively producing new seedling populations. There are pear breeding programs in many European and Asian countries, and efforts to import new cultivars and selections for evaluation are actively being pursued. There is considerable similarity among the major programs in breeding objectives for European as well as for Asian pears. The genetic diversity or relatedness of current cultivars and breeding selections has not been well documented. However, the genetic base for breeding for fire blight resistance is relatively restricted, with a reliance on 'Seckel' and 'Old Home' as the original sources of resistance. Efforts to broaden the base for resistance should be expanded. Sources of resistance to the pear psylla in East European and Asian cultivars and wild germplasm have been discovered and are being utilized in breeding.

Important single-gene traits are limited to short-internode dwarfing (derived from 'Nain Vert'), red leaf/fruit skin, self-incompatibility, susceptibility to Asian pear scab (*nashicola* Tan. et Yam.) and susceptibility to black spot (*Alternaria alternate* (Fr.) Keissler). The inheritance of most important fruit and tree traits has been characterized as polygenic.

Molecular genetic tools applied to *Pyrus* include genotyping, pedigree verification, and studies of genetic diversity. Molecular systems (RAPD, SSR, AFLP,

and RGAs) have been used to identify markers linked to major genes controlling susceptibility to Asian black spot and resistance to Asian pear scab, and for several self-incompatibility alleles. Markers linked to quantitative trait loci associated with fire blight resistance have been identified, and a genetic map of 150 loci was constructed. A genetic marker map of the interspecific cross of 'Bartlett' × 'Hosui' has also been constructed. Functional genomic studies have concentrated mostly on fruit expression studies and isolation of ripening and ethylene genes, and self-incompatibility alleles. Transformation and adventitious regeneration protocols for several European cultivars have been developed. Pears have been transformed to confer resistance to fire blight with genes for lytic peptides, lysozyme, lactoferrin, depolymerase, *Rhaphanus* defensin, harpin, and other antimicrobial genes. Genes evaluated for dwarfing in scions and rootstocks include *rolA*, *rolB*, and *rolC* from *Agrobacterium tumefaciens*.

Pear rootstocks

Rootstocks can be used to confer traits such as resistance to soil pathogens and pests, and adaptation to unfavorable soil pH or texture. In addition, one of the most pressing needs for pears are adapted rootstocks that will induce precocious bearing, reduce tree size, and thereby, promote efficient orchard production systems. Emerging concerns include water use efficiency and drought resistance. In much of Europe, quince (*Cydonia oblonga* L.) rootstocks have been used for their ability to reduce tree size by as much as 50% and to induce early and high yields. However, the major quince rootstocks are not well adapted to our major production regions, lacking cold hardiness and fire blight resistance.

The genetic base of *Pyrus* and *Cydonia* rootstocks is even narrower than that for scions. While seedling rootstocks were used almost exclusively in the United States until about 20 years ago, clonal rootstocks have become preferred. Seedlings of 'Bartlett' and 'Winter Nelis' predominate in older plantings. Both of these are highly susceptible to fire blight. Where high vigor is needed in clay or poorly drained soils, seedlings of *P. betulifolia* Bunge are used. These are also the predominant choice for Japanese (*P. pyrifolia*) cultivars. Growth-controlling clonal rootstocks selected from seedling populations of *P. communis* parentage have been widely planted in the last 20 years. Named for their parents, these 'Old Home' × 'Farmingdale' clonal rootstocks are moderately resistant to fire blight, and, depending on the clone, exhibit tree size control in a range of somewhat larger than the most vigorous quince (approximately 60% of the size produced on 'Bartlett' seedlings), to 20% more vigorous than the 'Bartlett' seedling rootstocks. While 'OH×F 333', perhaps the most easily propagated clone, was once the most widely planted, it has been surpassed by 'OH×F 87' and 'OH×F 97', with increased interest in 'OH×F 40'. Commercially available quince rootstocks are limited to a few genetic sources.

There is no pear rootstock breeding program in the U.S., although the most extensive evaluation program has been conducted by Oregon State University. New rootstocks developed by foreign breeding programs are being imported for evaluation. Many of these also are derived from 'Old Home' as a source of fire blight resistance, so there is a need to broaden the genetic base. Breeding programs in Europe emphasize fire blight resistance, induction of precocious bearing, dwarfing, high yield, ease of propagation, and resistance to lime-induced chlorosis.

Ornamental pears

Several small-fruited pear species are utilized as ornamental trees, with the Callery pear, *P. calleryana* Decne., being the most common. Other species include the Korean pea pear (*P. fauriei* Schneid.), the birch-leaf pear (*P. betulifolia*), the willow-leaf pear (*P. salicifolia* Pall.), and the evergreen pear (*P. kawakamii* Hayata). A breeding program is being conducted by the Landscape Plant Development Center in Minnesota.

Amygdaloideae

Peach and Nectarine

Hundreds of peach and nectarine [*Prunus persica* (L.) Batsch] cultivars are commonly grown, both in the U.S. and internationally. There is little cultivar name recognition during marketing. Cultivated germplasm typically falls into three main groups: fresh market peaches, nectarines, and canning peaches. In the U.S., fresh market peaches are mostly grown in California (over 50% of production), South Carolina, and Georgia, with a value of around \$300 million per year. Nectarines are mostly grown in California, valued at approximately half that of fresh market peaches. U.S. canning peaches are almost exclusively grown in California, valued at approximately \$120 million per year at harvest and \$500 million after processing. Simply inherited fruit traits for this species determine the fruit types currently available on the market. These traits are peach/nectarine (peach dominant), melting/non-melting flesh (melting dominant), white/yellow flesh color (white dominant), freestone/clingstone (freestone dominant), low/normal malic acid content (low dominant), and saucer/round shape (saucer dominant).

Peaches are susceptible to numerous pathogens and pests. Interest in breeding for disease and pest resistance has increased in recent years due to the concern over: (1) the cost of agricultural chemicals, (2) the potential negative impact of chemicals upon humans and animals, and (3) genetic uniformity as the basis of vulnerability to epiphytotics. Peach genotypes have been screened for resistance or tolerance to ring nematode (*Criconebella xenoplax*), a primary factor in Peach Tree Short Life syndrome (PTSL), Cytospora canker caused by *Leucostoma* spp., and brown rot (*Monilinia fructicola*). These studies have revealed somewhat low but potentially useful levels of disease resistance. Other studies examining the response of numerous peach and nectarine cultivars to *Stigmata carpophila*, *Monilinia laxa*, *Sphaerotheca pannosa*, *Tranzschelia pruni-spinosae*, *Taphrina deformans* and *Xanthomonas campestris* pv. *pruni*, found most cultivars susceptible to these pathogens. Major pests of peach include insects which attack fruit causing malformation, early fruit drop, or otherwise cause fruit to be unmarketable; insects which feed on foliage, weakening trees; insects that bore through twigs, stems, and trunk, debilitating trees; and virus vectors. Only a few cases of insect resistance in cultivated genotypes have been reported. Nematode feeding weakens trees and can cause severe decline syndromes such as "replant problem" and PTSL. Tomato ringspot virus, a serious disease in many peach-growing regions, particularly the

U.S. Mid-Atlantic states, is spread by the dagger nematode (*Xiphenema* spp.) and all peach rootstocks are susceptible to *Xiphenema*. Resistance to rootknot nematodes (*Meloidogyne* spp.) has been relatively easy to identify in peach rootstocks. Some peaches appear to be tolerant to the root lesion nematode (*Pratylenchus* spp.) that is associated with replant problems. Some tolerance of ring nematode (*Criconemella xenoplax*), a primary factor in PTSL, has been reported in peach. There are a number of virus diseases that affect peaches. Some have little noticeable effect on production and fruit quality and some cause devastating losses. Plum pox or Sharka is especially serious, affecting not only peach but all commercial stone fruits and many wild and ornamental species. The disease was recently found in the U.S. (Pennsylvania) and purportedly eradicated at great expense to state and federal governments and growers.

The most important factor limiting production in mid-continental and northern climates is the lack of flower bud hardiness. In peach, this has been shown to be a polygenic trait and is inherited quantitatively. Peach trees avoid low temperature injury through deep supercooling, a physical state which depresses the freezing point of cells. The degree of deep supercooling has been related to both xylem and flower bud cold hardiness in *Prunus*. Cultivated species generally supercool to a lesser degree than hardy wild species. The genetic control of this complex trait is not well understood.

A major cost of peach production is pruning. The genetic control of tree growth habit could reduce the need for pruning and allow for the development of more productive, more easily managed high-density production systems, systems that would be readily adapted to mechanization. Several loci have been shown to control peach tree size and canopy architecture producing compact, spur-type, semi-dwarf, columnar, dwarf and weeping trees. These simply inherited traits have a major impact on tree architecture and studies of these traits and their genetic control are just beginning.

Ultimately, it is consumer acceptance of fruit in the market that drives peach production. A common consumer complaint is that fresh peaches and apricots are large and attractive, but lack flavor and agreeable texture. While breeding programs have produced cultivars of high quality potential, much of this quality depends upon the fruit reaching physiological maturity. However, the process of softening begins at this stage, and soft fruit are difficult and expensive to keep from bruising during handling. Such fruit also tend to have a shorter shelf life, as senescence and decay occur sooner. The requirements for shipping and handling fruit for several weeks precludes the harvesting of fully mature fruit for all but local markets. Consumers therefore generally receive fruit that were harvested at the early stages of maturity, which are somewhat low in sensory qualities such as color intensity, flavor, and size. Peaches may also be harvested earlier than full maturity to fill gaps in market supply. Producers recognize that peach consumption is decreasing. In the 1960's, average per capita consumption of peaches in the U.S. was 4.4 kg. In the past 20 years the consumption level has remained flat at 2.0 kg. This low level of consumption in relation to other temperate fruits (e.g. 16 kg/yr/capita for apples) is due, at least in part, to the marketing of immature fruit. Historically, breeders have approached the problem by selecting for firmness in ripe fruit, allowing fruit to remain on the tree for longer without too much loss of firmness. This is apparent when comparing old and new cultivars. The gradual increase in firmness following generations of selection appears to be an additive gene effect. Major loci that dramatically affect fruit firmness in peach have also been identified. These include the

melting flesh, stony hard, and slow-ripening genes.

Another major reason for low quality fruit reaching consumers is the poor fruit storability of a large proportion of peach and nectarine varieties. When peach and nectarine fruit are stored at low temperatures, good appearance is maintained, but flavor and texture are seriously compromised for many varieties. The problem is known as chilling injury or internal breakdown, with the worst temperatures being 2-8°C, which are commonly encountered throughout the marketing chain and in home refrigerators. The main symptoms are mealiness (lack of juice and grainy texture), flesh browning, and poor flavor (lack of normal taste and development of off-flavors). Few varieties last more than five weeks of cold storage, even when painstakingly kept at the safer temperature of 0°C. One successful means of avoiding internal breakdown is to pre-ripen fruit before cold storage. However, this special treatment adds to the cost of production, further exacerbated by the softer fruit produced that require careful handling. Non-melting peaches are largely resistant to internal breakdown, and genetic resistance to this disorder is sought in melting flesh peaches and nectarines for the fresh market.

Peach is well suited to the application of molecular improvement techniques. It has the shortest juvenility period of the rosaceous tree fruits, the smallest genome, and is self-pollinating. Furthermore, essentially all commercial cultivars, of which nearly 100 are released per year worldwide, are produced through hybridization and selection by public or private breeding programs. Peaches are widely adapted throughout their range. Germplasm and cultivars developed in one growing region can be successfully utilized in many production regions. The investment in peach breeding worldwide and the expense and long-term nature of peach improvement programs calls for research into molecular genetics, to elucidate the genetic control of important tree and fruit traits, and to develop molecular technologies for peach improvement. The simply inherited characters particularly lend themselves to molecular studies of genetic control of these traits and marker-assisted selection. Additional alleles for these major genes may provide desirable quantitative effects. Molecular markers have been developed for a number of agronomic traits such as tree growth habit, leaf width and color, flower color, disease and nematode resistance, and for a number of fruit quality traits such as size and weight, shape, brix, epidermis color, melting flesh, and stone adhesion. Thus far, it appears that these markers are not being used in applied breeding programs. Genetic studies for most other important traits in peach and nectarine production are currently underway in laboratories and fields around the world.

Unfortunately, peaches lack an efficient genetic transformation system. Genes active during peach fruit ripening have been isolated and partially or fully sequenced, including genes for ACC oxidase, endopolygalacturonase, and ethylene receptors. The over-expression or repression of genes involved in fruit ripening and/or softening could allow for the direct manipulation of these processes through transfer of altered genes or gene promoters into peach cultivars or germplasm, but without an efficient transformation system this technology cannot be readily applied to produce improved cultivars. Genetic transformation of peach has been reported, but success has not been replicated in other laboratories. Peach transformation remains a major stumbling block to functional genomics studies and the improvement of this species through genetic engineering.

Peach cultivars that form the basis of commercial production worldwide represent only a small fraction of the genetic diversity in this species. The loss of peach germplasm is occurring at an alarming rate as urbanization, deforestation and the need for firewood accelerates in its center of origin in China. The cost of maintaining large collections of trees and the long-term nature of tree fruit breeding programs has discouraged germplasm collection and maintenance in many developing countries. Furthermore, Western stone fruit cultivars, which have a restricted germplasm base but high fruit quality, productivity, and generally superior handling characteristics, usually replace landrace cultivars that are adapted to local biotic and abiotic stress factors.

While many commercial peach cultivars have been developed from a restricted germplasm base, they remain heterozygous for many loci and cross-hybridization or selfing usually produces a phenotypically variable population of offspring. The effects of heterozygosity are most evident when cultivated and non-cultivated forms are hybridized. In most cases the characteristics that are desirable for commercial cultivars, including large fruit size, high coloration of the fruit epidermis, and firmness of the flesh, are recessive. Additional generations of hybridization and selection are required to produce commercial quality fruit with adaptive traits obtained from non-commercial genotypes. It may be in the initial rounds of selection from such “wide crosses” that marker-assisted selection can have its greatest impact allowing breeders to select those genotypes with the rare combinations of critical traits. Marker-assisted selection could also help widen the elite germplasm base for canning peaches and nectarines. The traits that are the genetic bases of these fruit types (non-melting and nectarine, respectively) are both recessive, which discourages the use of parents from other cultivated gene pools in traditional breeding programs. An even wider gene pool is available for the genetic improvement of peach, including related wild peach species (*Prunus davidiana*, *P. ferganensis*, *P. kansuensis*, and *P. mira*) and other inter-fertile members of subgenus *Amygdalus* (including almond, *P. dulcis*). Marker-assisted backcrossing would greatly aid in the introgression of novel and desirable traits from such germplasm.

Peach rootstocks

Peach rootstocks in the United States have almost exclusively been and still are open pollinated seedlings of peach. Currently these peach seedlings, derived primarily from the rootstock cultivars Lovell, Halford, Nemaguard, Nemared, Bailey and GuardianTM, constitute greater than 95% of the peach rootstocks used in the United States. Lovell (originally a drying cultivar) is a possible parent of Halford (originally a canning cultivar), and both Nemared and GuardianTM have Nemaguard as an ancestor. Bailey is not related by parentage to the other five seedling rootstocks. In field testing, these rootstocks differ in vigor, root-knot nematode resistance, and peach tree short life tolerance, but are similar in many other horticultural traits including economically important ones such as fruit growth and yield of scion cultivars. All of these peach seedling rootstocks are susceptible to the same soil diseases and conditions, which limit their productivity and longevity in many otherwise good production sites.

Within the U.S. a few clonal rootstocks are being used in commercial peach production on a limited scale. Atlas and Viking from California are interspecific *Prunus*

hybrids used on replant sites due to their replant tolerance, root-knot resistance and vigor. *P. americana* seedlings are used as rootstocks by some mail order nurseries for primarily home owner sales in cold winter climates. St. Julian A (*P. insititia*) has been used with limited success as a dwarfing rootstock, and Hiawatha (*P. besseyi* × *P. salicina*) is being evaluated for vigor control as a rootstock. Several other promising size controlling clonal rootstocks will be commercially released soon from California. These rootstocks are *P. salicina* × *P. persica* hybrids and will be named Controller 5 and Controller 9.

New peach rootstock cultivars have been imported into the U. S. during the past 10-15 years with the majority of them being complex *Prunus* hybrids that must be propagated vegetatively. The pedigrees of these hybrids contain many different *Prunus* species that confer traits that *P. persica* lacks such as adaptation or tolerance to heavy soils, waterlogging, alkalinity, drought, vigor control, and soil fungal diseases. Of these clonal rootstocks, the ones that are being licensed for limited grower testing include Empyrean #1 (Barrier 1) and Cadaman™ (both *P. persica* × *P. davidiana*), Krymsk™ 86 or Kuban 86 (*P. cerasifera* × *P. persica*), plum species Penta (Empyrean™ 2) and Tetra (Empyrean™ 3) (both *P. domestica*), Mr.S. 2/5 (*P. cerasifera* OP hybrid), plum hybrids Myran (*P. cerasifera* × *P. salicina*), Ishtara (*P. cerasifera* × (*P. persica* × *P. cerasifera*)), Julior (*P. insititia* × *P. domestica*), Krymsk™ 1 or VVA-1 (*P. cerasifera* × *P. tomentosa*), Krymsk™ 2 or VSV-1 (*P. incana* × *P. cerasifera*), peach-almond (*P. dulcis* × *P. persica*) hybrids Garnem (GxN15) and Felinem (GxN22), and PumiSelect (*P. pumila*).

Apricot

Apricot is the third most widely grown stone fruit crop, with world production in excess of 2,800,000 MT in 2005 (FAOSTAT, 2005). The primary areas with extensive apricot cultivation are generally limited to areas with a Mediterranean climate. Turkey, Spain, France, Italy, Morocco and Algeria are major producers in the Mediterranean area and collectively account for 40% of global production. In the U.S., apricot production was 81,790 MT in 2005, over 90% of which was grown in California. Layne et al. (1996) proposed that the cultivated apricots be classified into six ecogeographical groups: 1) Central Asian, 2) Iran-Caucasian, 3) European, 4) Dzhugar-Zailij, 5) North Chinese, and 6) East Chinese. The cultivars grown in the Mediterranean region and the U.S. belong to the European group and are especially low in genetic diversity (Badenes et al., 1998), probably because they originated from only a small subset of the genetic diversity from the Iran-Caucasian group. Cultivars in the European group tend to be larger, firmer, but have less sugar and more acidity than apricots of Central Asian and Iran-Caucasian groups. These cultivars also tend to have a lower chilling requirement, thereby limiting their cultivation to areas protected from spring frost during bloom. In contrast, apricots from the Central Asian group generally bloom later and are much richer in genetic diversity with greater variety in forms, flavors, colors, and season of fruit maturity. Research has shown that consumers would be willing to pay a premium for fruit with improved eating quality (Bruhn et al., 1991). The introgression of the Central Asian and other more diverse sources of germplasm into current apricot breeding programs in the U.S. could potentially develop apricots with improved quality and broader adaptation.

Cherry

The two main groups of cherries, sweet cherry (*Prunus avium* L.), and tart cherry (syn. sour cherry) (*P. cerasus* L.) originated in an area that includes Asia minor, Iran, Iraq, and Syria (Vavilov 1951, Watkins 1976). Sweet cherry is diploid ($2n=2x=16$) and tart cherry and the wild Russian ground cherry (*P. fruticosa* Pall.) are tetraploid ($2n=4x=32$). Tart cherry is believed to have arisen multiple times by sexual polyploidization between ground cherry and a $2n$ gamete from sweet cherry (Olden and Nybom 1968, Brettin et al. 2000).

Sweet cherries

Four states (Washington, California, Oregon and Michigan) produce over 95% of the U.S. sweet cherry production. In all states but Michigan, sweet cherry production is dominated by ‘Bing’, a chance seedling identified in Oregon during the late 19th century. Of the three major U.S. public sweet cherry breeding programs (Cornell University-NYSAES, University of California, and Washington State University), only Washington State University is currently active. A significant proportion of new sweet cherry cultivars released in the last 30 years has come from the breeding programs instituted by Agriculture and Agri-Food Canada.

The genetic base for current sweet cherry cultivars is narrow, particularly in those cultivars developed by North American breeding programs. Most of the new cultivars developed by these breeding programs in the last century are descended from five founding clones (Choi and Kappel, 2004). The exclusive use of one genetic source for self-compatibility has further contributed to the narrow genetic base.

Many of the major limitations to expansion of U.S. sweet cherry production can be addressed through breeding efforts supported by genomic research. Abiotic limitations, primarily the lack of cold-hardy or low-chill cultivars, result in low quality fruit or prevent sweet cherry production in many areas of the U.S. To date, little effort has been directed toward developing natural biotic pest resistance in sweet cherry. However, excellent sources of resistance to powdery mildew, the most prevalent pre-harvest sweet cherry, have been identified (Olmstead et al., 2001). Until recently, the lack of suitable dwarfing rootstocks has prevented the adoption of “pedestrian” orchards similar to apple production. Furthermore, tree architecture and fruit abscission traits desired for efficient adoption of orchard mechanization have yet to be incorporated into breeding efforts.

Tart cherries

The tart cherry industry in the U.S. has historically been a monoculture of the 400 year old cultivar named Montmorency. Despite its dominance in the U.S. industry, Montmorency has numerous shortcomings. These include poor fruit firmness, the necessity to add sugar and red coloring to the majority of processed products, and susceptibility to diseases, insects and climatic stresses.

The goal of the tart cherry breeding program at Michigan State University (MSU), the only tart cherry breeding program in the U.S., is the development of new tart cherry cultivars that are productive, cold hardy, disease resistant, and lend themselves to new

product development. After numerous collection trips to Eastern Europe, the center of diversity, the MSU tart cherry breeding program has the largest tart cherry germplasm collection in the world. One of the landrace varieties collected in Hungary that was tested and released in the U.S. through the MSU breeding program, is now in significant commercial production. This selection, Ujfehértói Fürtös but sold as Balaton® in the U.S. to protect intellectual property rights, has superior fruit quality compared to Montmorency (<http://www.hrt.msu.edu/balaton.html>). This indicates that the U.S. tart cherry industry is willing to adopt new cultivars if the benefits are compelling.

Other critical goals still must be met to improve the profitability and sustainability of U.S. tart cherry production. For example, in 2002, tart cherry production was the lowest it has been since 1945 due to spring frost damage, with a devastating affect on the industry and economy of the fruit growing regions. For example, the northwest region of Michigan produces an annual average of approximately 180 million pounds of tart cherries; yet, the 2002 production was only 3 million pounds (Kleweno and Matthews 2003). Montmorency flower buds were uniquely susceptible to the freeze damage as none of the MSU selections under test in the production region suffered such a devastating flower bud death (Iezzoni 2005). Another critical goal is resistance to cherry leaf spot, as more pesticides per acre are applied to control this disease than any other disease in tart cherry. Fortunately excellent sources of resistance to this pathogen have been identified (Wharton et al. 2003).

Cherry rootstocks

The most important rootstock species are *P. mahaleb* L. ($2n=2x=16$), wild *P. avium* commonly called mazzard, and more recently interspecific hybridizations between related *Prunus* species. Cherries are clonally propagated with the vast majority of trees propagated on seedling rootstocks. The most common seedling rootstocks that produce standard size trees are seedlings of *P. mahaleb* or *P. avium* mazzard. Dwarfing rootstocks such as GiSela® 5 and 6 that are triploid hybrids between sour cherry and the diploid *P. canescens* Bois ($2n=3x=24$) are vegetatively propagated. However, these dwarfing rootstocks have a tendency to induce over-cropping resulting in a reduced fruit size. Since reduced tree size and early cropping are critical needs for the fresh market sweet cherry industry there is a rootstock selection program at Michigan State University that is targeting these two goals.

Plum

Most of the plums grown in the US are either European (hexaploid) or Japanese (diploid) types. European plums (primarily *Prunus domestica*) are generally better adapted to cooler regions and include several groups of cultivars such as Green Gage, prunes, bullaces, damsons, mirabelles and St. Julien types. The bulk of European plum production is of 'French Prune', grown for dried fruit in California. The only recent breeding has been in California for prune types, and New York for fresh types. USDA-ARS in Kearneysville has engineered plums with resistance to PPV.

The ancestors of our fresh-market shipping plums were *Prunus salicina*, which originated in China. The designation “Japanese plum” now includes all the fresh market

plums developed by intercrossing various other diploid species with *P. salicina*. These plums were initially imported by Luther Burbank from Japan and released either as is ('Satsuma', 'Burbank'), or used to produce hybrids such as 'Santa Rosa'. Breeding and production are concentrated in California, and there has been little or no infusion of new germplasm since Burbank's time. The major public breeding program is that of USDA-ARS in Parlier. Private breeders have released many cultivars, although quite a few have been bud mutations or open-pollinated seedlings of popular cultivars. The latest trend is development of plum apricot hybrids, most of which are known under trademarks pluot® or aprium®. There is controversy over the interspecific nature of some of these "hybrids".

Elsewhere in the US native plum species were better adapted to the local climate, and were grown directly or crossed with Japanese plum. Most of this adapted germplasm has been lost and efforts to hybridize the material discontinued. The only major Japanese plum breeding program outside California is at USDA-ARS in Byron, GA, although smaller university and hobbyist efforts are on-going in several other states.

Emerging diseases also pose significant threats to US fruit and nut growers. One notable example is Sharka disease caused by an insect transmitted virus (PPV). Control of PPV requires eradication of infected trees coupled with pesticide applications targeted against aphid vectors. First discovered in 1915, plum pox has infected more than 100 million peach, plum, and apricot trees in Europe, crippling fruit production in some regions, and is widespread throughout Chile, another major fruit-producing nation (Gildow et al., 2000). Post-transcriptional silencing of potyvirus coat protein gene in transgenic European plum has resulted in C5 clone highly resistant to Sharka (Scorza et al. 2001). The clone was subsequently named "Honey Sweet". Possible deregulation of this cultivar is currently being reviewed by APHIS and other U.S. regulatory government agencies. Since the disease resistance is caused by gene silencing, there is no protein produced by the transgene. This fact makes this technology highly promising from the standpoint of grower and consumer acceptance. Irrespective of this fact, Scorza and his collaborators are testing new and even more environmentally friendly and consumer acceptable constructs that will not only impart resistance to Sharka but also to a number of other deadly viruses afflicting *Prunus* species. Much more work is needed, however, to bring the development of this technology to fruition.

Almond

Almond, *Prunus dulcis*, is the largest agricultural export crop from California and the largest US specialty crop export with a value of 1.4 billion dollars in 2004. California produces more than 80% of the world's almonds and virtually 100% of domestic product. Nonpareil is the major variety with approximately 38% of the acreage. With few exceptions, all remaining varieties are progeny from natural crosses between Nonpareil and the variety Mission, which is in a historically important pollinizer for the self-incompatible Nonpareil variety. Such inbred varieties include the commercially important Carmel, Butte, and Monterey varieties, which presently make up approximately 34% of the acreage. The combination of large plant size and long seed-to-seed breeding cycle have largely eliminated private breeding programs from almond improvement. Public (University and USDA-ARS) breeding programs have successfully incorporated new

germplasm into the highly inbred US commercial germplasm. Varieties released from these programs include Padre, Sonora, Solano, and Winters and are currently planted on approximately 10% of commercial acreage. The market dominance of California varieties has also resulted in their increased plantings in other producer countries, contributing to a loss in germplasm diversity worldwide. Current breeding efforts, in addition to incorporating useful commercial germplasm from European and Central Asian origins, have also been successful in incorporating valuable traits from related species including *Prunus persica*, *P. webbii*, *P. argentea*, and *P. mira*. Traits recovered include disease and pest resistance, improved phytonutrient content, and self-compatibility/self-fertility. Virtually all almond cultivars are grafted onto peach or plum rootstock. Almond x peach hybrid rootstocks, however, are becoming increasingly utilized owing to their greater vigor and disease resistance. While early hybrid rootstocks were seedlings from field crosses, more recent hybrid rootstock are vegetative propagation of breeding program selections.

Rosoideae

Strawberry

Strawberries (*Fragaria* × *ananassa*) are an important rosaceae crop in the United States and worldwide. More than \$1.4 billion of strawberries are sold in the U.S. each year, mostly through fresh market channels. Unlike most crops that are grown only in certain regions, every state has some strawberry production, although California and Florida are the largest producers. The vast majority of the fresh market fruit are produced in California (85%) nearly year-round in an annual plasticulture system with the other major growing region being Florida (8%) for winter production. The Pacific Northwest is the second most important production area after California for processed fruit; however, this fruit is produced in a perennial system much like that in the eastern U.S. However, every state has some strawberry production as small strawberry farms encircle most cities across the U.S. Nationally, approximately 6,800 farms are engaged in strawberry production. Consumers are willing to pay a relatively high price for strawberries, averaging \$2.57/lb retail, and the value of strawberries has increased more than 3-fold over the last 20 years. Strawberry farmers employ large numbers of workers since berries cannot be successfully harvested mechanically. In addition, a large percentage of farmers sell strawberries directly to the public either through farmers markets or pick-your-own, and by doing so, help maintain a fragile, direct connection between consumers and their food. Strawberries have an exceptionally high nutritional value and data suggest that consuming them can enhance health. For these reasons, strawberries have an impact far beyond their farm gate value.

Although strawberries have been quite successful as a domesticated crop, the potential still exists to make considerable genetic improvement. The wide distribution of native species bodes well for further enhancement of character traits. Seventeen wild species are recognized in various areas of the world and vary in ploidy from 2x to 8x. The vast majority of cultivated strawberries are derived from the interspecific hybridization of the 8x species *F. chiloensis* × *F. virginiana* first done by accident in the early 1700's. As

strawberry is a relatively new crop, introgression of traits from the progenitor species can produce a genotype of variety quality in as few as three backcross generations or twelve years before testing. Fifty three founding clones figure into the nuclear background of the 134 North American cultivars released since 1960 with 7 accounting for 50% of the nuclear genes (Sjulin and Dale, 1987; Luby et. al., 1991). The cultivars clustered into 11 groups mainly based on geographic origin. Only 17 founding clones contributed to their cytoplasm (Dale and Sjulin, 1990).

The challenging genomic complexity of the octoploid, cultivated strawberry has prompted the development of the diploid species *F. vesca* as a model system for strawberry genetics and genomics. *F. vesca* is the most widely distributed and most diverse of the diploid *Fragaria* species. Variants of *F. vesca*, selected for their novel, mutant traits such as day-neutrality, yellow/white fruit color, and runnerlessness, have been in cultivation in Europe for several hundred years. The everbearing (day-neutrality) trait is the defining characteristic of the 'semperflorens' or 'Alpine' form of ssp. *vesca*. Well know, commercially available varieties of the Alpine strawberry include red-fruited 'Baron Solemacher', and yellow-fruited 'Yellow Wonder'. Advantages of *F. vesca* as a diploid model species for strawberry include its self-fertility, fecundity, short generation time, ease of maintenance and propagation, amenability to genetic transformation, diverse germplasm base, and very small genome.

While *F. vesca* can be used a model to dissect the genomics of strawberry, there is still great need to evaluate the genetics of the octoploid crop. *Fragaria* × *ananassa* is composed of a complex set of progenitor species in addition to *F. vesca*, and these likely have their own unique genomes and genes. To employ marker assisted selection on the crop species, it will be necessary to test the segregation patterns of diagnostic markers in octoploid crosses. This approach has been successfully employed to identify QTL for the day-neutrality trait in *F. × ananassa* which have inheritance patterns that appear unique to those associated with day-neutrality in *F. vesca*.

Most strawberry growers rely on fumigation to reduce pathogen populations in soil prior to planting. Enhancing the tolerance or resistance of cultivars to root-rotting pathogens or nematodes could have tremendous environmental benefits as reliance on fumigation could be diminished. Similarly, considerable pesticide use is necessary to control fruit rots, mites and insects such as lygus bug. Observations of plant material suggest that tolerance or resistance exists within the genus, but incorporating it into the complex octoploid germplasm requires more knowledge than currently exists about the genetic basis for resistance.

Raspberry and blackberry

Worldwide, red raspberry (*Rubus idaeus* L.) production is concentrated in the former Yugoslavia and the Pacific Northwest of North America. In these regions, 'Meeker' and 'Willamette' developed in the mid-1900s are the primary cultivars although recent publicly developed cultivars 'Cowichan' and 'Coho' are being widely planted. Fresh market production of red raspberries is concentrated in California, Mexico and Chile in floricane and primocane fruiting cultivars developed by private and public breeding programs. Worldwide, 50 founding clones have been found to have contributed to the pedigrees of 137 red raspberry varieties released since 1960 (1993). These 137 varieties

cluster into 13 groups. Of the 50 founding clones, 31 appear in less than ten varieties, and 19 appear only one time. In modern varieties, 19 clones account for the vast majority of the germplasm with five founding varieties predominating, i.e., Lloyd George, Pyne's Royal, Cuthbert, Newburgh and Pruessen, (1989). Black raspberry (*R. occidentalis* L.) production has traditionally been concentrated almost completely in Oregon; however, a strong South Korean industry has developed over the past five years. With the recognition of the very high levels of anthocyanins/antioxidants contained in the fruit of this species consumption has rapidly been increasing. A total of ten species have been utilized but *R. idaeus* predominates for red raspberries and *R. occidentalis* for black raspberries. No commercially grown black raspberry cultivar is more than two generations from a wild selection (2002). Fall bearing red raspberries trace primocane fruiting to two founding clones with one exception. Currently less than 30 red raspberry varieties are cultivated to any extent in the U.S. and a single black raspberry cultivar accounts for over 95% of U.S. production. There are only five public and one or a few private programs, with Driscoll Fruit Associates being the most prominent devoting significant breeding effort to red raspberries and two public black raspberry breeding programs.

The two most significant problems facing the red and black raspberry processing industries are diseases. Red raspberries are generally very susceptible to phytophthora root rot, and the most important cultivars are susceptible to *Raspberry bushy dwarf virus* (RBDV). Marker assisted selections could greatly assist breeding for either disease as they are difficult to screen for and seem to be linked to unfavorable traits. The USDA-ARS (Corvallis, Ore.) has developed transgenic 'Meeker' red raspberries using coat and movement protein mediated resistance to RBDV. These genotypes have been through USDA screening but the industry has asked that they not be submitted for FDA approval until the public decides whether GMO raspberries are acceptable. Black raspberries are grown only for two cropping seasons before they must be replanted due to debilitating viruses. Identification of sources of virus resistance are being pursued in breeding programs.

Most red raspberries grown for the fresh market are grown for less than 18 months in the field and therefore have fewer problems with diseases particularly viruses. However, raspberry fruit are very perishable, and anything that can be done to increase their shelf life and decrease their susceptibility to botrytis fruit rot is desirable.

The blackberry industry continues to expand around the world, and an estimated 20,035 ha are planted and cultivated (Strik et al. 2006). While it is hard to point to one predominant reason for the continual expansion some of the reasons include: (1) blackberries are a new crop to many areas of the world, (2) they share many similarities to red raspberry and as raspberry production develops in an area, blackberries often follow, (3) blackberries are less expensive to produce than red raspberries because they do not have to be replanted as often and commonly do not have as many pest control inputs, (4) improved cultivars have been developed that ship better, extend the harvest season, taste better, are thornless etc., and (5) the growing awareness of the nutraceutical value of blackberries(they have higher levels of anthocyanins than many widely available fruits). North America is the leading producer of blackberries and production here is concentrated in the Pacific Northwest for processing and in Mexico for fresh market production. Blackberries can be divided into eastern types and western types in the U.S.

and are generally interspecific in makeup and extremely variable in ploidy with 4x, 6x, 7x, 8x, 9x, 12x and mixed aneuploid varieties available. Six or more North American native species have been used in breeding these. Western types are generally trailing while eastern ones are generally upright or semi-upright. Historically, the Eastern types have been bred for the fresh market and so attractive, firm fruit with good shelf life are highly desired, whereas the Western types have been bred for processing where machine harvestability, intense color, intense flavor, high titratable acidity, low pH, high soluble solid levels and low drip loss following freezing and thawing are important. The eastern types have a series of disease problems that need to be addressed and the western types need more thornless cultivars and greater adaptation to high and low temperatures. While there are several U.S. breeding programs with a small effort in blackberry, the two largest active public breeding programs are the USDA-ARS program in Corvallis (Ore.) led by Chad Finn and the University of Arkansas led by John Clark. Driscoll Fruit Association has the most substantial private program.

Rose

The rose industry is one of the largest ornamental industries in the USA, based on sales of rose bushes for landscaping, long-cut flower stems, and potted miniatures, with a value of about \$500 million annually (Streeper, 1990; U.S. International Trade Commission, 1995; USDA, 1998, 2002; Pertwee, 1992; Ferare, *The Conard-Pyle Company*, 2001).

Roses belong to the genus *Rosa* and have been cultivated as ornamental plants for more than two thousand years and are available in a range of distinct forms such as hybrid tea, floribunda, hybrid perpetual, grandiflora, shrubs, miniatures, old roses, and many others (Krussmann, 1981; Martin et al., 2001). There are about 120 wild rose species and more than 20,000 commercial cultivars. Most of the commercial cultivars are complex tetraploid ($x = 7$) or triploid hybrids derived from 8 to 10 wild diploid and a few tetraploid rose species. Intensive breeding during the last two centuries has resulted in a profusion of cultivars bred for color, fragrance and form; however, relatively little has been done for the development of resistance to the range of biotic and abiotic stresses (Gudin, 2001). To increase the level of biotic and abiotic resistance in the rose, breeding programs need to incorporate traits from “wild” germplasm, a very time consuming process via traditional methods.

Among ornamental woody plants, roses have a small genome, about 600 Mbp/haploid (Rajapakse et al., 2001a; Yokoya et al., 2000), which is only four times the genome size of *Arabidopsis*. Rose species and cultivars are highly polymorphic for morphological traits, isozymes, and DNA markers (Debener et al., 1996; 2000; Jan et al., 1999; Rajapakse et al., 1993; Martin et al., 2001; Esselink et al., 2003; Zhang et al., in prep.). In addition, roses have many traits preferred by consumers such as a wide range of flower types, fragrances, colors and sizes, availability of flowers throughout the year mainly due to the recurrent blooming ability, variety of growth habits ranging from miniatures to climbers, and good cut-flower keeping qualities. Most of these traits are not available in peach or other model crops. Furthermore, with a relatively short breeding cycle and easy vegetative propagation (Ma et al., 1996), rose is an excellent complementary model plant for the woody ornamentals within the Rosaceae family.

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