

**Microbial Genomic Sequencing
Perspectives of the
American Phytopathological Society
(Revised 2006)**



Healthy Plants • Healthy World

The American Phytopathological Society

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Background

Microorganisms play a critical role in plant health. Depending on the organism, they can cause multiple diseases or prevent them. Yet, on a genomic level, we know little about them (*The Microbe Project*, 2001, National Science and Technology Council, Office of Science and Technology Policy, Washington, D.C., 29 pg.). Genomic analyses of plant associated microorganisms are as essential to understanding the development and suppression of plant diseases. Analyses of microbial genomes will complement those done on plant genomes (e.g. for Arabidopsis, rice, etc) by providing new insights into the nature of plant-microbe interactions. The APS has consulted its members and constituencies on priority setting of microorganisms that should be sequenced. A first list was compiled in 2000-2001 which had significant impact in stimulating efforts leading to the sequencing of a number of microbial genomes, particularly bacterial and fungal. The list was revised in 2003. Researchers have been quite successful over the past two years in obtaining funding to sequence plant-associated microbes (see Existing sequencing projects with Plant-Associated Microbes), and therefore the list required a second revision in 2005. Nevertheless, there remains a critical need for greater information in microbial genomics. Thus it is with a sense of continued urgency that this revised list, created with extensive input from the membership of The American Phytopathological Society during 2005 is presented.

Plants for food, fiber, forestry and sport and amenity are subject to losses caused by a variety of physical and biological factors. Biological agents that cause losses estimated at 20-35%, over \$200 billion annually, are insects and microbes. Yet the biotic and abiotic variables that contribute to these losses are not fully understood. To date, much has been learned about the microbes that cause and suppress plant diseases, but genomic analyses will be needed to fully understand the nature of their interactions with plants. Due to multiple factors, such losses will continue to be a challenge. These factors include global climate change, plants grown in new ecosystems, mutation or gene transfer in pathogens, and spread of pathogens by nature or by commerce (shipping, transport, and storage). Such losses are considered unsustainable in view of projected needs of human and animal populations.

Using both traditional and innovative genetic approaches, plant breeding programs will continue to make a significant impact on reducing crop losses. However, little consideration is currently given to the diverse microbes that colonize plant tissues under field conditions. Continued huge economic and nutritional losses incurred are considered unsustainable given current projections for the growth of the human population and their increasing demand for food.

A complete understanding of disease susceptibility and resistance will require understanding the interactions between plant hosts and pathogen, and beneficial microorganisms. Sequence data from the genes for such microorganisms is essential to advance our knowledge of infection and the interaction of pathogens and host gene

products, and will provide knowledge on how these organisms reproduce and spread. Effective control will then be achieved through developing host resistance or through means that combat the pathogen directly or indirectly. Studies of microorganisms with biocontrol capacities may lead to further development of environmentally safe chemical controls for plant pathogens. The use of genomics has already been demonstrated through enhancing disease resistance by using viral components that can be incorporated into a host with current technology. Identifying critical genes in other pathogens will permit similar strategies to be developed for disease control. Similar strategies are receiving significant support for microbes of medical importance, as such efforts are identifying targets for drugs, and suggesting new targets for drug development and diagnostics. The genetic potential and sensitivity of pathogens must be understood to effectively combat current and future disease threats.

It should be noted that while not included in these lists parasitic plants such as members of the genera *Striga*, *Orobancha*, *Cuscuta* and *Viscum* represent some of the most destructive pests in world agriculture. Their non-inclusion here is primarily to maintain a focus on microbes. However, the society supports the sequence analysis of these important organisms.

Priority Setting and Criteria

A variety of organisms cause and prevent plant diseases. Fungi and viruses are the most significant and widespread. It is estimated that there are more than 10,000 pathogenic species of fungi and viruses, many of which are economically important. It is clear that it is not possible to obtain genomic sequences of all of them, at least based on current and anticipated technology. Thus, we suggest focusing on a representative set of significant microorganisms. Because of the taxonomic diversity of plant associated microbes and because the economic and/or research importance of specific species, continued microbial genomic sequencing is essential. To assist with this endeavor the following lists are a current consensus of up to 10 species of “Immediate Priority” and up to an additional 25 species considered of “high priority” within each biological category.

There have been additional substantial changes to the lists from the first version. Due to their relatively small genome size it is not useful to list individual plant viruses for sequencing, rather it is within technical and fiscal reach to sequence all known plant viruses, which of course would provide an extraordinary research resource to the scientific community. Additionally, because some genomes on the earlier list have been completed, are in progress, or substantial funding is in place, a list of these organisms follows each of the pertinent sections.

The listing has been developed using these criteria, essentially as outlined by the USDA (RFP for IFAFS, 2000):

- Economic importance and relevance to U.S. (and world-wide) plant health.
- Unique biological or environmental features.
- Broad interest to a significantly sized community of scientists or agriculturists.

- Genetic tractability, i.e. the ease with which genetic studies, such as crosses, genome modifications, etc. can be performed.
- Availability of tools and other biological resources, such as gene libraries, genetic maps, genetic tractability of the host so that the system could be addressed from both sides of the host-pathogen interaction, etc.

It is recognized that some organisms may be of critical agricultural importance but not easily cultured or subjected to genetic analysis, and therefore may be candidates for sequencing.

The taxonomic position of species of interest is recognized as of considerable significance in the choice of organisms to sequence. A broad representation of genomes of diverse taxa within each group is thought by many to be of importance. Thus sequencing of multiple closely related species prior to collection of data from the diversity of the group should be considered with due caution. This topic is discussed with focus on fungi and oomycetes the following article: Goodwin, S.B. Minimum phylogenetic coverage: An additional criterion to guide the selection of microbial pathogens for initial genomic sequencing efforts *Phytopathology* 94: 800-804.

Needs

Additional and new funding is of critical need. A growing number of research programs are at a major impasse due to lack of information about pathogen and biocontrol genomes. Cloning and characterization of individual genes is no longer cost effective. Microorganisms in general have compact genomes, in most cases a fraction of the size of plants and animals. Costs of genomic sequencing are still high, but decreasing. Functional and structural genomics will be the next phase of analysis. Some investment has occurred in the private sector, but relatively little. Very little has been publicly available for plant pathogens. The lack of sequence information for agriculturally important microorganisms in public databases has other serious consequences, such as those related to human resources, trade (phytosanitary) issues, and agroterrorism. Finally, although this list is primarily focused on initial structural genomics for these organisms continued funding is universally recognized by the membership to be essential for taking full advantage of this information. A plant-associated microbe genome initiative has been published (Leach *et al. Phytopathology*, 93:524-527) as a result of a workshop held in 2002 that recommends additional new funding for needed further research and education to fully leverage the value of the structural data obtained as advocated in this document.

Supplementary supporting documentation pertinent to some species on the “Immediate Priority” list can be found at

www.apsnet.org/media/ps/MicrobialGenomicsSequencingWhitePaperSupplement9_05.pdf

PLANT PATHOGENIC FUNGI AND STRAMENOPILES

**10 - IMMEDIATE PRIORITY SPECIES:
(Alphabetically, arranged - not ranked within the list)**

Species	Common Name	Genome Size	Rationale /Significance
<i>Aphanomyces euteiches</i>	Aphanomyces root rot	50 Mb???	<p>a) One of the most economically important pathogens on a diverse group of organisms including: pea, lentils and sugarbeet as well as fish and crayfish.</p> <p>b) A taxonomically primitive oomycete so genomic work done on other oomycetes such as <i>Phytophthora</i> species is not directly comparable. <i>Aphanomyces</i> can thus serve as the model species for primitive oomycetes such as <i>Saprolegnia</i> and <i>Achlya</i>.</p>
<i>Armillaria ostoyae</i>	Armillaria root rot	55 Mb	<p>a) In many forests, damage from pathogenic <i>Armillaria</i>, either directly or through predisposition to insect attack, accounts for a greater loss in forest productivity than that from any other forest pathogen.</p>
<i>Blumeria graminis</i>	powdery mildew	30-50 Mb	<p>a) Economically important pathogen of grain crops.</p> <p>b) Model for biotrophic fungal-plant interactions.</p>
<i>Cochliobolus heterostrophus</i>	southern corn leaf blight	35 Mb	<p>a) Necrotrophic pathogen model with classical and molecular genetic tractability and an historically significant disease.</p> <p>b) Representative of the <i>Cochliobolus/Alternaria</i> group of pathogens, notorious for production of host</p>

			selective toxins c) Loculoascomycete representative
<i>Colletotrichum graminicola</i>	anthracnose stalk rot of corn	48 mb	a) Representative species of a genus affecting a broad range of important crops. b) A serious pathogen of cool season turfgrasses as well as maize. Glomerella teleomorph
<i>Cronartium ribicola</i>	White pine blister rust		a) Introduced biotroph; ecologically and economically the most significant pathogen of North American conifers. b) Gene-for-gene and quantitative relationships with two different hosts: 5-needle pines and Ribes. c) Environment triggers several transitions in life cycle, allowing gene expression studies.
<i>Cryphonectria parasitica</i>	chestnut blight	Ca. 45 Mb	a) Causal agent of the economic extinction of the American chestnut. b) Model for fungal-mycovirus interactions, signal transduction and hypovirulence.
<i>Ophiostoma novo-ulmi</i>	Dutch elm disease	30-40 Mb	a) Responsible for the pandemic which has been decimating elm populations in North America and Europe since the 1960's.
<i>Rhizoctonia solani</i>	Rhizoctonia damping off and canker, etc.	37-46 Mb	a) Has a wide geographic distribution. b) Is an economically important pathogen of many plant species, including maize, potato, rice, soybean and wheat and turfgrasses used for sport and amenity.
<i>Verticillium dahliae</i>	Verticillium wilt	28.4 Mb	Vascular wilt disease on broad range of hosts.

PLANT PATHOGENIC FUNGI AND STRAMENOPILES

≤ 25 SPECIES - HIGH PRIORITY SPECIES:
(Alphabetically, arranged - not ranked within the list)

Species	Common Name	Genome Size	Rationale /Significance
<i>Armillaria mellea</i>	Armillaria root rot		
<i>Aspergillus ochraceus</i>		15.8 to 40 Mb	a) a major producer of ochratoxin A, a mycotoxin suspected (but not yet proven) to be a human carcinogen with widespread occurrence on a number of products b) The EU has proposed regulatory limits on ochratoxin A in products.
<i>Bremia lactucae</i>	lettuce downy mildew	50 Mb	a) Most important disease of lettuce. Lettuce is the eight most valuable crop in the US. b) Biotrophic member of the Oomycetes. c) Most experimentally tractable and studied of the downy mildews. Smaller genome size than some other oomycetes.
<i>Cercospora kikuchii</i>	Purple seed stain	28.4 Mb	a) Significant foliar and seed pathogen of soybean b) World-wide in occurrence.
<i>Colletotrichum higginsianum</i>	Anthracnose of crucifers	35-42 Mba	Significance: Although crucifer anthracnose disease itself is of only localized and sporadic importance, this pathogen is an excellent model for the entire genus of <i>Colletotrichum</i> fungi, which cause anthracnose diseases on nearly every crop of agronomic or horticultural importance in the world. Anthracnose diseases are particularly devastating on staples that are important for major populations in the developing world including cassava, maize, sorghum, millet, pulses, bananas, and yams. <i>C. higginsianum</i> is an important model because it causes a severe anthracnose disease on the model cruciferous plant <i>Arabidopsis thaliana</i> . <i>Colletotrichum</i> fungi are model hemibiotrophs, which produce primary "biotrophic" hyphae that cause relatively little damage to host tissues, followed by developmentally distinct secondary "necrotrophic" hyphae that induce massive tissue collapse and death.

<i>Crinipellis pernicioso</i>	Witches' Broom Disease of Cacao		The main factor limiting cocoa production in the Americas. A difficult to control disease causing pod losses of up to 90% in affected areas. This is a basidiomycete and thus its sequence will add to our knowledge on basidiomycete plant pathogens.
<i>Cronartium quercuum</i> f. sp. <i>fusiforme</i>	fusiform rust of pines		The major economic pathogen of pine trees in the southeastern U.S.
<i>Hemileia vastatrix</i>	coffee leaf rust		Critical pathogen of one of the world's most significant international commodities.
<i>Heterobasidium annosum</i>	Annosum/ Annosus root rot		
<i>Penicillium verrucosum</i>	Post-harvest mycotoxin producer	21 to 49 Mb	a) a major producer of ochratoxin A, a mycotoxin with widespread occurrence including economically important products (e.g. cereals, wine, coffee). b) Significance of ochratoxin A is increasing due to its perceived carcinogenic potential, and the proposal of regulatory limits on products in the EU.
<i>Labyrinthula terrestris</i>	rapid blight of turf		A new Stramenopile disease of turf. See http://www.apsnet.org/online/feature/rapid/
<i>Labyrinthula zosterae</i>	wasting disease of eelgrass		Important Stramenopile pathogen in marine ecosystems. See http://www.apsnet.org/online/feature/rapid/
<i>Levillula taurica</i>	Vegetable powdery mildew		Important wide host range disease in vegetables.
<i>Olpidium brassicae</i>	Soilborne virus vector		Transmitter of lettuce big vein virus. As a chytrid its genome sequence would be of high taxonomic value.
<i>Puccinia coronata</i>	oat crown rust	78 Mb?	a) One of most economically important pathogens of oat and barley. Is a pathogen of wide range of grasses. b) The Uredinales (rust fungi) represents one of largest groups of fungal plant pathogens (over 100 genera and 7,000 species). c) Genome sequence of <i>Puccinia graminis</i> (causal agent of stem rust of cereal and grasses, including wheat) is currently being done and having related rust fungi will be extremely beneficial for comparative analysis. d) Haploid chromosome number has been determined to be 17. cDNA libraries have been constructed to

			urediniospores, aeciospores and pycnial/aceial infected buckthorn leaf tissue.
<i>Puccinia striiformis</i>	wheat stripe rust	unknown	<ul style="list-style-type: none"> a) One of the most economically important pathogens of wheat and barley. In recent years has become the most important pathogen of wheat in Europe, Middle East and Northern Africa. In addition, has become a major disease in southern and central U.S., representing a major shift. In the past, stripe of wheat and barley was primarily confined to the Pacific Northwest. b) The Uredinales (rust fungi) represents one of largest groups of fungal plant pathogens (over 100 genera and 7,000 species). c) Genome sequence of <i>Puccinia graminis</i> (causal agent of stem rust of cereal and grasses, including wheat) is currently being done and having related rust fungi will be extremely beneficial for comparative analysis. d) Current resources: BAC library and cDNA library from urediniospores (approximately 40,000 clones).
<i>Puccinia triticina</i>	wheat leaf rust	90 Mb?	<ul style="list-style-type: none"> a) One of the most economically important pathogens of wheat, found worldwide. b) The Uredinales (rust fungi) represents one of largest groups of fungal plant pathogens (over 100 genera and 7,000 species). c) Genome sequence of <i>Puccinia graminis</i> (causal agent of stem rust of cereal and grasses, including wheat) is currently being done and having a related rust fungus would be extremely beneficial for comparative analysis. d) Current resources: 28,000-large EST database to be increased to 40,000 by the end of 2005; many life cycle stages sampled. Preliminary comparison to <i>P. graminis</i> indicates nucleotide similarities between homologs up to 90 – 95%. BAC library, genetic map

			and functional genomics tools in surrogate system under construction.
<i>Pythium aphanidermatum</i>	Damping off and root rot.	18.8 to 41.5 Mb	The most destructive <i>Pythium</i> species, attacking seedling to adult plants including both monocots and dicots in the field and in greenhouse operations.
<i>Sclerotium rolfsii</i>	Southern blight/ White mold		Important broad host range soil-borne fungal pathogen. Particularly damaging in warm environments.
<i>Tilletia caries</i>	Common bunt/ stinking smut	28-42 Mb	Causes Common bunt/stinking smut
<i>Ustilago hordei</i>	barley smut	20 Mb	Taxonomically and economically important smut species. Representative and model species of the bipolar mating type smuts. Many molecular tools already have been developed (genomic, sorted BAC and large cDNA libraries, and a physical map)
<i>Venturia inaequalis</i>	apple scab		

PLANT PATHOGENIC BACTERIA AND MOLLIICUTES
≤10 - IMMEDIATE PRIORITY SPECIES BACTERIA
AND
≤10 - IMMEDIATE PRIORITY SPECIES PHYTOPLASMAS and SPIROPLASMAS:
(Species are alphabetically, arranged - not ranked within the list)

Organism	Strain	Genome Size	Rationale /Significance
<u>Bacteria</u>			
<i>Burkholderia cepacia</i>	ATCC 25416	7.9 Mb incl 3.5, 3.1, 1.1, and 0.2 Mb replicons	Causes sour skin of onion, cavity disease of mushroom, brown spot of orchids, and rot of caladium bulbs. Strain ATCC 25416 is a plant-pathogen representative of genomovar I strains, which have rarely been isolated as human pathogens. Opportunity for direct genome comparison to genomovar III strains, which are more typically associated with cystic fibrosis patients exhibiting symptoms of Cepacia syndrome.
<i>Clavibacter michiganensis</i> subsp. <i>insidiosus</i>	NCPPB 1109	ca. 3.0	Causes an economically important disease on alfalfa. Very little known of its molecular biology due to the difficulty in genetic manipulation of the pathogen. Recent advances in the manipulation of related pathogens and the soon to be available genome sequences of <i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i> , <i>C. michiganensis</i> subsp. <i>michiganensis</i> and <i>Leifsonia xyli</i> will enable genomic and functional comparisons across phylogenetically related vascular pathogens..
<i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i>	Ecc71	ca. 5 Mb	Causes soft rot and related diseases of numerous crops worldwide, under temperate as well as tropical conditions and under field conditions, in storage and in transit. Opportunity for genome-scale comparison with enterobacterial pathogens (virulence factors and evolution of pathogenesis). Because this pathogen has world wide economic importance and has been a principal model organism for molecular studies of plant-microbe interactions, the scientific community who would benefit from the genomic sequence is particularly large.
<i>Pseudomonas marginalis</i>		ca 6.5 Mb	Causes soft rot. Sequence would be useful for comparison to other <i>Pseudomonas</i> spp. and to <i>Pectobacterium</i> spp. This bacterium represents a group of phytopathogenic pseudomonads and its sequence would be useful for exploring the similarities and differences among this important group of plant pathogens.

<i>Pseudomonas viridiflava</i>		ca. 6.0 Mb	Causes leaf spot (soybean and melon, among others) and bacterial blight (kiwi). This bacterium represents a group of phytopathogenic pseudomonads and its sequence would be useful for exploring the similarities and differences among this important group of plant pathogens.
<i>Rhodococcus fascians</i>	D188	5.8 Mb	Causes leafy gall formation on a broad array of monocot and dicot plants. It induces de novo cell division in cortical plant cells, leading to the formation of numerous shoot meristems. It is an adapted endophyte that possibly also enters the plant cells. This strain has been the model strain in molecular studies. As a close relative to <i>Rhodococcus equi</i> (virulent on horse) and Mycobacterium species (known human and animal pathogens), it is a good model for understanding general and specific pathogenesis factors from Actinomycetes, from both plant and animal pathogens.
<i>Streptomyces turgidiscabies</i>	Car8	10 Mb	Causes a severe version of potato scab in Japan and possibly in Europe. Not currently found in the United States. Contains a mobilizable pathogenicity island about 660 kb in size that includes the fas operon. This operon is homologous and colinear with the operon in <i>Rhodococcus fascians</i> and represents an introduction to the PAI in <i>Streptomyces</i> . A genome sequence will be highly useful for comparative genomics among pathogenic and nonpathogenic <i>Streptomyces</i> and investigation of the PAI within different genetic backgrounds.
<i>Xanthomonas axonopodis</i> <i>pv. malvacearum</i>		ca. 5.0-5.2 Mb	Causes cotton blight disease, which causes yield losses of up to 50%, with 10-30% losses occurring commonly. Cotton blight disease is a world-wide problem. The pathogen has served as a model bacterial gene-for-gene system with the highest level of race specificity of any xanthomonad (over 20 races described). The African strains are of particular interest because they are quarantined pathogens in the U.S., and they are capable of defeating most of the resistance genes that are known against the disease. The organism is amenable to standard microbial genetic tools, and the histology, biochemistry and physiology of the disease have been very well described, giving enormous leverage to the sequence information..
Phytoplasmas and Spiroplasmas			
<i>Clover Phyllody</i> <i>Phytoplasma</i>		ca. 0.8 Mb	Clover phyllody is widespread in North America and Europe where it is responsible for diseases in fruits and vegetables. Host plants damaged by this phytoplasma include <i>Trifolium</i> spp., <i>Fragaria</i> (strawberry), <i>Olea</i> (olive), <i>Poa pratensis</i> , <i>Anemone</i> , <i>Ranunculus</i> , and <i>Vitis</i> (grapevine). This phytoplasma is a

			member of subgroup C in group I (the aster yellows group) and is a distinct species from aster yellows phytoplasma strains.
<i>Spiroplasma citri</i>	BR3-3X	1.6 Mb	<p>Spiroplasmas are unique bacteria characterized by tiny cell and genome sizes, lack of a cell wall, helical morphology, and an unusual genetic code.</p> <p><i>Spiroplasma citri</i> causes disease in a number of plant species including citrus, and also colonizes its insect vectors. <i>S. citri</i> strain BR3-3X, isolated from brittle-root diseased horseradish plants in Illinois, has been the model system for U.S. research on spiroplasma-vector interactions for over 20 years</p>

PLANT PATHOGENIC BACTERIA AND MOLLICUTES ≤25 SPECIES - HIGH PRIORITY SPECIES 10 BACTERIA AND ≤25 SPECIES - HIGH PRIORITY SPECIES PHYTOPLASMAS and SPIROPLASMAS: (Species are alphabetically, arranged - not ranked within the list)			
Bacteria			
<i>Acidovorax avenae</i> subsp. <i>avenae</i>	CAa4		Infects many important crops including bacterial stripe of rice, bacterial stalk rot and blight of corn, leaf blight of oats, and red stripe of millet and sugarcane. These diseases have become very important in Asia, especially in seedlings. The closely related <i>A. avenae</i> subsp. <i>citrulli</i> causes severe losses in watermelon and other cucurbits.
<i>Brenneria rubrifaciens</i>		ca. 3.0 Mb	Causes deep bark canker of walnut. Former name is <i>Erwinia rubrifaciens</i> . Opportunity for comparative genomics with other Enterobacteriaceae, including those that cause other plant and animal diseases.
<i>Clavibacter michiganensis</i> subsp. <i>nebraskensis</i>	NCPPB 2581	ca. 3.0 Mb	Causes Goss's wilt of corn. Very little is known of its molecular biology. Availability of the <i>C. m.</i> subsp. <i>nebraskensis</i> genome sequence would enable genomic and functional comparisons across phylogenetically related vascular pathogens, which specifically infect either monocots or dicots.
<i>Pectobacterium betavasculorum</i>	Ecb168		Causes soft rot of sugar beet. Differs from other soft rot pathogens in having very narrow host range, and therefore provides opportunity for discovery of molecular basis of host specificity. Opportunity for genome-scale comparison with enterobacterial pathogens of humans.
<i>Pectobacterium rhapontici</i>			Causes crown rot of rhubarb. Produces pro-ferrosamine (pink iron+2 chelating pigment)
<i>Pseudomonas chicorii</i>		ca. 6.0 Mb	Center rot of "french endive" or wilt of chicory. This bacterium represents a group of phytopathogenic pseudomonads and its sequence would be useful for exploring the similarities and differences among this important group of plant pathogens.
<i>Pseudomonas corrugata</i>			The tomato pith necrosis pathogen, <i>Pseudomonas corrugata</i> , is a non-fluorescent pseudomonad that is closely allied to the fluorescent pseudomonads when compared using standard physiological tests. The bacterium is also a severe opportunistic pathogen of tomatoes but has a restricted host range. It can

			rapidly macerate tomato pith tissue but the actual mechanism of pathogenicity is still unknown. All is known of the genetics of the bacterium is a putative regulator of pathogenicity. Hence, sequence data would clarify taxonomic standing and elucidate potential pathogenicity pathways that can be explored through genomics and proteomics.
<i>Pseudomonas syringae</i> pv. <i>atropfaciens</i>		ca. 6.0 Mb	Causes basal glume blotch of cereals, and produces syringomycin and syringopeptin. This bacterium represents a group of phytopathogenic pseudomonads and its sequence would be useful for exploring the similarities and differences among this important group of plant pathogens.
<i>Pseudomonas syringae</i> pv. <i>coronofaciens</i>		ca. 6.0 Mb	Causes bacterial blight of soybean. Important model strain for studies of gene-for-gene interactions. Opportunity for comparative studies with other <i>Pseudomonas</i> spp. whose genomes are known.
<i>Pseudomonas tolaasii</i>			Causes bacterial blotch of mushrooms. Produces a variety of lipodepsipeptides and other secondary metabolites. Opportunity for comparative pathobiology of fungal vs. plant and animal pathogens.
<i>Rathayibacter toxicus</i>	ATCC 49908		Infects annual Wimmera ryegrass in South Australia. It is carried by a nematode (<i>Aguina</i> species) into developing seed heads and produces corynetoxin, which is a relative of tunicamycin, an antibiotic that blocks glycosylation. The toxin kills livestock grazing on the infected wild ryegrass. Control is to use herbicides to kill the ryegrass. <i>R. toxicus</i> distorts the seed heads (swelling) and produces an orange exudate. It could therefore be considered a plant pathogen of a weed grass, but <i>R. toxicus</i> is more economically important to the cattle and sheep industry, which would also benefit from having <i>R. toxicus</i> ' genome sequenced.
<i>Sphingomonas</i> (<i>Rhizomonas</i>) <i>suberifaciens</i>			Causes corky root. Genomic sequence information will provide insight into a plant pathogen in a distinct taxon from others whose sequences are known.
<i>Serratia marcescens</i>		ca. 5 Mb	Causes cucurbit yellow vine disease of watermelon, cantaloupe, and squash, associated with devastating losses in Oklahoma and Texas in recent years. Opportunity for genomic comparisons to related Enterobacteria that cause disease of humans. Also could provide insight into the relationship with the vector of this disease, the squash bug, <i>Anasa tristis</i> (De Geer) and phloem-limited lifestyle of this bacterial pathogen.

<i>Xanthomonas phaseoli</i>			Causes common bacterial blight (CBB) on <i>Phaseolus vulgaris</i> . <i>P. vulgaris</i> (common dry and snap beans) is notoriously susceptible to pathogens. CBB is one of the most economically important and widespread diseases of <i>P. vulgaris</i> and is a major constraint to the realization of high yields and high seed quality. CBB has been reported to cause significant yield losses in Michigan (10%-20%), in Canada (38%) and in Colombia (45%). Management of CBB is very difficult due, in part, to the pathogen's persistence. Although CBB is seed transmitted, seed programs have been only partially and inconsistently effective in controlling it in the U.S. and Canada.
<i>Xanthomonas campestris</i> pv. <i>translucens</i>		ca. 5.0 Mb	Causes bacterial blight or stripe of several cereals and streak of sorghum and maize. Important genus for comparative genomics due to extensive host-pathovar specificity and sequenced <i>Xanthomonas</i> and <i>Xylella</i> genomes.
<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i>	75-3	ca. 5.0 Mb	Causes bacterial spot of tomato and pepper, a significant disease constraining tomato and pepper production worldwide, especially in tropical and subtropical regions. Model organism for molecular studies on plant-microbe interactions, especially host-pathogen specificity because the <i>hrp</i> system has been most extensively characterized in this species of <i>Xanthomonas</i> . Important genus for comparative genomics due to extensive host-pathovar specificity and sequenced <i>Xanthomonas</i> and <i>Xylella</i> genomes. Large international research community.
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	PXO86	ca. 5.0-5.2 Mb	Causes bacterial blight of rice, the most important bacterial disease of rice worldwide and quarantined as a threat to US production. Model monocot-(vascular) bacterial pathosystem. By comparison with closely-related rice mesophyll parenchyma pathogen <i>X. o. oryzicola</i> , superb model to determine genetic requirements for vascular colonization. Important genus for comparative genomics due to extensive host-pathovar specificity and sequenced <i>Xanthomonas</i> and <i>Xylella</i> genomes. Important for understanding xanthan gum and pigment biosynthesis and utilization of plant compounds. International research community. Tractable for molecular studies, many tools and resources available. The genome of a different strain of <i>X. oryzae</i> pv. <i>oryzae</i> has been sequenced, and the availability of genome sequences for several strains will provide opportunity for comparative genomics of this important pathogen.

Phytoplasmas and Spiroplasmas

Elm Yellows Phytoplasma			Elm Yellows Phytoplasma is widespread in North America and Europe. This phytoplasma is lethal to American elm (<i>Ulmus americana</i>). A large percentage of American elm tree deaths that were originally attributed to Dutch elm disease are now believed to have been caused by the EY phytoplasma. This phytoplasma is also a major cause of the loss of our native American elm. EY phytoplasma is a member of group V subgroup A and is being named 'Candidatus Phytoplasma ulmi'.
Palm Lethal Yellowing Phytoplasma		0.67 kb	Palm lethal yellowing (LY) phytoplasma is responsible for devastating and recurrent losses of coconut and other palms species in Florida, the western Caribbean and, most recently, Central America. LY phytoplasma is a member of Group IV and phylogenetically distinct from other phytoplasmas in the Americas.
Pigeon Pea Witches' Broom		1 MB	Pigeon pea witches' broom (PPWB) phytoplasmas are found in many parts of the world and can cause significant losses. PPWB in Florida is caused by a phytoplasma that is phylogenetically distinct from other phytoplasmas found in North America. Comparative genomics of the PPWB phytoplasma with the other unrelated phytoplasmas that are being sequenced could provide significant insight into the genetic diversity of this unique group of plant pathogenic mollicutes.
Potato Witches Broom Phytoplasma			Potato witches' broom phytoplasma is responsible for serious disease in potato in North America. This phytoplasma is a member of group VI and represents a distinct species that is only distantly related phylogenetically to aster yellows and clover phyllody phytoplasmas.
<i>Spiroplasma melliferum</i>			Although not a plant pathogen, <i>S. melliferum</i> is a pathogen of bees, and thus is similar to plant pathogenic spiroplasmas in replicating in insects. The genomic sequence will be useful for comparative genomics to identify genes that are potentially involved in plant pathogenesis.
Walnut Witches Broom Phytoplasma		0.8 Mb	Walnut witches' broom phytoplasma causes economic losses in the southeastern U.S. This phytoplasma is phylogenetically related to the X-disease phytoplasma, however X-disease phytoplasma does not infect walnut nor does walnut witches broom infect stone fruit trees. Comparative genomics of X-disease, which is nearing completion, with walnut witches broom could provide insights into host specificity.

<i>Spiroplasma phoenicium</i>			Third of three known spiroplasmas that cause diseases of plants. Native host is unknown, causes disease of periwinkle. Value in comparison to other two species of plant pathogenic <i>Spiroplasma</i> as well as to the many of <i>Spiroplasma</i> that cause diseases of insects,
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PLANT ASSOCIATED BENEFICIAL PROKARYOTES AND EUKARYOTES

<10 - IMMEDIATE PRIORITY SPECIES:
(Alphabetically, arranged - not ranked within the list)

Organism	Strain	Genome Size Mb	Rationale/Significance
<u>Prokaryotes:</u>			
<i>Bacillus subtilis</i>	GB03	ca. 4.3	One of the most widely distributed bacterial species in agricultural systems. This rhizosphere isolate is used in biocontrol of soilborne root diseases. Well-established commercial applications. Excellent opportunity for genome-scale comparisons with saprophytic and pathogenic species in the genus.
<i>Enterobacter cloacae</i>	Ec501		A common, aggressive spermosphere and rhizosphere colonizer of several plant species. Strain Ec501 provides an excellent model system for colonization, biocontrol and metabolism, and would serve as an excellent choice for comparative genomics with other plant and non-plant associated enterics.
<i>Lysobacter enzymogenes</i>	C3	6.5 Mb	Common soil and water inhabitant with antagonistic activity towards various microorganisms, and demonstrated biocontrol activity towards several plant diseases. Producers of multiple forms of chitinases and glucanases and other extracellular, depolymerizing enzymes. Also produces antibiotics and contains a type III secretion system. No <i>Lysobacter</i> spp. has been sequenced to date.
<i>Pantoea agglomerans</i>	C9-1	ca 4.5	Common plant epiphyte. Registration is in progress for commercialization for biological control strain of fireblight. Opportunity for genome-scale comparison with enterobacterial pathogens.
<i>Pseudomonas fluorescens</i>	A506	ca. 6.5 Mb	Common plant epiphyte. Commercial biological control strain for fireblight. Opportunity for genome-scale comparison with other fluorescent pseudomonads.
<i>Pseudomonas fluorescens</i>	Q8r1-96	ca 6.5 Mb	Aggressive rhizosphere colonist and biological control agent of root diseases. Type strain for D genotype of DAPG producers. Biovar distinct from <i>P. fluorescens</i> Pf-5 which is currently being sequenced. Opportunity for comparisons with other fluorescent pseudomonads.

<i>Pseudomonas synxantha</i>	BG33R	ca. 6.5	Isolated from a nematode suppressive soil. Produces a compound that kills eggs of both <i>Mesocriconema xenoplax</i> (Ring nematode) and <i>Meloidogyne incognita</i> (Root Knot nematode). Extensive molecular analysis has been done, libraries and mapped sequence tags are available to support an accelerated, cost-effective sequencing effort.
<u>Eukaryotes:</u>			
<i>Cryptococcus nodaensis</i>	OH 182.9		Consistent field efficacy against Fusarium head blight and published accounts of fermentation, formulation, and field efficacy results alone or in combination with other antagonists and/or fungicides. Opportunity for genome-scale comparison with <i>Cryptococcus neoformans</i> (genome sequence completed).
<i>Fusarium oxysporum</i>	Fo47		
<i>Trichoderma harzianum</i>	T22	ca. 35	Active ingredient in commercial biocontrol products used on multiple crops. Subject of extensive genetic and ecological studies. Opportunity for genome-scale comparison with T. reesei strain which is currently being sequenced.

PLANT ASSOCIATED BENEFICIAL PROKARYOTES AND EUKARYOTES

**≤25 - HIGH PRIORITY SPECIES:
(Alphabetically, arranged - not ranked within the list)**

Prokaryotes:

<i>Bacillus licheniformis</i>	Type Strain		
<i>Bacillus licheniformis</i>	SB3086		Commericalized biocontrol strain used in Ecoguard (Novozymes). Type strain ATCC14580 already sequenced. Useful for genomic comparisons with biological control strains to identify genes unique to biocontrol.
<i>Bacillus mojavenis</i>	203-7		
<i>Bacillus mycoides</i>	ATCC 6482		Accepted type strain of species. Useful for genomic comparisons with biological control strains to identify genes unique to biocontrol.
<i>Bacillus mycoides</i>	BmJ		
<i>Bacillus pumilis</i>	ATCC 7061		Accepted type strain of species. Useful for genomic comparisons with biological control strains to identify genes unique to biocontrol. Note: <i>B. pumilis</i> strain FO-036b, non biocontrol strain is slated for sequencing in 2006.
<i>Bacillus pumilis</i>	GB34		Commercial biocontrol strain
<i>Bacillus pumilis</i>	QST 2808		Commercial biocontrol strain
<i>Bacillus subtilis</i>	MBI600		Commercial biocontrol strain
<i>Bacillus subtilis</i>	IN937a	ca. 4.3	Well-studied PGPR strain. Known inducer of plant host defenses against multiple diseases on different crops.

<i>Beuvaeria basiana</i>			Controls <i>Rhizoctonia</i>
<i>Pseudomonas aureofaciens</i>	ATCC 13985		Accepted type strain of species. Useful for genomic comparisons with biological control strains to identify genes unique to biocontro
<i>Pseudomonas aureofaciens</i>	30-84	ca 6.5	Phenazine producer and model strain for genetic studies of biological control and quorum sensing. Opportunity for genome-scale comparison with other fluorescent pseudomonads.
<i>Pseudomonas fluorescens</i>	CHA0	ca. 7.1	Well-studied cognate of Pf-5, differing in genomic and carbon utilization fingerprints. More similar to A-genotypes isolated from multiple locations in than Pf-5.
<i>Pseudomonas fluorescens</i>	Q2-87	ca. 6.5	
<i>Rhizobium etlii</i>	G12		
<i>Stenotrophomonas maltophilia</i>	34S1		The species is a common soil and rhizosphere inhabitant known to produce complex secondary metabolites and extracellular enzymes with antifungal activities. No species of this genus has been sequenced to date and would be of interest from both the diversity standpoint, as well as comparative purposes with taxonomically-related xanthomonads.
<u>Eukaryotes:</u>			
<i>Fusarium oxysporum</i>	Cs-20		
<i>Glomus sp.</i>	mycorrhizal fungus	100 Mb	a) Important symbiotic mycorrhizal fungus
<i>Paecilomyces lilaciuus</i>	251		

<i>Rhizoctonia</i> sp.			Binucleate <i>Rhizoctonia</i> useful for controlling pathogenic <i>Rhizoctonia</i> and other fungal and bacterial diseases.
<i>Trichoderma asperellum</i>	T-34		
<i>Trichoderma hamatum</i>	382		
<i>Trichoderma virens</i>	G1-21		

PLANT PATHOGENIC NEMATODES

≤10 - IMMEDIATE PRIORITY SPECIES: (Alphabetically, arranged - not ranked within the list)

Organism (by category)	Common Name	Genome Size	Rationale or Significance
<i>Bursaphelenchus xylophilus</i>	Pine wood Nematode		
<i>Globodera pallida</i>	Potato cyst nematode	1 x 10 ⁸	Most economically important nematode in Europe. Sedentary endoparasite of potato.
<i>Globodera rostochiensis</i>	Potato Cyst Nematode		
<i>Heterodera glycines</i>	Soybean cyst Nematode	9.2 x 10 ⁷	Most economically important pathogen on soybean. Chosen as a model nematode for plant parasites. Sedentary endoparasite.
<i>Heterodera schachtii</i>	Sugar beet Cyst Nematode		
<i>Meloidogyne arenaria</i>	Peanut Root Knot Nematode		
<i>Pratylenchus penetrans</i>	Lesion Nematode		An economically important migratory endoparasite. Wide host range with a different feeding habit.
<i>Radopholus similis</i>	Burrowing Nematode		An economically important migratory endoparasite on citrus and ornamentals in the Americas.
<i>Trichodorus spp.</i>	Stubby Root Nematodes		
<i>Xiphinema rivesi</i>	Dagger Nematode		An economically important nematode and a vector for plant viruses including tomato ringspot.

- Compiled by the nematology committee

PLANT PATHOGENIC NEMATODES

≤25 - HIGH PRIORITY SPECIES:

(Alphabetically, arranged - not ranked within the list)

Organism (by category)	Common Name	Genome Size	Rationale or Significance
<i>Anguina funesta</i>	(Seed Gall Nematode)		
<i>Aphelenchoides fragariae</i>	Foliar nematode, Spring Crimp Nematode		A leaf-inhabiting nematode that is a pathogen on ornamentals.
<i>Ditylenchus dipsaci</i>	Bulb and Stem Nematode		One of the most devastating nematodes on a wide range of crops worldwide. Feeds on the shoots of plants as a migratory endoparasite.
<i>Meloidogyne artiella</i>	Root Knot Nematode		
<i>Meloidogyne chitwoodi</i>	Columbia Root Knot Nematode		
<i>Meloidogyne fallax</i>	Root Knot Nematode		
<i>Meloidogyne javanica</i>	Javanese Root Knot Nematode		
<i>Nacobbus aberrans</i>	False root knot Nematode		Problems in Western US on potato, same family as <i>Pratylenchus</i> and <i>Radopholus</i> but sedentary.
<i>Rotylenchulus reniformis</i>	Reniform Nematode		Widely distributed sedentary semiendoparasitic nematode in the tropical and subtropical countries that is an important parasite with a wide host range.
<i>Xiphinema americanum</i>	Dagger Nematode		An economically important nematode and a vector for plant viruses including tomato ringspot.

- Compiled by the nematology committee

PLANT VIRUSES

Because the genome of plant viruses is small compared to cellular microbes the aps membership believes that rather than listing individual viruses a great deal of progress can be made by accomplishing the goal of sequencing all known plant viruses. Below is a statement prepared to this effect by the APS Virology Committee.

Because the genome of plant viruses is small compared to cellular microbes the APS membership believes that rather than listing individual viruses a great deal of progress can be made by accomplishing the goal of sequencing all known plant viruses. Below is a statement prepared to this effect by the APS virology committee.

The biodiversity among and between viruses is staggering. Viruses are microbes known to infect a majority of life forms. Among their genomes are single-stranded and double-stranded, linear and circular, DNA and RNA representatives. Viruses use a diversity of mechanisms to replicate in host cells, elucidation of such mechanisms has led to many major advances in biology. Yet, our understanding of viral genomes, driven by interests in human medicine and agriculture, has been limited mostly to economically important viruses. Still, the proportion of recognized viruses for which the genome has been completely sequenced is impressive. Completion of the genome sequencing of recognized viruses is within our grasp. An effort to complete the sequencing of the genomes of recognized plant viruses will have immediate significance for biotechnology, for molecular and cellular biology, and for virus diagnostics.

Given the importance of viral sequences to biotechnology, molecular biology, and virus detection and identification, it is surprising that virus sequencing projects have been underfunded by the Microbial Genome Sequencing program. The poor representation of viruses is due in part to the ease with which single virus sequences can be obtained and in part to the lack of an organized effort of obtaining complete coverage of a virome, such as the plant virome. An organized effort to determine the genomic sequences of viruses most diverged from those whose genomes have been already completely sequenced is needed. The plant viral genomes are eukaryotic in nature because they function in eukaryotic cells. However, selection for small genome sizes resulted in a high gene density, more dense than found in other microbes, including eukaryotic microbes. With rare exceptions there are no introns, no highly repeated sequences and no large intergenic regions. Often one finds overlapping genes. Thus, the yield per million base pairs (Mbp) of useful molecular biological information from a virome project should be far greater than from other genome projects.

Therefore, the long range goal of the proposed work is to obtain complete genome sequences of all recognized viruses. Understanding that reaching this goal efficiently requires considerable organization and cooperation, we propose to demonstrate the feasibility of the larger goal by concentrating on viruses that infect plants. The defined number of recognized but unsequenced viruses (572 species at last count), combined with the relatively small size of most of their genomes makes this an ideal pilot project. This number will increase slightly over time due to the continual emergence and recognition of new plant viruses species.

Sequencing the complete genomes of all known but as yet unsequenced plant viruses would take minimal effort and resources in comparison to sequencing the complete genomes of two bacterial species, while providing enormous amounts of useful data.

Existing sequencing projects with Plant-Associated Microbes.

PREVIOUSLY LISTED FUNGAL AND STRAMENOPILE PLANT PATHOGENS SEQUENCED/OR FUNDED (additional funding for completion may be needed):			
<i>Alternaria brassicicola</i>	black spot disease of crucifers	28 Mb	a) Relative to a number of other important pathogens. b) Necrotrophic fungal pathogen model.
<i>Aspergillus flavus</i>		~ 30 Mb	Important producer of aflatoxins, extremely potent carcinogenic mycotoxin.
<i>Botrytis cinerea</i>	gray mold	ca. 22Mb	a) Economically very significant pathogen. b) taxonomically distinct discomycete. Botryotinia teleomorph
<i>Epichloe sp.</i>	grass endophyte	29-35 Mb	a) Endophytes provide benefits to forage grasses but often reduce livestock productivity. b) The model endophyte, <i>E. festucae</i> is the most genetically tractable, plant-mutualistic fungus and has numerous agronomically important genes such as for bioprotective alkaloids. (Contact: Chris Schardl)
<i>Fusarium graminearum</i>	wheat head scab fungus	40 Mb	a) Causes one of the most important plant diseases in US, wheat head scab. b) Produces trichothecene mycotoxins. c) Studied by large number of investigators worldwide.
<i>Fusarium oxysporum</i>	Fusarium vascular wilt	43 MB	a) A model for soil-borne fungal diseases, a pathogen of <i>Arabidopsis thaliana</i> . b) Causes economically important diseases of a broad range of crops and ornamentals including tomato, banana, palm, cotton and many others. c) One of the dominant fungal species found in soil and endophytic on plant roots.
<i>Fusarium verticillioides</i>	Fusarium stalk rot of corn	46 Mb	a) Major pathogen of maize worldwide, causes both kernel and stalk rot. b) Produces fumonisin mycotoxins. Gibberella teleomorph

<i>Magnaporthe grisea</i>	rice blast fungus	40 Mb	a) Most devastating fungal disease of rice and a serious pathogen of turfgrasses used for sport and amenity. b) Amendable to classical and molecular genetics
<i>Mycosphaerella graminicola</i>	Septoria blotch	38-40 Mb	a) Largest genus of plant pathogenic fungi. b) Economically significant disease of wheat worldwide. c) Model system for the order Dothideales. d) Large, international research community.
<i>Mycosphaerella fijiensis</i>	black sigatoka pathogen of banana		Being sequenced by JGI, not previously on APS list. Contact: Steve Goodwin
<i>Phaeosphaeria nodorum</i> (anamorph <i>Stagonospora nodorum</i>)	leaf and glume blotch of wheat		Being sequenced by the Broad Institute, not previously on APS list. Funded by Australian wheat growers consortium in Contact: Steve Goodwin
<i>Phakopsora meibomia</i>	soybean rust	70 Mb	a) A major soybean pathogen, the less virulent species of <i>Phakopsora</i> .
<i>Phakopsora pachyrhizi</i>	soybean rust	70 Mb	a) A major soybean pathogen, listed as one of the "Agricultural Select Agents" by USDA and CDC.
<i>Phytophthora infestans</i>	potato late blight	237 Mb	a) Most important pathogen of potato b) Model system within the oomycetes c) Advanced genetics and transformation system and libraries
<i>Puccinia graminis</i>	stem rust	67 Mb	a) Causes rust disease on several agriculturally important cereal crops (barley, oat, rye and wheat) and turfgrasses used for sport and amenity. b) Distributed worldwide.
<i>Pyrenophora tritici-repentis</i>	tan spot of wheat	27 Mb	a) Broad distribution of disease and researchers worldwide. b) Produces proteinaceous host-selective toxins.
<i>Sclerotinia sclerotiorum</i>	white mold	26-44 Mb	a) Number 2 cause of yield loss in soybean in US. b) Major pathogen of canola, sunflower, edible beans, vegetable crops and more than 400 plant species.
<i>Ustilago maydis</i>	corn smut fungus	20 Mb	Important basidiomycete model system for the smuts which are economically important disease agents.

PROKARYOTIC PLANT PATHOGENS SEQUENCING PROJECT STATUS (additional funding for completion may be needed):

Species	Strain	Size (Mb)	status	Contact person	Sequencing Center	References
Bacteria						
<i>Acidovorax avenae</i> subsp. citrulli		in progress		JGI		
<i>Agrobacterium tumefaciens</i>	C58	5.7	completed		University of Washington Genome Center/Cereon	Wood et al. 2001; Goodner et al 2001
<i>Agrobacterium vitis</i>	CG78		in progress	Burr, Cornell	Monsanto	
<i>Burkholderia glumae</i>		8	in progress	Jaeger, Germany	Göttingen Genomics Laboratory	
<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	ATCC 33113	3.5	in progress	Ishimaru, Colorado	Sanger Institute	Bell et al 2004. PNAS 101:11105.
<i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i>	NCPB382	3.2	in progress	Eichenlaub, Germany		
<i>Erwinia amylovora</i>	Ea273	ca. 4.5	in progress	Beer, Cornell		
<i>Erwinia carotovora</i> subsp. <i>atroseptica</i>	SCRI1043	5.1	completed	Salmond, Cambridge, UK; Toth, Scotland, UK	Sanger Institute	Bell et al 2004. PNAS 101:11105.
<i>Erwinia</i>	3937	3.7	in progress	Perna, Wisconsin	TIGR	

<i>chrysanthemi</i>						
<i>Leifsonia xyli</i> <i>subsp. xyli</i>	CTCB07	3	completed		AEG, Brazil	Monteiro-Vitorello et al 2004. MPMI 17:827
<i>Pantoea citri</i>			completed	C. I. Kado, U.C. Davis	Genecor	
<i>Pantoea stewartii</i> <i>subsp. stewartii</i>	DC283	ca. 5.0	in progress	Perna, Wisconsin		
<i>Pseudomonas syringae</i> pv <i>tomato</i>	DC3000	5.6	completed	Collmer, New York	TIGR	Buell et al. 2003. PNAS 100:10181
<i>Pseudomonas syringae</i> pv <i>syringae</i>	B728a		completed	Lindow, California	JGI	Feil et al. 2005. PNAS 102:11064
<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i>	1448A	6.5	completed	Collmer, New York	TIGR	J. Bacteriology (in press)
<i>Pseudomonas viridiflava</i>			proposal submitted	Micheltmore, Greenberg, Collmer	DOE/JGI	
<i>Ralstonia solanacearum</i>	GMI1000	5.8	completed		Genoscope/INRA	Salanoubat et al. 2002. Nature 415:497.
<i>Ralstonia solanacearum</i>	1609		in progress		Genoscope	
<i>Ralstonia solanacearum</i>	Molk2		in progress		Genoscope	
<i>Ralstonia solanacearum</i>	UW551		8X completed	Gabriel, Florida		

race 3 biovar 2						
<i>Streptomyces scabies</i>	87.22	ca. 8.0	in progress	Loria, Cornell		
<i>Xanthomonas axonopodis</i> pv. <i>aurantifolii</i>	B		in progress		FAPESP, San Paulo University	
<i>Xanthomonas axonopodis</i> pv. <i>aurantifolii</i>	C		in progress		FAPESP, San Paulo University	
<i>Xanthomonas axonopodis</i> pv. <i>citri</i>	306	5.2	completed		ONSA/Brazilian consortium	da Silva et al. 2002. Nature 417:459.
<i>Xanthomonas campestris</i> pv. <i>armoraciae</i>			in progress	Bogdanove, Iowa State		
<i>Xanthomonas campestris</i> pv. <i>campestris</i>	ATCC 33913	5.1	in progress		ONSA/Brazilian consortium	da Silva et al. 2002. Nature 417:459.
<i>Xanthomonas campestris</i> pv. <i>campestris</i>	8004	5.1	in progress	Guangxi Univ, the Institute of Microbiology China	NCBI	Qian et al. 2005. Genome Res. 15:757
<i>Xanthomonas campestris</i> pv. <i>campestris</i>	B100		in progress		Bielefeld	
<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i>	85-10		in progress		Bielefeld	
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	KACC 10331	5	completed	Lee, Korea	National Institute of Agricultural Biotechnology,	Lee et al. 2005 Nucleic

					Korea	Acids Res 33:577-586
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	T7174	4.9	submitted	Kaku, Japan	Natl Inst Agrobiol Res, Japan	
<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>			in progress	Bogdanove, Iowa State		
<i>Xylella fastidiosa</i>	CVC9a5c	2.7	completed		ONSA/Brazilian consortium	Simpson et al. 2000. Nature 406:151.
<i>Xylella fastidiosa</i> -Pierce's disease strain	Temecula 1	2.6	completed		AEG	Van Sluys et al. 2003. J. Bacteriol. 185:1018.
<i>Xylella fastidiosa</i> -almond strain	Dixon	2.6	draft completed		JGI	
<i>Xylella fastidiosa</i> -oleander strain	ann1	2.6	completed		JGI	
<u>Phytoplasmas and Spiroplasmas</u>						
Candidatus <i>Phytoplasma asteris</i> (Aster yellows group 16SrIB)	Onion Yellows	0.86	Completed	Namba, Tokyo, Japan	The University of Tokyo	Oshima et al., 2004. Nature Genetics 36: 27-29
Candidatus <i>Phytoplasma asteris</i> (Aster	Aster Yellows-Witches'	0.8	Completed	Hogenhout, Ohio	Integrated Genomics Inc., Chicago	

yellows group 16SrIA)	Broom					
X-disease group 16SrIII	Western X	0.64	10 X draft completed	Kirkpatrick and Liefting, California	JGI	
Candidatus <i>Phytoplasma asteris</i> (Aster yellows group 16SrIB)	Maize Bushy Stunt	0.7	8 X draft completed	Hogenhout, Ohio	Integrated Genomics Inc., Chicago	
Candidatus <i>Phytoplasma asteris</i> Clover proliferation group 16SrVI	Beet Leafhopper Transmitted Virescence	0.7	4 X draft completed	Hogenhout, Ohio; and Kirkpatrick and Liefting, California	Integrated Genomics Inc., Chicago	
<i>Spiroplasma citri</i>	GII3		Completed	Bové	Bove, INRA, Bordeaux	
<i>Spiroplasma citri</i>					Central Washington University	
<i>Spiroplasma kunkelii</i>	CR2-3x	1.6	Draft completed	Davis, USDA-ARS	University of Oklahoma	

PLANT ASSOCIATED BENEFICIAL PROKARYOTES AND EUKARYOTES SEQUENCING PROJECT STATUS (additional funding for completion may be needed):

<i>Bacillus cereus</i>	UW85		in progress	Handelsman, Wisconsin	TIGR	
<i>Agrobacterium rhizogenes</i>	K84		in progress	Farrand, Illinois	Monsanto	
<i>Burkholderia ambifaria</i>	AMMD		in progress	Parke, Oregon	JGI	
<i>Pseudomonas fluorescens</i>	Pf-5		completed	Loper, Oregon	TIGR	Paulsen et al. 2005. Nature Biotechnology 23:873
<i>Pseudomonas fluorescens</i>	SBW25		in progress	Bailey, UK	Sanger	

PREVIOUSLY LISTED NEMATODE PLANT PATHOGENS SEQUENCED/OR FUNDED (additional funding for completion may be needed):

<i>Meloidogyne hapla</i>	Northern root knot nematode	5.5×10^7	Problems on wide range of crops such as alfalfa, vegetable; cool weather nematode. Has BAC library from inbred diploid strain.
<i>Meloidogyne incognita</i>	Southern rootknot nematode	5.1×10^7	Most economically important nematode worldwide. A sedentary endoparasite that has an extremely wide host range.