

6/15/07

Dear All:

This is a companion document to article entitled: "Microbe Genome Sequence List: 2008 Revision" in the June 2007 issue of Phytopathology News.

The following list indicates with strike through the species sequenced or funded that I could find to date. Note that I only identified fungi, but suspect some of the bacteria and even some of the nematodes may have had successful applications.

I ask for your assistance in identifying other species/strains that you are aware of that have an active genome project or are sequenced. If you know of additional species/strains please email me (sgold@uga.edu) and I will update the list. To date I have checked only through use of Gold Genomes Online Database and a few other sites but am sure to have missed several.

I encourage those committees interested in fungi to discuss amongst their membership replacements for those coming off the list. These could come from the High Priority species or from outside the list.

Please note that the lists of species already removed from the lists because they have already been sequenced are not included here but can be found on the document entitled "MicrobialGenomicsSeq06.pdf" under the heading APS Microbial Genomics Sequencing Report, Final 2006 at <http://www.apsnet.org/members/ppb/plantassocinitiative.asp>.

Thank you, Scott Gold

Lists from:

Microbial Genomic Sequencing

Perspectives of the American Phytopathological Society

(Revised 2006)

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???	a) One of the most economically important pathogens on a diverse group of organisms including: pea, lentils and sugarbeet as well

			<p>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> (JGI)	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 selective toxins</p> <p>c) Loculoascomycete representative</p>
<i>Colletotrichum graminicola</i> BI/MIT	anthracnose stalk rot of corn	48 mb	<p>a) Representative species of a genus affecting a broad range of important crops.</p> <p>b) A serious pathogen of cool season turfgrasses as well as maize.</p> <p>Glomerella teleomorph</p>
<i>Cronartium ribicola</i>	White pine blister rust		<p>a) Introduced biotroph; ecologically and economically the most significant pathogen of North American conifers.</p>

			<p>b) Gene-for-gene and quantitative relationships with two different hosts: 5-needle pines and Ribes.</p> <p>c) Environment triggers several transitions in life cycle, allowing gene expression studies.</p>
<i>Cryphonectria parasitica</i> JGI	chestnut blight	Ca. 45 Mb	<p>a) Causal agent of the economic extinction of the American chestnut.</p> <p>b) Model for fungal-mycovirus interactions, signal transduction and hypovirulence.</p>
<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	<p>a) Has a wide geographic distribution.</p> <p>b) Is an economically important pathogen of many plant species, including maize, potato, rice, soybean and wheat and turfgrasses used for sport and amenity.</p>
<i>Verticillium dahliae</i> BI/MIT	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>	Anthrachnose 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 perniciosa</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 <i>Mycobacterium</i> 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..
<u>Phytoplasmas and Spiroplasmas</u>			
<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	Spiroplasmas are unique bacteria characterized by tiny cell and genome sizes, lack of a cell wall, helical morphology, and an unusual genetic code. <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

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 betavascularum</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>atrofaciens</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 taxa 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> <i>pv. 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> <i>pv. 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> <i>pv. 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> <i>pv. oryzae</i> has been sequenced, and the availability of genome sequences for several strains will provide opportunity for comparative genomics of this important pathogen.
<u>Phytoplasmas and Spiroplasmas</u>			

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 phylogenically 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
Prokaryotes:			
<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 mojavensis</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: B. pumilus 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>Beauveria 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 biocontrol
<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 than Pf-5.
<i>Pseudomonas fluorescens</i>	Q2-87	ca. 6.5	
<i>Rhizobium etli</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 lilacinus</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>	Gl-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	1×10^8	Most economically important nematode in Europe. Sedentary endoparasite of potato.
<i>Globodera rostochiensis</i>	Potato Cyst Nematode		
<i>Heterodera glycines</i>	Soybean cyst Nematode	9.2×10^7	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.

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