China’s fungal genomics initiative: a whitepaper

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Fungal genomics is becoming one of the focal interests within the Chinese mycological community and advances in genomics will, no doubt, accelerate the pace of mycological research in China. Simultaneously, the challenge will be how to capture the full potential of genomics by maximizing and prioritizing the resources within the Chinese mycological community. The 2009 China Fungal Genome Initiative Symposium in Shanghai examined the status of China’s fungal genome research and, for the first time, focused attention in the extent, range and quality of fungal genomics in China. This whitepaper is the result. Following this whitepaper, a series of recommendations and actions will be put in motion within the coming months and years to coordinate the various genome projects, ranging from selection of fungi for sequencing, to the development of a bioinformatics infrastructure, and accompanying research ideas, funding and commercialization.

Keywords: genomics; genome project; sequencing

Introduction

China has a long history of fascination with fungi, where they have been used not only as food but also as traditional Chinese medicines (Kavaler, 1965; Rolfe, 1925). Chinese scientists have contributed to the science of mycology since ancient times and, in recent years, there has been a renaissance in mycological research. Among a wide spectrum of research areas, fungal genomics is a field of particular interest. By late 2009, more than two dozen fungal genome projects have been completed or are in progress in China. Many more are in the planning stages. The cost of genome sequencing has dropped so much that single laboratories can afford to initiate individual projects on their favorite species. Against this backdrop of unprecedented interest in fungal genomics research, the China Fungal Genome Initiative Symposium was proposed and organized by the Chinese Mycological Society and the Key Laboratory of Systematic Mycology and Lichenology, and held in Shanghai on September 20–22, 2009. About 100 scientists, including representatives from China’s major fungal genome projects and fungal genome experts from around the world attended the symposium. More than a genomics symposium, this meeting was a gathering of scientists and experts of diverse backgrounds and interests representing classical mycology, medical mycology, biological control, natural products chemistry, plant pathology, model systems, molecular biology, bioinformatics, food mycology, and genomics.

Short history and current status of fungal genomics research worldwide

The interest in fungal genomics research reflects the unique position that fungi occupy in biology. Fungi are nutrition-absorptive eukaryotes that exist in every ecological niche (Alexopoulos et al., 1996). Due to their ease of handling, rapid life cycle, haploid genetics and phylogenetic relationship to the animal kingdom, fungi are studied as model systems in every aspect of the life sciences (Baldauf and Palmer, 1993; Bennett, 2000). Aspergillus nidulans, Neurospora crassa and Saccharomyces cerevisiae are among the best known fungal models and have been used extensively in genetics and cell biology (Bos, 1996; Davis, 2000). Numerous fundamental discoveries and technological breakthroughs in the life sciences have been made from the studies of fungi. For example, the one gene–one protein theory, proposed by George Beadle and Edward Tatum and based on their work on Neurospora crassa (Beadle, 1948), was one of the milestones in modern biology and earned them the 1958 Nobel Prize in Physiology or Medicine. Similarly, breakthrough work on the cell cycle was conducted in both budding and fission yeasts (Lee and Nurse, 1987), resulting in the 2001 Nobel Prize in Physiology or Medicine for Lee Hartwell and Paul Nurse. The economic importance of fungi is equally impressive, with uses in the food and beverage industries, agriculture, the pharmaceutical and agrochemical industries.

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and medicine (An, 2005; Dijksterhuis and Samson, 2007; Tkacz and Lange, 2004; West and Godfrey, 1996).

It is natural that the first fungal genomes sequenced were model organisms due to the availability of physical maps and genomic libraries for these organisms. In fact, the budding yeast *Saccharomyces cerevisiae* was the first eukaryotic organism to have its complete genomic sequence determined (Goffeau et al., 1996). After the completion of yeast, the genomes of other model organisms, such as *Neurospora crassa* (Borkovich et al., 2004; Galagan et al., 2003) and *Aspergillus nidulans* (Galagan et al., 2005), followed. These early genome projects were huge undertakings. For example, the yeast genome project was a global collaborative effort of more than 600 scientists from over 100 laboratories. Similarly, the early filamentous fungal genome projects were initially slow, expensive, and intermittent. Most of the projects were organized by large consortia and the sequencing was conducted at a few professional genome centers (Bennett and Arnold, 2001; Nierman and Nelson, 2002). The pace of the genome projects picked up rapidly when the cost of genome sequencing decreased exponentially. Currently, there are over 200 fungal genomes in the public databases (see, for example: http://genomesonline.org/index2.htm and http://www.ncbi.nlm.nih.gov/projects/genome/guide/fungi/).

**Landscape of China’s fungal genome research**

Throughout China’s long history of mycological research, the focus has been on practical aspects. Not surprisingly, the emphasis on economically important fungi continues. Table 1 is a partial list of advanced fungal genome projects in China. The list not only demonstrates the breadth of China’s fungal genome research, but it also reflects the landscape of mycological research as a whole in China. China’s fungal genome projects can be divided into the following areas: plant and human pathogenic fungi, fungal–host interactions, fungi as biocontrol agents, food fungi, and medicinal fungi.

**Plant pathogenic fungi**

Fungi are the number one cause of plant diseases with over 8000 fungal species shown to cause diseases in an array of crop, forestry and wild species (Agrios, 2005). The importance of fungi as plant pathogens has spurred scientists worldwide to study their biology and this focus on plant pathogens is particularly true in China. China has about 21% of the world’s population, but only 7% of the world’s arable land. Controlling crop loss caused by fungi is critical to sustain a successful agricultural sector and provide self sufficiency in food production. Genomic information will speed up the understanding of plant pathogenic fungi in many areas: host range and specificity, pathogenicity factors, fungicide resistance, epidemiology, evolution, and control. Examples of plant pathogenic fungi with on-going genome projects in China include the following species.

*Magnaporthe oryzae*, formerly *M. grisea*, is the most important fungal pathogen of rice, with a high degree of host specificity. It largely affects above-ground plant parts, causing huge crop loss across the globe. Being associated with different rice varieties, there are many genetically distinct strains within the species, which makes it an ideal species for comparative genome studies. In addition to rice, this fungus infects more than 50 other species within the grass and sedge families. The most effective control strategy is breeding for plant resistance (Skamnioti and Gurr, 2009).

*Ustilago hordei* is the causal agent of covered smut of barley and the disease is found worldwide, especially in areas where chemical seed treatment is not implemented. In infected plants, barley kernels are replaced with masses of smut spores (Agrios, 2005).

The soil borne fungus *Verticillium dahlia* is a pathogen of over 300 woody and herbaceous plant species including cotton, eggplant, pepper, potato, raspberries, strawberries, and tomatoes as well as many other fruits and vegetables. The disease, verticillium wilt, is problematic in temperate areas of the world, especially in irrigated regions and there are no curative measures once a plant is infected. Once established in a field, it becomes difficult to control the spread of the pathogen (Klosterman et al., 2009).

*Puccinia striiformis* var. *striiformis* causes stripe rust on both winter and spring wheat. The main symptom is the formation of yellow pustules that occur in stripes parallel to the veins in the leaves. Infection can cause losses of up to 40% in wheat; other members of the Poaceae (grass) family are also susceptible (Agrios, 2005).

*Fusarium oxysporum* causes fusarium wilt disease in more than a hundred species of plants. It colonizes the water-conducting vessels (xylem) of the plant. As a result of this blockage and breakdown of xylem, plants exhibit wilting and yellowing of leaves and eventually die (Kvas et al., 2009).

*Rhizoctonia solani* is another plant pathogenic fungus with a wide host range and worldwide distribution. It especially affects below-ground plant parts, such as seeds and roots. Infected seedlings die off as they emerge from the soil in a disease commonly called damping off. Many legumes such as beans and peanuts are susceptible to *R. solani* as are a wide range of other food crops such as eggplant and papaya (Anderson, 1982).

**Fungal–host interactions**

In addition to plants, fungi can interact with almost all higher life forms including vertebrates, nematodes, insects and other fungi. The relationship can be mutualistic, pathogenic, parasitic, or otherwise (Mueller et al., 2004).
### Table 1. Fungal species that have been or are being sequenced by Chinese mycologists.

| No. | Species | Institution | Contact |
|-----|---------|-------------|---------|
| 1   | *Metarhizium anisopliae* var. *anisopliae* ARSEF 23 | Shanghai Institutes for Biological Sciences Chinese Academy of Sciences (CAS) Shanghai, China | Dr Chengshu Wang cswang@sibs.ac.cn |
| 2   | *Metarhizium anisopliae* var. *acridum*, CQMa102 | Shanghai Institutes for Biological Sciences Chinese Academy of Sciences (CAS) Shanghai, China | Dr Chengshu Wang cswang@sibs.ac.cn |
| 3   | *Beauveria bassiana* | Zhejiang University Hangzhou, China | Prof. Mingguang Feng mgfeng@zau.edu.cn |
| 4   | *Cordyceps militaris* | Shanghai Institutes for Biological Sciences Chinese Academy of Sciences (CAS) Shanghai, China | Dr Chengshu Wang cswang@sibs.ac.cn |
| 5   | *Cordyceps sinensis* (Ophiocordyceps sinensis) | Shanghai Institutes for Biological Sciences Chinese Academy of Sciences (CAS) Shanghai, China | Dr Chengshu Wang cswang@sibs.ac.cn |
| 6   | *Arthrobotrys oligospora* (ATCC 24927) | Yunnan University Kunming, China | Prof. Keqin Zhang kqzhang1@yahoo.com.cn |
| 7   | *Drechslerella stenobrocha* YNWS02-9-1 | Institute of Microbiology Chinese Academy of Sciences (CAS) Beijing, China | Prof. XingZhong Liu liuxz@im.ac.cn |
| 8   | *Hirsutella minnesotensis* | Institute of Microbiology Chinese Academy of Sciences (CAS) Beijing, China | Prof. XingZhong Liu liuxz@im.ac.cn |
| 9   | *Pestalotiopsis fici* | Institute of Microbiology Chinese Academy of Sciences (CAS) Beijing, China | Prof. Liang-Dong Guo guold@im.ac.cn |
| 10  | *Acremonium chrysogenum* | Chinese National Human Genome Center at Shanghai Shanghai, China | Dr Shuangxi Ren rensx@chgc.sh.cn |
| 11  | *Lentinula edodes* | The Chinese University of Hong Kong Hong Kong, China | Prof. Hoi Shan Kwan hskwan@eservices.cuhk.edu.hk |
| 12  | *Volvariella volvacea* | Shanghai Academy of Agricultural Sciences Shanghai, China | Dr Dapeng Bao bao.dp@hotmail.com |
| 13  | *Magnaporthe oryzae* | China Agricultural University Beijing, China | Prof. Youliang Peng pengyl@cau.edu.cn |
| 14  | *Ustilago hordei* | Sun Yat-Sen University Guangzhou, China | Prof. Xiongjie He hexiong@mail.sysu.edu.cn |
| 15  | *Verticillium dahliae* Kleb | Chinese Academy of Agricultural Sciences Beijing, China | Prof. Xiaofeng Dai dxf@caas.net.cn |
| 16  | *Puccinia striiformis* West. f. sp. *tritici* | Northwest Agriculture and Forest Science and Technology University Xi’an, China | Prof. Zhensheng Kang kangzs@nwusuaf.edu.cn |
| 17  | *Fusarium oxysporum* f. sp. *cubense* race 4 | Chinese Academy of Tropical Agricultural Sciences Haikou, China | Dr Junshen Huang h888111@126.com |
| 18  | *Rhizoctonia solani* | Sichuan Agricultural University Chengdu, China | Dr Aiping Zheng aipingzh@yahoo.cn |
| 19  | *Penicillium decumbens* | Shandong University Jinan, China | Prof. Quyin Bo quyinbo@sdu.edu.cn |
| 20  | *Nosema bombycis* | Southwest University Chongqing, China | Dr Guoqing Pan gpan@swu.edu.cn |
| 21  | *Coniothyrium mimitans* | Huazhong Agricultural University Wuhan, China | Dr Donghong Liang daohongjiang@mail.hzau.edu.cn |
| 22  | *Trichoderma koningii* SMF2 | Shandong University Jinan, China | Dr Yuzhong Zhang zhangyz@sdu.edu.cn |
| 23  | *Candida albicans* | Institute of Microbiology Chinese Academy of Sciences (CAS) Beijing, China | Dr Fengyan Bai baify@im.ac.cn |
Examples of on-going genome projects on nematode-trapping and insect-infecting fungi in China include the following species.

Entomopathogenic species of *Metarhizium anisopliae* grow naturally in soils throughout the world and cause disease in various insects by acting as parasites. The fungus has green spores so the diseases it causes are sometime called green muscardine disease. The fungus produces a number of secondary metabolites including insecticidal cyclic peptides such as destruxins (Wang et al., 2009). Owing to its broad host range, *M. anisopliae* is being used as a biological insecticide to control a number of pests such as beetles and termites. The species *M. acridum*, however, is locust specific and has been used to control locusts and grasshoppers in large-scale in China, Africa and Australia.

*Beauveria bassiana* is another well known entomopathogenic fungus that grows naturally in soils throughout the world and acts as a parasite on various insect species. Similar to *M. anisopliae*, the fungus also infects its insect hosts by cuticle penetration. *B. bassiana* has been developed as mycoinsecticides against different insect pests, including sucking insect pests such as mosquitoes, aphids and plant hoppers (St. Leger and Wang, 2010). Sexual reproduction of ascomycetes *Metarhizium* and *Beauveria* occurs infrequently, but all have been identified as *Cordyceps* spp. *B. bassiana* is the anamorph of *Cordyceps bassiana*. *C. bassiana*, the teleomorph, has been collected and used as a medicinal fungus in eastern Asia.

*Cordyceps sinensis* (now renamed as *Ophiocordyceps sinensis*) is another insect parasitic fungus which infects larva of the ghost moth. Known as the Chinese caterpillar fungus, or “winter worm, summer grass”, *C. sinensis* is one of the most famous traditional Chinese medicines, said to provide relief for a variety of ailments from tuberculosis to impotence. The entire fruit body–caterpillar at high altitudes on the Himalayan Plateau. Due to its restricted geography and substrate, and the difficult of harvesting it, its has been expensive since ancient times and remains expensive today. The fruiting body of *C. sinensis* contains many secondary metabolites including cyclic peptides such as destruxins (Wang et al., 2009).

**Fungi as biocontrol agents**

There is significant overlap between the lists of pathogenic fungi and the list of fungi as biocontrol agents. Certain pathogens can be developed as effective biocontrol agents that are variously called “myco-herbicides” and “myco-insecticides.” For example, the entomopathogenic *Metarhizium* and *Beauveria* fungi are being developed as insecticides (St. Leger and Wang, 2010). Commercial products that deliver *Metarhizium* have been developed for the control of cockroaches, grubs, locusts, termite and other insect pests. *Coniothyrium mimitans* is used to treat soil to control the common plant pathogens, *Sclerotinia sclerotiorum* and *Sclerotinia minor*, which cause white mold, pink rot, and water soft rot. *Trichoderma koningii* is being developed for control of the take-all fungus, *Gaeumannomyces graminis* var. *tritici*. See Butt et al. (Butt et al., 2001) for a review of the fungi that have been used as biocontrol agents as well as a discussion of their production and formulation, environmental fate, and regulatory issues.

**Food fungi**

*Lentinula edodes*, commonly known as the Shiitake, is an edible mushroom native to East Asia, which is cultivated and consumed in many Asian countries, as well as being dried and exported to countries around the world. It is a feature of many Asian cuisines including Chinese, Japanese, Korean and Thai. In the East, the Shiitake mushroom has long been considered a culinary delicacy as well as a medicinal mushroom. Consumption is said to boost life energy or *qi* (Chang and Miles, 1989; Stamets, 2000).

*Volvariella volvacea* (also known as the straw mushroom or paddy straw mushroom; syn. *Volvariola volvacea*, *Agaricus volvaceus*, *Amanita virgata*, *Vaginata virgata*) is a species of edible mushroom that is cultivated throughout East and Southeast Asia and used extensively in Asian cuisines (Chang and Miles, 1989; Stamets, 2000).

**Medicinal fungi**

Many Chinese medicines have a fungal component; however, the caterpillar fungus *Cordyceps sinensis* is perhaps the single best representative of a Chinese medicinal fungus. *Cordyceps* grows on one species of subterranean caterpillar at high altitudes on the Himalayan Plateau. Due to its restricted geography and substrate, and the difficult of harvesting it, *Cordyceps* has been expensive since ancient times and remains expensive today. The fruiting body of *C. sinensis* contains many secondary metabolites including...
alkaloids, polyketides and nonribosomal peptides (Zhou et al., 2009). Additional species of Cordyceps such as C. militaris, C. ophioglossoides and others also are used as health supplements or for therapeutic purposes. There is considerable research on developing methods to cultivate Cordyceps. Cordyceps has been used to treat conditions that range from renal, liver and cardiovascular diseases, as well as immune system disorders, as an aphrodisiac, to boost energy, and to ward off fatigue. Both athletes and the elderly are among the more avid consumers. Clinical trials to identify the physiological basis of the pharmacological effects of Cordyceps are in their early stages (Holliday and Cleaver, 2008).

**Fungi used for biotransformations**

*Penicillium decumbens* is an example of industrial fungus and its cellulolytic enzymes are being explored for biorefinery and biodegradation. In addition to biorefinery and biodegradation, genomics will benefit industrial mycology in areas of food microbiology, biopolymer production, and waste biotreatment. It is expected that the genomes of other industrially important fungi will be sequenced and analyzed in China in the not too distant future (Sun et al., 2008).

**Challenges and opportunities facing China’s fungal genome projects**

A 2-h brainstorming session was devoted to discussing the challenges and opportunities facing China’s fungal genome projects. There was consensus that the direction of the Chinese fungal genomics should be determined by the genomic community and that there was a need for developing centralized data bases.

While the cost of DNA sequencing has decreased logarithmically, there has not been a corresponding decrease in the cost of annotation. Funding agencies are more likely to provide resources for sequencing than for doing adequate annotation or for maintaining well curated databases. Furthermore, even at well-established genomics centers, numerous difficulties remain with automated annotation. There is a high error rate in many published fungal genomes and there is an acute need for developing better gene-finding algorithms. On the other hand, it was felt that existing tools were sufficient for solving many problems. The disciplinary gap between individuals trained in biology and those trained in bioinformatics poses an international challenge. To maximize the utility of the vast datasets produced by genomics, each group needs to learn more about the jargon, methods and limitations of their respective fields of expertise. Nevertheless, because “biologists cannot become computer programmers,” it is important for consortia of scientists with complementary skills to work together. Experimental biologists need to collaborate effectively with sequencing centers and bioinformatics experts. For example, expressed sequence tags (ESTs) are one of the best ways to clean up errors introduced by automated annotation methods. Biologists should do the EST experiments and then work with bioinformaticists to improve gene-calling programs.

Another world wide challenge concerns bureaucracy and regulation. By definition, genomic projects are examples of “big science” that require support from government and industry. Governmental agencies and large companies tend to have accompanying bureaucracies that can impede scientific research and divert economic resources. Furthermore, governments and companies each have characteristic, incompatible and/or competing agendas. They generate obstacles to creating open systems for sharing data and maximizing the utility of genomics projects.

In the past, the benefits of genomic research have often been oversold, with unachievable promises of finding new miracle drugs and clean fuels, and of developing revolutionary control measures for plant and animal diseases. Politicians generally do not have the technical expertise to separate hype from attainable biotechnological goals. It is important for molecular mycologists to recognize that, even though our resources are limited, we should devote some of them to strengthening our own organizational profile so as best to provide expert advice to governmental agencies on the development of realistic policies and recommendations. International meetings such as this symposium are a good way of communicating within the scientific community. However, better ways of communicating with politicians and entrepreneurs need to be devised.

**Fungi to sequence and the importance of collaboration**

Sequencing of a fungal genome is just the beginning of a genome project. To maximize the scientific and economic output of the limited resources available to the Chinese mycological community, it was recommended that selection of fungi to be sequenced should be made carefully. Criteria for sequencing a fungal genome include but are not limited to the following considerations: What scientific and practical questions could be addressed? Is the organism agricultural, industrially or medically important? Is there a source of pure DNA? Are there genetic resources such as markers, maps and an available transformation system? How hard will it be to extract sufficient pure DNA, develop ESTs, and develop various kinds of genomic libraries? Can a consortium of experts be formed to tackle different aspects of the genome? Are there enough financial and human resources to annotate the genome? Is there a broad scientific user community to form a “critical mass” of interested scientists? Is there a focused and dedicated principle investigator with the leadership skills to keep the project together?
Model systems

The twentieth century advances in fungal molecular biology and genetics were driven largely by discoveries made within a few model systems such as *S. cerevisiae*, *A. nidulans*, and *N. crassa*. State of the art protocols in molecular biology, bioinformatics, genetics and biochemistry, such as those available in model organisms, are needed to harvest fully the fruits of the vast amounts of data coming from genome projects. Even though China has a long history of mycological research, expertise in molecular biology and genetics on model systems is relatively scarce because the emphasis has been on practical aspects of mycology. Applied scientists cannot always take full experimental advantage of findings from fungal species that lack easily manipulated genetic systems. It would be advantageous to develop both international exchange programs, and Chinese education programs and centers of excellence, for training scientists on genetic models to advance China’s fungal genome projects to their full utility.

Bioinformatics infrastructure

Data resources are at the core of genomics. The single biggest challenge facing China’s genomics projects is to design the appropriate bioinformatics infrastructures for deciphering the information in the sequenced fungal genomes. Globally, due to the cost and expertise required, bioinformatics infrastructures have been concentrated in a few large genome centers and academic institutions around the world. Table 2 lists selected websites with a fungal genome focus. Meeting participants agreed that it is not practical to design a one-shoe-fits-all bioinformatics infrastructure, but a streamlined effort should be coordinated by an organization such as a “China Fungal Genome Consortium.” Such a coordinated effort could maximize access to the existing resources and foster the exchange of information and expertise. The entire research community would benefit from a bioinformatics infrastructure that supports data mining and facilitates comparative genomic studies.

Areas of research, funding, and biotechnology

Fungal genome research in China has the potential to contribute to some of the most interesting basic and applied research areas that include, but are not limited to, the following: evolution/coevolution, natural products discovery (Traditional Chinese Medicine), biological control, medical mycology (disease mechanisms/virulence factors), plant pathology (disease mechanisms/virulence factors), biodegradation and bioremediation, biofuel production, genetic manipulation of “valuable gene(s)**, “fit-for purpose”

| Table 2. Selected databases that focus on fungi. |
|---|---|
| Name | Note |
| Fungal Genomes Central at NCBI http://www.ncbi.nlm.nih.gov/projects/genome/guide/fungi/ | Contains more than 210 completed and in-progress fungal genomes. |
| Fungal Genome Initiative, the Broad Institute http://www.broadinstitute.org/science/projects/fungal-genome-initiative/fungal-genome-initiative | Over 25 fungi have been sequenced or are being sequenced, including human and plant pathogens, as well as fungi that serve as basic models for molecular and cellular biology. |
| Genomes Online Database, GOLD http://genomesonline.org/index2.htm | Contains genome project information for some 443 fungal species. |
| DOE Joint Genome Institute http://www.jgi.doe.gov/ | Includes about 150 fungal genome project information and databases. |
| J. Craig Venter Institute http://www.jcvi.org/cms/research/groups/microbial-environmental-genomics/ | More than 100 microbe genomes completed including fungi. Currently focusing on environmental genomics. |
| Sanger fungal genome projects http://www.sanger.ac.uk/Projects/Fungi/ | Emphasis on genomes of model fungal species. |
| Génolevures http://www.genolevures.org/ | The genomes of eighteen species of hemiascomycete yeasts. |
| The Fungal Genomics Laboratory, North Carolina State University http://www.fungalgenomics.ncsu.edu/ | Plant fungal pathogens including the rice blast fungus *Magna porthe grisea*. |
| Database and website constructed and maintained by Darren Soanes (University of Exeter) http://cogeme.ex.ac.uk/ | Phytopathogenic Fungi and Oomycete EST Database. |
| Website maintained by Jason Stajich (University of California – Riverside) http://fungalenomes.org/ | List of in-progress and published fungal genomes and genome tools and links. |
| *Aspergillus fumigatus* DB http://www.genedb.org/chedb/asp/ | The *Aspergillus fumigatus* database is an example of a well curated database devoted to a single medically important species. |
| Comparative Fungal Genomics Platform http://cfgp.riceblast.snu.ac.kr/main.php | Tools and databases for comparative genomics analysis. |
| SGD, Saccharomyces Genome Database http://www.yeastgenome.org/ | A comprehensive scientific database of *Saccharomyces cerevisiae*. |
| CGD, Candida Genome database http://www.candidagenome.org/ | A comprehensive resource for genomic sequence data and gene and protein information for *Candida albicans*. |
strain engineering, and industrial enzymes. While basic research is of interest to every scientist, it is important to keep in mind that converting basic science to practical applications should be a major objective of most fungal genome research. Moreover, it is also important to remember that genomics is not a panacea. The full utility of genomic projects is achieved only when combined with systemic “wet lab” approaches.

Ultimately, commercialization of genome discoveries will supplement the funding from government and not-for-profit funding sources. There are numerous possibilities for new fungal genome projects that can lead to breakthroughs in both fundamental and applied biology. Many important groups of fungi have not been studied, including several groups that have high economic importance. The early twenty-first century is likely to be remembered as a “Golden Era for Fungal Genomics.”

Summary
Fungal genome sequencing technology has reached the point that genome sequencing projects are going on within individual laboratories and small consortia as well at large genome centers. Following the publication of this whitepaper, a series of recommendations and actions will be put in motion within the coming months and years to coordinate the various genome projects ranging from selection of fungi for sequencing, to the development of bioinformatics infrastructure, and accompanying research ideas, funding, and commercialization. The companion paper by Dr Li-Jun Ma (Broad Institute, USA) and Dr. Natalie Fedorova (J. Craig Venter Institute) entitled “A blueprint for initiating a fungal genome project” is an example of one of the ongoing discussions on China’s fungal genome projects. The group is planning to meet again in October, 2011.

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