

Chapter 2

Fungal Genomics for Energy and Environment

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2.1 Introduction

The finite resource of fossil fuels and the adverse ecological impacts of their exploration and use pose significant challenges for mankind. Development of alternative energy sources goes hand in hand with restoring ecological balance. This requires knowledge of how natural biological systems work. One such system includes fungi that interact with plants as symbionts, pathogens, or decomposers. These interactions, first, determine growth of biomass and, second, provide clues toward efficient conversion of plant-produced lignocellulose into energy, offering real alternatives to fossil fuels. Understanding these processes at the molecular level is therefore a critical challenge.

The tools of molecular biology and genomics can help us meet this challenge. Over the past decades, genomics, and genome sequencing in particular, have emerged as powerful tools for biological research. In the last few years, due to the introduction of the next-generation sequencing (NGS) technologies, these tools went through dramatic transformations. The first genome projects like sequencing the genome of *Saccharomyces cerevisiae* were colossal multi-institutional, multi-national sequencing efforts (Goffeau et al. 1996), which reached their culmination with the Human Genome Project (Lander et al. 2001). Though deemed an extremely large quantity of data several years ago, the 3×10^9 base pairs of the human genome represent only a fraction of the data produced from just a single lane of an Illumina sequencer these days. Genomics technologies are thus poised to help us study not just individual organisms but entire ecological systems.

With technology breakthroughs, the scope of the projects has evolved accordingly. Genomics projects have reached an unprecedented scale like the 1000 human genomes (2010) or ENCODE (2004) and enable scientists to ask new types of

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questions. How can genomics help to obtain a sustainable growth of biomass? What is the role of microbial association with plants? Do genome features determine if a fungus is a friend (symbiont) or a foe (pathogen)? How do microbes efficiently convert biomass into energy? What biological mechanisms govern ecological balance? Here, in the context of fungal genomics for energy and the environment, we discuss tools, applications, and the most recent developments available to explore the biology of soil fungi at the molecular level.

2.2 The Tools of Genome Sequencing

The first sequencing experiments were very laborious. Not long ago, a scientist would have to make a significant effort to sequence a single gene. At the end of the twentieth century, Sanger sequencing (Sanger et al. 1977) became the dominant way to sequence genomes, including the human genome. At the beginning of the twenty-first century, suddenly several new NGS platforms were introduced (Metzker 2010). First, 454 (now Roche) offered a new technique called pyrosequencing as a way to read DNA fragments in a high-throughput fashion and for just a fraction of the cost of Sanger sequencing. Shortly after, Solexa (later acquired by Illumina) developed a new way to produce very large numbers of very short (initially 25 bp) reads at a much less cost. More recently, Pacific Biosciences presented a single molecule sequencing approach to produce long reads but with a relatively high error rate (up to 15 %). These are just a few among the larger collection of sequencing platforms that are available today. Each of them dramatically improved characteristics of the produced sequence reads—length, error rate, throughput, and GC bias—during just the last few years. Innovation continues as new players like Oxford Nanopore promise groundbreaking solutions in the near future (Pennisi 2012).

Many sequence analysis tasks have been solved in the era of Sanger sequencing. Genome assemblers like Arachne (Batzoglou et al. 2002) are capable of putting together Sanger reads into assemblies for both small bacteria-size and large plant-size genomes. However, some sequencing and analysis problems remain quite challenging. Sequencing shows some platform-dependent bias. Repetitive sequences make it difficult to place reads uniquely into an assembly. Polymorphism and polyploidy interfere with clean separation of haplotypes.

A few dozen fungal genomes were sequenced using the Sanger platform and have draft assemblies available in public databases like GenBank (<http://www.ncbi.nlm.nih.gov/genbank>). Using multiple iterations of targeted Sanger sequencing, many gaps in several draft genomes were closed in a process called genome finishing. This resulted in at least a dozen small yeast-size finished genomes (Dujon et al. 2004) starting with *S. cerevisiae* and only a couple of finished genomes of filamentous fungi (Berka et al. 2011; Goodwin et al. 2011). Many others including the model fungus *Neurospora crassa* went through multiple rounds of

genome improvements but continue to keep “secret messages” in some as-yet unresolved parts of their genomes (Galagan et al. 2003).

Genes encoded in the sequenced and assembled genomes can be predicted and functionally annotated using different computational approaches (Grigoriev et al. 2006; Haas et al. 2011). The complex intron-exon structure of a eukaryotic genome makes annotation a challenge in comparison to the simpler problem of calling ORFs in compact, gene-dense prokaryotic genomes (in which genes typically lack introns). Eukaryotic gene prediction usually combines several methods including transcriptome-based (deriving genes from ESTs mapped to a genome assembly), homology-based (based on proteins from other genomes mapped to a translation of the assembly), and ab initio gene predictors. For the latter, which sometimes is the last resort (since preference is usually given to genes predicted from experimental data or similarity to known proteins), gene structure features are derived from a collection of known genes and then are searched for in the entire genome to predict new genes using these features. Gene structures or models predicted using these methods also require annotation methods to predict possible gene functions. For a given protein encoded in a genome, function can be inferred from known proteins or protein domains if their protein sequences are sufficiently similar as determined by various alignment programs like BLAST or HMMER (Altschul et al. 1990; Bateman et al. 1999). The problem is that despite the quickly growing number of sequenced genes, the number of biochemically characterized proteins grows very slowly. In addition, computational methods for gene prediction and annotation as well as reference databases themselves are error prone. Therefore, both structural and functional annotations are often followed by manual inspection in which trained analysts look at genomes, predicted genes and available lines of evidence in genome browsers. The largest scale efforts in manual curation have been achieved for the human genome, although several model fungi including *S. cerevisiae*, *S. pombe*, and *N. crassa* also have curators devoted to iterative improvement of these datasets (Howe et al. 2008).

The new sequencing technologies have brought new types of data, for example, very short reads in large numbers from Illumina or longer and error-prone reads from 454 and Pacific Biosciences sequencers. Variation in read sizes and numbers demands completely different analytical approaches. Various implementations of de Bruijn graph have been used in new assemblers such as Newbler, Velvet, and AllPathsLG that were tuned for different platforms (Earl et al. 2011). Hybrid sequencing and assembly has become the norm, with assemblies often being constructed from Illumina, 454, and Sanger reads all pooled together, often with different assembly algorithms used for the different kinds of reads. However, even though NGS was much cheaper than Sanger sequencing, the resulting genomes are generally of lower quality. To compensate for this, the questions posed and the applications of these platforms were adjusted accordingly. For example, NGS has given rise to massive re-sequencing and transcriptomics applications. Annotation methods have changed as well using RNA-seq data as a primary source of data.

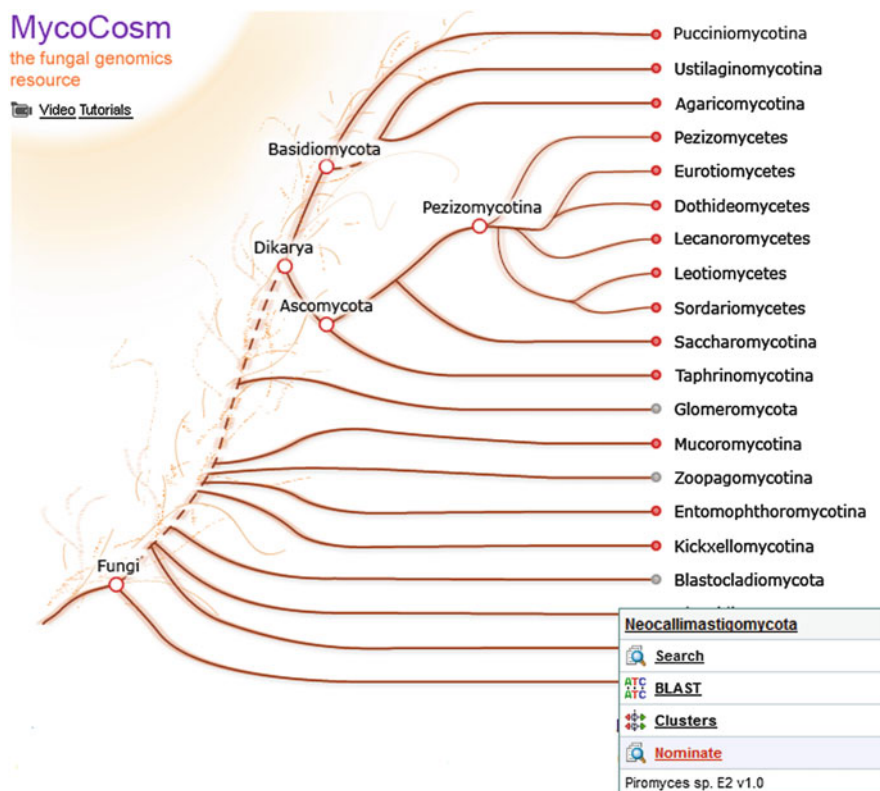


Fig. 2.1 JGI fungal genome portal MycoCosm (<http://jgi.doe.gov/fungi>) with 200+ fungal genomes and tools for their comparative analysis and nomination of new fungal species for sequencing

Data integration and visualization problems formulated during the human genome era from the need to put genome sequences, gene predictions, ESTs, and protein homologs on one screen became even more complex when confronting massive amounts of sequence data and large numbers of sequenced genomes. While GenBank offers a large collection of sequenced genomes and many bioinformatics tools are open access, the lack of their integration makes them difficult and time-consuming to use. One solution has been developed specifically for fungal genomes by the US Department of Energy (DOE) Joint Genome Institute (JGI): the web-based fungal genome portal MycoCosm, which offers 200+ fungal genomes and tools for their comparative analysis and manual curation (Grigoriev et al. 2012; Fig. 2.1).

2.3 Plant–Microbe Interactions and Evolution of Fungal Lifestyles

The Human Genome Project started a revolution in health care. Similarly, plant genomics became a game changer in plant breeding. The poplar genome (Tuskan et al. 2006), for example, led to research investigating the role of various transcription factors on plant growth. However, the genome only reflects the organism's potential to develop, while the actual growth and development depends on interaction with the environment including microbial interactions. Fungal symbionts and pathogens are important players in these interactions. The majority of plant species are dependent on mycorrhizal associations. Pathogens can destroy a significant share of agricultural and bioenergy crops like the Southern corn leaf blight, which in the 1970s destroyed the entire corn crop in several US states. Decomposers recycle dead materials to provide nutrients for the new generations of primary producers and microbes associated with them. These lifestyles—symbiosis, pathogenicity, and saprotrophism—are encoded in genomes. Thus, genome analysis and comparison of different genomics features are essential for understanding fungal lifestyles, their evolution, and interactions to possibly lead to better management practices.

Genomes of several organisms involved in interactions with each other in natural ecosystems have been sequenced. One such system includes a poplar tree and associated ectomycorrhizal symbiont *Laccaria bicolor* and pathogenic rust *Melampsora laricis-populina*. Interestingly, genomes of these symbiotic and pathogenic fungi share several things in common: large genomes inflated with repeats and expanded gene families, the most interesting of which is a large number of small secreted proteins (Martin et al. 2008; Duplessis et al. 2011). Despite being very abundant, small secreted proteins are frequently lineage specific. They may share some functional domains between symbionts and pathogens but hardly show any sequence similarity even between closely related poplar rust and wheat rust. Interestingly, in all these fungi, genes encoding the small secreted proteins are among the most expressed in planta, during infection of the plant host.

Another important part of both plant symbiont and pathogen gene sets is CAZymes, the carbohydrate-active enzymes (Cantarel et al. 2009) involved in lignocellulose degradation, fungal cell wall reconstruction, and other important processes. In contrast to pathogens, whose expanded CAZy families aim to modify and destroy the host plant, the genome of symbiotic *L. bicolor* contains a relatively limited arsenal of CAZymes and a lack of those involved in plant cell wall degradation, which results in a protection mechanism to minimize the impact on the plant host. The symbionts thus evade the plant's defense responses (Martin et al. 2008). Interestingly, this reduction is similar to the reduced CAZy profiles of one group of saprobic, wood-decaying fungi called brown rot fungi. In contrast to the white rot fungi (the second and dominant type of wood decay), brown rot fungi have evolved to employ a less “expensive” mechanism for lignocellulose degradation (Eastwood 2011; Martinez et al. 2004, 2009). Instead of enzymatic attack typical for white rot fungi, brown rot relatives are thought to use Fenton chemistry

to generate highly reactive hydroxyl radicals to break cellulose chains. They also do not degrade lignin and thus lack the corresponding genes in their genomes.

For some wood decayers, it is not always obvious if white or brown rot is their natural mode of decay (R. Blanchette, pers. comm.) and their genomes may provide some hints. On the other hand, the genome of *Agaricus bisporus* apparently encodes enzymes involved in lignin degradation, though the fungus has not been observed to do so in nature (Morin et al. 2012). Fungi efficiently combine different lifestyles. *L. bicolor* as a saprobe extracts nutrients from decaying organic matter to provide them to the host plant, with which it also forms mycorrhizal association. The white rot fungus *Heterobasidion irregulare*, also a pathogen of conifers and other trees, encodes both of these lifestyles into its genome and balances between these lifestyles even when growing on the same host (Olson et al. 2012). Thus, interactions between plants and fungi are complex, and lifestyles of members of these interactors—symbionts, parasites, and saprobes—are hard to define with clear boundaries. A better understanding of the genomics basis of different lifestyles will require more complex analyses and large-scale comparative genomics studies.

2.4 Large-Scale Comparative Genomics

Discoveries based on the analysis of individual genomes become stronger in the context of comparative analysis. Instead of sequencing genomes one after another, analysis of groups of phylogenetically divergent fungi that share common traits or lifestyles may enable mapping of these traits to a specific set of genes and genomics features. JGI is one of the institutes partnering with numerous scientific groups around the world to explore the diversity of fungi, which are important for solving energy and environmental problems. Starting with the first sequenced basidiomycete, the white rot fungus *Phanerochaete chrysosporium* in 2004, by 2012 JGI has contributed to over a half of all fungal genome projects worldwide. After delivering several “first of its kind” fungal genomes—wood decayers, ectomycorrhizae, and thermophiles—JGI launched a project called the Genomic Encyclopedia of Fungi (Grigoriev et al. 2011) devoted to several areas of plant health and biotechnological applications for energy and the environment, the DOE mission areas. By 2012, the first two chapters of the encyclopedia, the large-scale comparative genomics studies, were published (Floudas et al. 2012; Ohm et al. 2012), while sequencing for several others was nearly complete.

Understanding the mechanisms of lignocellulose degradation by wood-decay fungi is important to finding new ways for processing biomass into biofuels. The first sequenced white and brown rot fungi, as mentioned earlier, revealed completely different mechanisms of wood decay encoded in their genomes and justified more extensive sequencing of this group of fungi. About 30 species of wood-decay fungi were selected for sequencing at JGI, and recently 12 of them were analyzed and reported in the context of 31 other sequenced fungal genomes (Floudas et al. 2012). This work has catalogued the largest collection of genes

encoding CAZymes while focusing on the analysis of the class II peroxidases involved in lignin decay. The ancestor of both white and brown rot fungi (as well as mycorrhizal *L. bicolor*) was capable of processing lignin, which was produced by plants and converted into coal in prehistoric times. Molecular clock analysis suggested that the white rot ancestor evolved approximately at the end of Carboniferous, i.e., potentially in time to contribute to the significant decline of coal accumulation observed at that time. In other words, what could have contributed to the decline in fossil fuel accumulation ~300 Mya can help us today to make progress in developing biofuels.

In order to convert biomass into biofuels, the former needs to be produced in a sustainable fashion. Pathogenic fungi are notorious for destroying a significant fraction of agricultural crops and can destroy bioenergy crops to the same or greater extent. In order to protect plants, we should better understand the molecular basis of different strategies of pathogenicity. The Dothideomycetes are an example of a diverse class of fungi that contains a large number of plant pathogens. Several independent research groups at various genome centers have been sequencing fungal genomes from this class and converged in 2008 at JGI to consolidate the genomics data for comparative analysis and propose a much larger set of sequencing targets. As a result of this effort, 14 newly sequenced Dothideomycete genomes were compared with each other and fungi sequenced earlier to explore different modes of pathogenicity and patterns of their evolution (Ohm et al. 2012). This revealed common features of genome organization across the entire class: an inversion-based mechanism for mesosynteny or gene reshuffling within the boundaries of chromosomes; a variable number of dispensable chromosomes with unclear role in pathogenesis; and blocks of genes conserved in most of these species and expressed during plant infection in some of them. Gene family expansions and contractions were traced along the evolution of major groups of Dothideomycetes, Capniodiales, and Pleosporales and revealed larger sets of genes involved in secondary metabolism and plant cell wall degradation in necrotrophs vs. biotrophs with stealth pathogenesis like *Mycosphaerella graminicola* (Goodwin et al. 2011). This global genome comparison was followed by several functional studies focused on specific gene families (Condon et al. 2013), plant-pathogen systems (Manning et al. 2013), and functional platforms (Cho et al. 2012). One of them suggested that differences in gene regulation may be the key in determining host specificity even in very closely related species such as *Dothistroma* and *Cladosporium fulvum* (de Wit et al. 2012) and that functional genomics would be the next critical step in understanding fungal biology.

Besides the Agaricomycetes and Dothideomycetes, large-scale comparative analysis of other groups of fungi has been progressing quickly: these include 30+ mycorrhizal fungi (Chap. 8), 20+ yeasts of biotechnology and taxonomic importance, and 10+ species of *Aspergillus* and *Penicillium* for various biotech applications (Chap. 5). Finally, the desire to ask bigger questions through larger scale sequencing transformed one of the chapters, fungal diversity, into a project of unprecedented scale: the 1000 fungal genome project.

2.5 The 1000 Fungal Genome Project

Advances in genome sequencing have allowed scientists to launch very large-scale genomics projects like 1000 human genomes (2010), 1001 *Arabidopsis* genomes (Weigel and Mott 2009), and GEBA (Wu et al. 2009). *The 1000 fungal genome project* is one of the latest JGI large-scale genomics initiatives aimed at highly divergent fungal species to obtain a comprehensive list of reference genomes, to better assess fungal diversity, to explore evolutionary processes driving this diversity, and to provide a comprehensive vocabulary for studying complex metagenomes.

The Kingdom Fungi is estimated to contain over a million species. These organisms developed a tremendous natural arsenal of enzymes, chemicals, deconstruction, and synthesis mechanisms over millions of years of evolutionary history, which are poorly understood. Despite the growing number of fungal genome sequencing projects, the phylogenetic diversity of fungi covered by these projects is still very limited. Ascomycetes of medical importance remain dominant among the sequenced fungal genomes. In contrast, lower fungi are hardly represented among the currently available reference genomes.

The goal of the 1000 fungal genome project is to sequence genomes for on average two species for each of the about 500 known fungal families within 5 years. The project started in close collaborations with several culture collections and research groups providing DNA and RNA samples. JGI accepts nominations for new species for sequencing and DNA/RNA samples from the scientific community worldwide at <http://jgi.doe.gov/fungi> (Fig. 2.1). These will serve as references in ecological genomics.

2.6 Ecological Genomics

Having a large collection of reference genomes may set a stage for eukaryotic metagenomics. Metagenomes of bacterial and archaeal communities have been successfully analyzed previously (Tringe and Rubin 2005; Kalyuzhnaya et al. 2008). Even when metagenomes are poorly assembled but dominated by prokaryotes, the assembled pieces provide sufficient information to predict genes. Unlike gene-dense bacterial genomes, eukaryotic genomes, with their complex gene structure and genome organization, present a significant bottleneck for metagenomics. Assembled DNA pieces lack sufficient information to train *ab initio* gene predictors. Homology-based methods may work but require a representative collection of reference genomes. While this collection is being built over time, approaches to assess complexity of fungal communities, for example, in soil, are being explored (Buée et al. 2009).

A standard method to identify fungal species is by their Internal Transcribed Sequences (ITS). Targeted ITS sequencing can be applied to fungal communities

composed of multiple species to assess their composition. Here transition to the NGS imposes some challenges. In the days of Sanger sequencing, long sequence reads would cover the entire region which is ~1 kb long. The first NGS products were too short to cover the entire ITS, although several studies used 454 pyrosequencing to obtain ITS fragments, ITS1 or ITS2 regions (Buée et al. 2009). The latest generation of Illumina machines, the benchtop MiSeq, offers sequencing in the format of 2×250 bp reads, which with sufficiently short inserts may overlap and produce contigs long enough to cover one of these regions. The cycle time of these machines (1 day instead of 18 for HiSeq) allows sequencing a multitude of samples.

Another strategy to overcome the complexity of fungal gene structure is metatranscriptomics, which gives a functional portrait of the community as a biological system and captures its dynamics. The challenge is the poly (A) enrichment in complex communities like soil where fungi make up just a few percent of the entire microbial transcriptome. Furthermore, total eukaryotic RNA consists of only a few percent of mRNA.

2.7 Functional Genomics

The increased throughput in genome sequencing has created a situation where the number of sequenced genes and genomes grows dramatically each year but does not necessarily help us to better understand their functions. A thorough biochemical characterization is required to determine gene functions, but its throughput is not on par with sequencing.

Analysis of gene and protein expression under different conditions may suggest roles of these genes in an organism's growth, while genes' co-regulation can be inferred from patterns of their co-expression. Large-scale transcriptomics has been broadly successful for a number of fungi and quickly progressed from in-depth characterization of genes in single species to multispecies comparative functional genomics, as with fission yeasts (Wilhelm et al. 2008; Rhind et al. 2011). Proteomics of different flavors offer approaches complementary to gene expression analysis and allows the characterization of proteins, protein complexes, and post-translational modifications. Among fungi, this was applied to the greatest extent to *S. cerevisiae* (e.g., Ho et al. 2002; Ptacek et al. 2005; Krogan et al. 2006). The combination of transcriptome and proteome analyses is becoming more and more often a part of genomics studies of many fungi (e.g., Berka et al. 2011; Martinez et al. 2009).

The roles of genes can be also determined by turning genes on and off using various techniques at reasonably high throughput. Transcriptomics and proteomics studies of gene deletion mutants, especially transcription factors, can point to their roles in an organism's regulatory cascades. Several studies along these lines have been done for fungi. For example, novel virulence factors have been identified in the plant pathogen *Alternaria brassicicola* (Cho et al. 2009, 2012), factors

influencing cellulose production have been studied in the industrial workhorse *Trichoderma reesei* (Schuster et al. 2012), the role of transcription factors has been explored for mushroom development in the basidiomycete *Schizophyllum commune* (Ohm et al. 2010, 2011), and a much broader approach is taken in the model ascomycete *Neurospora crassa* (Colot et al. 2006). For the models *N. crassa* and *S. cerevisiae*, extensive collections of deletion mutants along with microarrays and other functional genomics resources have been developed (Winzeler et al. 1999; Giaever et al. 2002; Dunlap et al. 2007), which created a solid basis for future experiments.

A different context for gene function studies comes from the analysis of interactions of fungi with other organisms. Analysis of the transcriptome at different stages of plant infection (O'Connell et al. 2012) or of interactions with a fungal prey (Atanasova et al. 2013) has been revealing for the dynamics of such interactions. However, looking at both partners at once can give more complete and, therefore, more accurate picture. Indeed, transcriptomes of the fungus *L. bicolor* and poplar tree upon their interaction provided clues for a metabolic model of nutrient exchange between them (Larsen et al. 2011). For pathogens, Skibbe et al. (2010) have shown that infection of maize by corn smut (*Ustilago maydis*) depends on organ-specific gene expression by both host and pathogen. Proteomics of such interactions was also studied in several different systems (reviewed by El Hadrami et al. 2012). Much larger-scale transcriptomics studies of several host-pathogen and mycorrhizal systems are also currently in progress at JGI. Finally, along the lines of the human ENCODE, which recently generated a very large amount of functional data (Skipper et al. 2012), *N. crassa* is a target of fungal ENCODE at JGI to further understand this model organism and project this knowledge to other fungi (Chap. 14).

2.8 Conclusion

Fungal diversity is enormous and so far poorly explored. Soil is the most abundant ecosystem on Earth, enriched in microbial life including a large number of fungal species. Very few microbial species inhabiting soil have been characterized. Genomics and transcriptomics offer new ways to identify these poorly characterized species and understand their function and interactions with environment, hosts, and other fungi. Metagenomics approaches can help to better understand the complexity of microbial communities in soil, how they are formed, and how they change in response to various environmental factors. Communities of pathogens and symbionts are components of the rhizosphere and determine the success of plant growth. Genomics analysis of these interactions will help us to better understand natural biological systems and can lead to applications for environmental protection and bioenergy production.

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References

- 1000 Genomes Project Consortium (2010) A map of human genome variation from population-scale sequencing. *Nature* 467:1061–1073
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. *J Mol Biol* 215(3):403–410
- Atanasova L, Le Crom S, Gruber S, Couplier F, Seidl-Seiboth V, Kubicek CP, Druzhinina IS (2013) Comparative transcriptomics reveals versatile strategies of *Trichoderma mycoparasitism*. *BMC Genomics* 14:121
- Bateman A, Birney E, Durbin R, Eddy SR, Finn RD, Sonnhammer EL (1999) Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins. *Nucleic Acids Res* 27(1):260–262
- Batzoglou S, Jaffe DB, Stanley K, Butler J, Gnerre S, Mauceli E, Berger B, Mesirov JP, Lander ES (2002) ARACHNE: a whole-genome shotgun assembler. *Genome Res* 12(1):177–189
- Berka RM, Grigoriev IV, Otillar R, Salamov A, Grimwood J, Reid I, Ishmael N, John T, Darmond C, Moisan MC, Henrissat B, Coutinho PM, Lombard V, Natvig DO, Lindquist E, Schmutz J, Lucas S, Harris P, Powlowski J, Bellemare A, Taylor D, Butler G, de Vries RP, Allijn IE, van den Brink J, Ushinsky S, Storms R, Powell AJ, Paulsen IT, Elbourne LD, Baker SE, Magnuson J, Laboissiere S, Clutterbuck AJ, Martinez D, Wogulis M, de Leon AL, Rey MW, Tsang A (2011) Comparative genomic analysis of the thermophilic biomass-degrading fungi *Myceliophthora thermophila* and *Thielavia terrestris*. *Nat Biotechnol* 29(10):922–927
- Buée M, Reich M, Murat C, Morin E, Nilsson RH, Uroz S, Martin F (2009) 454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. *New Phytol* 184(2):449–456
- Cantarel BL, Coutinho PM, Rancurel C, Bernard T, Lombard V, Henrissat B (2009) The Carbohydrate-Active EnZymes database (CAZy): an expert resource for glycogenomics. *Nucleic Acids Res* 37:D233–D238
- Cho Y, Kim KH, La Rota M, Scott D, Santopietro G, Callihan M, Mitchell TK, Lawrence CB (2009) Identification of novel virulence factors associated with signal transduction pathways in *Alternaria brassicicola*. *Mol Microbiol* 72(6):1316–1333
- Cho Y, Srivastava A, Ohm RA, Lawrence CB, Wang KH, Grigoriev IV, Marahatta SP (2012) Transcription factor Amr1 induces melanin biosynthesis and suppresses virulence in *Alternaria brassicicola*. *PLoS Pathog* 8(10):e1002974
- Colot HV, Park G, Turner GE, Ringelberg C, Crew CM, Litvinkova L, Weiss RL, Borkovich KA, Dunlap JC (2006) A high-throughput gene knockout procedure for *Neurospora* reveals functions for multiple transcription factors. *Proc Natl Acad Sci U S A* 103(27):10352–10357
- Condon BJ, Leng Y, Wu D, Bushley KE, Ohm RA, Otillar R, Martin J, Schackwitz W, Grimwood J, MohdZainudin N, Xue C, Wang R, Manning VA, Dhillon B, Tu ZJ, Steffenson BJ, Salamov A, Sun H, Lowry S, LaButti K, Han J, Copeland A, Lindquist E, Barry K, Schmutz J, Baker SE, Ciuffetti LM, Grigoriev IV, Zhong S, Turgeon BG (2013) Comparative genome structure, secondary metabolite, and effector coding capacity across *Cochliobolus* pathogens. *PLoS Genet* 9(1):e1003233
- de Wit PJ, van der Burgt A, Okmen B, Stergiopoulos I, Abd-Elsalam KA, Aerts AL, Bahkali AH, Beenen HG, Chettri P, Cox MP, Datema E, de Vries RP, Dhillon B, Ganley AR, Griffiths SA, Guo Y, Hamelin RC, Henrissat B, Kabir MS, Jashni MK, Kema G, Klaubauf S, Lapidus A, Levasseur A, Lindquist E, Mehrabi R, Ohm RA, Owen TJ, Salamov A, Schwelm A, Schijlen E,

- Sun H, van den Burg HA, van Ham RC, Zhang S, Goodwin SB, Grigoriev IV, Collemare J, Bradshaw RE (2012) The genomes of the fungal plant pathogens *Cladosporium fulvum* and *Dothistroma septosporum* reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. *PLoS Genet* 8(11):e1003088
- Dujon B, Sherman D, Fischer G, Durrens P, Casaregola S, Lafontaine I, De Montigny J, Marck C, Neuveglise C, Talla E, Goffard N, Frangeul L, Aigle M, Anthouard V, Babour A, Barbe V, Barnay S, Blanchin S, Beckerich JM, Beyne E, Bleykasten C, Boisramé A, Boyer J, Cattolico L, Confanioli F, De Daruvar A, Despons L, Fabre E, Fairhead C, Ferry-Dumazet H, Groppi A, Hantraye F, Hennequin C, Jauniaux N, Joyet P, Kachouri R, Kerrest A, Koszul R, Lemaire M, Lesur I, Ma L, Muller H, Nicaud JM, Nikolski M, Oztas S, Ozier-Kalogeropoulos O, Pellenz S, Potier S, Richard GF, Straub ML, Suleau A, Swennen D, Tekai F, Wésolowski-Louvel M, Westhof E, Wirth B, Zeniou-Meyer M, Zivanovic I, Bolotin-Fukuhara M, Thierry A, Bouchier C, Caudron B, Scarpelli C, Gaillardin C, Weissenbach J, Wincker P, Souciet JL (2004) Genome evolution in yeasts. *Nature* 430(6995):35–44
- Dunlap JC, Borkovich KA, Henn MR, Turner GE, Sachs MS, Glass NL, McCluskey K, Plamann M, Galagan JE, Birren BW, Weiss RL, Townsend JP, Loros JJ, Nelson MA, Lambrechts R, Colot HV, Park G, Collopy P, Ringelberg C, Crew C, Litvinkova L, DeCaprio D, Hood HM, Curilla S, Shi M, Crawford M, Koerhsen M, Montgomery P, Larson L, Pearson M, Kasuga T, Tian C, Bastürkmen M, Altamirano L, Xu J (2007) Enabling a community to dissect an organism: overview of the *Neurospora* functional genomics project. *Adv Genet* 57:49–96
- Duplessis S, Cuomo CA, Lin YC, Aerts A, Tisserant E, Veneault-Fourrey C, Joly DL, Hacquard S, Amselem J, Cantarel BL, Chiu R, Coutinho PM, Feau N, Field M, Frey P, Gelhaye E, Goldberg J, Grabherr MG, Kodira CD, Kohler A, Kües U, Lindquist EA, Lucas SM, Mago R, Mauceli E, Morin E, Murat C, Pangilinan JL, Park R, Pearson M, Quesneville H, Rouhier N, Sakthikumar S, Salamov AA, Schmutz J, Selles B, Shapiro H, Tanguay P, Tuskan GA, Henrissat B, Van de Peer Y, Rouzé P, Ellis JG, Dodds PN, Schein JE, Zhong S, Hamelin RC, Grigoriev IV, Szabo LJ, Martin F (2011) Obligate biotrophy features unraveled by the genomic analysis of rust fungi. *Proc Natl Acad Sci USA* 108(22):9166–9171
- Earl D, Bradnam K, St John J, Darling A, Lin D, Fass J, Yu HO, Buffalo V, Zerbino DR, Diekhans M, Nguyen N, Ariyaratne PN, Sung WK, Ning Z, Haimel M, Simpson JT, Fonseca NA, Birol I, Docking TR, Ho IY, Rokhsar DS, Chikhi R, Lavenier D, Chapuis G, Naquin D, Maillet N, Schatz MC, Kelley DR, Phillippy AM, Koren S, Yang SP, Wu W, Chou WC, Srivastava A, Shaw TI, Ruby JG, Skewes-Cox P, Betegon M, Dimon MT, Solovyev V, Seledtsov I, Kosarev P, Vorobyev D, Ramirez-Gonzalez R, Leggett R, MacLean D, Xia F, Luo R, Li Z, Xie Y, Liu B, Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Yin S, Sharpe T, Hall G, Kersey PJ, Durbin R, Jackman SD, Chapman JA, Huang X, DeRisi JL, Caccamo M, Li Y, Jaffe DB, Green RE, Haussler D, Korf I, Paten B (2011) Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Res* 21(12):2224–2241
- Eastwood DC, Floudas D, Binder M, Majcherzyk A, Schneider P, Aerts A, Asiegbu FO, Baker SE, Barry K, Bendiksby M, Blumentritt M, Coutinho PM, Cullen D, de Vries RP, Gathman A, Goodell B, Henrissat B, Ihrmark K, Kauserud H, Kohler A, LaButti K, Lapidus A, Lavin JL, Lee YH, Lindquist E, Lilly W, Lucas S, Morin E, Murat C, Oguiza JA, Park J, Pisabarro AG, Riley R, Rosling A, Salamov A, Schmidt O, Schmutz J, Skrede I, Stenlid J, Wiebenga A, Xie X, Kües U, Hobbitt DS, Hoffmeister D, Högborg N, Martin F, Grigoriev IV, Watkinson SC (2011) The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. *Science* 333(6043):762–765
- El Hadrami A, El-Bebany AF, Yao Z, Adam LR, El Hadrami I, Daayf F (2012) Plants versus fungi and oomycetes: pathogenesis, defense and counter-defense in the proteomics era. *Int J Mol Sci* 13(6):7237–7259
- ENCODE Project Consortium (2004) The ENCODE (ENCyclopedia Of DNA Elements) project. *Science* 306:636–640

- Floudas D, Binder M, Riley R, Barry K, Blanchette RA, Henrissat B, Martínez AT, Ortilar R, Spatafora JW, Yadav JS, Aerts A, Benoit I, Boyd A, Carlson A, Copeland A, Coutinho PM, de Vries RP, Ferreira P, Findley K, Foster B, Gaskell J, Glotzer D, Górecki P, Heitman J, Hesse C, Hori C, Igarashi K, Jurgens JA, Kallen N, Kersten P, Khajamohiddin A, Kohler A, Kues U, Kumar TKA, Kuo A, LaButti K, Larrondo LF, Lindquist E, Ling A, Lucas S, Lundell T, Martin R, McLaughlin DJ, Morgenstern I, Morin E, Murat C, Nolan M, Ohm RA, Patyshakuliyeva A, Rokas A, Ruiz-Dueñas FJ, Sabat G, Salamov A, Samejima M, Schmutz J, Slot JC, John FS, Stenlid J, Sun H, Sun S, Tsang A, Wiebenga A, Young D, Pisabarro A, Eastwood DC, Martin F, Cullen D, Grigoriev IV, Hobbett DS (2012) The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* 336(6089):1715–1719
- Galagan JE, Calvo SE, Borkovich KA, Selker EU, Read ND, Jaffe D, FitzHugh W, Ma LJ, Smirnov S, Purcell S, Rehman B, Elkins T, Engels R, Wang S, Nielsen CB, Butler J, Endrizzi M, Qui D, Ianakiev P, Bell-Pedersen D, Nelson MA, Werner-Washburne M, Selitrennikoff CP, Kinsey JA, Braun EL, Zelter A, Schulte U, Kothe GO, Jedd G, Mewes W, Staben C, Marcotte E, Greenberg D, Roy A, Foley K, Naylor J, Stange-Thomann N, Barrett R, Gnerre S, Kamal M, Kamvysselis M, Mauceli E, Bielke C, Rudd S, Frishman D, Krystofova S, Rasmussen C, Metzenberg RL, Perkins DD, Kroken S, Cogoni C, Macino G, Catchside D, Li W, Pratt RJ, Osmani SA, DeSouza CP, Glass L, Orbach MJ, Berglund JA, Voelker R, Yarden O, Plamann M, Seiler S, Dunlap J, Radford A, Aramayo R, Natvig DO, Alex LA, Mannhaupt G, Ebbole DJ, Freitag M, Paulsen I, Sachs MS, Lander ES, Nusbaum C, Birren B (2003) The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature* 422(6934):859–868
- Giaever G, Chu AM, Ni L, Connelly C, Riles L, Véronneau S, Dow S, Lucau-Danila A, Anderson K, André B, Arkin AP, Astromoff A, El-Bakkoury M, Bangham R, Benito R, Brachat S, Campanaro S, Curtiss M, Davis K, Deutschbauer A, Entian KD, Flaherty P, Foury F, Garfinkel DJ, Gerstein M, Gotte D, Güldener U, Hegemann JH, Hempel S, Herman Z, Jaramillo DF, Kelly DE, Kelly SL, Kötter P, LaBonte D, Lamb DC, Lan N, Liang H, Liao H, Liu L, Luo C, Lussier M, Mao R, Menard P, Ooi SL, Revuelta JL, Roberts CJ, Rose M, Ross-Macdonald P, Scherens B, Schimmack G, Shafer B, Shoemaker DD, Sookhai-Mahadeo S, Storms RK, Strathern JN, Valle G, Voet M, Volckaert G, Wang CY, Ward TR, Wilhelmy J, Winzeler EA, Yang Y, Yen G, Youngman E, Yu K, Bussey H, Boeke JD, Snyder M, Philippsen P, Davis RW, Johnston M (2002) Functional profiling of the *Saccharomyces cerevisiae* genome. *Nature* 418(6896):387–391
- Goodwin SB, M'barek SB, Dhillon B, Wittenberg AH, Crane CF, Hane JK, Foster AJ, Van der Lee TA, Grimwood J, Aerts A, Antoniw J, Bailey A, Bluhm B, Bowler J, Bristow J, van der Burgt A, Canto-Canché B, Churchill AC, Conde-Ferràez L, Cools HJ, Coutinho PM, Csukai M, Dehal P, De Wit P, Donzelli B, van de Geest HC, van Ham RC, Hammond-Kosack KE, Henrissat B, Kilian A, Kobayashi AK, Koopmann E, Kourmpetis Y, Kuzniar A, Lindquist E, Lombard V, Maliapaard C, Martins N, Mehrabi R, Nap JP, Ponomarenko A, Rudd JJ, Salamov A, Schmutz J, Schouten HJ, Shapiro H, Stergiopoulos I, Torriani SF, Tu H, de Vries RP, Waalwijk C, Ware SB, Wiebenga A, Zwiers LH, Oliver RP, Grigoriev IV, Kema GH (2011) Finished genome of the fungal wheat pathogen *Mycosphaerella graminicola* reveals dispensome structure, chromosome plasticity, and stealth pathogenesis. *PLoS Genet* 7(6): e1002070
- Goffeau A, Barrell BG, Bussey H, Davis RW, Dujon B, Feldmann H, Galibert F, Hoheisel JD, Jacq C, Johnston M, Louis EJ, Mewes HW, Murakami Y, Philippsen P, Tettelin H, Oliver SG (1996) Life with 6000 genes. *Science* 274(5287):546, 563–567
- Grigoriev IV, Martinez DA, Salamov AA (2006) Fungal genomic annotation. In: Aurora DK, Berka RM, Singh GB (eds) *Applied mycology and biotechnology*, vol 6, Bioinformatics. Elsevier, Philadelphia, PA, pp 123–142

- Grigoriev IV, Cullen D, Goodwin SB, Hibbett D, Jeffries TW, Kubicek CP, Kuske C, Magnuson JK, Martin F, Spatafora JW, Tsang A, Baker SE (2011) Fueling the future with fungal genomics. *Mycology* 2(3):192–209
- Grigoriev IV, Nordberg H, Shabalov I, Aerts A, Cantor M, Goodstein D, Kuo A, Minovitsky S, Nikitin R, Ohm RA, Otillar R, Poliakov A, Ratnere I, Riley R, Smirnova T, Rokhsar D, Dubchak I (2012) The genome portal of the Department of Energy Joint Genome Institute. *Nucleic Acids Res* 40(1):D26–D32
- Haas BJ, Zeng Q, Pearson MD, Cuomo CA, Wortman JR (2011) Approaches to fungal genome annotation. *Mycology* 2(3):118–141
- Ho Y, Gruhler A, Heilbut A, Bader GD, Moore L, Adams SL, Millar A, Taylor P, Bennett K, Boutillier K, Yang L, Wolting C, Donaldson I, Schandorff S, Shewnarane J, Vo M, Taggart J, Goudreault M, Muskat B, Alfaro C, Dewar D, Lin Z, Michalickova K, Willems AR, Sassi H, Nielsen PA, Rasmussen KJ, Andersen JR, Johansen LE, Hansen LH, Jespersen H, Podtelejnikov A, Nielsen E, Crawford J, Poulsen V, Sørensen BD, Matthiesen J, Hendrickson RC, Gleeson F, Pawson T, Moran MF, Durocher D, Mann M, Hogue CW, Figgeys D, Tyers M (2002) Systematic identification of protein complexes in *Saccharomyces cerevisiae* by mass spectrometry. *Nature* 415(6868):180–183
- Howe D, Costanzo M, Fey P, Gojobori T, Hannick L, Hide W, Hill DP, Kania R, Schaeffer M, St Pierre S, Twigger S, White O, Rhee SY (2008) Big data: the future of biocuration. *Nature* 455 (7209):47–50
- Kalyuzhnaya MG, Lapidus A, Ivanova N, Copeland AC, McHardy AC, Szeto E, Salamov A, Grigoriev IV, Suciu D, Levine SR, Markowitz VM, Rigoutsos I, Tringe SG, Bruce DC, Richardson PM, Lidstrom ME, Chistoserdova L (2008) High-resolution metagenomics targets specific functional types in complex microbial communities. *Nat Biotechnol* 26(9):1029–1034
- Krogan NJ, Cagney G, Yu H, Zhong G, Guo X, Ignatchenko A, Li J, Pu S, Datta N, Tikuisis AP, Punna T, Peregrín-Alvarez JM, Shales M, Zhang X, Davey M, Robinson MD, Paccanaro A, Bray JE, Sheung A, Beattie B, Richards DP, Canadien V, Lalev A, Mena F, Wong P, Starostine A, Canete MM, Vlasblom J, Wu S, Orsi C, Collins SR, Chandran S, Haw R, Rilstone JJ, Gandi K, Thompson NJ, Musso G, St Onge P, Ghanny S, Lam MH, Butland G, Altaf-Ul AM, Kanaya S, Shilatifard A, O'Shea E, Weissman JS, Ingles CJ, Hughes TR, Parkinson J, Gerstein M, Wodak SJ, Emili A, Greenblatt JF (2006) Global landscape of protein complexes in the yeast *Saccharomyces cerevisiae*. *Nature* 440(7084):637–643
- Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W, Funke R, Gage D, Harris K, Heaford A, Howland J, Kann L, Lehoczky J, LeVine R, McEwan P, McKernan K, Meldrim J, Mesirov JP, Miranda C, Morris W, Naylor J, Raymond C, Rosetti M, Santos R, Sheridan A, Sougnez C, Stange-Thomann N, Stojanovic N, Subramanian A, Wyman D, Rogers J, Sulston J, Ainscough R, Beck S, Bentley D, Burton J, Clee C, Carter N, Coulson A, Deadman R, Deloukas P, Dunham A, Dunham I, Durbin R, French L, Grafham D, Gregory S, Hubbard T, Humphray S, Hunt A, Jones M, Lloyd C, McMurray A, Matthews L, Mercer S, Milne S, Mullikin JC, Mungall A, Plumb R, Ross M, Shownkeen R, Sims S, Waterston RH, Wilson RK, Hillier LW, McPherson JD, Marra MA, Mardis ER, Fulton LA, Chinwalla AT, Pepin KH, Gish WR, Chissole SL, Wendl MC, Delehaunty KD, Miner TL, Delehaunty A, Kramer JB, Cook LL, Fulton RS, Johnson DL, Minx PJ, Clifton SW, Hawkins T, Branscomb E, Predki P, Richardson P, Wenning S, Slezak T, Doggett N, Cheng JF, Olsen A, Lucas S, Elkin C, Uberbacher E, Frazier M, Gibbs RA, Muzny DM, Scherer SE, Bouck JB, Sodergren EJ, Worley KC, Rives CM, Gorrell JH, Metzker ML, Naylor SL, Kucherlapati RS, Nelson DL, Weinstock GM, Sakaki Y, Fujiyama A, Hattori M, Yada T, Toyoda A, Itoh T, Kawagoe C, Watanabe H, Totoki Y, Taylor T, Weissenbach J, Heilig R, Saurin W, Artiguenave F, Brottier P, Bruls T, Pelletier E, Robert C, Wincker P, Smith DR, Doucette-Stamm L, Rubenfield M, Weinstock K, Lee HM, Dubois J, Rosenthal A, Platzer M, Nyakatura G, Taudien S, Rump A, Yang H, Yu J, Wang J, Huang G, Gu J, Hood L, Rowen L, Madan A, Qin S, Davis RW, Federspiel NA, Abola AP, Proctor MJ, Myers RM, Schmutz J, Dickson M, Grimwood J, Cox DR, Olson MV, Kaul R, Raymond C, Shimizu N, Kawasaki K,

- Minoshima S, Evans GA, Athanasiou M, Schultz R, Roe BA, Chen F, Pan H, Ramser J, Lehrach H, Reinhardt R, McCombie WR, de la Bastide M, Dedhia N, Blöcker H, Hornischer K, Nordsiek G, Agarwala R, Aravind L, Bailey JA, Bateman A, Batzoglu S, Birney E, Bork P, Brown DG, Burge CB, Cerutti L, Chen HC, Church D, Clamp M, Copley RR, Doerks T, Eddy SR, Eichler EE, Furey TS, Galagan J, Gilbert JG, Harmon C, Hayashizaki Y, Haussler D, Hermjakob H, Hokamp K, Jang W, Johnson LS, Jones TA, Kasif S, Kasprzyk A, Kennedy S, Kent WJ, Kitts P, Koonin EV, Korf I, Kulp D, Lancet D, Lowe TM, McLysaght A, Mikkelsen T, Moran JV, Mulder N, Pollara VJ, Ponting CP, Schuler G, Schultz J, Slater G, Smit AF, Stupka E, Szustakowski J, Thierry-Mieg D, Thierry-Mieg J, Wagner L, Wallis J, Wheeler R, Williams A, Wolf YI, Wolfe KH, Yang SP, Yeh RF, Collins F, Guyer MS, Peterson J, Felsenfeld A, Wetterstrand KA, Patrinos A, Morgan MJ, de Jong P, Catanese JJ, Osoegawa K, Shizuya H, Choi S, Chen YJ, International Human Genome Sequencing Consortium (2001) Initial sequencing and analysis of the human genome. *Nature* 409(6822):860–921
- Larsen PE, Sreedasyam A, Trivedi G, Podila GK, Cseke LJ, Collart FR (2011) Using next generation transcriptome sequencing to predict an ectomycorrhizal metabolome. *BMC Syst Biol* 5:70
- Manning VA, Pandelova I, Dhillon B, Wilhelm LJ, Goodwin SB, Berlin AM, Figueroa M, Freitag M, Hane JK, Henrissat B, Holman WH, Kodira CD, Martin J, Oliver RP, Robbertse B, Schackwitz W, Schwartz DC, Spatafora JW, Turgeon BG, Yandava C, Young S, Zhou S, Zeng Q, Grigoriev IV, Ma LJ, Ciuffetti LM (2013) Comparative genomics of a plant-pathogenic fungus, *Pyrenophora tritici-repentis*, reveals transduplication and the impact of repeat elements on pathogenicity and population divergence. *G3* 3(1):41–63
- Martin F, Aerts A, Ahrén D, Brun A, Danchin EG, Duchaussoy F, Gibon J, Kohler A, Lindquist E, Pereda V, Salamov A, Shapiro HJ, Wuyts J, Blaudez D, Buée M, Brokstein P, Canbäck B, Cohen D, Courty PE, Coutinho PM, Delaruelle C, Detter JC, Deveau A, DiFazio S, Duplessis S, Fraissinet-Tachet L, Lucic E, Frey-Klett P, Fourrey C, Feussner I, Gay G, Grimwood J, Hoegger PJ, Jain P, Kilaru S, Labbé J, Lin YC, Legué V, Le Tacon F, Marmeisse R, Melayah D, Montanini B, Muratet M, Nehls U, Niculita-Hirzel H, Oudot-Le Secq MP, Peter M, Quesneville H, Rajashekar B, Reich M, Rouhier N, Schmutz J, Yin T, Chalot M, Henrissat B, Kües U, Lucas S, Van de Peer Y, Podila GK, Polle A, Pukkila PJ, Richardson PM, Rouzé P, Sanders IR, Stajich JE, Tunlid A, Tuskan G, Grigoriev IV (2008) The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature* 452:88–92
- Martinez D, Larrondo LF, Putnam N, Gelpke MD, Huang K, Chapman J, Helfenbein KG, Ramaiya P, Detter JC, Larimer F, Coutinho PM, Henrissat B, Berka R, Cullen D, Rokhsar D (2004) Genome sequence of the lignocellulose degrading fungus *Phanerochaete chrysosporium* strain RP78. *Nat Biotechnol* 22(6):695–700
- Martinez D, Challacombe J, Morgenstern I, Hibbett D, Schmoll M, Kubicek CP, Ferreira P, Ruiz-Duenas FJ, Martinez AT, Kersten P, Hammel KE, Vanden Wymelenberg A, Gaskell J, Lindquist E, Sabat G, Bondurant SS, Larrondo LF, Canessa P, Vicuna R, Yadav J, Doddapaneni H, Subramanian V, Pisabarro AG, Lavín JL, Oguiza JA, Master E, Henrissat B, Coutinho PM, Harris P, Magnuson JK, Baker SE, Bruno K, Kenealy W, Hoegger PJ, Kües U, Ramaiya P, Lucas S, Salamov A, Shapiro H, Tu H, Chee CL, Misra M, Xie G, Teter S, Yaver D, James T, Mokrejs M, Pospisek M, Grigoriev IV, Brettin T, Rokhsar D, Berka R, Cullen D (2009) Genome, transcriptome, and secretome analysis of wood decay fungus *Postia placenta* supports unique mechanisms of lignocellulose conversion. *Proc Natl Acad Sci U S A* 106:1954–1959
- Metzker ML (2010) Sequencing technologies – the next generation. *Nat Rev Genet* 11(1):31–46
- Morin E, Kohler A, Baker AR, Foulongne-Oriol M, Lombard V, Nagy LG, Ohm RA, Patyshakuliyeva A, Brun A, Aerts AL, Bailey AM, Billette C, Coutinho PM, Deakin G, Doddapaneni H, Floudas D, Grimwood J, Hildén K, Kües U, Labutti KM, Lapidus A, Lindquist EA, Lucas SM, Murat C, Riley RW, Salamov AA, Schmutz J, Subramanian V, Wösten HA, Xu J, Eastwood DC, Foster GD, Sonnenberg AS, Cullen D, de Vries RP, Lundell T, Hibbett DS, Henrissat B, Burton KS, Kerrigan RW, Challen MP, Grigoriev IV, Martin F (2012) Genome

- sequence of the button mushroom *Agaricus bisporus* reveals mechanisms governing adaptation to a humic-rich ecological niche. *Proc Natl Acad Sci USA* 109(43):17501–17506
- O'Connell RJ, Thon MR, Hacquard S, Amyotte SG, Kleemann J, Torres MF, Damm U, Buiate EA, Epstein L, Alkan N, Altmüller J, Alvarado-Balderrama L, Bauser CA, Becker C, Birren BW, Chen Z, Choi J, Crouch JA, Duvick JP, Farman MA, Gan P, Heiman D, Henrissat B, Howard RJ, Kabbage M, Koch C, Kracher B, Kubo Y, Law AD, Lebrun MH, Lee YH, Miyara I, Moore N, Neumann U, Nordström K, Panaccione DG, Panstruga R, Place M, Proctor RH, Prusky D, Rech G, Reinhardt R, Rollins JA, Rounsley S, Schardl CL, Schwartz DC, Shenoy N, Shirasu K, Sikhakolli UR, Stüber K, Sukno SA, Sweigard JA, Takano Y, Takahara H, Trail F, van der Does HC, Voll LM, Will I, Young S, Zeng Q, Zhang J, Zhou S, Dickman MB, Schulze-Lefert P, Ver Loren van Themaat E, Ma LJ, Vaillancourt LJ (2012) Lifestyle transitions in plant pathogenic *Colletotrichum* fungi deciphered by genome and transcriptome analyses. *Nat Genet* 44(9):1060–1065
- Ohm RA, Jong JF, Lugones LG, Aerts A, Kothe E, Stajich JE, de Vries RP, Record E, Levasseur A, Baker SE, Bartholomew KA, Coutinho PM, Erdmann S, Fowler TJ, Gathman AC, Lombard V, Henrissat B, Knabe N, Kües U, Lilly WW, Lindquist E, Lucas S, Magnuson JK, Piumi F, Raudaskoski M, Salamov A, Schmutz J, Schwarze FW, van Kuyk PA, Horton JS, Grigoriev IV, Wösten HAB (2010) Formation of mushrooms and lignocellulose degradation encoded in the genome sequence of *Schizophyllum commune*. *Nat Biotechnol* 28(9):957–963
- Ohm RA, de Jong JF, de Bekker C, Wösten HA, Lugones LG (2011) Transcription factor genes of *Schizophyllum commune* involved in regulation of mushroom formation. *Mol Microbiol* 81(6):1433–1445
- Ohm RA, Feau N, Henrissat B, Schoch CL, Horwitz BA, Barry KW, Condon BJ, Copeland AC, Dhillon B, Glaser F, Hesse CN, Kosti I, Labutti K, Lindquist EA, Lucas S, Salamov AA, Bradshaw RE, Ciuffetti L, Hamelin RC, Kema GH, Lawrence C, Scott JA, Spatafora JW, Turgeon BG, de Wit PJ, Zhong S, Goodwin SB, Grigoriev IV (2012) Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen dothideomycetes fungi. *PLoS Pathog* 8(12):e1003037
- Olson A, Aerts A, Asiegbu F, Belbahri L, Bouzid O, Broberg A, Canbäck B, Coutinho PM, Cullen D, Dalman K, Defflorio G, van Diepen LT, Dunand C, Duplessis S, Durling M, Gonthier P, Grimwood J, Fossdal CG, Hansson D, Henrissat B, Hietala A, Himmelstrand K, Hoffmeister D, Höglberg N, James TY, Karlsson M, Kohler A, Kües U, Lee YH, Lin YC, Lind M, Lindquist E, Lombard V, Lucas S, Lundén K, Morin E, Murat C, Park J, Raffaello T, Rouzé P, Salamov A, Schmutz J, Solheim H, Ståhlberg J, Véléz H, de Vries RP, Wiebenga A, Woodward S, Yakovlev I, Garbelotto M, Martin F, Grigoriev IV, Stenlid J (2012) Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. *New Phytol* 194(4):1001–1013
- Pennisi E (2012) At long last, nanopore sequencing seems poised to leave the lab, promising a new and better way to decode DNA. *Science* 336:534–537
- Ptacek J, Devgan G, Michaud G, Zhu H, Zhu X, Fasolo J, Guo H, Jona G, Breitkreutz A, Sopko R, McCartney RR, Schmidt MC, Rachidi N, Lee SJ, Mah AS, Meng L, Stark MJ, Stern DF, De Virgilio C, Tyers M, Andrews B, Gerstein M, Schweitzer B, Predki PF, Snyder M (2005) Global analysis of protein phosphorylation in yeast. *Nature* 438(7068):679–684
- Rhind N, Chen Z, Yassour M, Thompson DA, Haas BJ, Habib N, Wapinski I, Roy S, Lin MF, Heiman DI, Young SK, Furuya K, Guo Y, Pidoux A, Chen HM, Robbertse B, Goldberg JM, Aoki K, Bayne EH, Berlin AM, Desjardins CA, Dobbs E, Dukaj L, Fan L, FitzGerald MG, French C, Gujja S, Hansen K, Keifenheim D, Levin JZ, Mosher RA, Müller CA, Pfiffner J, Priest M, Russ C, Smialowska A, Swoboda P, Sykes SM, Vaughn M, Vengrova S, Yoder R, Zeng Q, Allshire R, Baulcombe D, Birren BW, Brown W, Ekwall K, Kellis M, Leatherwood J, Levin H, Margalit H, Martienssen R, Nieduszynski CA, Spatafora JW, Friedman N, Dalggaard JZ, Baumann P, Niki H, Regev A, Nusbaum C (2011) Comparative functional genomics of the fission yeasts. *Science* 332(6032):930–936

- Sanger F, Nicklen S, Coulson AR (1977) DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci U S A* 74(12):5463–5467
- Schuster A, Bruno KS, Collett JR, Baker SE, Seiboth B, Kubicek CP, Schmoll M (2012) A versatile toolkit for high throughput functional genomics with *Trichoderma reesei*. *Biotechnol Biofuels* 5(1):1
- Skibbe DS, Doehlemann G, Fernandes J, Walbot V (2010) Maize tumors caused by *Ustilago maydis* require organ-specific genes in host and pathogen. *Science* 328(5974):89–92
- Skipper M, Dhand R, Campbell P (2012) Presenting ENCODE. *Nature* 489(7414):45
- Tringe SG, Rubin EM (2005) Metagenomics: DNA sequencing of environmental samples. *Nat Rev Genet* 6(11):805–814
- Tuskan GA, Difazio S, Jansson S, Bohlmann J, Grigoriev I, Hellsten U, Putnam N, Ralph S, Rombauts S, Salamov A, Schein J, Sterck L, Aerts A, Bhalarao RR, Bhalarao RP, Blaudez D, Boerjan W, Brun A, Brunner A, Busov V, Campbell M, Carlson J, Chalot M, Chapman J, Chen GL, Cooper D, Coutinho PM, Couturier J, Covert S, Cronk Q, Cunningham R, Davis J, Degroove S, Déjardin A, Depamphilis C, Detter J, Dirks B, Dubchak I, Duplessis S, Ehlting J, Ellis B, Gendler K, Goodstein D, Gribskov M, Grimwood J, Groover A, Gunter L, Hamberger B, Heinze B, Helariutta Y, Henrissat B, Holligan D, Holt R, Huang W, Islam-Faridi N, Jones S, Jones-Rhoades M, Jorgensen R, Joshi C, Kangasjärvi J, Karlsson J, Kelleher C, Kirkpatrick R, Kirst M, Kohler A, Kalluri U, Larimer F, Leebens-Mack J, Leplé JC, Locascio P, Lou Y, Lucas S, Martin F, Montanini B, Napoli C, Nelson DR, Nelson C, Nieminen K, Nilsson O, Pereda V, Peter G, Philippe R, Pilate G, Poliakov A, Razumovskaya J, Richardson P, Rinaldi C, Ritland K, Rouzé P, Ryaboy D, Schmutz J, Schrader J, Segerman B, Shin H, Siddiqui A, Sterky F, Terry A, Tsai CJ, Uberbacher E, Unneberg P, Vahala J, Wall K, Wessler S, Yang G, Yin T, Douglas C, Marra M, Sandberg G, Van de Peer Y, Rokhsar D (2006) The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313(5793):1596–1604
- Weigel D, Mott R (2009) The 1001 genomes project for *Arabidopsis thaliana*. *Genome Biol* 10(5):107
- Wilhelm BT, Marguerat S, Watt S, Schubert F, Wood V, Goodhead I, Penkett CJ, Rogers J, Bähler J (2008) Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. *Nature* 453(7199):1239–1243
- Winzeler EA, Shoemaker DD, Astromoff A, Liang H, Anderson K, Andre B, Bangham R, Benito R, Boeke JD, Bussey H, Chu AM, Connelly C, Davis K, Dietrich F, Dow SW, El Bakkoury M, Foury F, Friend SH, Gentale E, Giaever G, Hegemann JH, Jones T, Laub M, Liao H, Liebundguth N, Lockhart DJ, Lucau-Danila A, Lussier M, M'Rabet N, Menard P, Mittmann M, Pai C, Rebischung C, Revuelta JL, Riles L, Roberts CJ, Ross-MacDonald P, Scherens B, Snyder M, Sookhai-Mahadeo S, Storms RK, Véronneau S, Voet M, Volckaert G, Ward TR, Wysocki R, Yen GS, Yu K, Zimmermann K, Philippsen P, Johnston M, Davis RW (1999) Functional characterization of the *S. cerevisiae* genome by gene deletion and parallel analysis. *Science* 285(5429):901–906
- Wu D, Hugenholtz P, Mavromatis K, Pukall R, Dalin E, Ivanova NN, Kunin V, Goodwin L, Wu M, Tindall BJ, Hooper SD, Pati A, Lykidis A, Spring S, Anderson IJ, D'haeseleer P, Zemla A, Singer M, Lapidus A, Nolan M, Copeland A, Han C, Chen F, Cheng JF, Lucas S, Kerfeld C, Lang E, Gronow S, Chain P, Bruce D, Rubin EM, Kyrpides NC, Klenk HP, Eisen JA (2009) A phylogeny-driven genomic encyclopaedia of bacteria and archaea. *Nature* 462(7276):1056–1060

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