Microbial host interactions: a double-edge sword

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Wonderful diversity of fungi



Functional diversity of fungi



What is mycorrhiza?

Symbiosis between plant roots and the fungus



Evolution of mycorrhiza



From I to 1000 genomes

LETTERS

nature

The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis

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5 symbiotic genomes



Ascomycota; Pezizomycotina; Pezizomycetes; *Tuber* Ascomycota; Pezizomycotina;

Leotiomycetes; Oidiodendron

Oidma1

Paxin1

Tubme1

Basidiomycota; Agaricomycotina; Agaricomycetes; Boletales; *Paxillus*

Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricales; *Hebeloma*

Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricales; *Laccaria*

Lacbi2

Hebcy1

Armed and Dangerous

These fungi, weeds, and viruses are among the more serious biological threats to food security—so researchers are working hard on countermeasures





BLACK SIGATOKA

Pest: Mycosphaerella fijiensis Crops: Bananas, plantains Whereabouts: This fungus, first detected in Fiji in 1964, is now found in 100 countries in the Americas, Africa and South Asia.

RICE BLAST

Pest: Magnaporthe oryzae Crops: Rice, 50 species of grasses and sedges



ASIAN SOYBEAN RUST

Pest: Phakopsora pachyrhizi Crops: At least 31 legume species, notably soybeans

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POTATO BLICHT Pest: Phytophthora infestans Crops: Potatoes; also tomatoes and other solanaceous crops WHEAT STEM RUST

Pest: *Puccinia graminis* Ug99 Crop: Wheat

Use genomics to understand microbe-host interactions



Genome sequencing

- Extract DNA from the organism
- Fragment and sequence the DNA (millions of pieces)
- Assemble the sequences to a genome
- Find genes in the genome
- Perform functional analyses

Computational challenges

- Rapidly moving field requires novel tools and algorithms
- Data analyses, transfer and storage
- Bioinformaticians

Assembly

- Overlap Consensus Layout OLC
- De Bruijn Graphs





Sequencing technologies



Roche / 454 GS FLX Titanium Series 1,2 million reads Read length approx. 400 bp 400 million bp per run

Applied BioSystems (ABI) 3730xl DNA Analyzer (Sanger) 96 samples in parallel (reads) Read length approx. 800 bp - 80.000 bp per run

> Illumina / Solexa HiSeq 2000

- >2 billion reads
- Read length approx. 70 bp
- 200 Gbp per run





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Cumulative sequence output



Rokas presentation Workshop in Genomics 2012

Microprocessor (MIPS) Sequencing (kbases/day) Compact HDD storage capacity (MB) 199° 1002 2002 2003 Kahn, Science 2011 Year

BILS – Bioinformatics Infrastructure for Life Sciences

- Distributed national research infrastructure supported by the Swedish Research Council
- BILS provides bioinformatics support in various projects, e.g. in large-scale sequencing, proteom systems biology, metabolomics, metagenomics
- BILS provides infrastructure and tools for bioinformatics analyses
- Bioinformatics network
 - nodes at each of the 6 large university cities
 - annual workshop
 - training
- Bioinformatics computation and data storage provided in collaboration with SNIC
- Swedish node in ELIXIR
- Current staff of 11 people will during 2012 expand to 26 persons





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