# Welcome To the First Fungal Bioinformatics Workshop













# House keeping!





## Introductions for all of us!

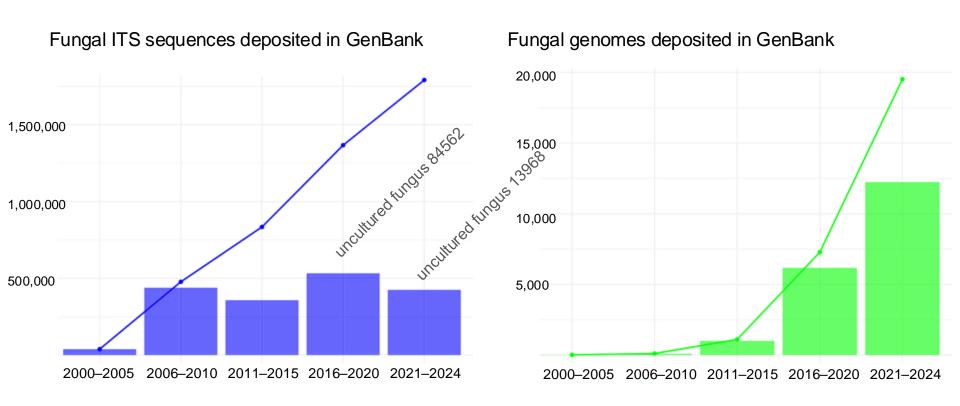
- √ Your name
- √ Your organisation
- ✓ Group of fungi you work with.
- ✓ One thing you want to get out of the workshop?
- ✓ One fun fungal fact of your life.

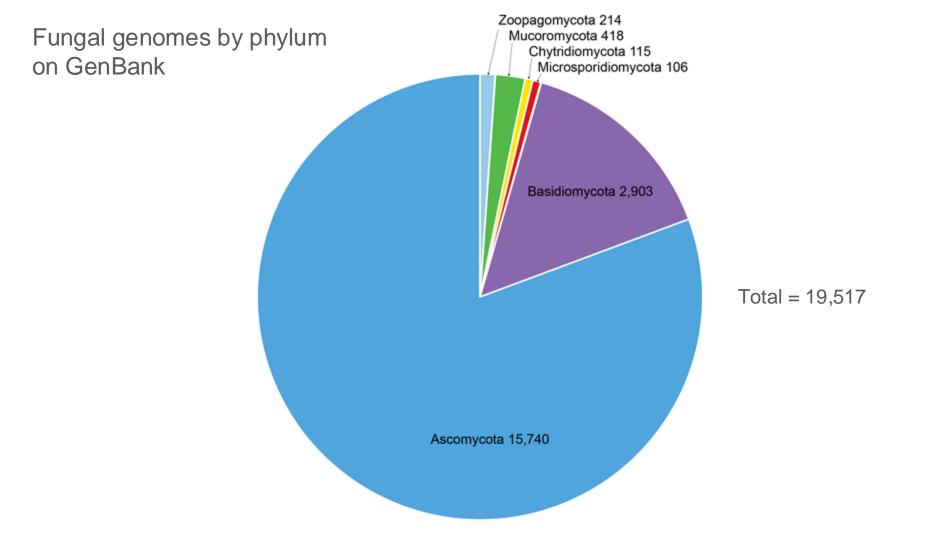




# High-throughput sequencing is the new normal for Fungi

#### Cumulative data on GenBank



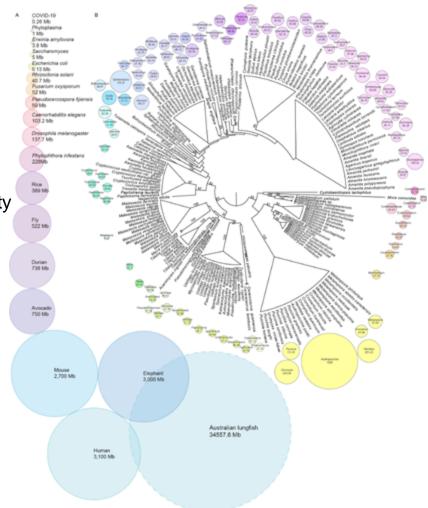


### Fungal genome size

Fungal genome size varies among species, genera... subphyla

Genome size dictates amount of required data and complexity of downstream analyses

Genera may be a 'ballpark' of genome size



## Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*

Li-Jun Ma, H. Charlotte van der Does, Katherine A. Borkovich, Jeffrey J. Coleman, Marie-Josée

Daboussi, Antonio Di Pietro, Marie Dufresne, Michael Freitag, Manfred Grabherr, Bernard Henrissat,

Petra M. Houterman, Seogchan Kang, Won-Bo Shim, Charles Woloshuk, Xiaohui Xie, Jin-Rong Xu, John

Antoniw, Scott E. Baker, Burton H. Bluhm, Andrew Breakspear, Daren W. Brown, Robert A. E. Butchko,

Sinead Chapman, Richard Coulson, ... Martijn Rep 

+ Show authors

Nature 464, 367-373 (2010) | Cite this article

#### The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes

Dimitrios Floudas, <sup>1</sup> Manfred Binder, <sup>1</sup> Robert Riley, <sup>2</sup> Kerrie Barry, <sup>2</sup> Robert A. Blanchette, <sup>3</sup> Bernard Henrissat, <sup>4</sup> Angel T. Martínez, <sup>5</sup> Robert Otillar, <sup>2</sup> Joseph W. Spatafora, <sup>6</sup> Jagjit S. Yadav, <sup>7</sup> Andrea Aerts, <sup>2</sup> Isabelle Benoit, <sup>6</sup> 9 Alex Boyd, <sup>6</sup> Alexis Carlson, <sup>1</sup> Alex Copeland, <sup>2</sup> Pedro M. Coutinho, <sup>4</sup> Ronald P. de Vries, <sup>6</sup> 9 Patricia Ferreira, <sup>10</sup> Keisha Findley, <sup>11</sup> Brian Foster, <sup>2</sup> Jill Gaskell, <sup>12</sup> Dylan Glotzer, <sup>1</sup> Pawel Górecki, <sup>13</sup> Joseph Heitman, <sup>11</sup> Cedar Hesse, <sup>6</sup> Chiaki Hori, <sup>14</sup> Kiyohiko Igarashi, <sup>14</sup> Joel A. Jurgens, <sup>3</sup> Nathan Kallen, <sup>1</sup> Phil Kersten, <sup>12</sup> Annegret Kohler, <sup>15</sup> Ursula Kües, <sup>16</sup> T. K. Arun Kumar, <sup>17</sup> Alan Kuo, <sup>2</sup> Kurt LaButti, <sup>2</sup> Luis F. Larrondo, <sup>18</sup> Erika Lindquist, <sup>2</sup> Albee Ling, <sup>3</sup> Vincent Lombard, <sup>4</sup> Susan Lucas, <sup>2</sup> Taina Lundell, <sup>19</sup> Rachael Martin, <sup>3</sup> David J. McLaughlin, <sup>17</sup> Ingo Morgenstern, <sup>20</sup> Emanuelle Morin, <sup>15</sup> Claude Murat, <sup>15</sup> Laszlo G. Nagy, <sup>3</sup> Matt Nolan, <sup>2</sup> Robin A. Ohm, <sup>2</sup> Aleksandrina Patyshakuliyeva, <sup>9</sup> Antonis Rokas, <sup>21</sup> Francisco J. Ruiz-Dueñas, <sup>5</sup> Grzegorz Sabat, <sup>22</sup> Asaf Salamov, <sup>2</sup> Masahiro Samejima, <sup>14</sup> Jeremy Schmutz, <sup>23</sup> Jason C. Slot, <sup>21</sup> Franz St. John, <sup>12</sup> Jan Stenlid, <sup>28</sup> Hui Sun, <sup>2</sup> Sheng Sun, <sup>11</sup> Khajamohiddin Syed, <sup>7</sup> Adrian Tsang, <sup>20</sup> Ad Wiebenga, <sup>9</sup> Darcy Young, <sup>1</sup> Antonio Pisabarro, <sup>25</sup> Daniel C. Eastwood, <sup>26</sup> Francis Martin, <sup>15</sup> Dan Cullen, <sup>12</sup> Igor V. Grigoriev, <sup>2\*</sup> David S. Hibbett<sup>1\*</sup>

## Obligate biotrophy features unraveled by the genomic analysis of rust fungi

Sébastien Duplessis , Christina A. Cuomo , Yao-Cheng Lin, +46, and Francis Martin Authors Info & Affiliations

Edited by Paul Schulze-Lefert, Max Planck Institute for Plant Breeding Research, Cologne, Germany, and approved March 31, 2011 (received for review January 5, 2011)

May 2, 2011 108 (22) 9166-9171 https://doi.org/10.1073/pnas.1019315108

## A thousand-genome panel retraces the global spread and adaptation of a major fungal crop pathogen

Alice Feurtey, Cécile Lorrain, Megan C. McDonald, Andrew Milgate, Peter S. Solomon, Rachael Warren, Guido Puccetti, Gabriel Scalliet, Stefano F. F. Torriani, Lilian Gout, Thierry C. Marcel, Frédéric Suffert,

Julien Alassimone, Anna Lipzen, Yuko Yoshinaga, Christopher Daum, Kerrie Barry, Igor V. Grigoriev,

Stephen B. Goodwin, Anne Genissel, Michael F. Seidl, Eva H. Stukenbrock, Marc-Henri Lebrun, Gert H.

J. Kema, ... Daniel Croll 
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Review Article | Free

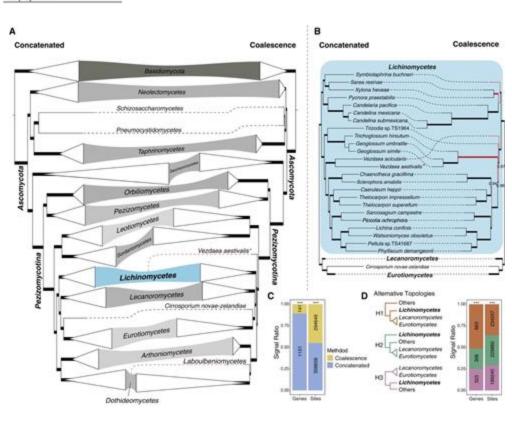
#### **Toward a Fully Resolved Fungal Tree of Life**

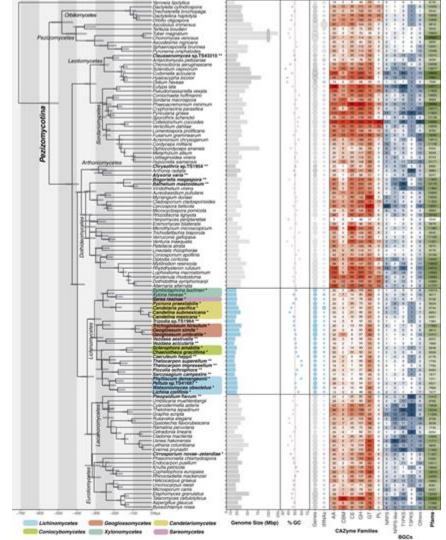
Timothy Y. James<sup>1</sup>, Jason E. Stajich<sup>2</sup>, Chris Todd Hittinger<sup>3</sup>, and Antonis Rokas<sup>4</sup>

◆ View Affiliations

# Genome-level analyses resolve an ancient lineage of symbiotic ascomycetes

David Díaz-Escandón <sup>1</sup>, Gulnara Tagirdzhanova <sup>1</sup>, Dan Vanderpool <sup>2</sup>, Carmen C.G. Allen <sup>1</sup>, André Aptroot <sup>3</sup>, Oluna Češka <sup>4 14</sup>, David L. Hawksworth <sup>5 6 7</sup>, Alejandro Huereca <sup>1</sup>, Kerry Knudsen <sup>8</sup>, Jana Kocourková <sup>8</sup>, Robert Lücking <sup>9</sup>, Philipp Resl <sup>10 11 12</sup>, Toby Spribille <sup>1 11 12 13 15</sup>  $\stackrel{>}{\sim}$   $\stackrel{>}{\bowtie}$ 

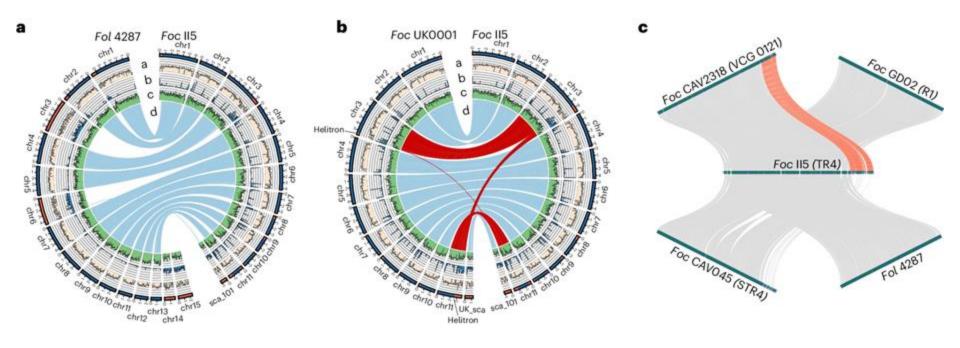




#### Virulence of banana wilt-causing fungal pathogen Fusarium oxysporum tropical race 4 is mediated by nitric oxide biosynthesis and accessory genes

Yong Zhang, Siwen Liu, Diane Mostert, Houlin Yu, Mengxia Zhuo, Gengtan Li, Cunwu Zuo, Sajeet Haridas, Katie Webster, Minhui Li, Igor V. Grigoriev, Ganjun Yi, Altus Viljoen ☑, Chunyu Li ☑ & Li-Jun Ma ☑

Nature Microbiology 9, 2232-2243 (2024) | Cite this article







## The Effects of Herbarium Specimen Characteristics on Short-Read NGS Sequencing Success in Nearly 8000 Specimens: Old, Degraded Samples Have Lower DNA Yields but Consistent Sequencing Success

**OPEN ACCESS** 

Edited by: Michael R. McKain, Heather R. Kates<sup>1\*†</sup>, Joshua R. Doby<sup>1†</sup>, Carol M. Siniscalchi<sup>2</sup>, Raphael LaFrance<sup>1</sup>, Douglas E. Soltis<sup>1,3,4,5</sup>, Pamela S. Soltis<sup>1,4,5</sup>, Robert P. Guralnick<sup>1,5\*†</sup> and Ryan A. Folk<sup>2\*†</sup>

### Fungal genomics is more and more accessible

#### 10 years ago

- Hardware and software were bottlenecks
- Needed competency in linux and at least one other language
- High-throughput sequencing data were expensive and limiting

#### Now

- Automated pipelines on Galaxy
- Server size increases
- With publicly available data, and creativity, there is unlimited capacity for large datasets

# One workshop for all of us!

√ Theory > Toy Practice > Real examples

✓ Let us know what you need more/less of

✓ Community building

✓ Ask question

√ Share your knowledge

✓ Have some fun hanging out with fun(gi) people

# One workshop for all of us!

https://tinyurl.com/BPAFunFungi

