An insight into the genome of *Sporisorium scitamineum*

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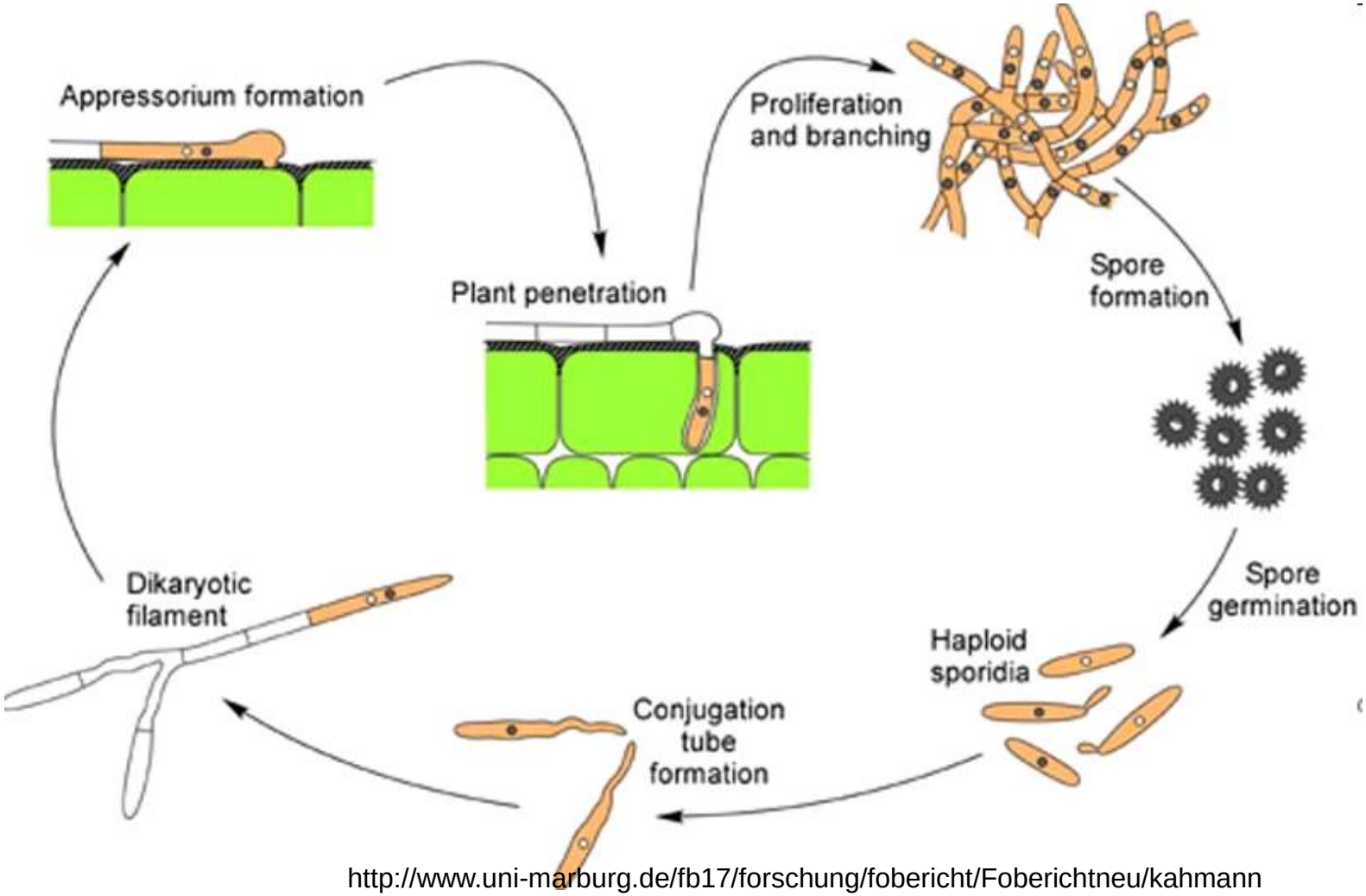
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- Sugarcane smut is world wide disease caused by *Sporisorium scitamineum*

Sporisorium scitamineum



http://www.uni-marburg.de/fb17/forschung/foberichtneu/kahmann





- JG35 and JG36 are opposite mating types isolated in Guangxi

Fungal genome project

- 360 fungal genome project registered in NCBI by 5/2011
  413 fungal genome project registered in NCBI by 4/2012

- *Ustilago maydis* FB1 and 521 sequenced by Broad Institute

- *Ustilago maydis* 521: 19.8015Mb, 23 chromasomes

Sporisorium scitamineum Guangxi strains

The genome project of JG36 and JG35 strains were initiated in April, 2010.



JG36: haploid genome (100X)

JG35: haploid genome (100X)

JG36: haploid transcriptome

JG36: diploid transcriptome



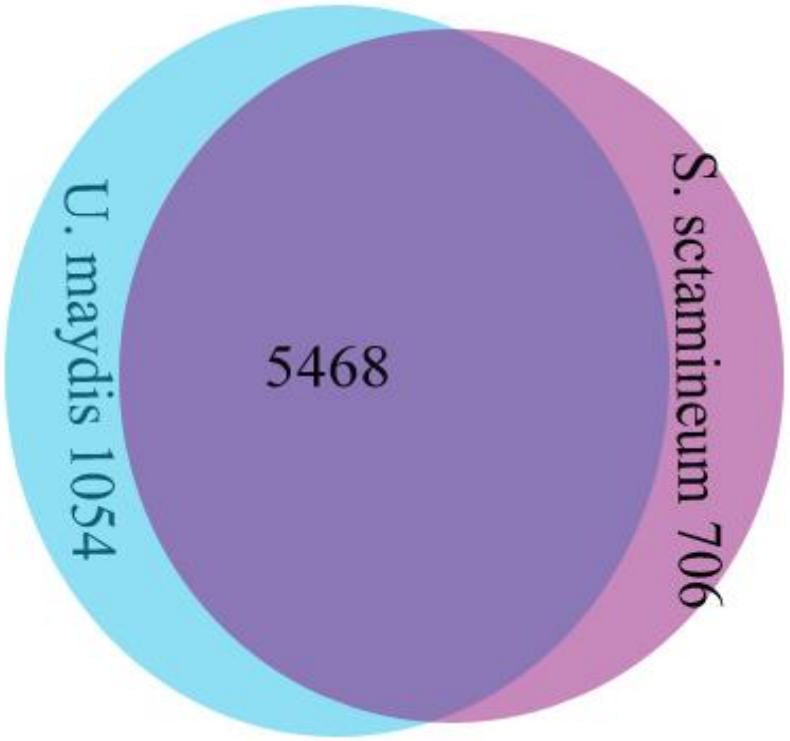
Sequencing

- **JG36 strain**
  - Roche 454: 8kb mate-paired reads 473Mb ~23X
  - Solexa: 3kb pair-end reads 0.95Gb ~48X
  - Solexa: 500bp pair-end reads 1.88Gb ~94X
  - Sanger: Fosmid-end reads 6.4Mb ~ 0.3X
- **JG35 strain**
  - Solexa: 500bp pair-end reads 1.97Gb ~98X

Assembly data

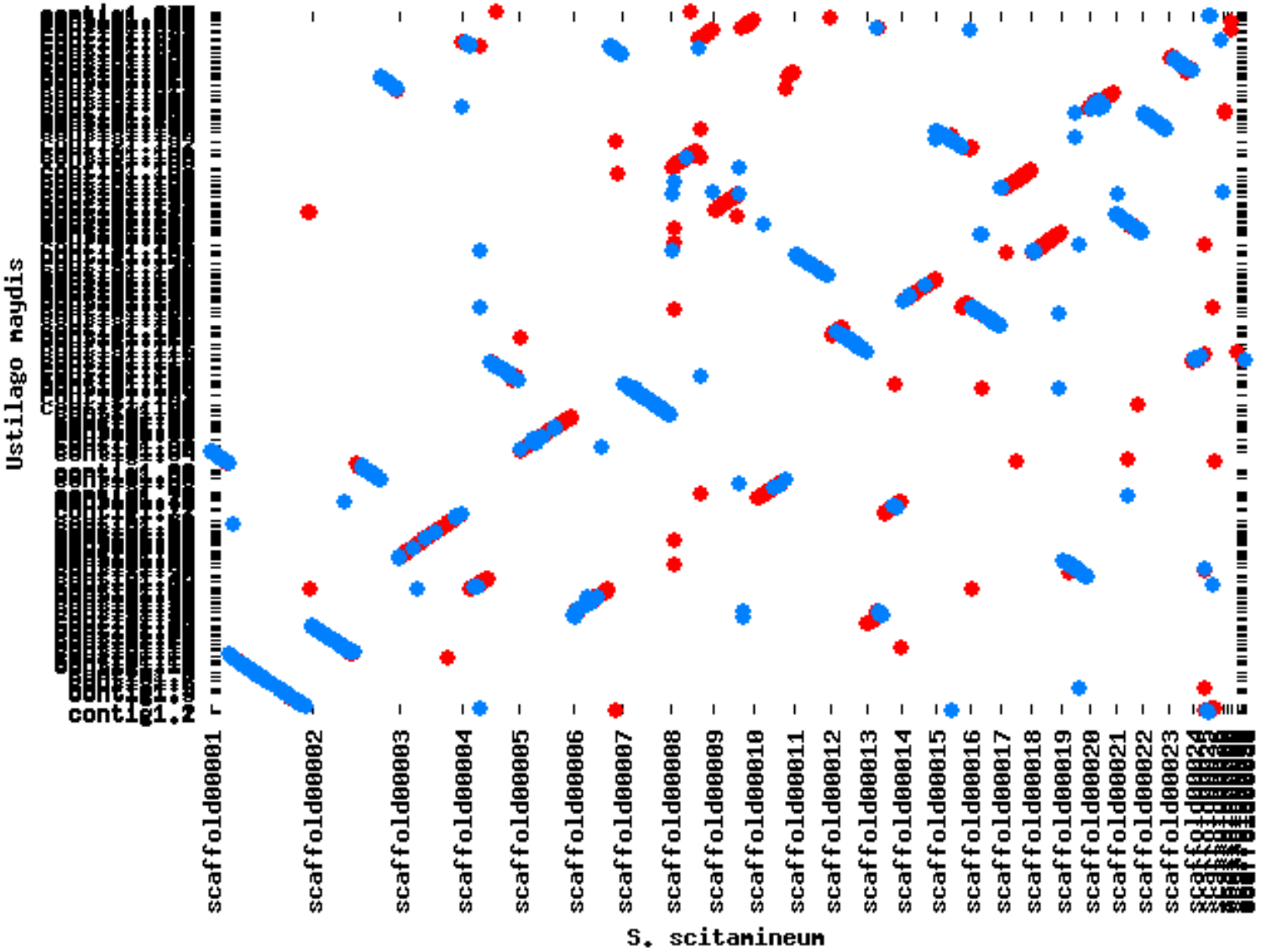
- JG36: 1486 contigs
  total length: 19.58 Mb
- Largest contig: 194.91kb
  N50 size: 40.86kb
- 40 scalffolds: largest scalffold size 1.92 Mb
  N50 size 793.11 kb
- 495 inner gaps, estimate in 345kb
  15 inner gap over 3 kb
  267 inner gaps, less than 8 kb

Comparison with *U. maydis*



- JG36: 6174 predicted genes
- 5468 genes with high similarity to *U. maydis*

Comparison with *U. maydis*



But, not so conserved in nucleotide level

Transcriptomes of *S. scitamineum*

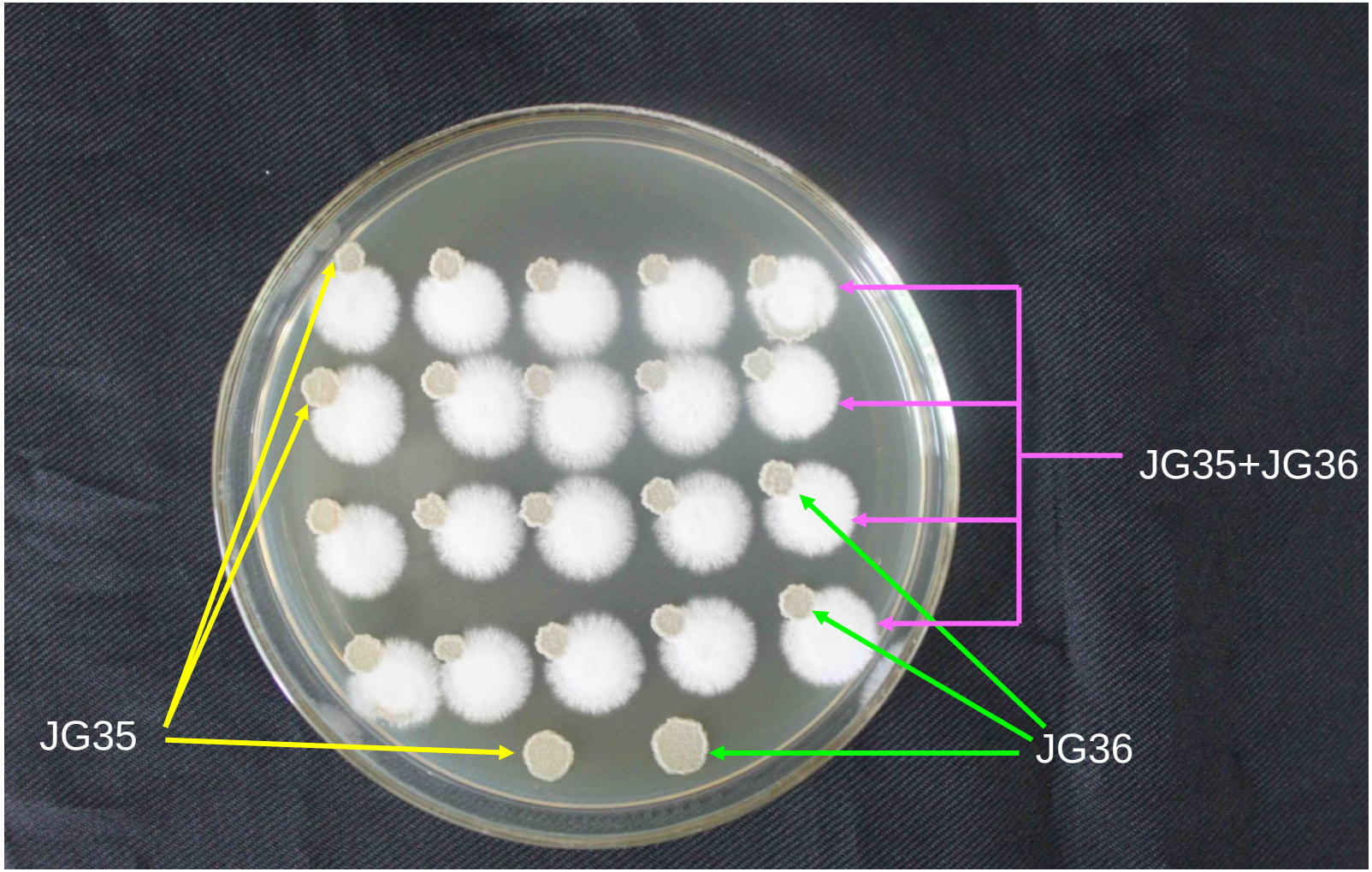
- Haploid

  Media culture , yeast-like cells

- Diploid

  Complicated

Diploid hyphae on PDA plate



Artificial infection

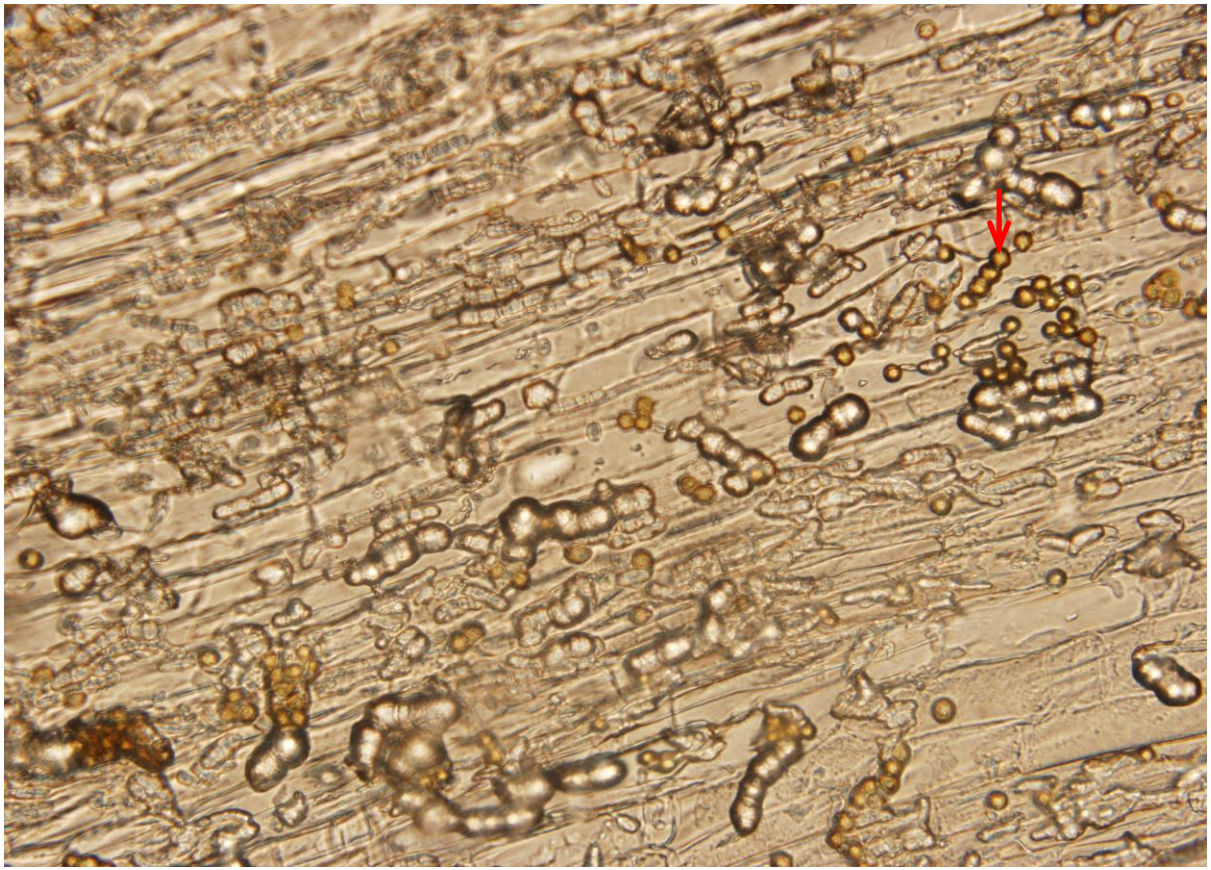






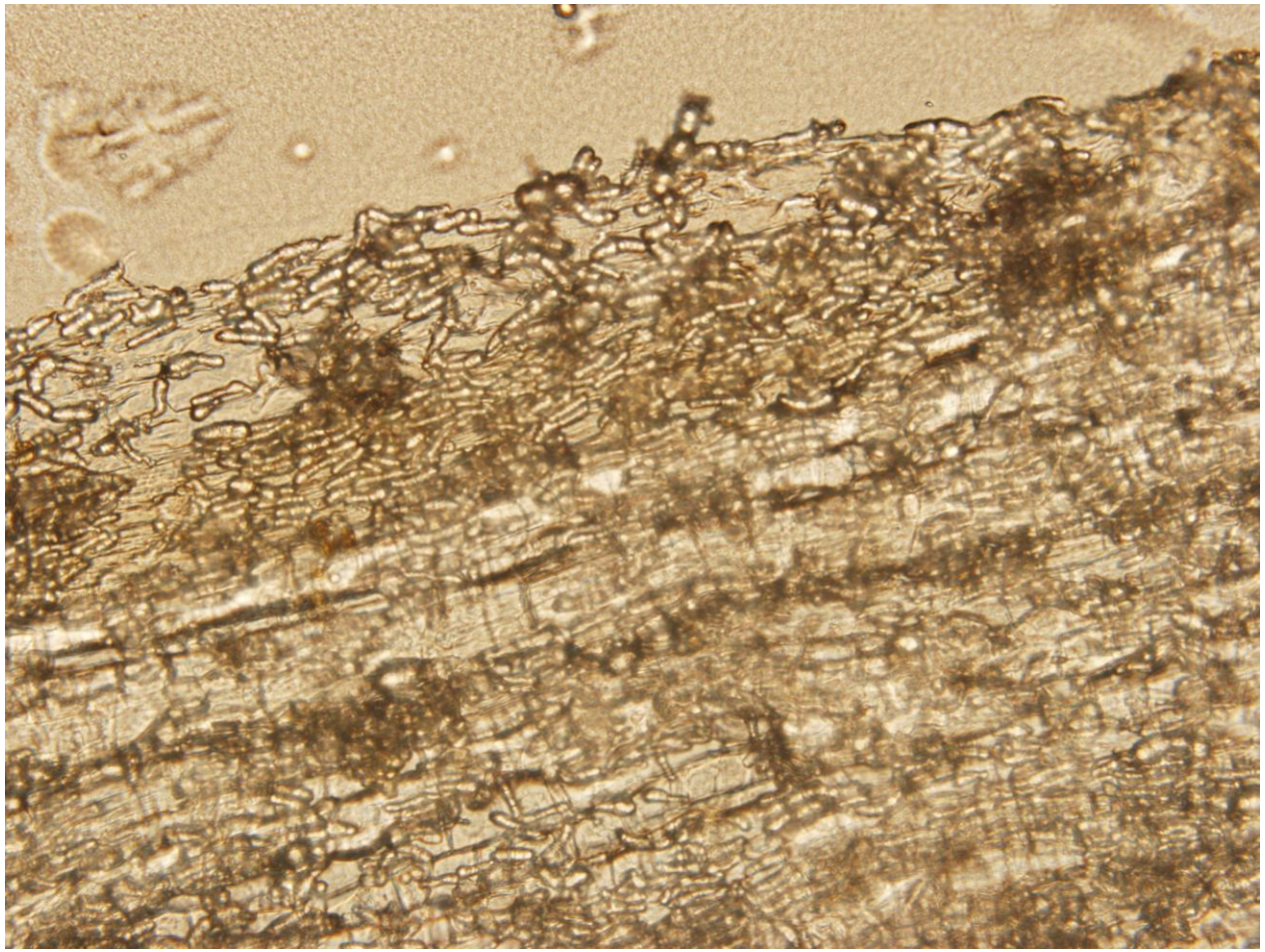
Mycelium identification

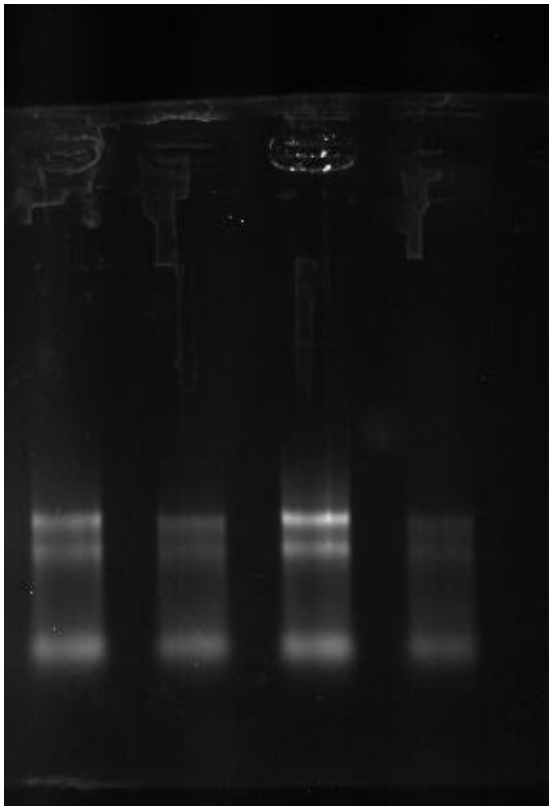




100 days after artificial infection

Mycelium identification





The mix tissues of white and grey smut-infected cones were used for RNA extraction

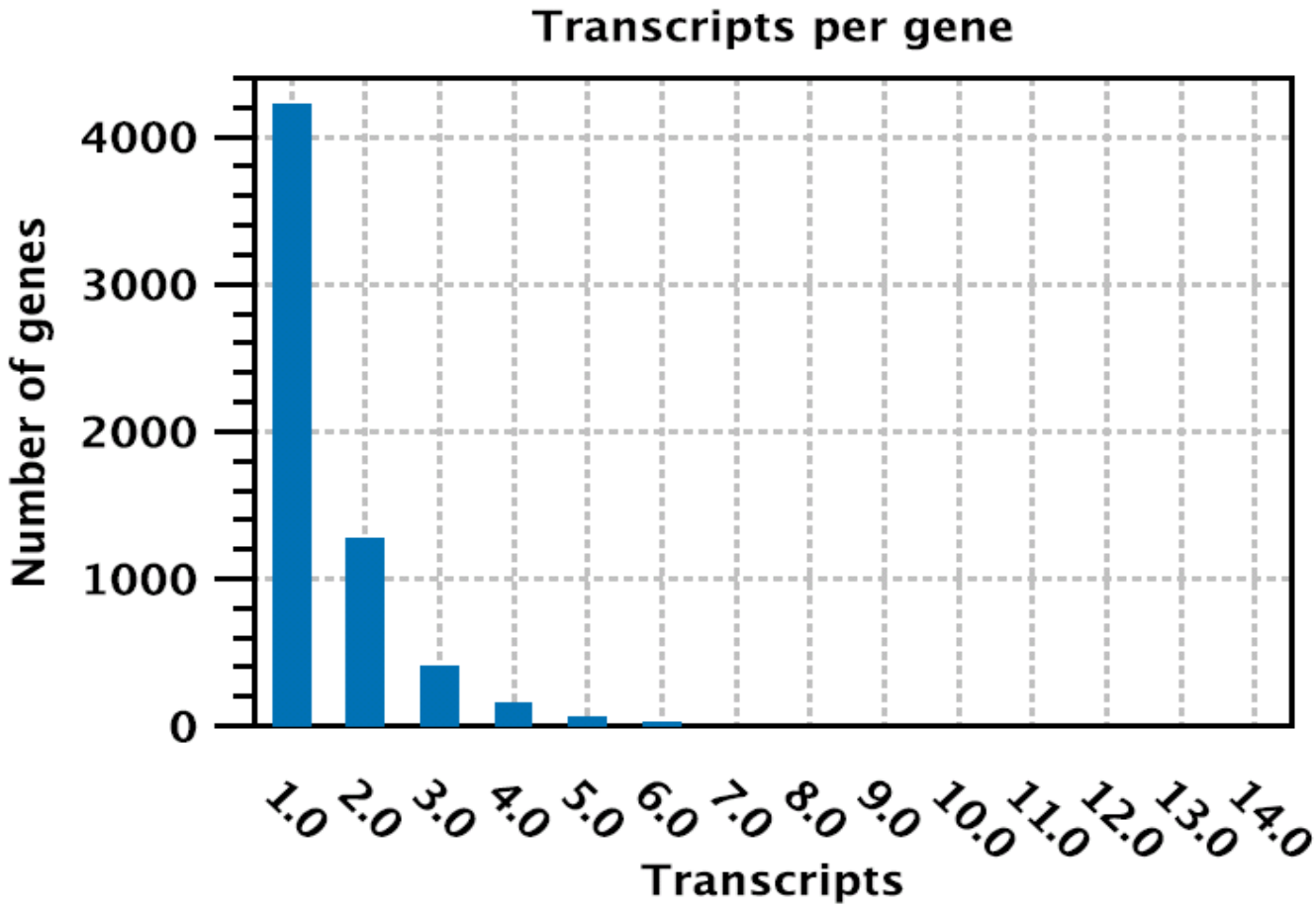
mRNA-seq

- **mRNA sequenced by Solexa GAIIx**

- JG35 1.24 Gb
- JG36 1.12 Gb

- Diploid mixed with sugarcane mRNA
  - White tissue: 3.86 Gb, 0.69Gb mapped on Ss genome
  - Grey tissue: 2.96 Gb, 1.94Gb mapped on Ss genome

mRNA-seq analysis

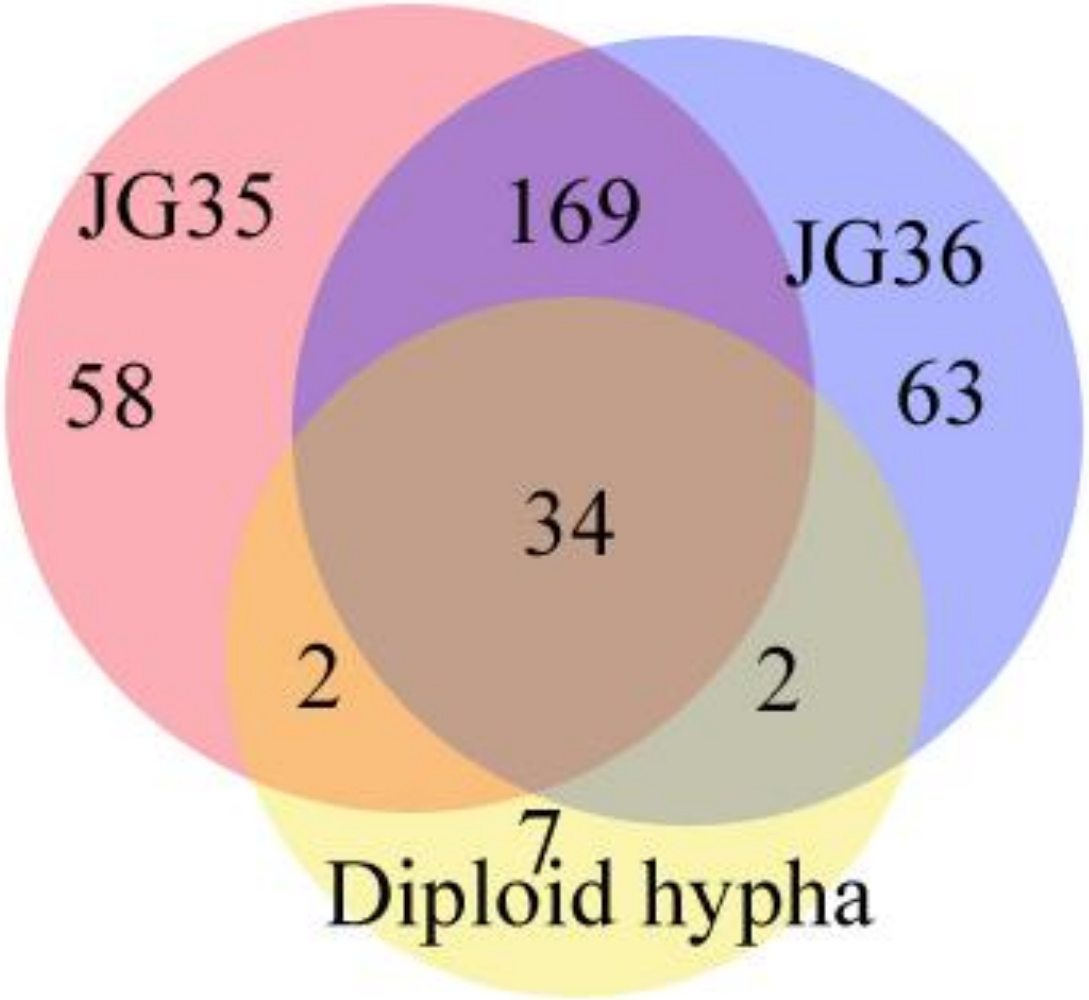


Using the genome as reference, more transcripts

Gene expression

	No. Transcripts	No. New exon	No. Alternative splicing
JG35	**7904**	**669**	**66**
JG36	**7900**	**649**	**69**
Diploid	**8035**	**474**	**61**

Gene expression Profiles- not expressed genes



How many genes in Ss?

- Genome annotation: 6174-34= 6140
- Transcripts: 8035
- New exons
- Alternative splicing
- What else?

Next,

- Gap closing
- Functional Genomics
- Disease Control Strategies
- …

Acknowledgement

This project was supported by

NSFC (grant No. NSF31160364)

Guangxi NSF
(2009GXNSFD0991205 ,2010GXNSFD013026)

Facility and Capability Upgrade Grants for Research Base from Guangxi Department of Science and Technology (grant No. 1116-02)



- Zhiqiang Wang
- Jiaorong Meng
- Jinjie Shang
- Liming Shi
- Jinzi Wang

Yongmei Liao
Chengwu Zou
Qi Chen
Yingzhi Chen



- Guining Zhu



- Lei Wang
- Yan Ren
- Shaojing Wang

Zhemin Zhou
Yang Li

Thank you

