# In search for the causal agent of faba bean gall disease in herbarium samples

Theo van der Lee Workshop on the use of NGS technologies for plant pest diagnostics,

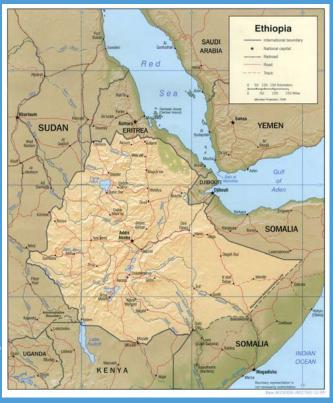




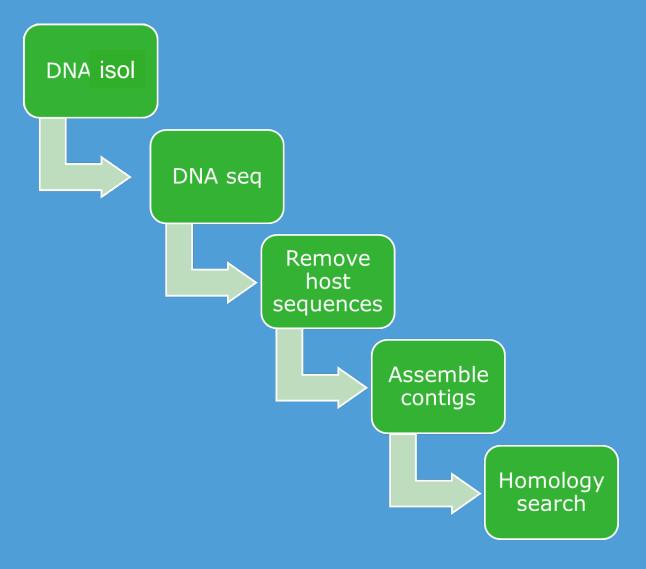
# Identification of a potential new pathogen from herbarium samples



Faba bean gall disease



# Faba bean gall research strategy



# Exp 1 - DNA extraction Faba Bean Gall

13/01/2015

### Faba Bean samples Ethiopia

- 002 healthy leaf	→ 2A	= 0.0014 g
- 002 FBG leaf	→ 2B	= 0.0026 g
- 003 healthy leaf	→ 3A	= 0.0016 g
- 003 FBG leaf	→ 3B	= 0.0040 g
- 004 healthy leaf	→ 4A	= 0.0021 g
- 004 FBG leaf	→ 4B	= 0.0033 g

- From each sample we took  $\pm$  0.5 cm<sup>2</sup> leaf
- For the FBG samples we took 50% clean & 50% FBG symptoms

## Protocol 1

### DNeasy® Plant Mini Kit

The DNeasy Plant Mini Kit (cat. nos. 69104 and 69106) can be stored at room temperature (15-25°C) for up to 1 year.

For more information, please refer to the DNeasy Plant Handbook, which can be found at www.qiagen.com/handbooks.

For technical assistance, please call toll-free 00800-22-44-6000, or find regional phone numbers at www.giagen.com/contact.

#### Notes before starting

- Perform all centrifugation steps at room temperature (15-25°C).
- If necessary, redissolve any precipitates in Buffer AP1 and Buffer AW1 concentrates.
- Add ethanol to Buffer AW1 and Buffer AW2 concentrates.
- Preheat a water bath or heating block to 65°C.
- 1. Disrupt samples (≤100 mg wet weight or ≤20 mg lyophilized tissue) using the TissueRuptor®, the TissueLyser II, or a mortar and pestle.
- 2. Add 400  $\mu$ I Buffer AP1 and 4  $\mu$ I RNase A. Vortex and incubate for 10 min at 65°C. Invert the tube 2-3 times during incubation.

Note: Do not mix Buffer AP1 and RNase A before use.

- Add 130 µl Buffer P3. Mix and incubate for 5 min on ice.
- Recommended: Centrifuge the lysate for 5 min at 20,000 x g (14,000 rpm).
- 5. Pipet the lysate into a QIAshredder spin column placed in a 2 ml collection tube. Centrifuge for 2 min at 20,000 x g.
- Transfer the flow-through into a new tube without disturbing the pellet if present. Add 1.5 volumes of Buffer AW1, and mix by pipetting.

- Transfer 650 μI of the mixture into a DNeasy Mini spin column placed in a 2 ml collection tube. Centrifuge for 1 min at ≥6000 x g (≥8000 rpm). Discard the flow-through. Repeat this step with the remaining sample.
- 8. Place the spin column into a new 2 ml collection tube. Add 500  $\mu$ l Buffer AW2, and centrifuge for 1 min at ≥6000 x g. Discard the flowthrough.
- Add another 500 μl Buffer AW2. Centrifuge for 2 min at 20,000 x g.

Note: Remove the spin column from the collection tube carefully so that the column does not come into contact with the flow-through.

- 10. Transfer the spin column to a new 1.5 ml or 2 ml microcentrifuge tube.
- 11. Add 100  $\mu$ I Buffer AE for elution. Incubate for 5 min at room temperature (15-25°C). Centrifuge for 1 min at ≥6000 x g.
- 12. Repeat step 11.

Step 1. Disrupt samples using RVS beats in Tissuelyser (2 min, 30 hertz)

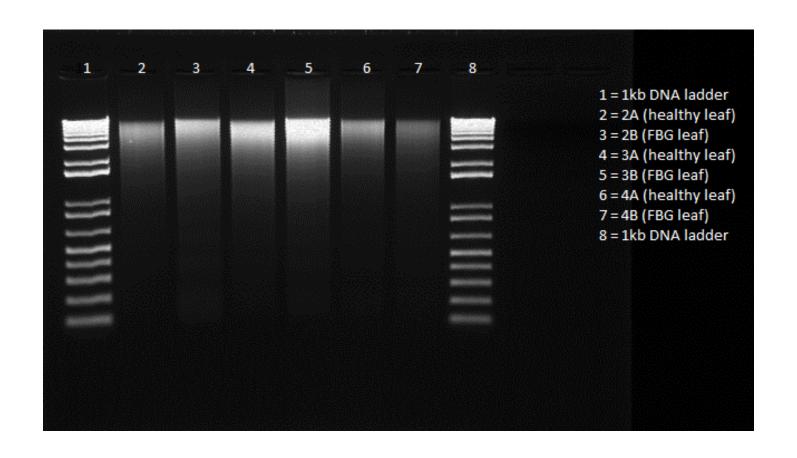
For up-to-date licensing information and productspecific disclaimers, see the respective QIAGEN kit handbook or user manual.

Trademarks: QIAGEN®, DNeasy®, TissueRuptor® (QIAGEN Group). 1071299 04/2012 @ 2011-1012 QIAGEN, all rights reserved.





# Results on 1% agarosegel





# Results Picogreen

Samples	DNA concentrations (ng/μl)	Yield (ng)
2A - healthy leaf	10.16	914
2B - FBG leaf	13.95	1256
3A - healthy leaf	15.00	1350
3B - FBG leaf	24.56	2211
4A - healthy leaf	9.28	835
4B - FBG leaf	6.03	543

Total volume → 90 µl
70 µl to Greenomics (10/02/2016)
Data received on 09/03/2016
Data no mismatches 07/04/2016

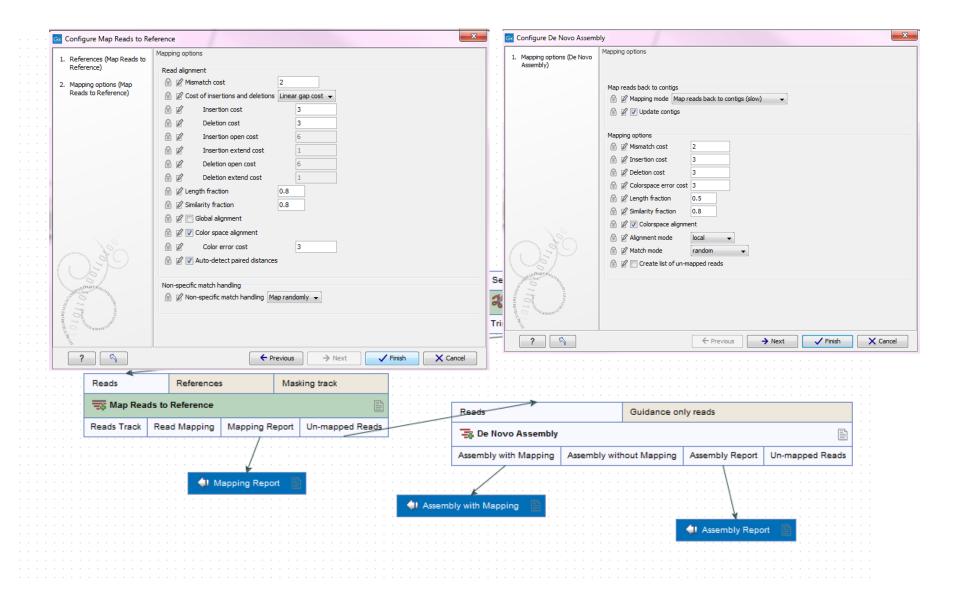


# Samplesheet

quotation	2016-02-01_HiSeq_Theo_	_vd_Lee_6_Faba_bear	n_gal_disease_DNA_seq_3	3740090100_quotation
Full name project leader	Theo van der Lee			
e-mail project leader	theo.vanderlee@wur.nl			
project name	6_Faba_bean_gal_disease	e_DNA_seq		
project number	3740091100			
samples delivered by	Ilse Houwers			
expected sample(s) delivery date (dd/mm/yy):	12/02/2016			
requested sequencing	HiSeq			
requested read length	125PE			
requested lanes	1			
no. of samples	6			
concentration based on nanodrop/qubit/other	Picogreen			
sample ID	concentration ng/uL	OD 260/280	OD 260/230	volume uL
2A_healthy_leaf	10.16			70
2B_FBG_leaf	13.95			70
3A_healthy_leaf	15.00			70
3B_FBG_leaf	24.56			70
4A_healthy_leaf	9.28			70
4B_FBG_leaf	6.03			70



# Data analysis - Workflow



# De novo assembly unmapped reads— 2A Healthy leaf

CLC → FBG analysis → Mapping faba bean\_assembly unmapped reads\_TL

Rows: 53,810				Filter	] =
Name	Conse	Total read	Reads in	Average cov	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	405	258	60	68.16	6
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	1562	21509	9936	1,553.93	3
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	1879	25907	12992	1,627.6	
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	494	408	58	88.74	4
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	258	228	6	87.7	1
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	292	68	2	22.80	0
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	232	147	2	64.8	5
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads (run0189 2A-healthy-leaf S	604	694	62	122.40	0
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	3257	12614	4754	451.76	6
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	374	593	34	169.30	0
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	389	507	4	94.7	
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	318	6	0	2.38	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	389	12062	_	3,551.9	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	662	147		23.9	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	971	986	152	105.7	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	447	3990	498	989.4	
un0189 2A-healthy-leaf S6 L002 R1 001.nophix (paired) trimmed (paired) un-mapped reads [run0189 2A-healthy-leaf S	578	1194	392	250.99	
uno 189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	822	940	156	137.6	
In 0.189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	337	1505		5	-
uno 189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	2441	847	390		
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	451	1470	402	394.1	-
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_(run0189_2A-healthy-leaf_S	232	121	0	45.40	
uno 189_2A-healthy-leaf_S6_Loo2_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_(runo 189_2A-healthy-leaf_S6	207	152	_	73.3	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_(run0189_2A-healthy-leaf un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_(run0189_2A-healthy-leaf_S	1395	9400	3410	786.98	
in0189_2A-healthy-leaf_S6_L002_k1_001.nophix_(paired)_uninned_(paired)_un-mapped_reads_(run0189_2A-healthy-leaf_S	205	2832		1,471.6	
_ , , _ , _ , _ , _ , _ , _ , _ , _	596	516	66	103.5	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S					
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	1331	2114		181.36	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	344	12053	948	4,129.50	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	317	1559	64	540.5	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	489	17088	1556	3,881.16	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	378	131	_	29.9	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	1959	18288	13842	1,145.76	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	332	5827	2970	2,040.10	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	794	2982		422.13	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	4697	40429	33118	1,065.1	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	587	15002		2,802.3	
in0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	365	93		23.79	
n0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	250	45	0	16.0	
n0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	286	102		33.0	
n0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	1170	173	82	16.76	
n0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	5313	50391		1,184.9	
in0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	205	13		5.7	
in0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	296	2440	174	929.19	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	243	3355	52	1,305.66	5
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	208	30	0	13.0	
un0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	1087	285	48	25.58	8
n0189_2A-healthy-leaf_S6_L002_R1_001.nophix_(paired)_trimmed_(paired)_un-mapped_reads_[run0189_2A-healthy-leaf_S	448	4360	384	1,141.36	6

Extract 1 contig from assembly subset → contig 2

## 2B FBG leaf

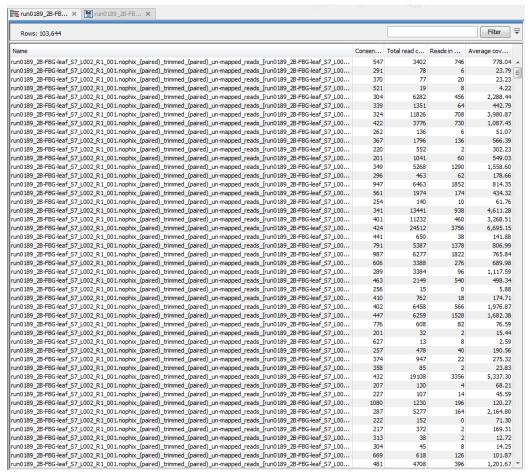
### Used references for mapping:

#### Originates from:

E CSVX01.1 (history)

xun0189\_2A-healthy-leaf\_S6\_L002\_R1\_001.nophix\_(paired)\_trimmed\_(paired)\_un-mapped\_reads\_[run0189\_2A-healthy-leaf\_S6\_L002\_R1\_001.nophix]\_(single)\_contig\_2 (history)

### De novo assembly unmapped reads:



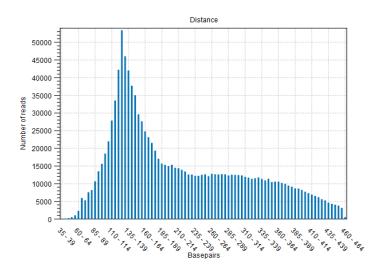
#### 1.2 Contig measurements (including scaffolded regions)

	Length
N75	287
N50	347
N25	444
Minimum	126
Maximum	7,502
Average	348
Count	103,644
Total	36,088,890

#### 1.5 Summary statistics

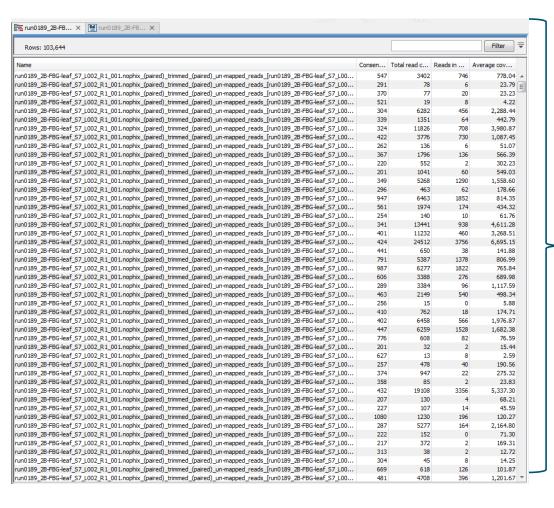
	Count	Average length	Total bases
Reads	45,878,868	125.38	5,752,241,086
Matched	28,218,747	125.37	3,537,779,935
Not matched	17,660,121	125.39	2,214,461,151
Contigs	103,644	348	36,088,890
Reads in pairs	2,353,566	215.37	
Broken paired reads	20,045,284	125.46	

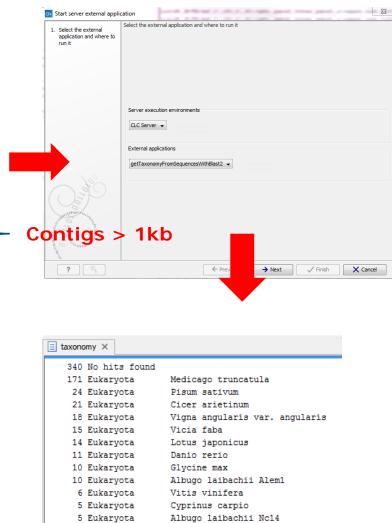
#### 1.9 Paired reads distance distribution



## 2B FBG leaf

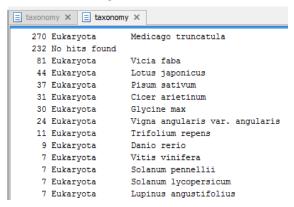
### Extract contigs > 1kb







### 2A healthy leaf



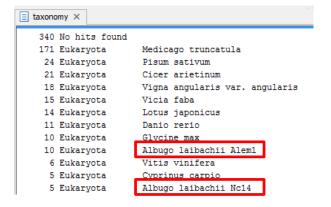
### 3A healthy leaf



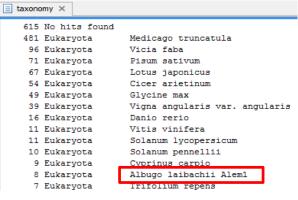
### 4A healthy leaf



#### 2B FBG leaf



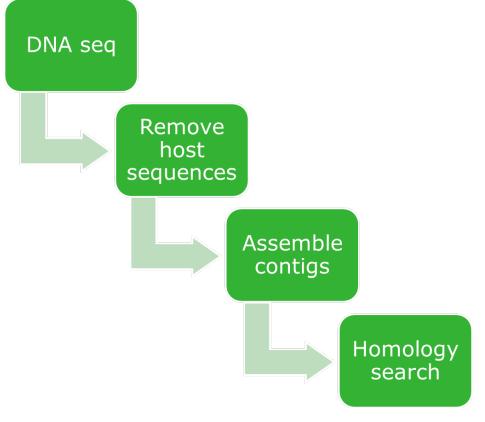
#### 3B FBG leaf



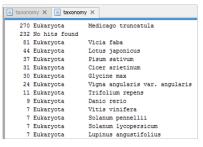
#### 4B FBG leaf

<b>■</b> taxono	omy ×	
380	No hits found	
328	Eukaryota	Medicago truncatula
82	Eukaryota	Vicia faba
53	Eukaryota	Pisum sativum
43	Eukaryota	Lotus japonicus
40	Eukaryota	Cicer arietinum
38	Eukaryota	Vigna angularis var. angularis
34	Eukaryota	Glycine max
9	Eukaryota	Solanum pennellii
9	Eukaryota	Solanum lycopersicum
9	Eukaryota	Danio rerio
7	Eukaryota	Lens culinaris
7	Eukaryota	Albugo laibachii Nc14
6	Eukaryota	Trifolium renens
6	Eukaryota	Albugo laibachii Alem1

# Faba bean gall disease



#### 2A healthy leaf



#### 3A healthy leaf

a taxono	my ×	
435	Eukaryota	Medicago truncatula
410	No hits found	
99	Eukaryota	Vicia faba
73	Eukaryota	Pisum sativum
63	Eukaryota	Cicer arietinum
54	Eukaryota	Vigna angularis var. angularis
51	Eukaryota	Glycine max
44	Eukaryota	Lotus japonicus
11	Eukaryota	Vitis vinifera
11	Eukaryota	Trifolium repens
9	Eukaryota	Lens culinaris
8	Eukaryota	Solanum lycopersicum
8	Eukaryota	Danio rerio
6	Eukaryota	Solanum pennellii

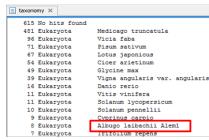
#### 4A healthy leaf

■ taxono	omy ×	
369	Eukaryota	Medicago truncatula
309	No hits found	
80	Eukaryota	Vicia faba
54	Eukaryota	Lotus japonicus
46	Eukaryota	Pisum sativum
46	Eukaryota	Cicer arietinum
36	Eukaryota	Vigna angularis var. angularis
23	Eukaryota	Glycine max
14	Eukaryota	Danio rerio
8	Eukaryota	Solanum pennellii
8	Eukaryota	Lens culinaris
6	Eukaryota	Vitis vinifera
6	Eukaryota	Trifolium repens
5	Eukaryota	Lupinus angustifolius
5	Eukaryota	Cyprinus carpio

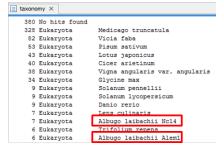
#### 2B FBG leaf

■ taxonomy ×	
340 No hits found	
171 Eukaryota	Medicago truncatula
24 Eukaryota	Pisum sativum
21 Eukaryota	Cicer arietinum
18 Eukaryota	Vigna angularis var. angularis
15 Eukaryota	Vicia faba
14 Eukaryota	Lotus japonicus
11 Eukaryota	Danio rerio
10 Eukaryota	Glycine max
10 Eukaryota	Albugo laibachii Alem1
6 Eukaryota	Vitis vinifera
5 Eukaryota	Cyprinus carpio
5 Eukaryota	Albugo laibachii Nc14

#### 3B FBG leaf

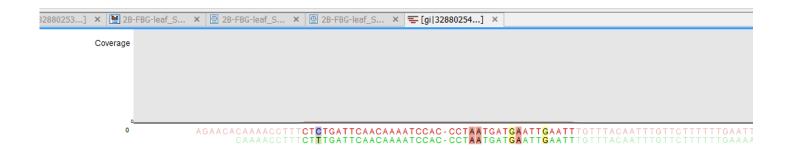


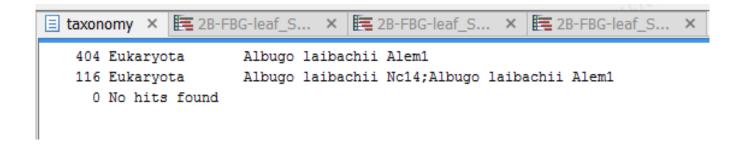
#### 4B FBG leaf





# Low homology but best fit to Albugo laibachii







# Faba bean gall disease candidate

- Albugo species
- White rust
- Not a bacterium, virus or fungus but an oomycete
- Possibly spreads quickly by zoospores
- Possibly seed transmitted
- Likely obligate biotroph so it may not be possible to obtain a pure culture
- Many of our genomic sequences are probably derived of this potential pathogen (estimated >500 contigs). These can be used to develop fast diagnostics and the genome may help to understand the pathogen.



# Acknowledgements

**Ilse Houwers** 



Theo van der lee (PhD)

Contact: theo.vanderlee@wur.nl

Research initiated by

Woubit Dawit (PhD) Associate Professor Ambo University, Ethiopia

