

# Cereal grain mycoflora on single seeds

Comparison of metabarcoding and  
VideometerLab for pathogen detection on  
cereal grain

Mogens Nicolaisen, Merete H Olesen, Birte Boelt, Johannes Ravn Jørgensen

Søren Knudsen  Carlsberg Group

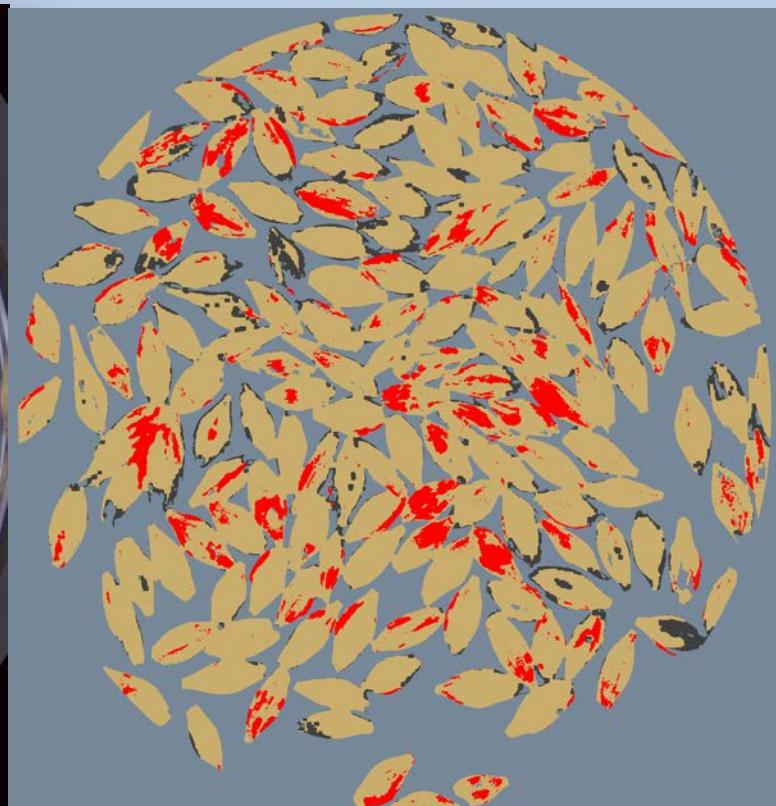
Kim Jørgensen  
Dorte Rennebjerg



Jens Michael Carstensen



# Videometer image

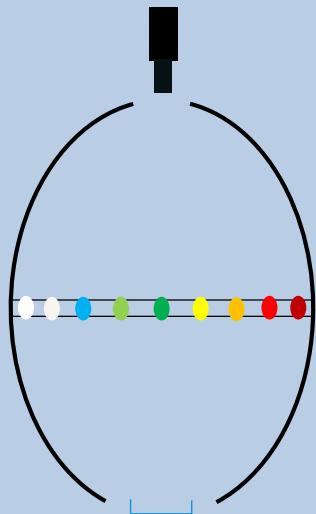


Red color = *Fusarium*

Gray color = grey and black moulds

Brown = barley without moulds

# Videometer Spectral Imaging



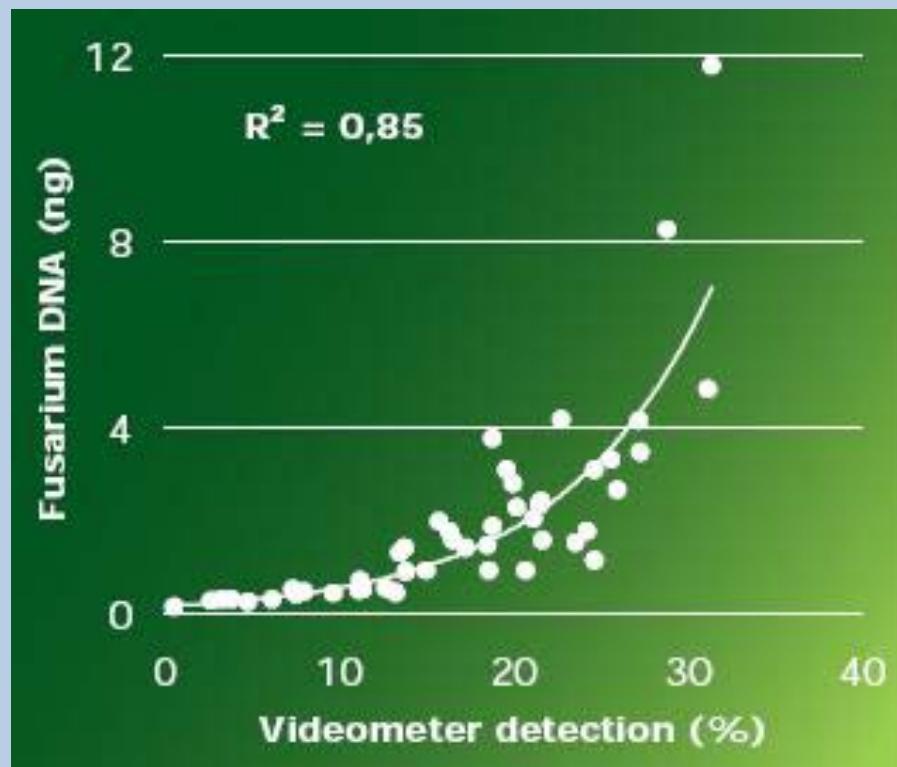
Camera  
Lens  
Integrating sphere  
LEDs of multiple wavelengths  
Sample is placed in target opening



- LEDs: Stable, durable, large selection, rapidly developing technology
- Up to 20 different high-resolution bands acquired sequentially in 0.5-1.5 seconds depending on camera
- May be combined with emission filters, backlight, and darkfield illuminant

# Validation by Carlsberg Research Center:

Comparison between VideometerLab® measurements and the level of Fusarium DNA quantified by real-time PCR on batches of seed



Excellent correlation with Fusarium DNA level  
( $R^2=0,85$ )

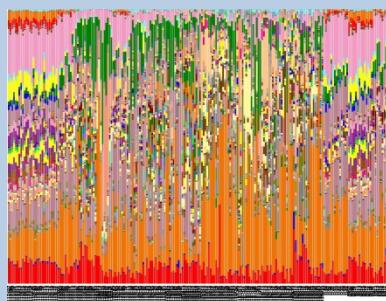
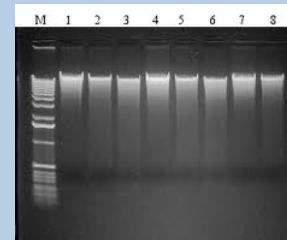


# Metabarcoding workflow

Sample



DNA extraction



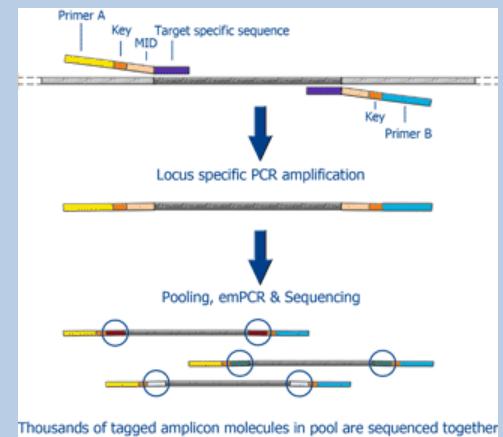
Fusarium qPCR



Data analysis

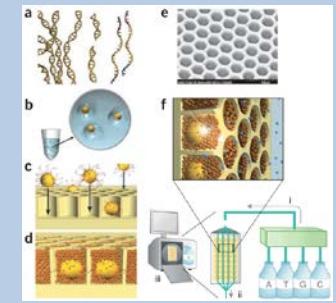
PCR amplification of ITS1

(ITS1-F/58A2R)



Amplicon 454 sequencing

~200.000 sequences



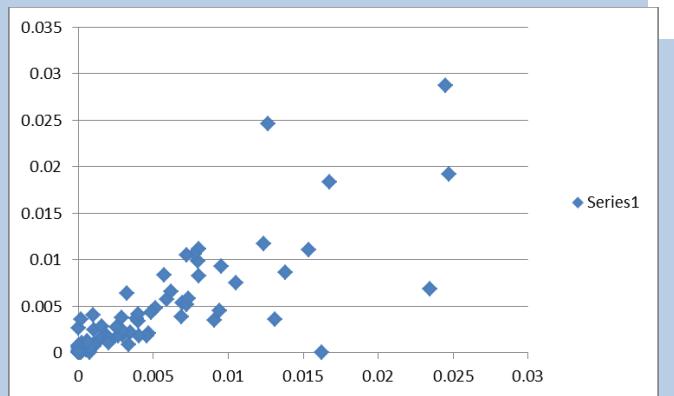


# Metabarcoded samples



# *Fusarium* qPCR

11 assays for individual *Fusarium* species, one generic



## Summarized



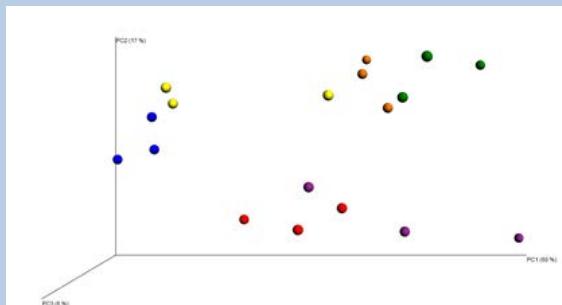
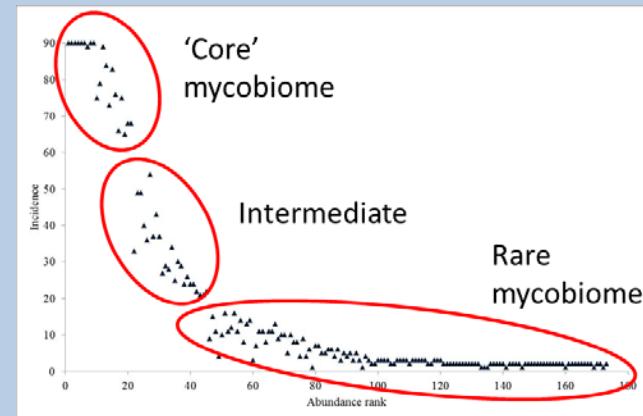
## Real-time PCR for quantification of eleven individual *Fusarium* species in cereals

Mogens Nicolaisen <sup>a,\*</sup>, Skairé Supronienė <sup>b</sup>, Linda Kærgaard Nielsen <sup>a</sup>, Irene Lazzaro <sup>a</sup>,  
Niels Henrik Spliid <sup>a</sup>, Annemarie Feier Justesen <sup>a</sup>

Aarhus University, Faculty of Agricultural Sciences, Department of Integrated Pest Management, Denmark

# Metabarcoding

Wheat seed lots from ~200 conventional farms at harvest



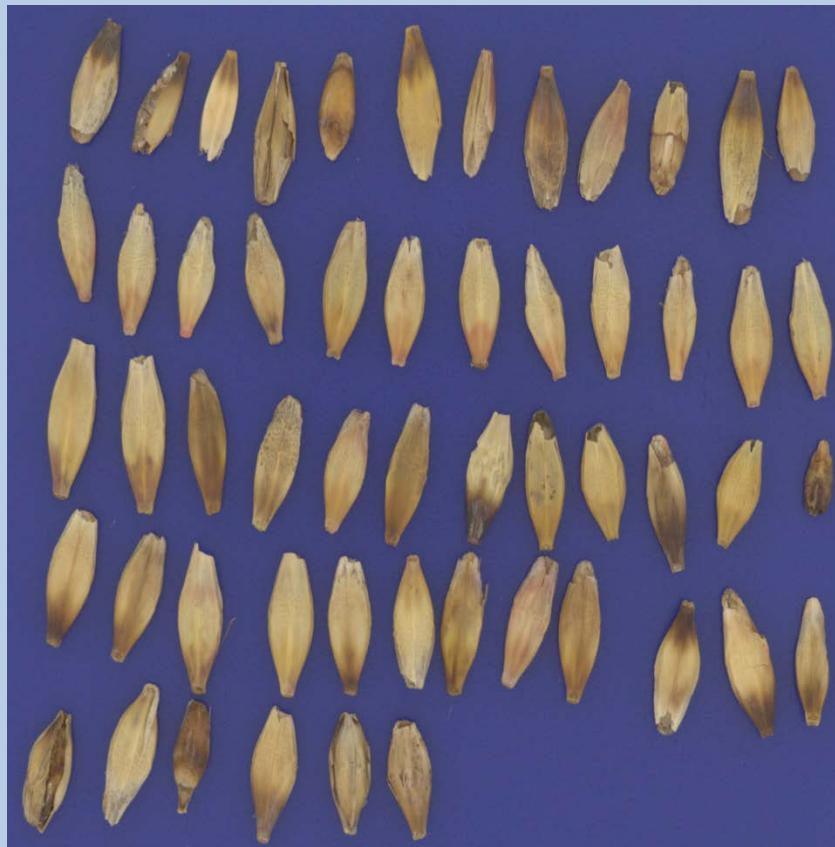
Cultivar effect

	Sequences	BLAST Id	Disease in wheat
OTU1	48161	<i>F. graminearum</i> group (Fgr)	Fusarium head blight
OTU2	45980	<i>Lewia infectoria</i>	Black head mold
OTU3	36072	<i>Cladosporium herbarum</i>	Black head mold
OTU4	22066	<i>Didymella exitialis</i>	Ascochyta leaf scorch
OTU5	16215	<i>Fusarium avenaceum</i> (Fav)	Fusarium head blight
OTU6	9959	<i>Epicoccum nigrum</i>	Black head mold
OTU7	9327	<i>Microdochium nivale</i>	Fusarium head blight
OTU8	2607	<i>Alternaria alternata</i>	Black head mold
OTU9	2241	<i>Cladosporium cladosporioides</i>	Black head mold
OTU10	2139	<i>Pyrenophora tritici-repentis</i>	Tan spot
OTU11	1870	<i>Fusarium poae</i> group (Fpo)	Fusarium head blight
OTU12	1822	<i>Mycosphaerella graminicola</i>	Septoria tritici blotch
OTU13	1421	<i>Botrytis cinerea</i>	Gray mold
OTU14	1404	<i>Phaeosphaeria nodorum</i>	Stagonospora nodorum blotch
OTU15	1209	<i>Cryptococcus victoriae</i>	non pathogenic
OTU16	745	<i>Sporobolomyces</i> sp	Black head mold
OTU17	493	<i>Stemphylium</i>	Black head mold
OTU18	374	<i>Cryptococcus tephrensis</i>	non pathogenic
OTU19	327	<i>Alternaria</i> sp.	Black head mold
OTU20	312	<i>Phaeosphaeria avenaria</i> f.sp. tr	Stagonospora nodorum blotch
OTU21	289	<i>Dioszegia hungarica</i>	non pathogenic



# Malting barley seeds with visible signs of fungal infection

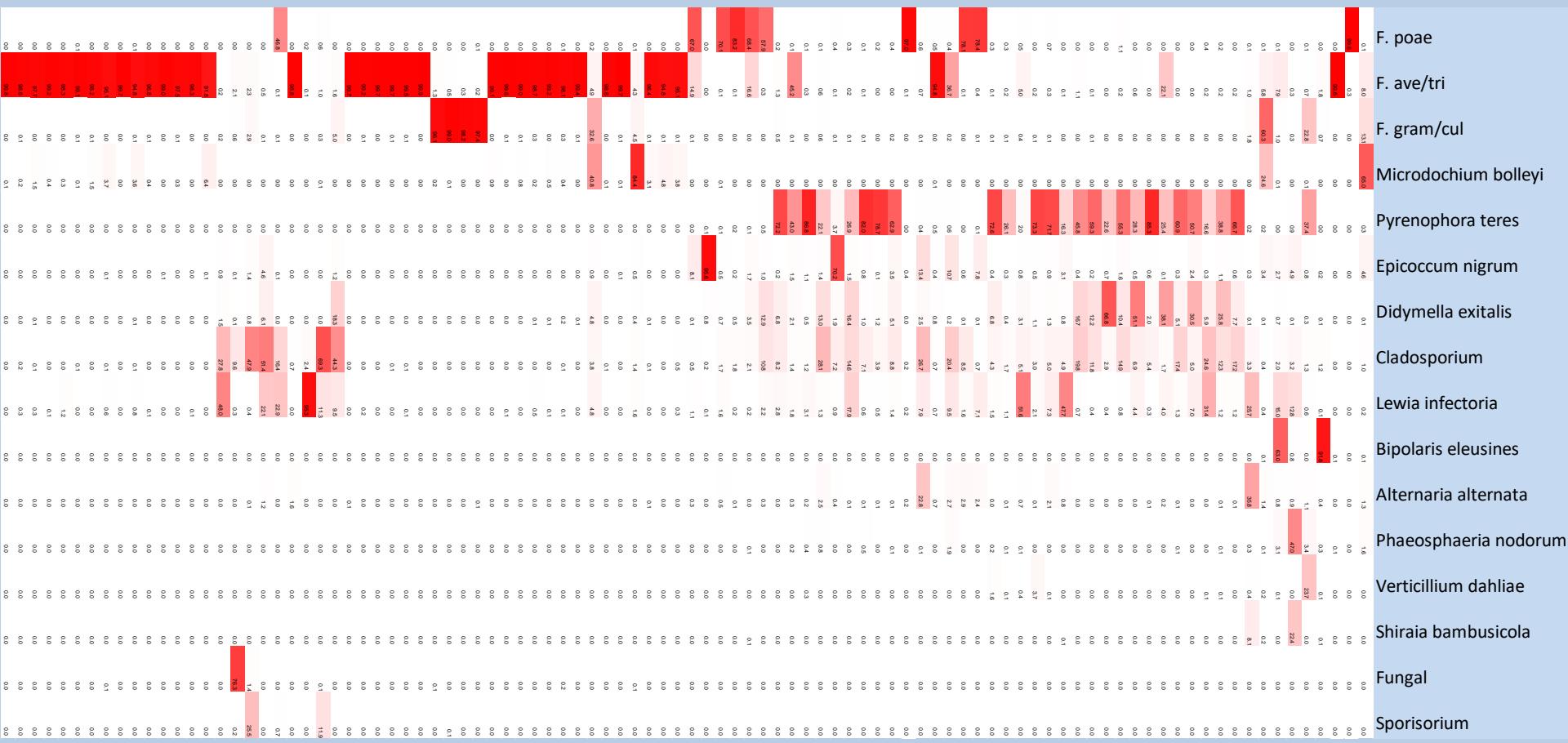
Dorsal



Ventral



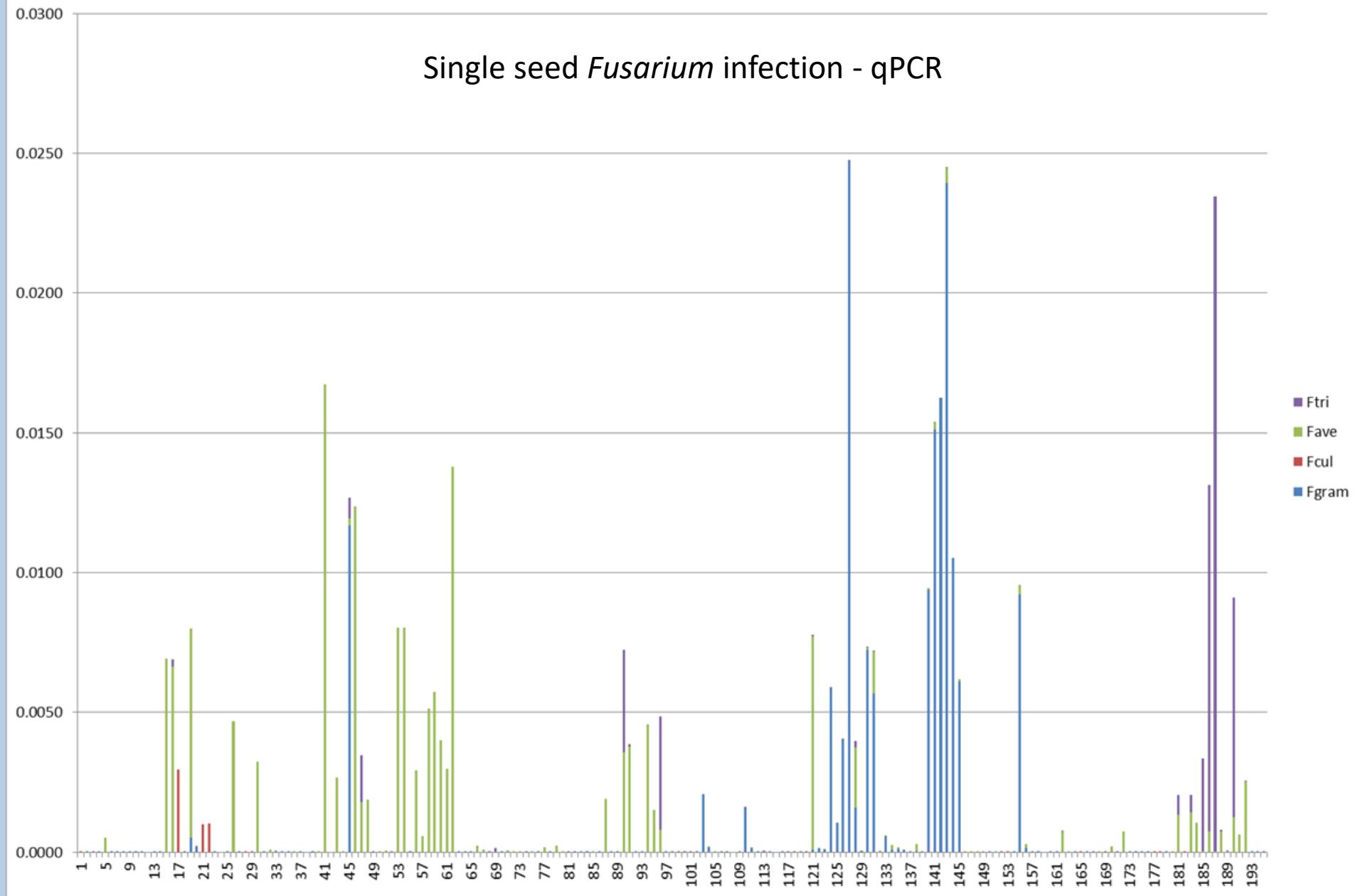
# Single seed infections



Generally one species/seed



# Single seed *Fusarium* infection - qPCR

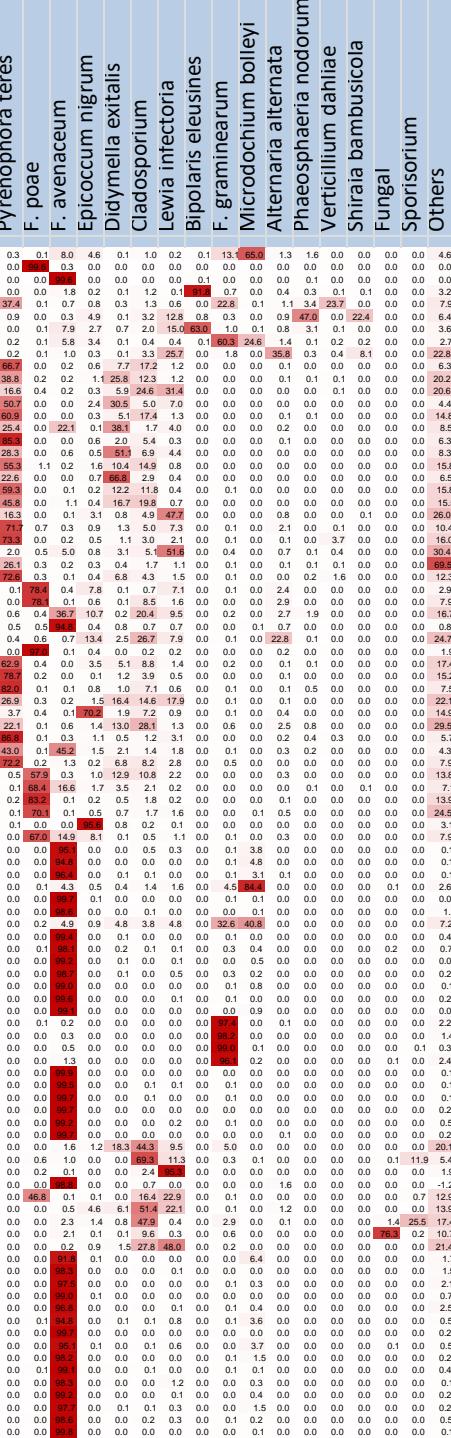


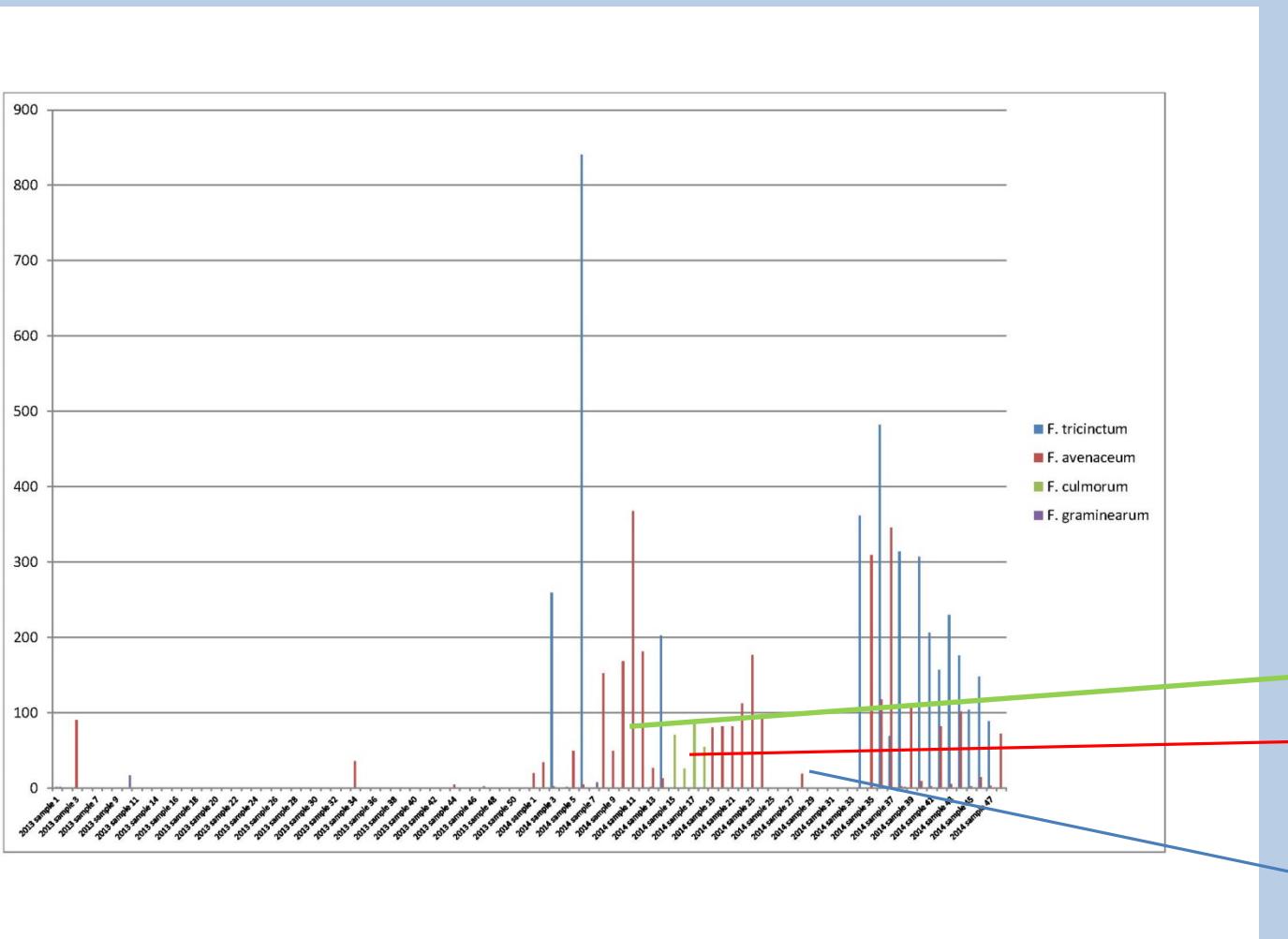
# Sequences from entire dataset

	% abundance
<i>avenaceum</i>	38.814835
<i>renophora teres</i>	13.932855
<i>poae</i>	7.868754
<i>adosporium</i>	6.3350191
<i>graminearum</i>	5.6560397
<i>ewia infectoria</i>	5.2410193
<i>idymella exitalis</i>	4.0651601
<i>picoccum nigrum</i>	2.7365175
<i>licrodochium bolleyi</i>	2.5928317
<i>polaris eleusines</i>	1.6260415
<i>ternaria alternata</i>	0.8952025
<i>ungal(?)</i>	0.8139792
<i>phaeosphaeria nodorum</i>	0.6314249
<i>oorisorium</i>	0.4012329
<i>hiraiabambusicola</i>	0.3250396
<i>erticillium dahliae</i>	0.3247018

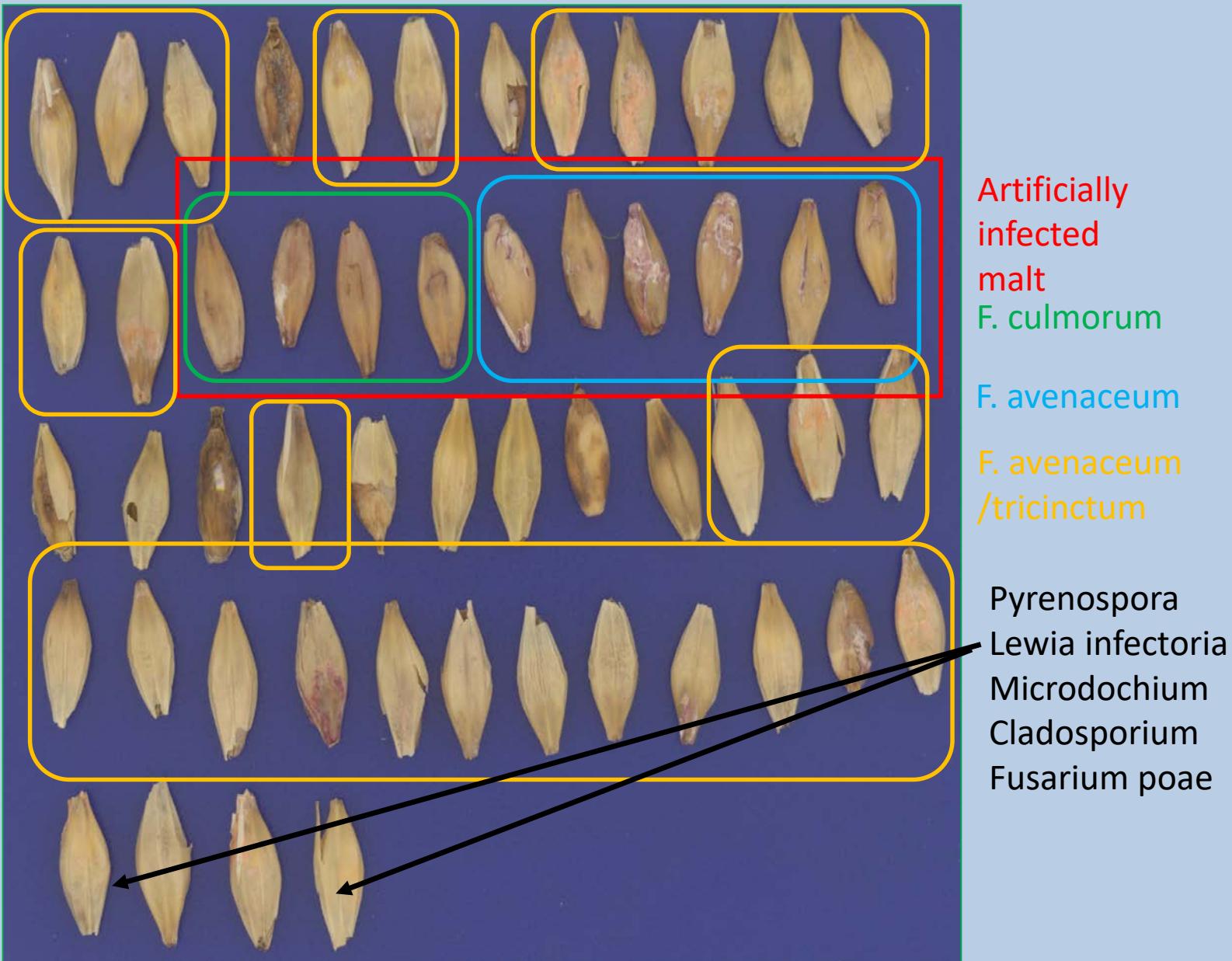
## Field inoculated samples

Inoculation in field	<i>Pyrenophora teres</i>	<i>F. poae</i>	<i>F. avenaceum</i>	<i>Epicoccum nigrum</i>	<i>Didymella exitalis</i>	<i>Cladosporium</i>	<i>Lewia infectoria</i>	<i>Bipolaris eleusiniae</i>	<i>F. graminearum</i>	<i>Microdochium bolleyi</i>	<i>Alternaria alternata</i>	<i>Phaeosphaeria nodorum</i>	<i>Verticillium dahliae</i>	<i>Shiraiia bambusicola</i>	<i>Sporisorium</i>	Visual
<i>F. culmorum</i>	0.0	0.1	0.2	0.0	0.0	0.0	0.0	0.0	97.4	0.0	0.1	0.0	0.0	0.0	0.0	Pinkish red
<i>F. culmorum</i>	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	98.2	0.0	0.0	0.0	0.0	0.0	0.0	Pinkish red
<i>F. culmorum</i>	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	99.0	0.1	0.0	0.0	0.0	0.0	0.1	Pinkish red
<i>F. culmorum</i>	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	96.1	0.2	0.0	0.0	0.0	0.0	0.0	Pinkish red
<i>F. avenaceum</i>	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Pink
<i>F. avenaceum</i>	0.0	0.0	99.5	0.0	0.0	0.1	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	Pink
<i>F. avenaceum</i>	0.0	0.0	99.7	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	Pink
<i>F. avenaceum</i>	0.0	0.0	99.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Pink
<i>F. avenaceum</i>	0.0	0.0	99.2	0.0	0.0	0.0	0.2	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	Pink
<i>F. avenaceum</i>	0.0	0.0	99.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	Pink

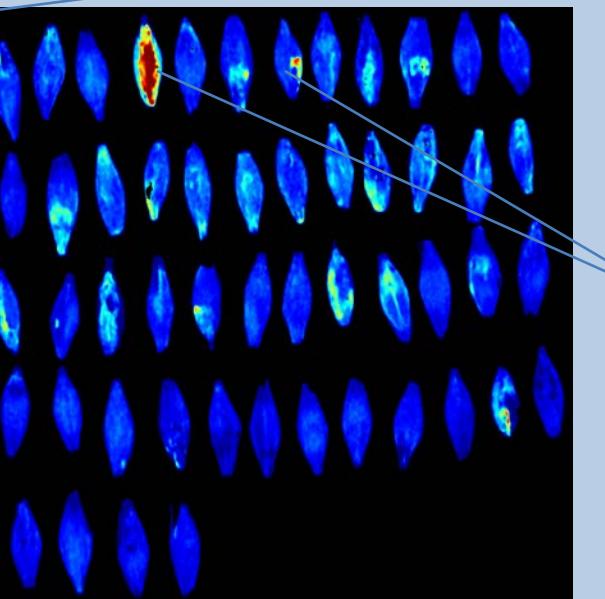
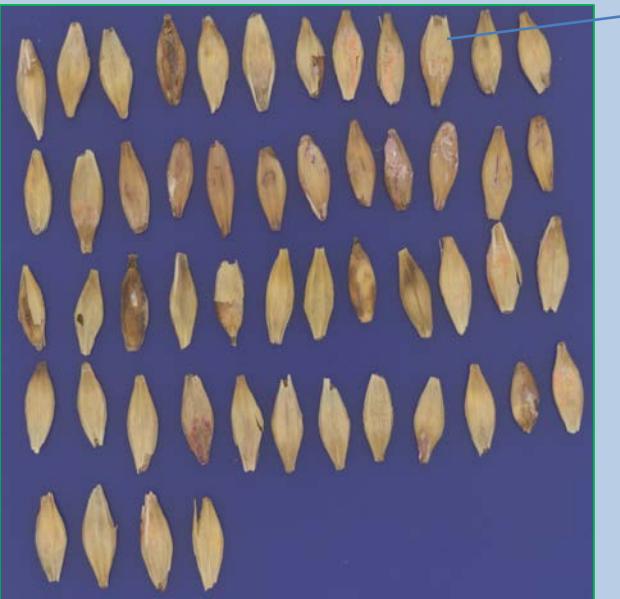




# 52 “red” kernels (dorsal)



# Microdochium detection



# Conclusions

- **Metabarcoding** is suitable for studying the microbial composition of seeds – our next aim is to study gushing
- **VideometerLab** detects *Fusarium* on single seeds – in agreement with qPCR and NGS
- Seeds generally infected by only **one species**
- ‘Black’ seeds are mostly ***Pyrenophora teres***
- Videometer *Fusarium* model may be improved and extended to other species e.g. ***Microdochium***



# Thanks!

*Mogens Nicolaisen  
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*Søren Knudsen*

*Kim Jørgensen  
Dorte Rennebjerg*

*Jens Michael Carstensen*



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