

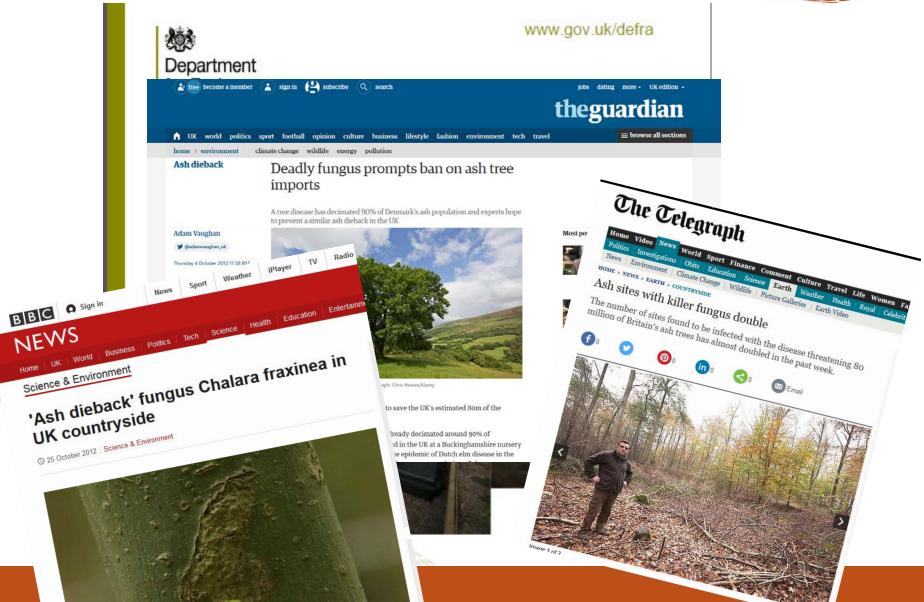
Tree disease surveillance: metabarcoding to identify fungi in spore traps

Ian Adams, Ummey Hany, Rachel Glover, Mel Sapp, Ian Brittain, Judith Turner, Rick Mumford, Neil Boonham



UK Plant Biosecurity Strategy







Task force recommendations

Increase the capacity of the Plant Health Services to undertake surveillance

 Development of new approaches to; find pests through new detection and identification methods (for example, studying sentinel plants planted at key locations or using molecular techniques for identification of new pest threats in samples from existing networks)

Non-targeted method to detect Airborne fungal spores

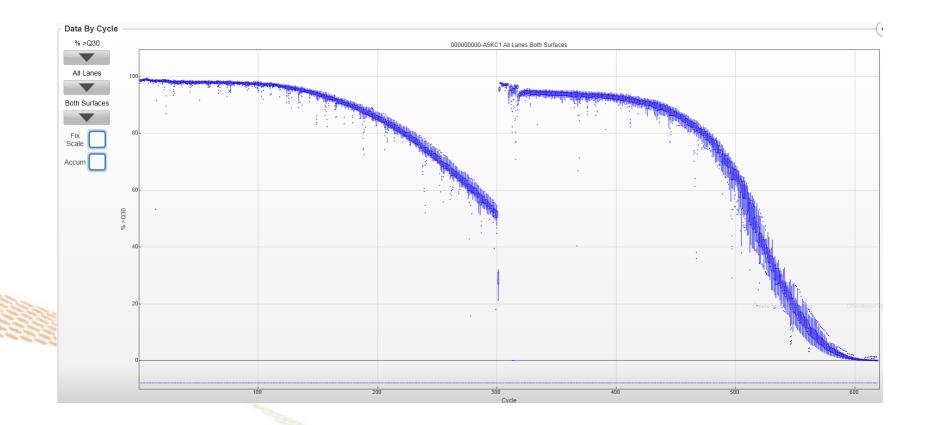


- Use NGS to determine species present in mixed populations of bacteria, fungi, insects, nematodes, woodchips
- Move from 454 (expensive, time consuming, phased out 2016) to MiSeq (cheap, simple, BUT.....)

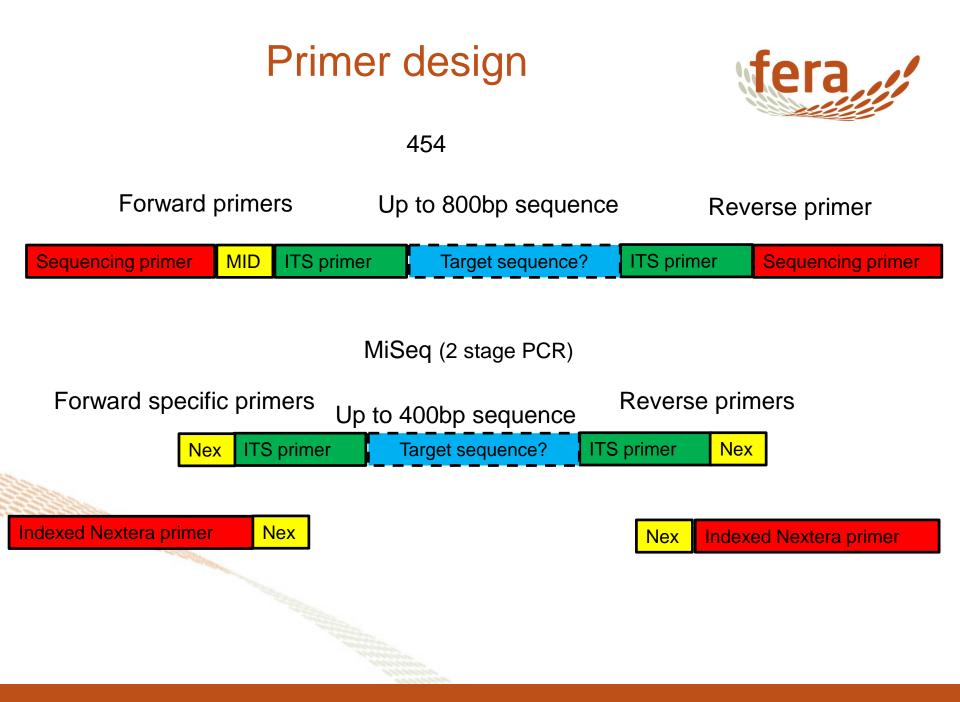




MiSeq Error profile



Corrected by combining 2 300bp reads =400bp (PEAR)





Samples tested

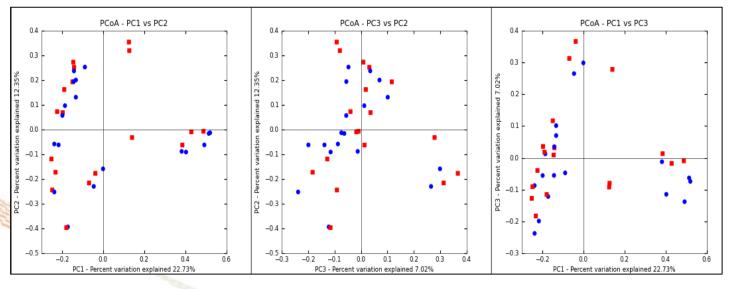
48 sample (sequenced with 454 and MiSeq)

- Chalara out break samples
- Fusarium spiked samples
- Chalara spiked samples
- UK air spore samples



Comparison between platforms

• ITS-1 sequenced range of spore trap samples. (454/MiSeq)



PCA betadiversity (Miseq / 454).

T-test alpha diversity asking if two platforms sampled from same population p=0.91



Detection of known fungi

Wide range of fungi detected Ferry sample 98 (454)-105 (MiSeq) different species

Taxon	Ferry S	Sample	-	ow levels xinea	Spore (Seed <i>fraxi</i>	led C.	Spore (Seeded F	e tape Fusarium)	<i>C. fra</i> outbre	
	454	MiSeq	454	MiSeq	454	MiSeq	454	MiSeq	454	MiSeq
Chalara Fraxinea	nd	nd	nd	0.004%	0.233%	0.067%	nd	nd	0.069%	0.010%
Fusarium Spp.	0.327%	0.251%	0.067%	0.098%	0.003%	0.001%	12.64%	19.90%	nd	0.005%

Fungal populations



	Ferry sample		
-	(all species above		
Таха	1%)	comment	
	MiSeq		
Mycosphaerellaceae	0.2%	family including plant pathogens	
Periconia spp	0%	wind dispersed fungi	
Xenobotryosphaeria calamagrostidis	1%	?	
Epicoccum nigrum	5%	plant saprophyte	
uncultured Ascochyta	6%	?	
Botryotinia fuckeliana	3%	common plant pathogen	
Monographella nivalis	2%	grass pathogen	
Peniophoraceae spp	1%	wood saprophyte	
Cryptococcus albidosimilis	0%	common yeast found in soil	
Cladosporium spp	71%	Common airborne fungus	





Mock Community fungi

- Puccinia striiformis, Puccinia triticina, Fusarium culmorum, Alternaria brassicae, Phytophthora kernoviae, Ceratocystis platani, Phytophthora ramorum, Cladosporium herbarum, Phomopsis sp., Microdochium nivale, Microdochium Majus, Alternaria tenuissima, Alternaria mali, Ceratocystis parasdoxa, Gibberella circinata, Pestalotiopsis guepinii, Hymenoscyphus pseudoalbidus, Mycosphaerella graminicola, Glomerella cingulata, Fusarium graminearum.
- Optimum primers for ITS1 ? / Proof reading / non-proof reading Taq?



Task 1: Smaller amplicons

Primer name	Forward/Reverse	Sequence (5-3)	Reference
ITS1	Forward	TCCGTAGGTGAACCTGCGG	White et al, 1990
ITS2	Reverse	GCTGCGTTCTTCATCGATGC	White et al, 1990
ITS3	Forward	GCATC GAT GAAGA ACGC AGC	White et al, 1990
ITS4	Reverse	TCCTCCGCTTATTGATATGC	White et al, 1990
ITS5	Forward	GGAA GTA AAAGTCG TAA CAAGG	White et al, 1990
ITS1-F	Forward	CTTGGTCATTTAGAGGAAGTAA	Gardes & Bruns, 1993
ITS4-B	Reverse	CAGGAGACTTGTACACGGTCCAG	Gardes & Brus, 1993
5.8S	Reverse	CGCTGCGTTCTTCATCG	Vilgalys lab (Googlecache pdf of webpage attached below)
5.8SR	Forward	TCGATGAAGAACGCAGCG	Vilgalys lab (Googlecache pdf of webpage attached below)
SR6R	Forward	AAGWAAAA GTC GTAACAAGG	Vilgalys lab (Googlecache pdf of webpage attached below)
ITS1-F_KYO2f	Forward	TA GAGGA AGTAAAAGTC GTA A	Toju et al, 2012
ITS2_KYO2r	Reverse	TTYRCTRCGTTCTTCATC	Toju et al, 2012
ITS4r	Reverse	CCTCCGCTTATTGATATGC	Toju et al, 2012
Scibetta_wobble	Reverse	GCARRGACTTTCGTCCCYRC	Scibettaetal, 2012



Primer and polymerase choices

- Higher chao1
 - Higher number of 'rare' OTUs
 - Potentially more amplification and sequencing errors rather than true 'rare' OTUs
- Chosen:
 - Polymerase = phusion
 - Forward primer = Ky02F
 - Reverse primer = its1wobble

Polymerase	observed_species	chao1	shannon
phusion	257851	4026393.443	3.613001552
gold	367985	5908409.965	3.613045931
p.'			
Primer			
	observed_species	chao1	shannon
ky02f-its1wobble	270419	4577996.03	3.567338981
ky02f-its1wobble	270419	4577996.03	3.567338981



QC strategy

- Standard QC strategy:
 - 16.2 million merged reads passed QC
 - Resulted in >600,000 OTUs when clustered at 97%
 - Only 20 species in the mock community...
- Revised QC strategy:
 - 14.2 million merged reads passed QC
 - Resulted in 9,000 OTUs when clustered at 97% much better!
 - Standard Taxonomic assignment identified the mock community species (although frequently not to Species)

Species-level identification



- QIIME standard tool for metabarcoding analysis
- Species-level identification not that important for community comparisons (most are genus level or above)
- To use community profiling techniques effectively for surveillance, species level identifications are required
- Currently developing new methods to provide accurate species level identification

Current work



Plant Biosecurity Strategy

Development of new approaches to; find pests through new detection and identification methods (for example, studying sentinel plants planted at key locations or using molecular techniques for identification of new pest threats in samples **from existing networks**)

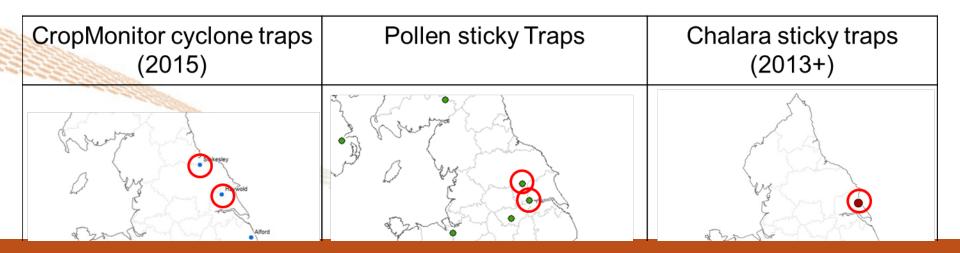
Potential to use existing networks (pollen network / air quality network / targeted spore traps) to monitor for invasive fungal species



Current work



- 1. Complete comparison of existing and "new" analysis methods on mock community
- 2. Compare fungal communities measurable from specialist fungal traps and geographically related spore traps on defined dates.





Acknowledgments

Funding: Defra Plant Health, BBSRC tree health initative





Department for Environment Food & Rural Affairs