

Improved pathogen management in crops using rapid in-field diagnostics

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Septoria the disease

- *Mycosphaerella graminicola* (*Septoria tritici*, leaf blotch) is the most common foliar disease of wheat in Europe.
- Most fungicides used on wheat are targeted against its control.



Economic losses due to leaf blotch



- Up to 16% of the global harvest is lost to plant diseases.
- In the UK, foliar diseases of wheat account for losses of up to 12%.
- Septoria tritici residual yield losses £43-53 million p.a. UK
- Estimated than £82million p.a. UK is targeted against its control.



Azole resistance

- Azoles are the primary control method in the UK.
- CYP51 gene is important in the biosynthesis of a fungal cell membrane component.
- 33 known mutations on the CYP51 gene.





Aim of project

- To develop a rapid, in-field test to detect fungicide resistant genotypes.
- To enhance decision making, achieving effective disease control and more responsible use of chemicals in crops.
- The tests will be deployed on a hand held platform with automated result calling.

Septoria population evaluation



- Evaluate the population structure of pathogens to enable effective sampling in the field.
- How common are the known mutations.
- How variable are populations:
 - From farm to farm
 - From field to field
 - Within a field



Septoria sampling plan

- To establish a sampling strategy
- 4 Farms
- 3 fields per farm
- 20 samples from each field using a W grid
- 2 intensive sampling points
- Total 2160 samples





Septoria sequencing process



Sequence variation



DNA Sequences Translated Protein Sequences

Species/Abbrv A	<u>Gr</u>
1. SEPT0320 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GT</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
2. SEPT0379 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
3. SEPT0382 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
4. SEPT0384 consensus	CTCCTGTCTTTGGCAAGG <mark>G</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
5. SEPT0387 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
6. SEPT0415 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>TG</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
7. SEPT0416 consensus	CTCCTGTCTTTGGCAAGG <mark>G</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
8. SEPT0420 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
9. SEPT0425 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
10. SEPT0427 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
11. SEPT0429 consensus	CTCCTGTCTTTGGCAAGG <mark>G</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
12. SEPT0434 consensus	CTCCTGTCTTTGGCAAGG <mark>G</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
13. SEPT0444 consensus	CTCCTGTCTTTGGCAAGG <mark>G</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
14. SEPT0445 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GT</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
15. SEPT0450 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GC</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:
16. SEPT0452 consensus	CTCCTGTCTTTGGCAAGG <mark>A</mark> TGTG <mark>GT</mark> TTATGATTGTCCCAATTCGAAGCTCATGGAGCAGAAGAAGG:

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	6. SEPT0415 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>D</mark> VCVDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA
	7. SEPT0416 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>C</mark> V <mark>A</mark> YDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA?
	8. SEPT0420 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>D</mark> VAYDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA
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	13. SEPT0444 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>G</mark> V <mark>A</mark> YDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA?
	14. SEPT0445 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>D</mark> V <mark>V</mark> YDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA?
	15. SEPT0450 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK <mark>O</mark> VAYDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA
	16. SEPT0452 consensus	KGNDFILNGKLKDVNAEEIYSPLTTPVFGK U V <mark>V</mark> YDCPNSKLMEQKKFVKYGLTTSALQSYVTLIA



Mutation combinations found

	50	134	136	188	379	381	461	459-461	% isolated
Wild type	L	D	V	S	А	I	Y		
Type 1	S	G	А	S	А	V	Н		47.23
Type 2	S	D	А	Ν	G	V	Y	deletion	24.52
Туре 3	S	D	V	Ν	А	V	Y	deletion	18.87
Type 4	S	D	А	S	А	V	Н		5.65
Type 5	S	D	А	Ν	А	V	Y	deletion	3.73







Importance of mutations found

- D134G Causes reduced Azole sensitivity in combination with changes at 459-461
- V136A Causes reduced Azole sensitivity in combination with changes at 459-461
- A379G Found in resistant strains in combination with 381
- I381V– Causes reduced Azole sensitivity in combination with changes at 459-461



Importance of mutations found

- Y461H Found in resistant strains in combination with other changes
- 459-461- deletion causes azole sensitivity
- 50 and 188 No effect on azole sensitivity



The assay requirements

- The assay is a DNA based LAMP assay
- Must be able to detect SNPs (single nucleotide polymorphisms).
- Ideally be a multiplex reaction.
- Must be rapid (less than 20 minutes)
- Must be able to be performed in the field.



New developments required

- To develop new probe methods to enable SNP detection and multiplexing. (Fera and GeneSys Biotech)
- Improved LAMP chemistry/reagents (GeneSys Biotech).

To develop improved software for LAMP probe assays (OptiSense).



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Initial method comparison



LAMP for detection of Septoria tritici





Acknowledgments

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- Project partners
 - Agrii
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 - Emily Roberts PhD student Fera