

PATHOGEN POPULATIONS

Diagnostics and surveillance

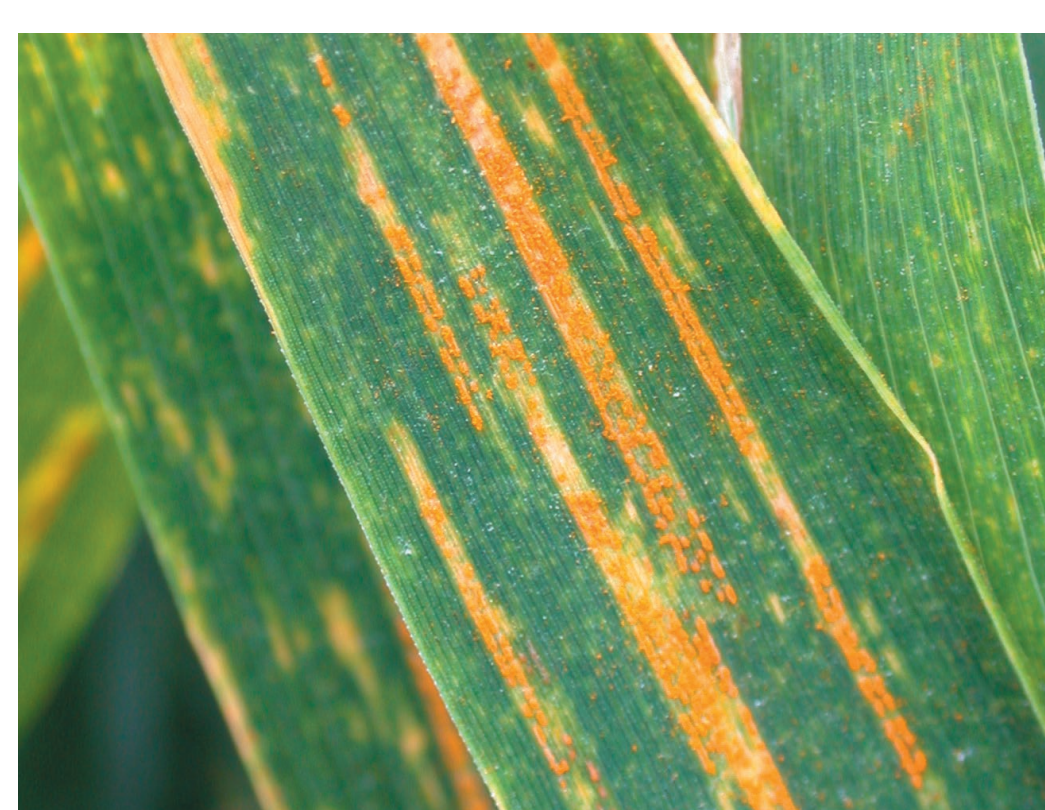
Deploying pathogen resistance in new varieties of crop plants is an essential element of integrated control strategies, but genetic variation in many pathogens creates the constant threat of new virulences arising which break down or overcome resistance. The ability to monitor and characterise this variation rapidly is a critical part of maintaining crop health in both developed and developing areas of the world.

Focus on NIAB research

NIAB is deploying new technologies in pathogenomics to understand variation in wheat yellow rust within the UKCPVS programme, and is also applying similar methods to many other diseases of national and international relevance including:



Septoria leaf blotch (*Zymoseptoria tritici*) is the major disease of wheat in the UK. *Z. tritici* is highly variable and has quickly overcome many resistance genes.



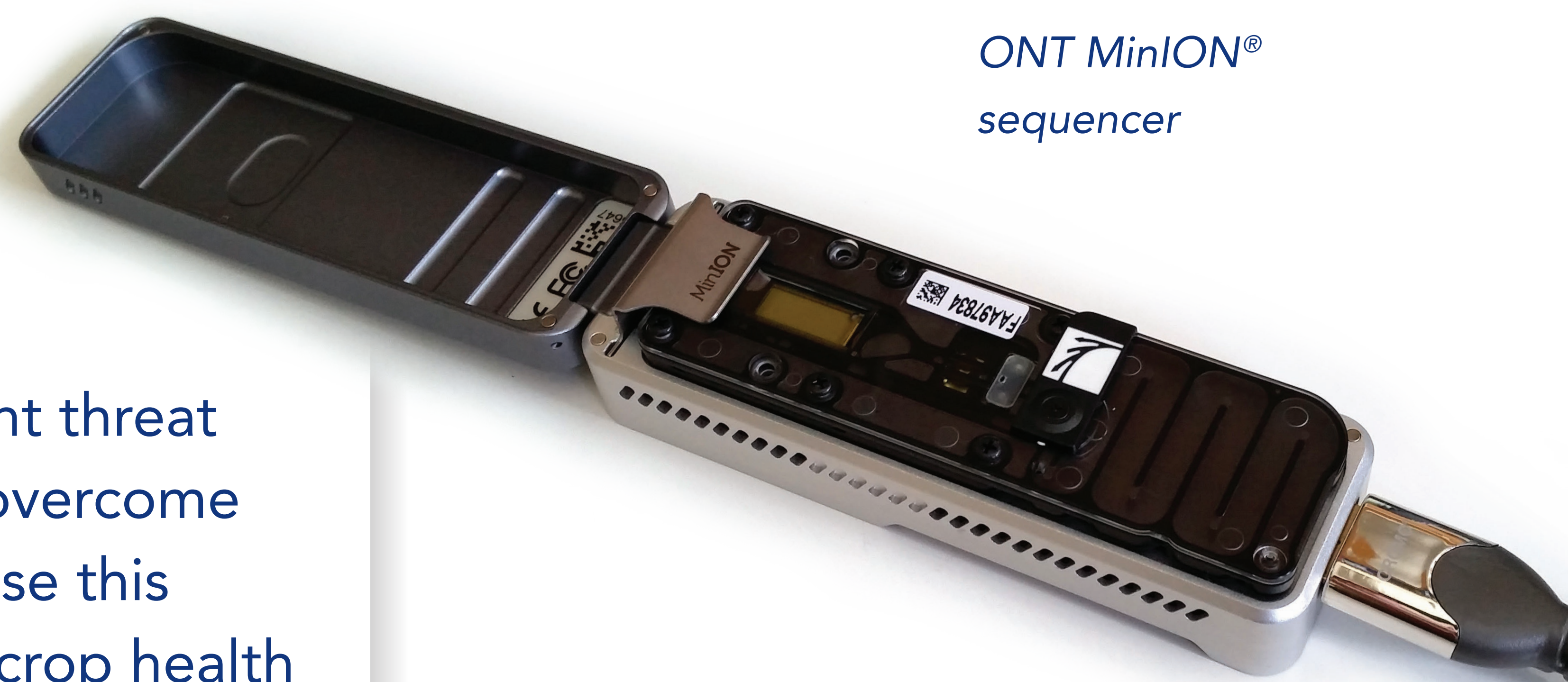
Yellow rust (*Puccinia striiformis* f. sp. *tritici*) is a major fungal disease of wheat. It is a diverse and dynamic disease in the UK and new virulent races can readily evolve.



Pea downy mildew (*Peronospora viciae*) is a highly specific oomycete infecting vining and combining peas. Novel variants have caused loss of variety resistance in UK field crops.



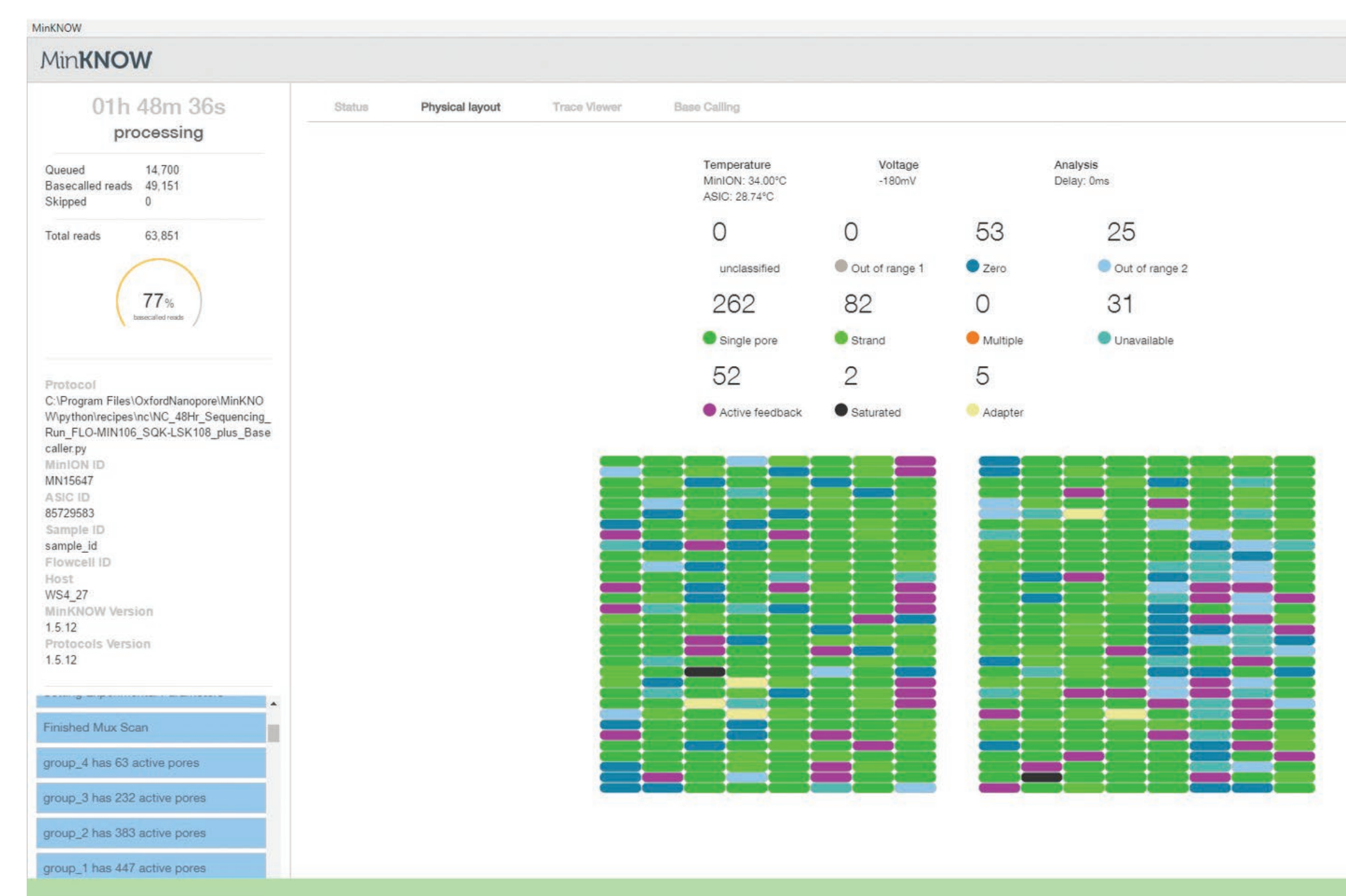
Angular leaf spot (*Pseudocercospora griseola*) causes devastating losses in common bean in east Africa. A complex race structure means that intensive surveillance is needed to identify the most damaging variants.



ONT MinION® sequencer

Using nanopore technologies for septoria surveillance

Oxford Nanopore Technologies MinION®, and other similar methods, now make it possible to characterise disease samples from differences in their DNA sequence within a few days and predict whether new and potentially damaging variants have arisen. This helps growers to react with different management approaches and plant breeders to understand the value of different resistance sources.



An ONT MinION® sequencing run of Septoria leaf blotch taking 48 hours. The green ovals represent 'pores' actively sequencing pathogen DNA