

## Developing new tools for interrogating cereal invaders

*Diane G.O. Saunders<sup>1,2</sup>*

<sup>1</sup>The Genome Analysis Centre, Norwich Research Park, Norwich, UK, NR4 7UH

<sup>2</sup>John Innes Centre, Norwich Research Park, Norwich, UK, NR4 7UH

Emerging and re-emerging diseases of humans, animals and plants pose a significant hazard to public health and food security. With recent advances in sequencing technology, bacteriologists and virologists are now integrating high-resolution genotypic data into pathogen studies. However, the application of genomics to emerging filamentous plant pathogens has lagged. To address this, we are leading the genome sequencing of hundreds of isolates of the wheat yellow rust pathogen *Puccinia striiformis* f. sp. *tritici* (PST), aimed at improving our understanding of the molecular mechanisms that drive PST evolution. Furthermore, we have developed a robust and rapid “field pathogenomics” strategy to improve filamentous pathogen surveillance. We applied this method in 2013 to PST, using gene sequencing of PST-infected wheat leaves taken directly from the field to gain insight into the population structure of an emerging pathogen. Our analysis uncovered a dramatic shift in the PST population in the UK and supports the hypothesis that recent introduction of a diverse set of exotic PST lineages may have displaced the previous populations. Working with cross-institutional and industrial partners we are now developing this technique further to reduce its cost so it can be applied routinely within our UK pathogen surveillance program for agroecosystems.