

# USING FIELD PATHOGENOMICS TO TEST FOR YELLOW RUST

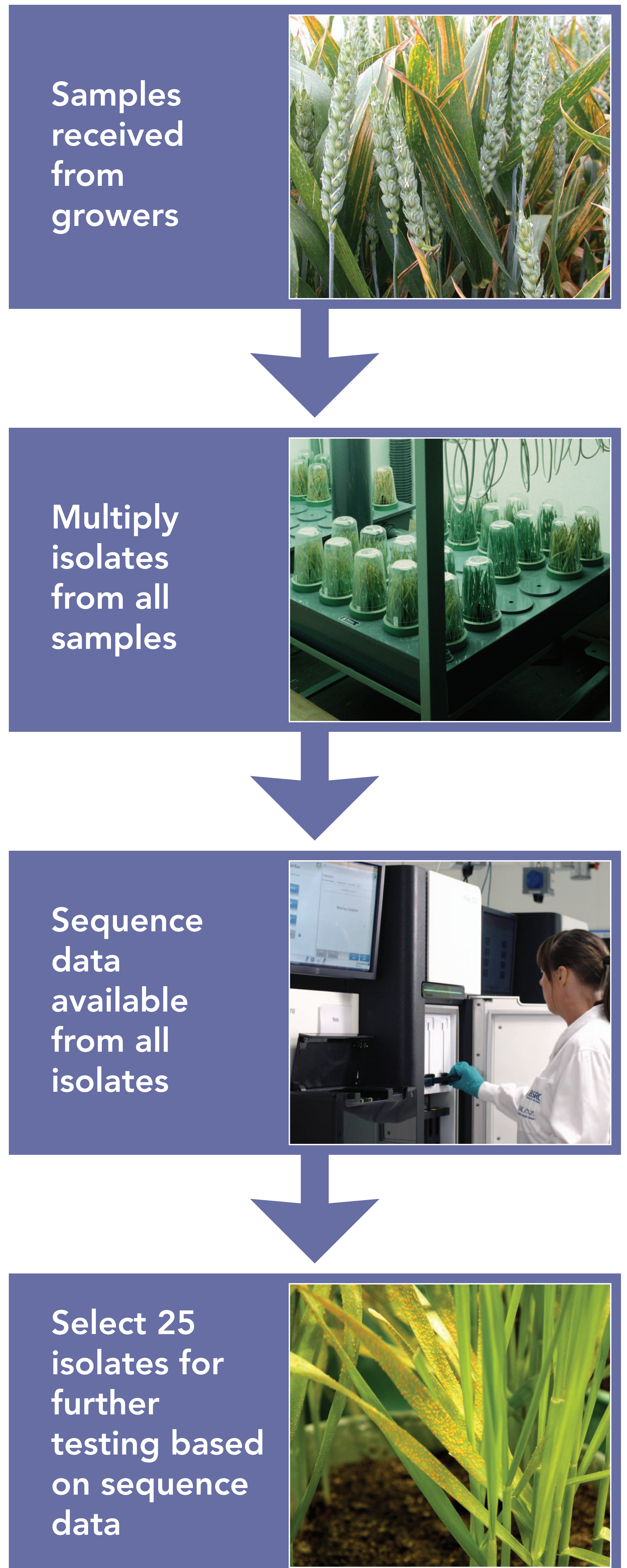


For almost 50 years NIAB has been monitoring the population of wheat yellow rust in the UK through the UK Cereal Pathogen Virulence Survey (UKCVPS), detecting and warning industry and growers of new races of disease emerging on resistant varieties, and funded by APHA and AHDB Cereals and Oilseeds.

During this time there have been minor modifications to the testing methods but none as big as the potential created by a new approach called Field Pathogenomics. This new method, developed as a partnership between NIAB, The Genome Analysis Centre and John Innes Centre, utilises existing methods used by UKCPVS and complements it with new sequencing techniques that have only recently been available for use on the yellow rust pathogen.

By using these two sets of information together researchers can understand the population in much more detail, with differences between isolates collected in any one year being seen at a much higher resolution.

Another advantage of this new approach is the reduction in cost and time associated with the sequencing aspect; ultimately UKCPVS could obtain sequence data on every sample received. Currently UKCPVS can only pathotype 25 isolates per year, with the isolates selected based on host variety and geographical location only. It is hoped that, in the next two to three years, by having sequence data on all isolates it will allow a more informed choice of isolates for further testing.



# USING FIELD PATHOGENOMICS IN PRACTICE



UKCPVS and TGAC research using field pathogenomics have been instrumental in understanding the recent changes in the wheat yellow rust population after the incursion of the Warrior population.

The old UK isolates found in the years prior to this incursion were very closely related, indicated by how tight they are together in Figure 1. The new population however is very diverse, shown by the wider spaces between the different isolates.

Using field pathogenomics' isolates collected in the years after the incursion are added to the analysis to see if they are still related to this wider Warrior group or if they are different again.

Aside from surveillance, field pathogenomics can be used to answer fundamental questions about how the yellow rust develops over time and space. For example, are isolates found in the autumn the same ones that cause epidemics later in June? Are isolates found in one part of the field the same as those found a few metres away?

Figure 1. Relationship between yellow rust isolates – infected leaves contain both wheat and yellow rust DNA that can be extracted and sequenced. Comparing sequence data from the pathogen across different isolates reveals how related they are and can highlight any novel variants such as the Warrior group (grouped in yellow)

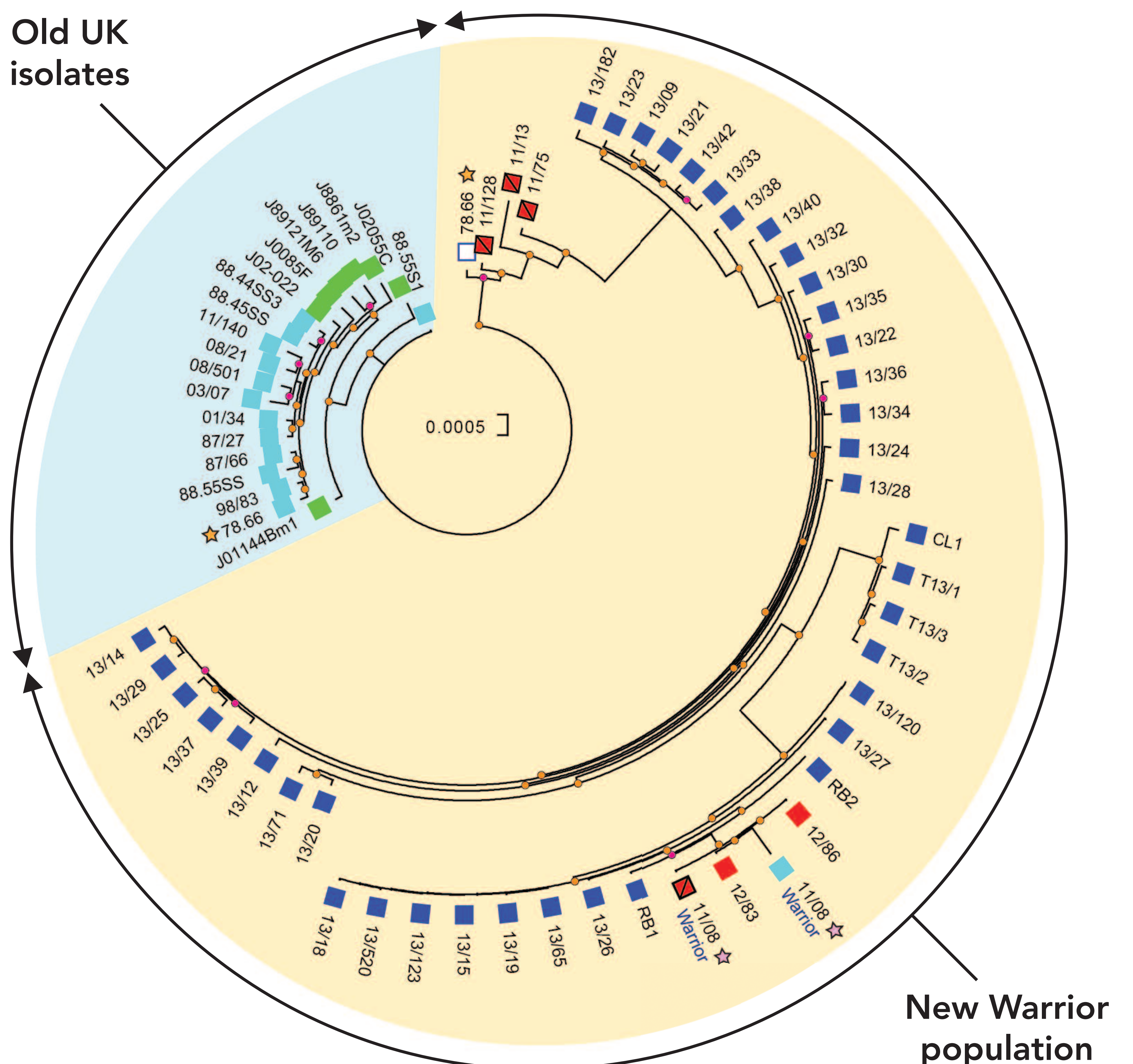


Figure 2. Is the isolate found in one part of the a field the same as the one a few metres away?

