

Introduction

Wheat stem rust, inflicted by the pathogen *Puccinia graminis* f. sp. *tritici* (*Pgt*), has a devastating effect upon wheat yield but since influx of new germplasm during the Green Revolution and the routine application of fungicides this disease was largely consigned to historical records for the past half century in western Europe. However, in recent years serious outbreaks of the disease have been occurring with increasing frequency across western Europe.

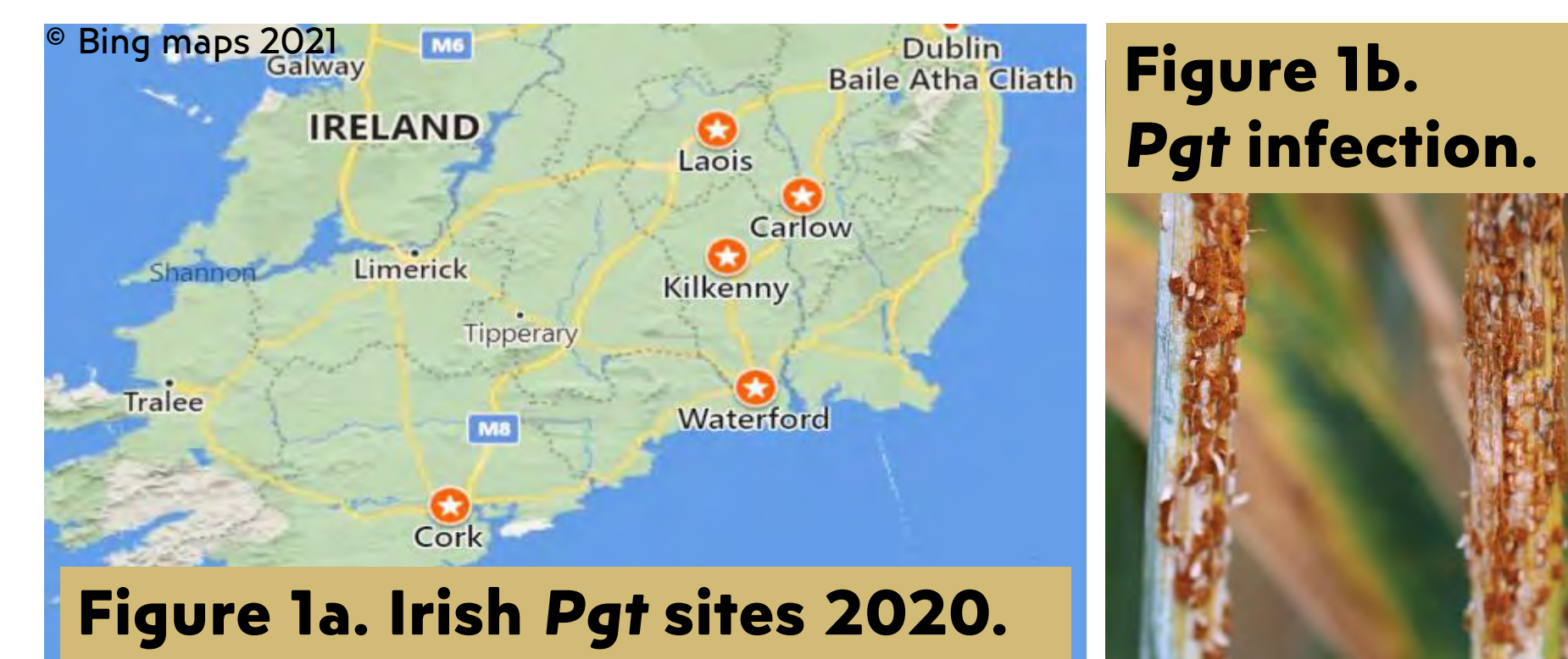
Aims

In June 2020 wheat stem rust was recorded in some southern counties of Ireland for the first time since the 1960s.

- Where did it originate from?
- What race/clade could it be?
- What prompted the outbreak?

Materials and Methods

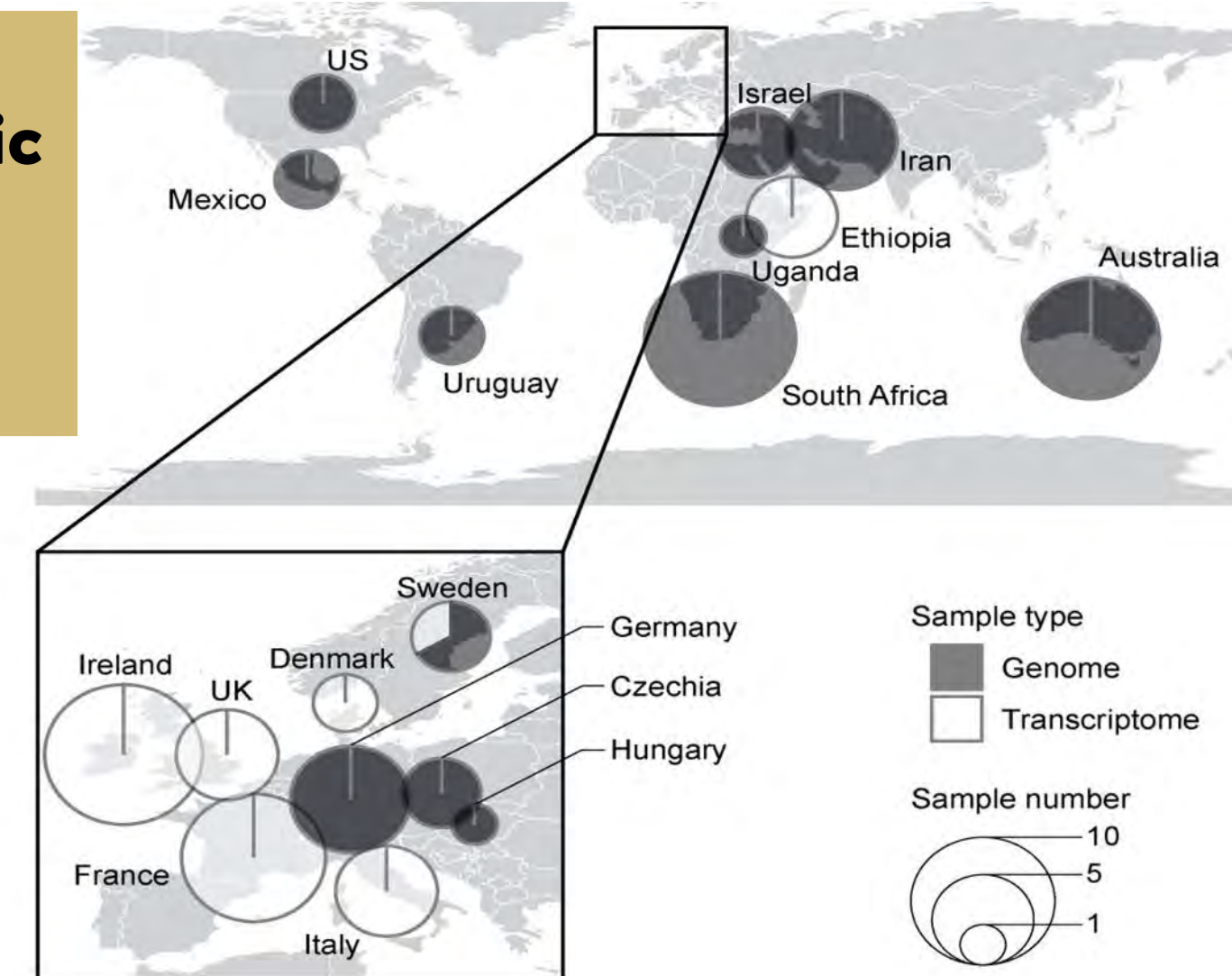
Pgt infected wheat stem tissue was collected from 5 locations in the Irish Republic (Fig 1a/b).



Pgt isolates were purified and multiplied from 2 Irish locations (Cork; IE-01 and Laois; IE-12), one from the UK (UK-02) and one from France (FR-11) were used for race profiling.

Pgt isolates collected at all five Irish locations (Figure 1a) and 76 further *P. graminis* isolates were also used for phylogenetic and population genetic analyses (Figure 2).

Figure 2. Geographic source of Pgt isolates.



Results

Race profiling

Pgt isolates IE-01, IE-12, FR-11 and UK-02 were screened across the BGRI international set of core differentials. This analysis designated all four *Pgt* isolates to the TKTTF race group (Figure 3).

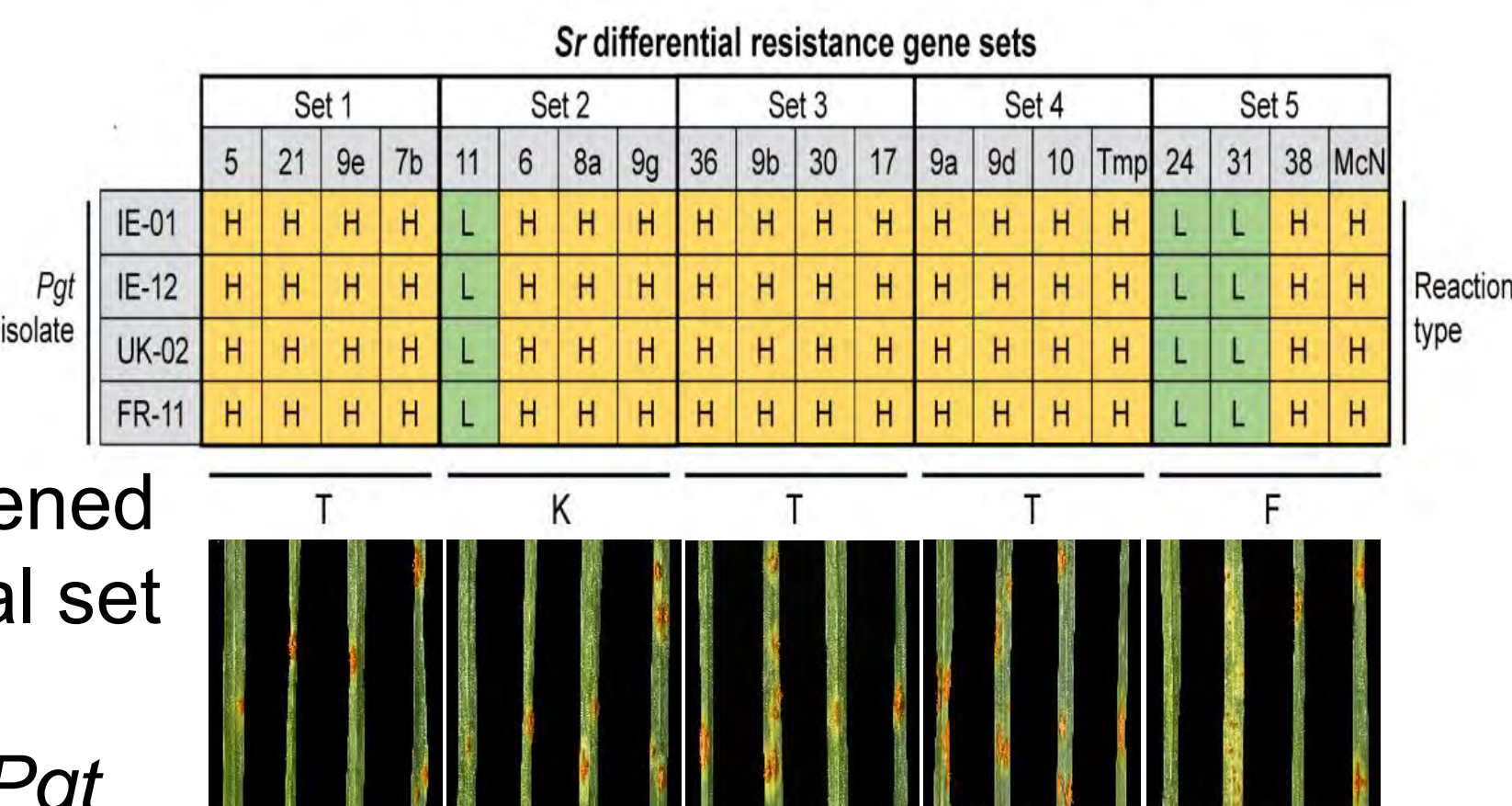


Figure 3. The 2020 isolates all have the TKTTF race profile.

Phylogenetic analysis

Phylogenetic analysis using the third codon position of 7,812 gene models and a maximum likelihood approach (rooted with 2 oat stem rust isolates as outliers) revealed that the isolates IE-01, IE-12, UK-02 and FR-11 grouped closely with Ethiopian isolates ET-03 and ET-04 and the UK isolate UK-01 (Figure 4). ET-03, ET-04 and UK-01 were all previously assigned to race group TKTTF [1] [2].

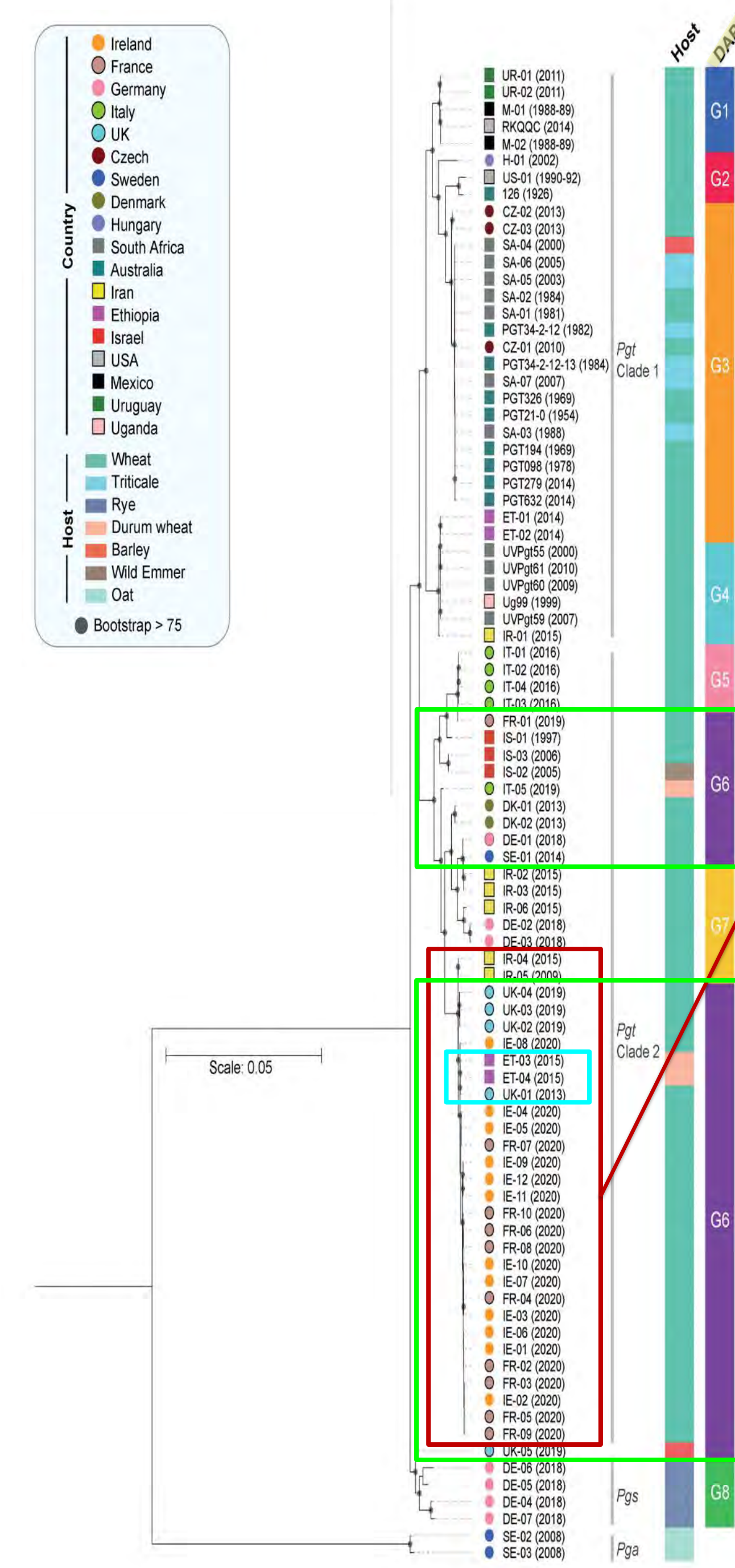


Figure 4. The 2020 Irish Pgt isolates are closely related to the TKTTF race group.

Population genetic analysis

Discriminant analysis of principal components (DAPC) performed on 16,639 biallelic synonymous SNP sites grouped all isolates into eight distinct populations clusters (G1-G8 in Figure 4).

IE-01, IE-12, UK-01, UK-02, FR-11, ET-03 and ET-04 all group in cluster G6, plus additional isolates from Israel, Italy, Denmark, Germany, France and Sweden.

Conclusions

The Irish *Pgt* isolate(s) belong to the TKTTF race group and likely arrived as urediniospores from western Europe where this race is currently present. It is believed that an usually humid summer experienced in this region during 2020 enabled the disease to proliferate although it arrived too late in the season to spread widely and impact yield.

References

- [1] DOI: 10.1094/PHYTO-11-14-0302-F
[2] DOI: 10.1038/s42003-018-0013-y
This research: Tsushima et al., 2021 (under review)