

UTILISING PATHOGENOMICS FOR SEPTORIA LEAF BLOTCH SURVEILLANCE

Septoria (*Zymoseptoria tritici*) is the major foliar disease affecting wheat in the UK.

In 2015/16 a breakdown in virulence was observed on the wheat variety Cougar (Figure 1). A similar breakdown was observed in 20/21 in varieties with Cougar in their pedigree.

84 samples of Septoria were collected in 2015/16 from various host wheat varieties, including Cougar (Figure 2). The isolates were tested for pathogenicity on Cougar and Gallant to confirm their identity (Figure 3).

Genome resequencing was used to screen 35 Cougar/non-cougar types to see if genetic profiles could be used to distinguish between the two types (Figure 4); profiles are being compared with newly collected isolates from RGT Saki and KWS Firefly in 2021.

A mapping population was subsequently developed by crossing virulent and avirulent Septoria isolates. Of the 71 isolates phenotyped, 34 were Cougar-type and 37 non-Cougar, indicating a single major effect gene could be responsible for virulence.

This work will help to contribute to monitoring for race changes in the Septoria population, enabling breeders to select for the most effective sources of resistance and growers to deploy the best-suited varieties.

Quantitative PCR (qPCR) strategies have also been developed to monitor the amount of Septoria in leaves during the period of latent infections to assess control treatment efficacy.

Figure 1. Septoria symptoms from new/old isolates on the wheat varieties Cougar and Solstice

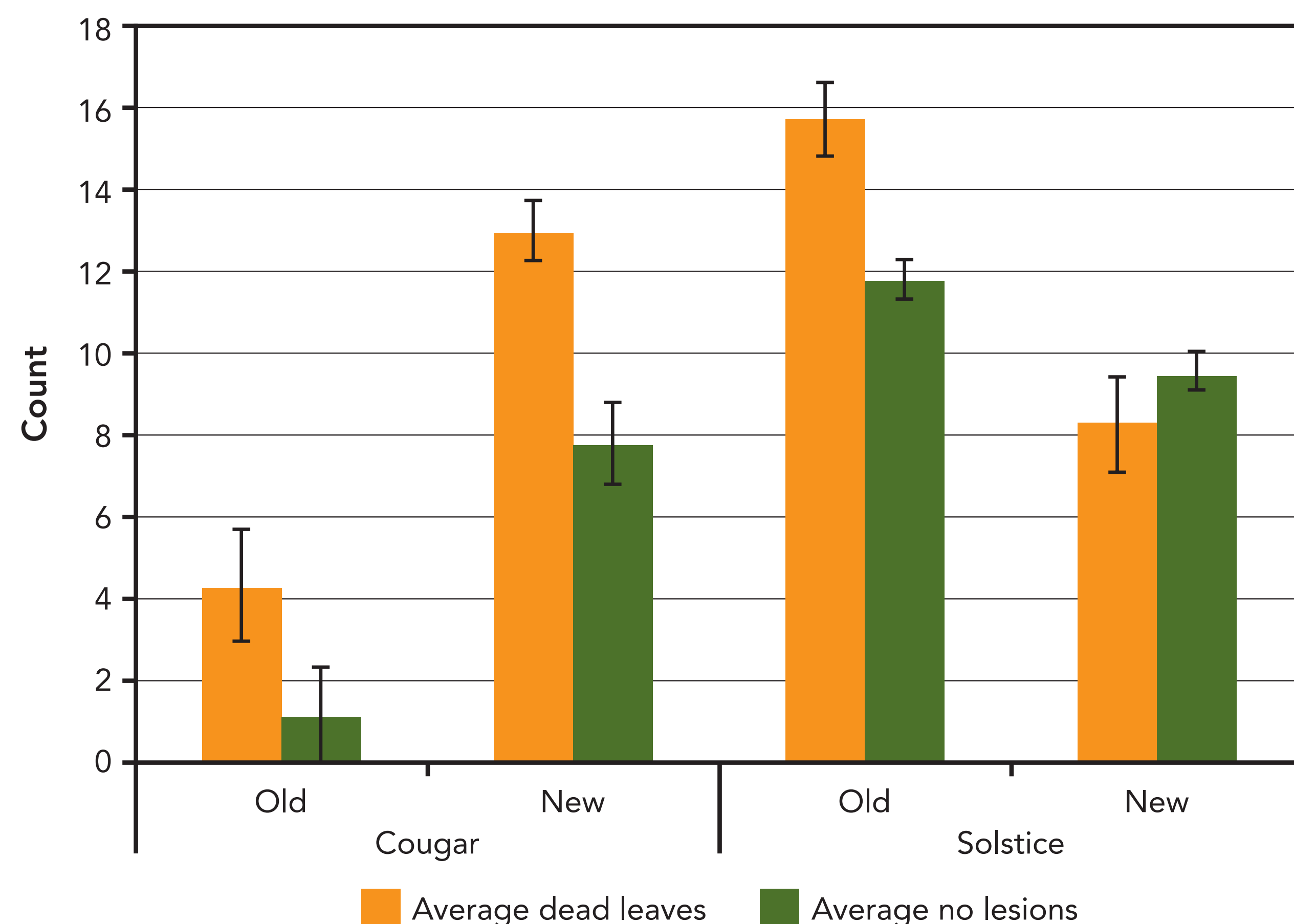


Figure 2. The origin of collected Septoria isolates across the UK

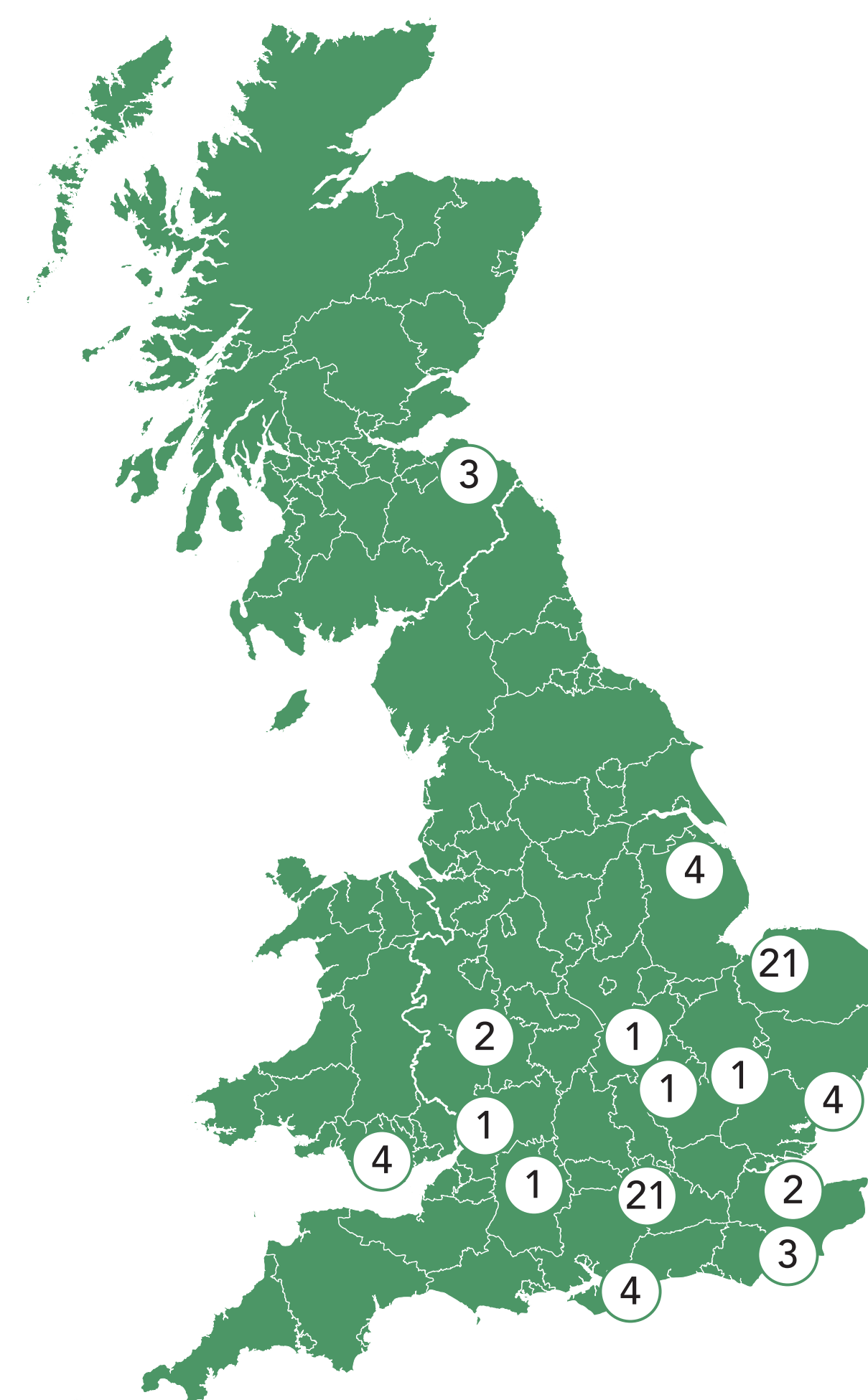


Figure 3. Cougar plants inoculated with Septoria in pathogenicity testing



Figure 4. Phylogenetic tree demonstrating the genetic relationship between the tested Septoria isolates

