Role of indigenous barberry species and accessory hosts on stem rust variability in Spain

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Objective

- To investigate the functionality of indigenous barberry species *(Berberis vulgaris* subsp. *seroi* and *B. vulgaris* subsp. *australis*) as alternate hosts for rust pathogens infecting cereals and grasses.

Materials and methods

- Barberry leaves bearing aecia were collected from several provinces of Spain **(Fig. 1)**.

Fig.1. Barberry leaves bearing aecia of *Berberis vulgaris* subsp. *seroi*.

- DNA sequencing of the EF1α gene was performed on 100 single aecial clusters **(Fig. 2)**.
- SSR genotyping using primers targeting *Puccinia graminis* complex was performed on 30 single aecial clusters **(Fig. 2)**.

Fig. 2. Single aecial clusters were used for DNA sequencing and SSR genotyping

- Host specificities on cereal crops and grasses were investigated by pooled inoculations on varieties of wheat, barley, rye, oat, ryegrass and cock's-foot using aeciospores from barberry leaves.

Results

- DNA sequencing of 100 single aecial clusters confirmed *Pgt/Pgs* (*P. graminis* f.sp. *tritici* and *P. graminis* f. sp. *secalis*) and *Pga* complexes *(P. graminis* f.sp. *avenae*). Both also infecting grasses of the *Poaceae* family (**Fig. 3**).

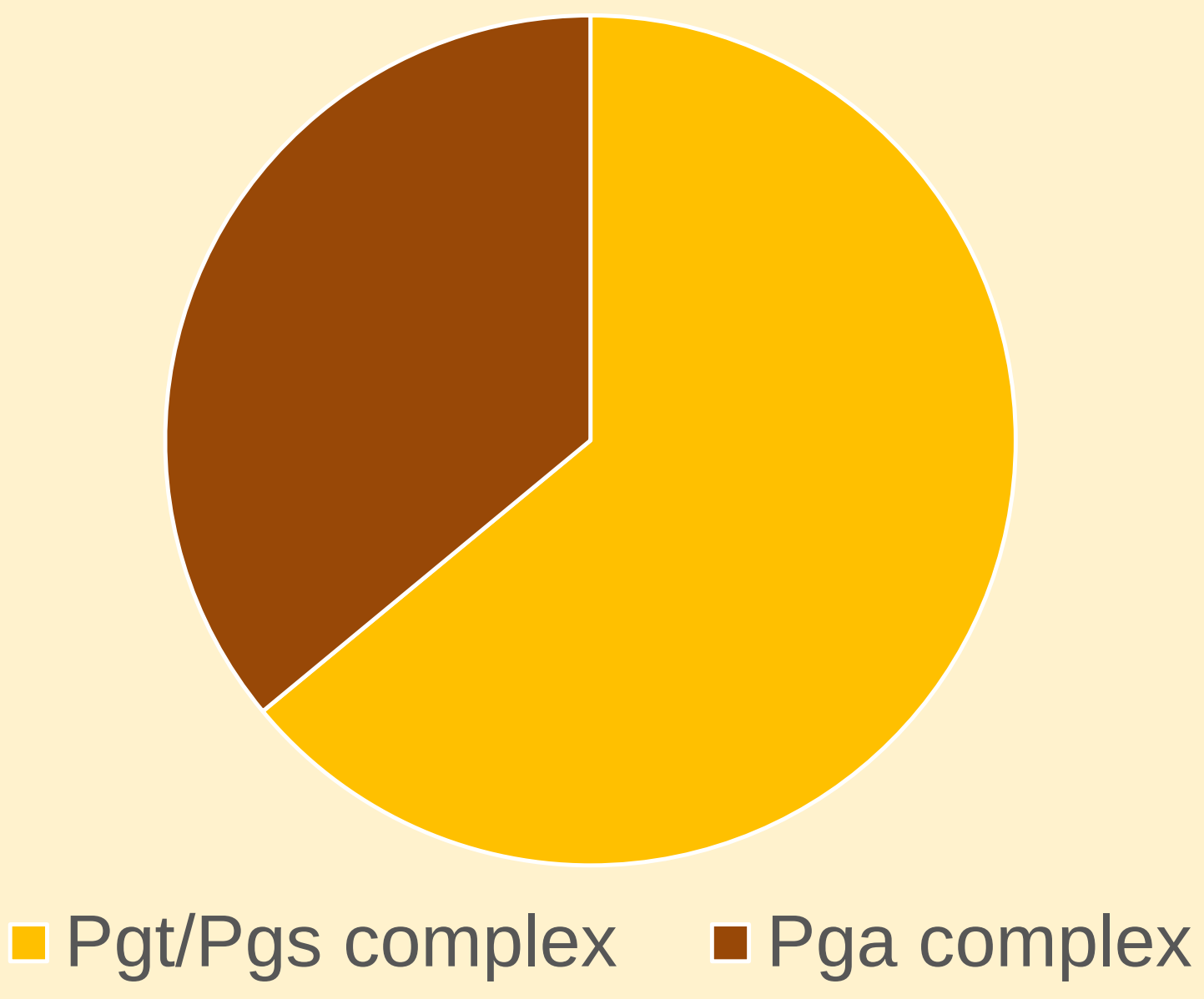

Fig 3. *Puccinia* specie identification by DNA sequencing of single aecial clusters.

- SSR genotyping of 30 aecial clusters resulted in 30 unique MLGs.
- A total of 681 single-pustule isolates of *Puccinia graminis* were recovered on cereal hosts and grasses, *i.e.*, wheat, barley, rye, oat, ryegrass and cock's-foot (**Fig. 4**).

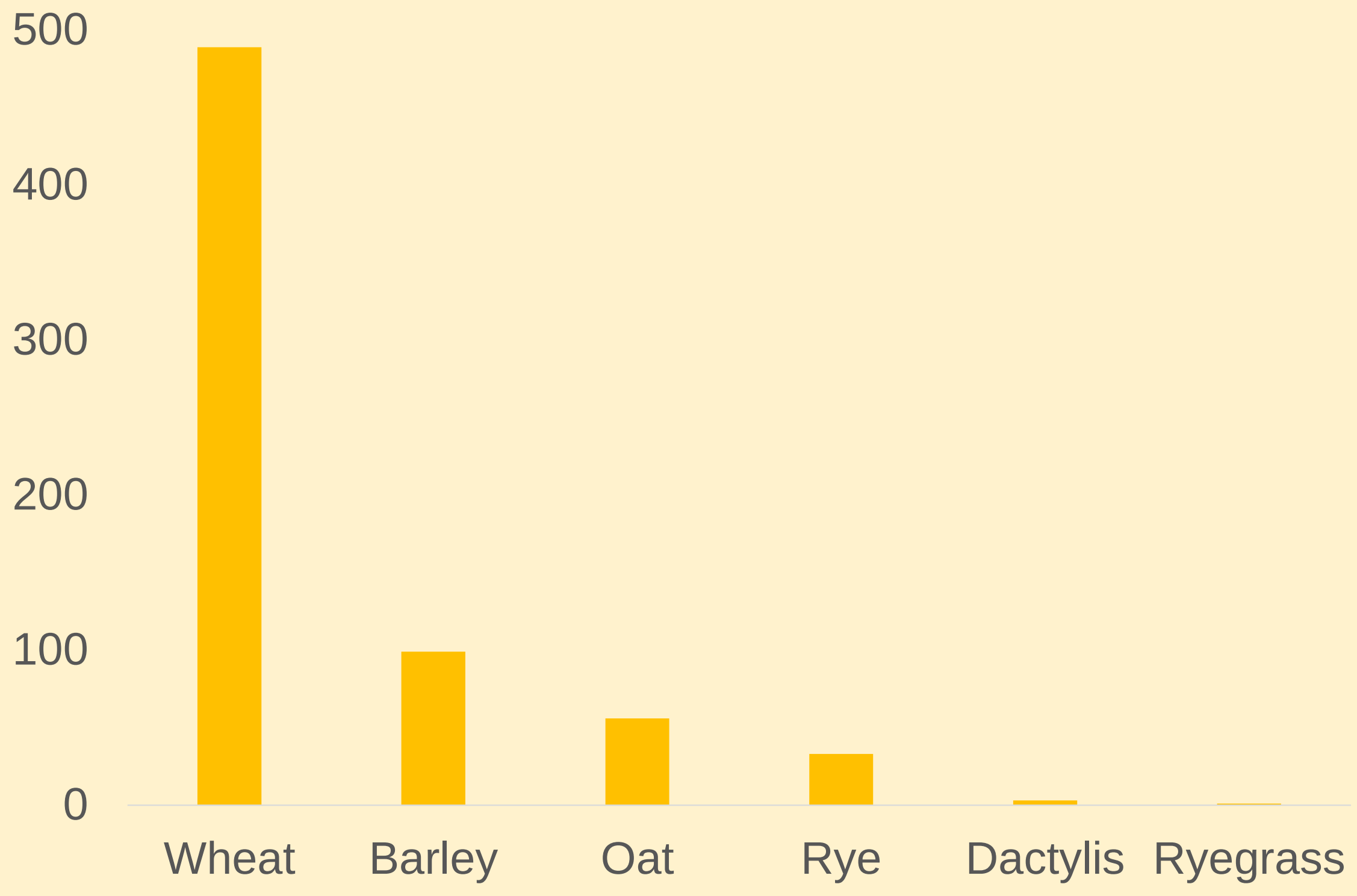

Fig. 4. Proportion of Sr isolates recovered on cereal crops and grasses.

- Race analyses of 190 single-pustule isolates resulted in the identification of 148 unique *Pgt* races.
- Stem rust infections were sampled from cereal crops and grasses of the *Poaceae* family in close proximity to infected barberries **(Fig. 5)**.

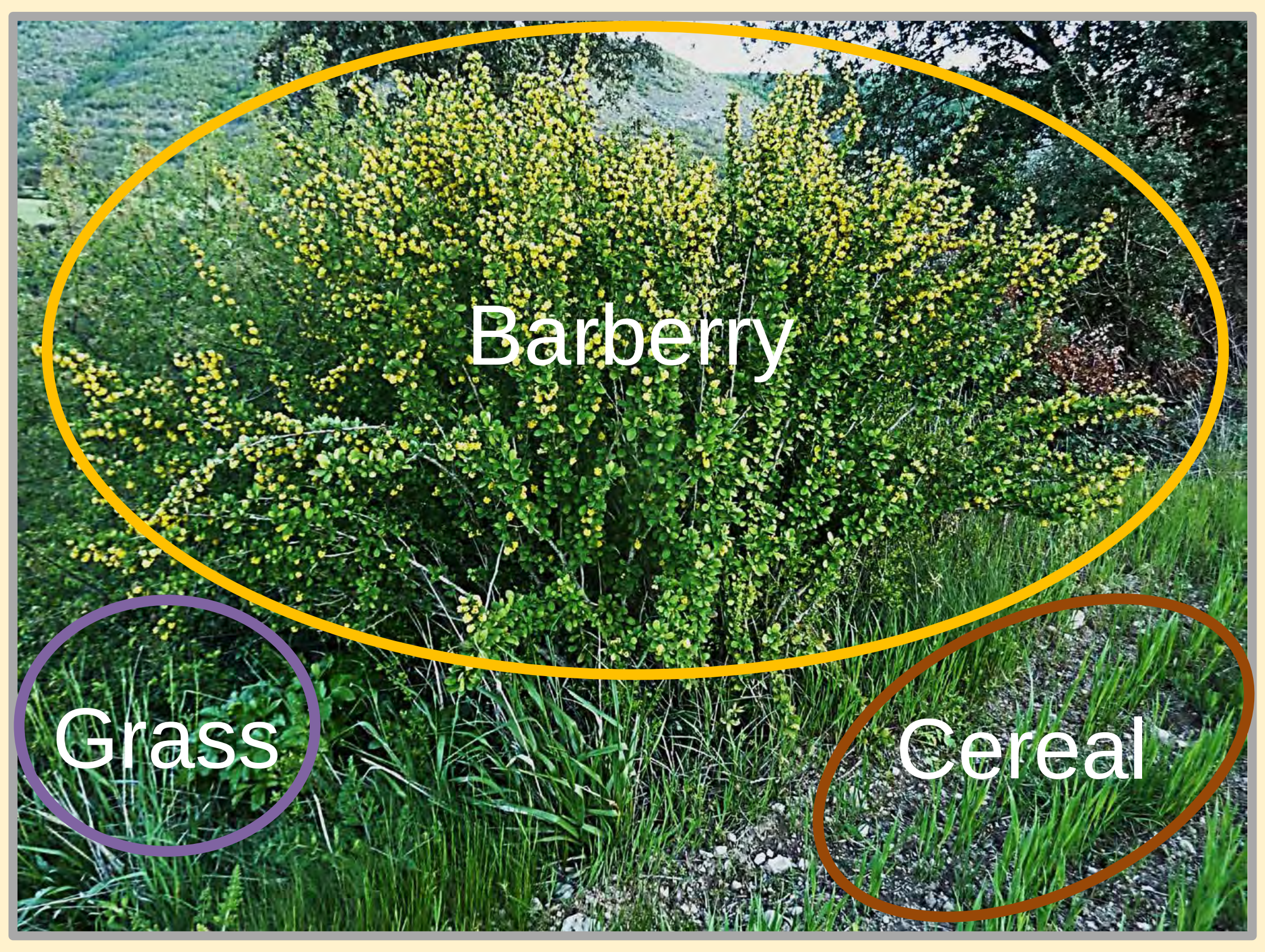

Fig. 5. Coexistence of *Berberis vulgaris* subsp. *seroi,* cereal crops and grasses in the Huesca province of Spain.

Conclusions

- DNA sequencing and SSR genotyping confirmed that *Berberis* spp. may function as alternate hosts and contribute to the genetic diversity of *Puccinia graminis* in Spain.
- Stem rust pustules recovered on cereal and grasses indicated that *Berberis* spp. are functional as alternate hosts for rust pathogens in Spain.
- Stem rust infections sampled from cereal and grasses next to infected barberries indicated that the sexual cycle has likely contributed to stem rust infections and generated unique virulence combinations (e.g., **Fig. 6**) (for more information see presentations by Villegas et al. and Patpour et al. and poster by Olivera et al.).

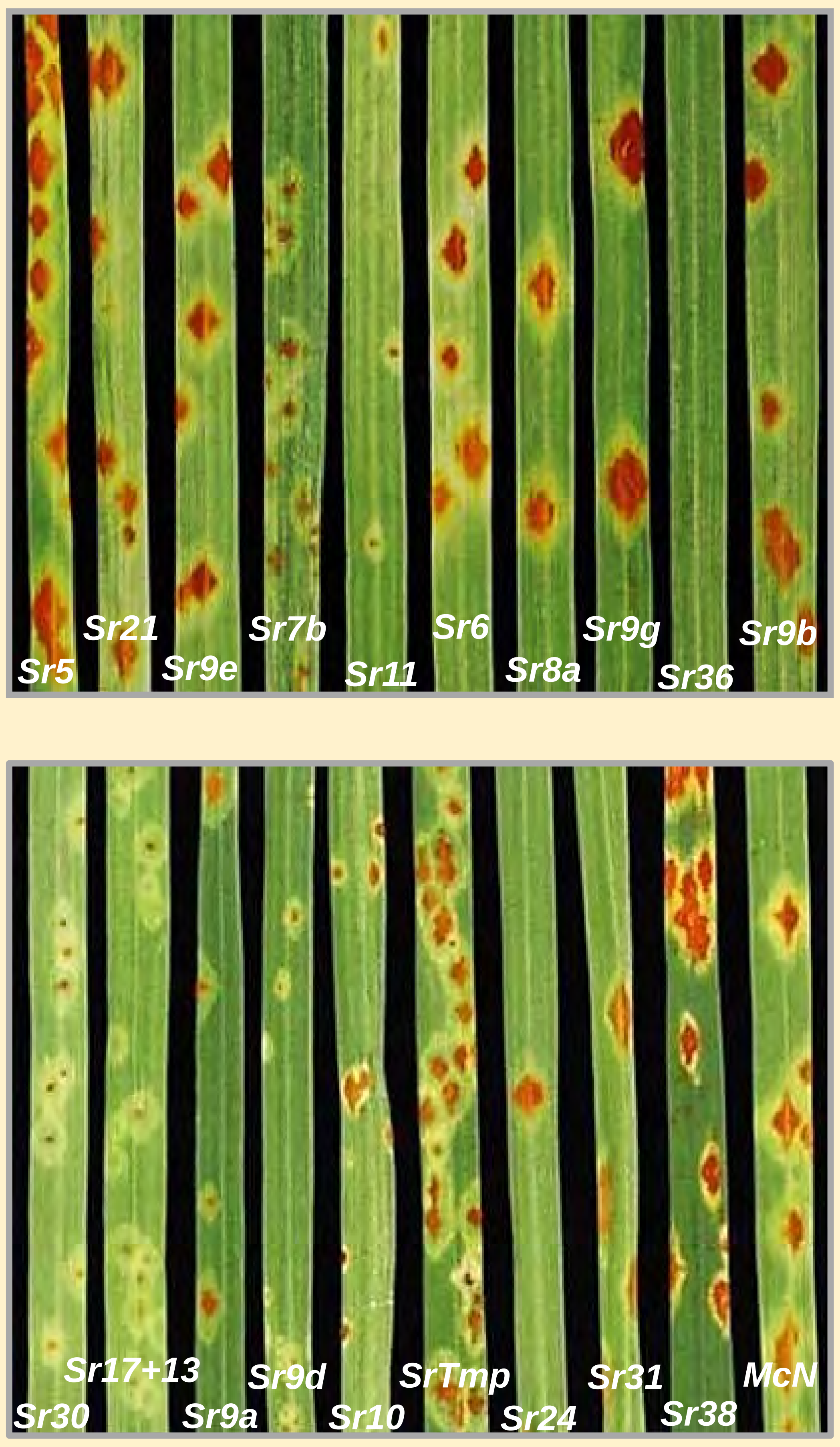

Fig. 6. Race typing of an isolate recovered from *Elymus repens* confirmed unique virulence combinations on wheat differentials.

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