RUSTWATCH

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SUMMARY

Based on observations in field and greenhouse, it is known that some *Puccinia striiformis* strains produce teliospores more abundantly than others, e.g., highly diverse isolates originating from sexual recombining populations in the Himalayas, in contrast to isolates originating from clonal populations in Europe (Ali et al. 2010). PstS7 (Warrior race), widely detected in Europe since 2011 , which has a putative origin in the near Himalayan region (Hovmøller et al. 2016), was capable of producing teliospores and undergo sexual reproduction on the alternate host, *Berberis vulgaris,* under experimental conditions (Rodriguez-Algaba et al. 2014).

In two articles recently published in the European Journal of Plant Pathology (https://doi.org/10.1007/s10658-019-01919-4) and Plant Disease (https://doi.org/10.1094/PDIS-02-21-0269-SC), scientists at Aarhus University have demonstrated that two races of the yellow rust fungus (termed "Kranich" and "PstS15"), both detected in several European countries since 2011 and 2018, respectively, were able to complete sexual reproduction on *Berberis vulgaris,* but also on *B. vulgaris* subspp. *sero*i and *australis*, which are indigenous in Spain. In both studies, novel genetic diversity was generated on these *Berberis* species, which was confirmed by the recovery of segregating progeny isolates on the wheat host (Table 1, Fig. 1). The experiments demonstrated that the two indigenous barberry subspecies from Spain were indeed susceptible to yellow rust, i.e., they can now be added to the approximately 50 Berberis species, which have been confirmed susceptible to yellow rust under natural or experimental conditions (Fig. 2).

Table 1. Sizes of alleles (a1: allele 1, a2: allele 2 given in base pairs) at 8 heterozygous simple sequence repeat (SSR) loci in parental isolate (DK02d/12, "Kranich" race) and in 23 segregating progeny isolates of *Puccinia striiformis* f.sp. *tritici*. Genetic segregation of progeny isolates is presented based on the number of segregated markers and the corresponding multilocus genotype (MLG).

MLG ID	Isolate(s)	No. of segregated SSR loci	RJO24 a1	RJO24 a2	RJN3 a1	RJN3 a2	RJN11 a1	RJN11 a2	RJO27 a1	RJO27 a2	RJN6 a1	RJN6 a2	RJN10 a1	RJN10 a2	RJN4 a1	RJN4 a2	RJN5 a1	RJN5 a2
-	DK02d/12	-	284	293	336	340	176	180	232	242	315	318	221	224	253	255	222	226
1	69a	1	284	293	336	340	176	180	242	242	315	318	221	224	253	255	222	226
2	35a, 37a	3	284	293	336	336	176	180	242	242	315	318	221	224	255	255	222	226
3	100a	3	284	293	340	340	176	180	242	242	315	318	221	224	253	255	222	222
4	1a	4	293	293	340	340	176	180	242	242	315	318	221	224	253	255	222	222
5	61a	4	284	284	336	340	176	180	242	242	318	318	224	224	253	255	222	226
6	77a	4	284	293	336	340	176	176	242	242	315	318	224	224	253	255	222	222
7	91a ,92a	4	284	284	340	340	176	180	242	242	318	318	221	224	253	255	222	226
8	114a	4	284	293	336	340	176	180	242	242	318	318	224	224	253	255	222	222
9	8a, 10a	5	293	293	340	340	176	180	242	242	315	315	221	224	255	255	222	226
10	30a, 34a	5	284	284	340	340	176	180	242	242	315	318	221	221	253	255	222	226
11	55a	5	284	284	336	340	176	180	242	242	315	315	221	221	255	255	222	226
12	81a	5	293	293	336	340	176	176	242	242	315	315	221	224	253	253	222	226
13	2a	6	293	293	340	340	176	180	242	242	315	315	224	224	255	255	222	226
14	47a, 51a	6	284	284	336	336	180	180	242	242	318	318	221	224	255	255	222	226
15	94a	6	284	284	336	336	180	180	242	242	315	318	221	221	253	255	222	222
16	15a	7	284	284	336	336	176	176	242	242	315	315	224	224	253	255	222	222
17	41a	7	284	284	336	336	180	180	242	242	315	318	221	221	253	253	222	222
18	74a	7	293	293	336	336	176	180	242	242	315	315	224	224	255	255	226	226
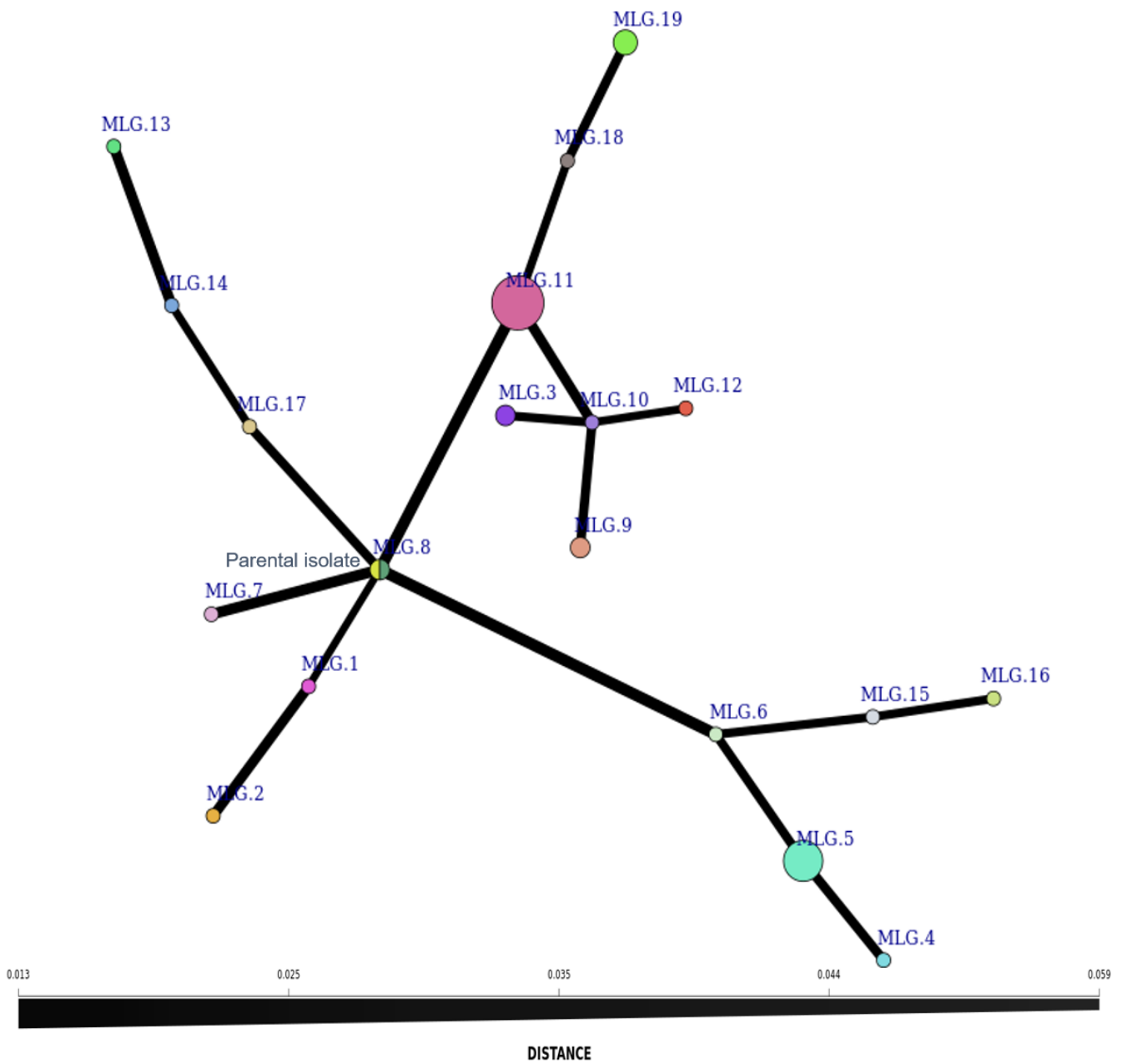
Fig. 1. Minimum distance spanning tree of the parental isolate (in yellow) and the 19 multilocus genotypes (MLG) detected among the 43 progeny isolates compared to parental isolate (DK219_19, "PstS15" race). Sizes of nodes are proportional to the number of progeny isolates detected on each MLG, which are indicated by different colours
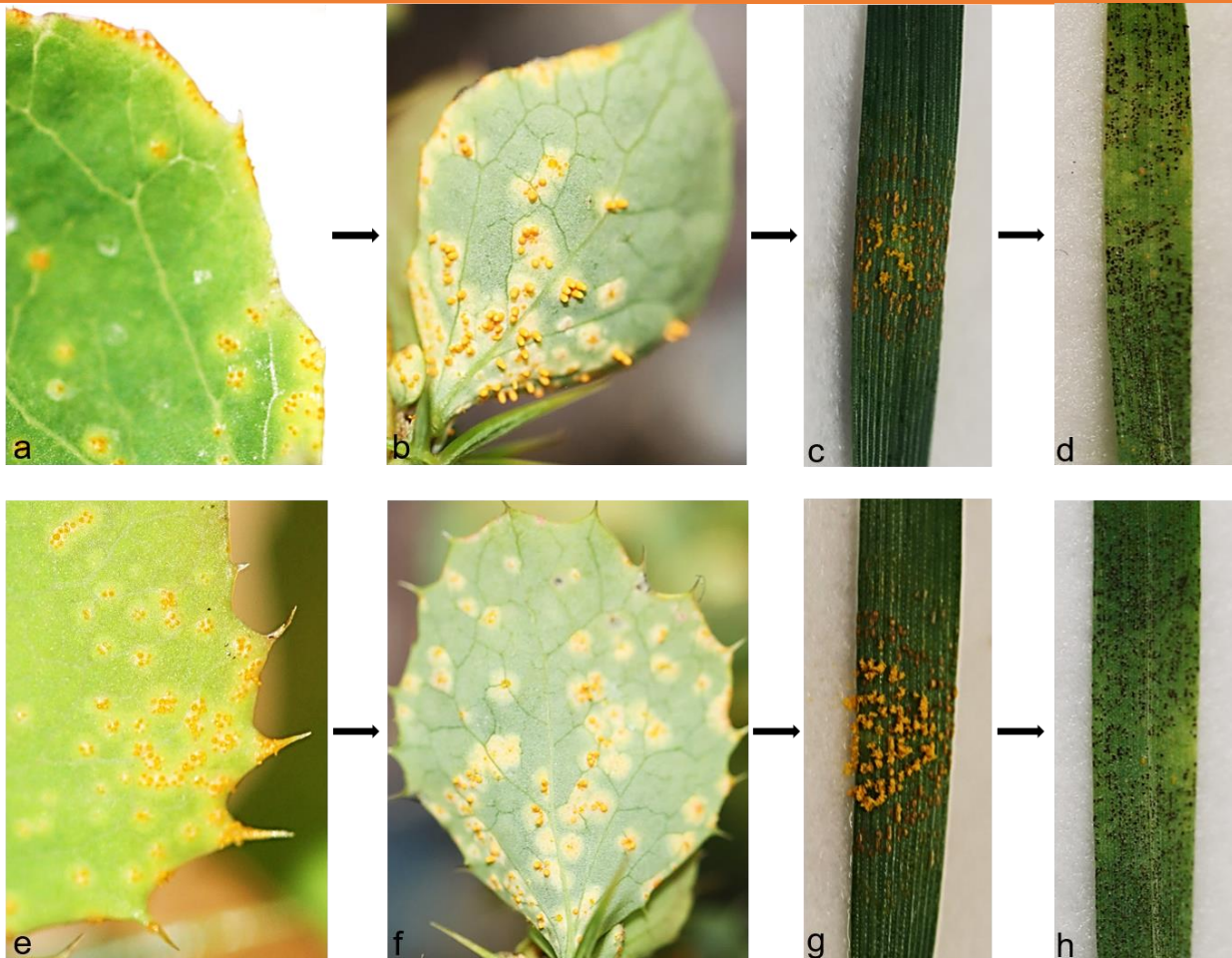
Fig. 2. Pycnia and aecia developed on *Berberis vulgaris* subspp*. seroi* (top) and *australis* (bottom) and uredinia and telia observed on wheat seedlings, **a,e:** Pycnia observed on the adaxial side of the leaf at 10 days after inoculation (dai), **b,f:** Aecia observed on the abaxial side of the leaf at 20 dai, **c,g:** Uredinia observed on wheat seedlings of cultivar 'Morocco' at 14 days after aeciospore recovery, **d,h:** Telia observed on wheat seedlings of cultivar 'Morocco' at 28 days after aeciospore recovery.

CONCLUSION

The two strains, PstS8 (Kranich race) and PstS15 detected in several European countries, were able to undergo sexual reproduction on *Berberis vulgaris* as well as on *B. vulgaris* subspp. *sero*i and *australis*, which are indigenous in Spain. In terms of risk assessment, we have detected *P. striiformis* isolates collected in Europe, which are prone to undergo sexual reproduction, and we have detected susceptible plants of the alternate host, Berberis spp. Currently we have no indications of sexual reproduction in the contemporary European *P. striiformis* population. There may be various reasons for the absence of the sexual life cycle of *P. striiformis* in Europe, e.g., lack of synchrony and proximity of alternate and primary host plants and the required environmental conditions for teliospore germination, infection of the alternate host and subsequent completion of the life cycle on susceptible wheat plants. However, the results stress the importance of rust surveillance in areas where barberry species and wheat coexist and suitable conditions for completion of the sexual cycle are present. Sexual reproduction could result in novel and unique virulence combinations that can have negative consequences for wheat production.

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