

Virulence Surveys of the Barley Leaf Rust Pathogen (*Puccinia hordei*) in the United States and Screening of Breeding Germplasm for Resistance

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Introduction

- Barley leaf rust is caused by the basidiomycete and heteroecious fungus, *Puccinia hordei* Otth [1].
- Yield losses due to the disease can range from 30–60% in susceptible varieties [2,3].
- P. hordei* may acquire new virulences through mutation, sexual recombination on its alternate host (*Ornithogalum* spp.), and somatic hybridization [4,5].
- Routine monitoring of pathogen virulence is necessary to detect the emergence of new pathotypes and support plant breeding programs.
- This study examined the virulence dynamics of *P. hordei* in two survey periods: 1989–2000 and 2010–2020 and evaluated barley breeding germplasm for resistance.

Materials and Methods

- The 1989–2000 surveys were conducted at North Dakota State University, Fargo, ND, while the 2010–2020 surveys were performed at the USDA-ARS Cereal Disease Laboratory, St. Paul, MN.
- Single pustule isolates were collected, increased, and phenotyped using the barley leaf rust differential set, comprised of 15 unique *Rph* genes from *Rph1.a*–*Rph15.ad*. Raw infection type scores were converted to 0–9 linearized scale for statistical analyses.
- For detecting regional patterns, isolates from each survey period were grouped into five regions in the United States: Pacific/West (PW), Southwest (SW), Midwest (MW), Northeast (NE) and Southeast (SE) (Fig. 1).
- Barley germplasm from breeding programs across the United States were screened using a relatively avirulent isolate, 17TX10b.

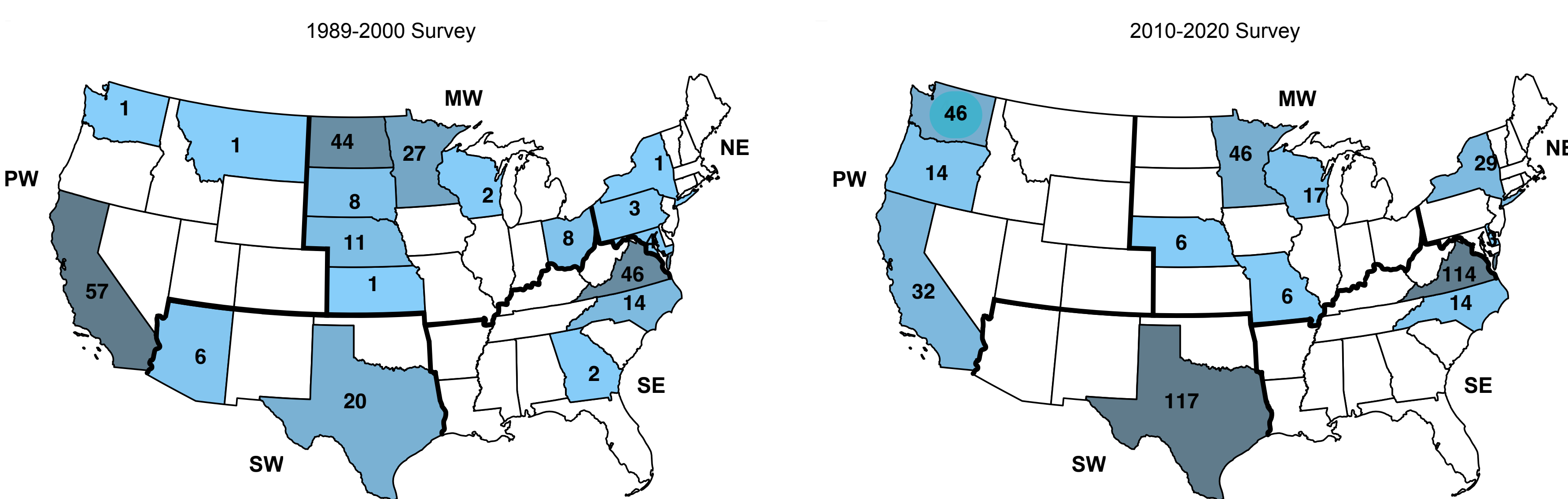


Fig 1. Number of isolates collected from the 1989–2000 survey period (N= 256), and B) 2010–2020 survey period (N= 444). Bold lines denote divisions of the country into five geographic regions.

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Results and Discussion

- A total of 700 *P. hordei* isolates were collected from the two survey periods (Fig 1).
- High virulence frequencies (60.9–96.9%) were observed for *Rph1.a*, *Rph2.b*, *Rph4.d*, and *Rph8.h* in both survey periods (Table 1).
- Low virulence frequencies (0 to 14.9%) were noted for *Rph5.e*, *Rph5.f*, *Rph9.z*, *Rph14.ab*, and *Rph15.ad*.
- Virulence for *Rph3.c*, *Rph5.e*, *Rph5.f*, *Rph9.i*, *Rph9.z*, and *Rph14.ab* increased from 1989–2000 to 2010–2020 (9.4–33.7%).

Rph Gene	1989–2000 Survey					2010–2020 Survey				
	PW	SW	MW	NE	SE	PW	SW	MW	NE	SE
<i>Rph1.a</i>	100	100	100	87.5	88.7	92.3	96.4	76	68.8	81.9
<i>Rph2.b</i>	84.7	80.8	33.7	62.5	74.2	47.8	75.2	57.5	59.4	62.5
<i>Rph3.c</i>	0	3.8	0	0	0	8	42.5	10.7	54.8	54
<i>Rph4.d</i>	94.9	100	100	87.5	93.5	73.3	80	64.7	73.3	64.5
<i>Rph5.e</i>	0	0	2	0	0	35.6	2.7	21.7	3.6	5.7
<i>Rph5.f</i>	1.7	0	12	12.5	0	38.6	4.5	27.5	4	2.6
<i>Rph7.g</i>	3.4	0	8.9	25	64.5	9.1	7.8	24	19.4	45.2
<i>Rph8.h</i>	84.7	80.8	96	100	96.8	65.2	75.2	63.9	41.9	61.6
<i>Rph9.i</i>	0	0	0	0	0	8.7	33	8	16.7	16
<i>Rph10.o</i>	8.5	11.5	55.4	37.5	17.7	40	8.7	27.4	10.3	15.3
<i>Rph11.p</i>	47.5	34.6	74.3	50	82.3	25.6	22.6	41.2	36.7	42.6
<i>Rph9.z</i>	0	0	0	0	0	5.8	16.5	3.1	10.7	13.6
<i>Rph13.x</i>	89.8	84.6	28.7	62.5	79	18.5	75.2	35.1	28.1	44.9
<i>Rph14.ab</i>	0	0	0	12.5	4.8	22	3.6	13.5	18.8	14.8
<i>Rph15.ad</i>	0	0	0	0	0	0	0	0	0	0

Fig. 2. Virulence frequencies of *P. hordei* isolates for 15 *Rph* genes across five geographical regions of the United States in the 1989–2000 and 2010–2020 survey periods.

- In the 1989–2000 survey period, MW had lower virulence frequency for *Rph2.b* and *Rph13.x* compared to other regions. Virulence to *Rph10.o* was also higher in MW and NE compared to the rest of the country (Fig. 2).
- In the 2010–2020 survey period, SW, NE, and SE had higher virulence for *Rph3.c* than PW and MW. In contrast, virulence for *Rph5.e* and *Rph5.f* was higher in PW and MW than SW, NE, and SE.
- Virulence for *Rph7.g* was higher in MW, NE, and SE, while *Rph9.i* and *Rph9.z* virulence was higher in SW, NE, and SE, and *Rph14.ab* virulence was higher in all regions except SW.

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Table 1. Virulence frequencies of *P. hordei* isolates collected from the 1989–2000 and 2010–2020 survey periods.

Resistance Allele	1989–2000 Survey Period (n= 256)							2010–2020 Survey Period (n= 444)						
	# vir	% vir	# int	% int	# avr	% avr	Ave linearized IT	# vir	% vir	# int	% int	# avr	% avr	Ave linearized IT
<i>Rph1.a</i>	248	96.9	4	1.6	4	1.6	7.8	375	85.8	61	14.0	1	0.2	7.8
<i>Rph2.b</i>	156	60.9	94	36.7	6	2.3	6.3	269	61.7	158	36	9	2.1	7.0
<i>Rph3.c</i>	1	0.4	0	0	255	99.6	1	147	34.1	49	11.4	235	54.5	3.7
<i>Rph4.d</i>	248	96.9	5	2	3	1.2	7.3	300	71.1	112	26.5	10	2.4	7
<i>Rph5.e</i>	2	0.8	24	9.4	230	89.8	1.7	57	13.7	22	5.3	337	81.0	2
<i>Rph5.f</i>	14	5.5	81	31.8	160	62.7	2.8	60	14.9	24	6.0	319	79.2	2.2
<i>Rph7.g</i>	53	20.7	1	0.4	202	78.9	2.4	98	22.5	48	11.0	290	66.5	2.9
<i>Rph8.h</i>	236	92.2	20	7.8	0	0	7.2	281	64.9	145	33.5	7	1.6	7
<i>Rph9.i</i>	0	0	202	78.9	54	21.1	4.2	77	17.6	229	52.4	131	30.0	4.5
<i>Rph10.o</i>	78	30.5	178	69.5	0	0	5.9	88	20.4	218	50.6	125	29.0	4.7
<i>Rph11.p</i>	167	65.2	89	34.8	0	0	6.6	129	33.2	239	61.4	21	5.4	6.1
<i>Rph9.z</i>	0	0	24	9.4	232	90.6	1.5	39	10.5	102	27.3	232	62.2	3.2
<i>Rph13.x</i>	158	61.7	69	27	29	11.3	6.1	194	44.3	166	37.9	78	17.8	5.8
<i>Rph14.ab</i>	4	1.6	192	75	60	23.4	3.9	59	13.5	190	43.5	188	43.0	3.9
<i>Rph15.ad</i>	0	0	0	0	256	100	1	0	0	3	0.7	435	99.3	1
Average	91	35.6	66	25.6	99	38.8	4.4	145	33.9	118	27.8	161	38.3	4.6

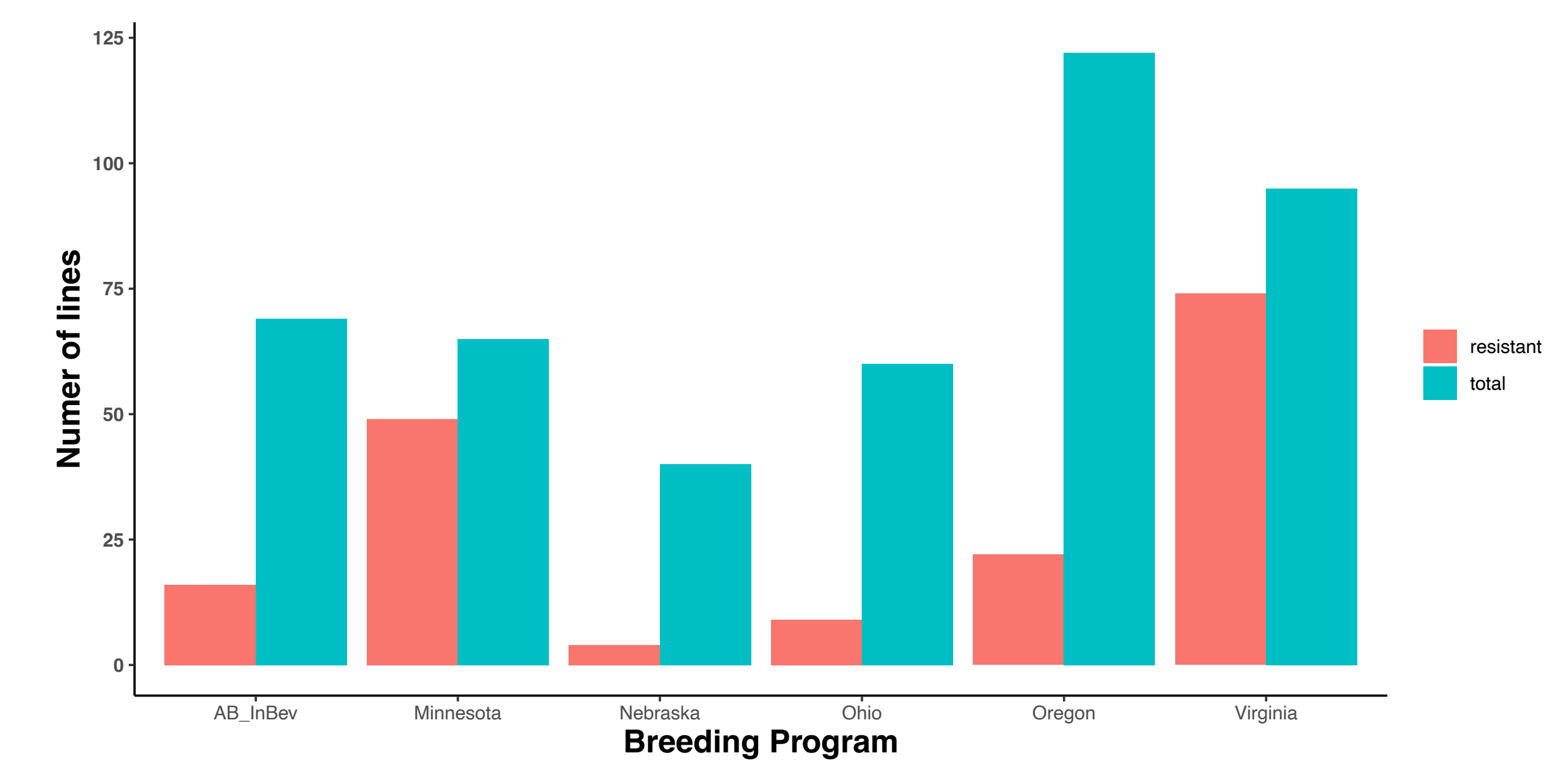


Fig. 3. Number of barley leaf rust resistant lines from germplasm samples received from different US barley breeding programs.

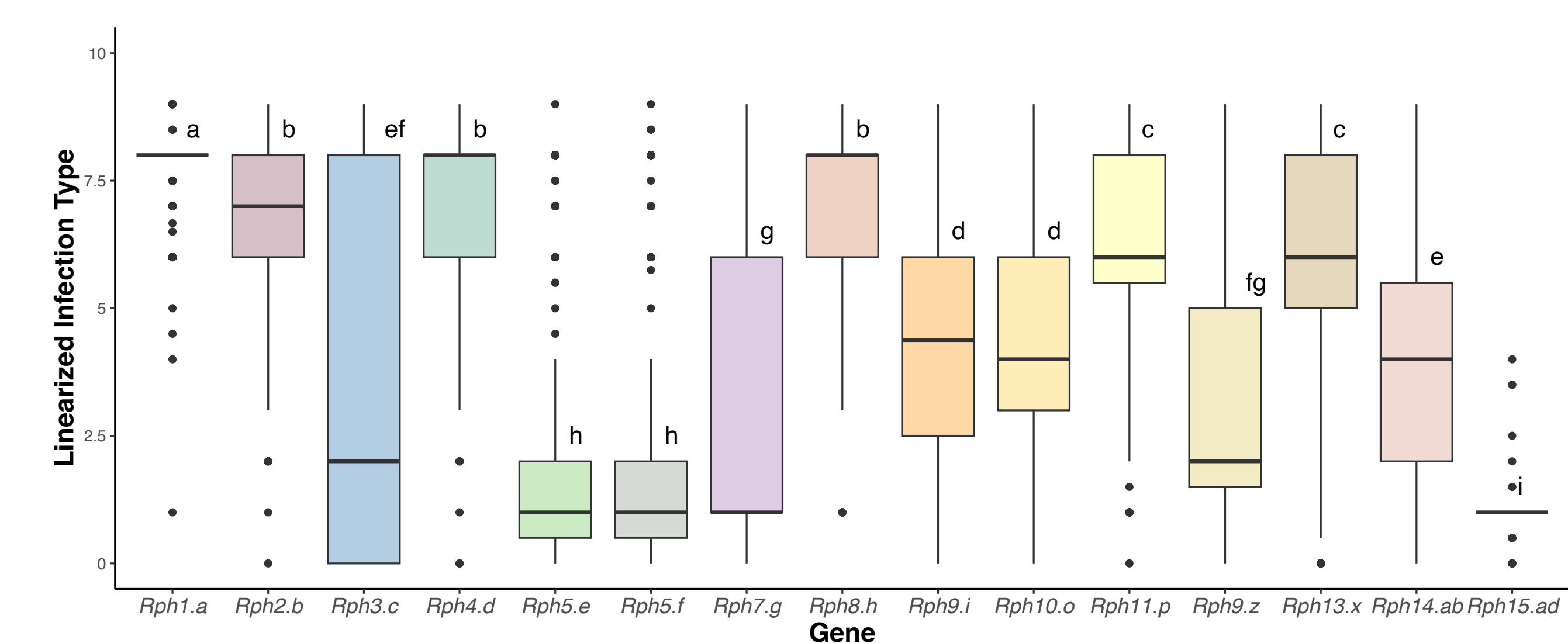


Fig. 4. Linearized infection type data of *Puccinia hordei* isolates from the 2010–2020 survey period on 15 *Rph* genes in the barley leaf rust differential set.

- Resistance to leaf rust is not common in U.S. barley breeding germplasm (Fig. 3.). Currently, the most effective resistance genes against leaf rust in the United States are *Rph15.ad*, *Rph5.e*, *Rph5.f*, *Rph7.g*, *Rph9.z*, *Rph9.i*, *Rph14.ab*, and *Rph3.c* (Fig. 4). The introgression of one or more of these genes together with adult plant resistance should result in the successful control of leaf rust in deployed cultivars.