## Fargo sugar beet germplasm evaluated for Rhizoctonia crown and root rot resistance in Idaho, 2022.

Forty sugar beet (*Beta vulgaris* L.) lines from the USDA-ARS Fargo sugar beet program and two check cultivars were screened for resistance to *Rhizoctonia solani*. The Rhizoctonia crown and root rot evaluation was conducted at the USDA-ARS North Farm in Kimberly, ID which has Portneuf silt loam soil and had been in barley in 2021. In the spring the field was plowed and fertilized (110 lb N and 160 lb  $P_2O_5/A$ ) and roller harrowed on 6 Apr. The germplasm was planted at the density of 114,048 seeds/A on 3 May. The plots were one row 10-ft long with 22-in. between-row spacing and arranged in a randomized complete block design with 6 replicates. The crop was managed according to standard cultural practices for southern Idaho. The trial was inoculated with dried barley inoculum (0.02 oz of inoculum/plant of with strain F521 = *R. solani* AG2-2 IIIB) at the 10-leaf growth stage on 30 Jun. The plots were lifted with a single row lifter and rated for rhizoctonia root rot development (percentage of root surface area covered by root rot) on 2 Aug. The percentage root data were analyzed in SAS (Ver. 9.4) using the general linear model (Proc GLM) procedure, and Fisher's protected least significant difference ( $\alpha = 0.05$ ) was used for mean comparisons. The categorical root data were rank transformed prior to analysis with mixed linear models (Proc MIXED) and mean separation was based on PDIFF ( $\alpha = 0.05$ ). For transformed data, the non-transformed means have been presented in the table.

Rhizoctonia symptom development was uniform and other disease problems were not evident in the plot area. Entry 38 had 97% of its root area covered in rot and none of the roots were considered harvestable. Thus, the potential for root disease in the nursery was considerable. The rhizoctonia susceptible check had 76% of its root area covered in rot and 5% of its roots were harvestable. In contrast, the resistant check had only 30% rot and 64% of its roots were harvestable. Entries 14 and 18 had a level of rhizoctonia resistance similar to the resistant check based on root rot, disease index, and harvestable roots. Entries 14 and 18 should be evaluated again since they may serve as a starting point for identifying additional sources of resistance to *R. solani*. Rhizoctonia resistance in sugar beet is considered a multi-gene trait and thus some of the other lines that performed well may contain a smaller complement of resistance genes.

			Disease	Healthy	Harvestable	Root rot
Entry <sup>z</sup>	Line	Description	index (0-7) <sup>y</sup>	(% in 0-1)	(% in 0-3)	(%)
14	17N0043-12	Line R376-43 crossed with a Beta maritima	3.0 j	8 ab	70 a	24 p
R3	B-80	resistant sugar beet check	3.3 j	10 ab	64 a	30 op
18	17N0043-16	Line R376-43 crossed with a Beta maritima	3.9 ij	2 bc	40 ab	39 no
4	10N0034	Multi-parent population crossed with Y577	4.0 ij	8 ab	41 a	43 mn
6	15N0057	Line R376-43 crossed with a Beta maritima	4.3 h-j	13 a	31 a-d	54 lm
13	17N0043-10	Line R376-43 crossed with a Beta maritima	4.9 g-j	3 bc	32 a-c	62 kl
21	F1033	Sugar beet crossed with Beta maritima	4.8 g-j	2 bc	21 c-g	63 kl
23	F1035	Sugar beet crossed with <i>Beta maritima</i>	5.1 f-i	2 bc	24 b-e	64 j-l
25	F1037	Sugar beet crossed with <i>Beta maritima</i>	5.1 f-i	2 bc	19 c-h	67 i-k
16	17N0043-11	Line R376-43 crossed with a <i>Beta maritima</i>	5.0 f-i	5 bc	15 e-i	68 h-k
15	17N0043-13	Line R376-43 crossed with a Beta maritima	5.4 f-h	6 bc	17 e-i	69 h-k
17	17N0043-14	Line R376-43 crossed with a <i>Beta maritima</i>	5.1 f-h	3 bc	20 c-h	70 g-k
31	F1045	Sugar beet crossed with <i>Beta maritima</i>	5.4 f-h	2 bc	21 c-h	70 g-k
37	F1051	Sugar beet crossed with <i>Beta maritima</i>	5.3 f-h	0 c	13 f-i	70 g-k
35	F1049	Sugar beet crossed with <i>Beta maritima</i>	5.1 f-h	3 b	15 f-i	71 g-k
8	16N0029-01	Line R376-43 crossed with a <i>Beta maritima</i>	5.4 e-g	6 b	22. c-9	72 f-k
27	F1039	Sugar beet crossed with <i>Beta maritima</i>	5.3 e-g	3 b	17 e-i	72 f-k
36	F1050	Sugar beet crossed with <i>Beta maritima</i>	5.4 e-g	0 c	14 f-i	73 e-k
1	10N0031	F1024/Y577 Y577 a cross with <i>B</i> maritima	5.4 e-g	5 b	10 f-i	73 e-k
R2	Crystal 539R	susceptible sugar beet check	5.6 d-f	0 c	5 ii	76 d-i
11	17N0043-07	Line R376-43 crossed with a <i>Beta maritima</i>	5.4 c-f	12 ab	24 h-f	77 d-i
5	13N0018	Selection from multi-parent population	5.8 c-e	0 c	13 f-i	78 c-i
32	F1046	Sugar beet crossed with <i>Beta maritima</i>	5.5 c-e	4 bc	12 f-i	79 c-i
22	F1034	Sugar beet crossed with <i>Beta maritima</i>	5.7 с-е	0 c	8 f-i	79 c-i
9	16N0029-19	Line R376-43 crossed with a <i>Beta maritima</i>	5.7 с-е	0 c	8 f-i	80 c-h
28	F1040	Sugar beet crossed with <i>Beta maritima</i>	5.8 c-e	0 c	6 ii	80 c-h
3	10N0033	Two selections from multi-parent population	5.9 с-е	2 bc	7 f-i	82 c-g
10	17N0043-04	Line R376-43 crossed with a <i>Beta maritima</i>	5.6 c-e	0 c	5 ii	82 c-g
39	F1053	Sugar beet crossed with <i>Beta maritima</i>	5.9 с-е	0 c	4 ii	82 c-g
7	15N0059	Line R376-43 crossed with a <i>Beta maritima</i>	5.9 с-е	0 c	4 ii	84 b-f
12	17N0043-08	Line R376-43 crossed with a Beta maritima	5.8 c-e	2 bc	18 e-i	84 b-f
2	10N0032	Two selections from multi-parent population	5.7 с-е	0 c	11 f-i	84 b-f
20	17N0043-18	Line R376-43 crossed with a <i>Beta maritima</i>	6.0 cd	2 bc	3 ii	85 a-e
26	F1038	Sugar beet crossed with <i>Beta maritima</i>	6.0 cd	8 ab	8 h-i	85 a-e
24	F1036	Sugar beet crossed with <i>Beta maritima</i>	6.0 cd	0 c	10 f-j	86 a-d
19	17N0043-17	Line R376-43 crossed with a <i>Beta maritima</i>	6.1 cd	0 c	5 ij	86 a-d
30	F1044	Sugar beet crossed with Beta maritima	6.0 cd	2 bc	6 ij	87 a-d
33	F1047	Sugar beet crossed with <i>Beta maritima</i>	6.0 bc	0 c	5 ij	87 a-d
29	F1041	Sugar beet crossed with <i>Beta maritima</i>	6.1 a-c	0 c	6 ij	90 a-c
34	F1048	Sugar beet crossed with <i>Beta maritima</i>	6.0 a-c	0 c	0 j	90 a-c
40	F1054	Sugar beet crossed with <i>Beta maritima</i>	6.6 ab	0 c	0 j	95 ab
38	F1052	Sugar beet crossed with <i>Beta maritima</i>	6.7 a	0 c	0 i	97 a
$P > F^{x}$			< 0.0001	< 0.0001	<0.0001	< 0.0001
LSD			Trans	Trans	Trans	13

<sup>z</sup>All lines were *Beta vulgaris* subsp. *vulgaris*. Two commercial cultivars (R2 and R3) were included as checks.

<sup>y</sup>Root rot = the percent of root surface area covered by fungal growth or rot was determined on 10 roots per plot. Percentage root rot was also converted to a categorical scale of 0-7 (0 = healthy and 7 = dead) as suggested by Ruppel et al. (Plant Dis. Reptr. 63:518-522). The percentage of healthy (0-1 categories) and harvestable (0-3 categories) roots were determined as well.

 ${}^{x}P > F$  was the probability associated with the F value. The percentage of root area data were analyzed in SAS (Ver. 9.4) using the general linear model (Proc GLM) procedure, and Fisher's protected least significant difference (LSD;  $\alpha = 0.05$ ) was used for mean comparisons. The categorical root ratings were rank transformed (Trans) prior to analysis with mixed linear models (Proc MIXED) and mean separation was based on PDIFF ( $\alpha = 0.05$ ). For transformed data, the non-transformed means have been presented in the table.