BEET (*Beta vulgaris* L.)
Rhizomania; *Beet necrotic yellow vein virus*

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USDA-ARS sugar beet germplasm developed in Salinas, CA, evaluated for rhizomania resistance in Idaho, 2005.

Thirty-one sugar beet germplasm breeding lines and releases produced by the USDA-ARS sugarbeet program at Salinas, CA, and one line from the USDA-ARS sugarbeet program at East Lansing, MI, were evaluated for resistance to rhizomania under south-central Idaho conditions at Twin Falls, ID. The field had been identified as having *Beet necrotic yellow vein virus* (BNYVV), which overcomes resistance conditioned by the *Rz1* gene. Single-row plots 10 ft long with 22-in. spacing were planted on 23 May 05. Plants were thinned to 4 to 6-in. spacing in mid-Jun. The materials were predominantly multigerm; they were hand thinned to single plants during the first week of Jul. The trial layout was a randomized complete block with eight replicates, however, the blocks were divided into 16 sub-blocks of six rows in which single-row plots of two entries and four control lines were randomized. The control lines were Beta4430R (*Rz1* gene), GO17R (*Rz2* gene), Angelina (*Rz1+Rz2* genes) and Beta6600 (no resistance to rhizomania). This allowed each entry plot to have its own control (Local Control). This was necessary given the uneven distribution in the field of resistance breaking strains of BNYVV. Naturally occurring *Curly top virus* infection was found throughout the field early in the season. Many plants of the rhizomania susceptible control were killed apparently by curly top and therefore this should be considered when evaluating the results. Plants were scored 19 Sep for curly top using a 0-9 scale with 0 showing no symptoms and 9 being dead. Plants were topped, roots lifted then scored on 12-13 Oct. Four teams evaluated the trial for rhizomania with each team rating two replicates. Each root was scored based on the traditional 0 to 6 scale which was converted to a 0 to 9 scale. The categories were 0, 1, 3, 5, 6, 7 and 9 with 0-3 being resistant, 5-7 susceptible and 9 was dead. The average disease severity was determined to create a disease index (DI) for each entry and control. A second index (DI2) was calculated for each entry-plot to evaluate the entry relative to the mean of the *Rz2* and *Rz1+Rz2* Local Controls (DI of entry/mean DI of the *Rz2* and *Rz1+Rz2* Local Controls). The percent healthy roots (categories 0-3 combined) and the percent of healthy roots relative to *Rz2* and *Rz1+Rz2* Local Controls were calculated (PR and PR2, respectively). The DI and DI2 were transformed with the inverse square-root and analyzed using PROC MIXED - SAS with Dunnett's test ($P = 0.05$) option and PROC GLM – SAS with Fisher's protected LSD test ($P = 0.05$) option, respectively. PR and PR2 were analyzed with PROC GLM –SAS using Dunnett's test ($P = 0.05$) and Fisher's protected LSD ($P = 0.05$) test, respectively. The analysis of variance of DI2 showed that block effects were significant, therefore Spearman's partial correlation (PROC CORR Spearman partial - SAS) was used to analyze the relationship of D1, PR, DI2, PR2, and curly top. PROC CORR Spearman -SAS was used to analyze the relationship between DI and DI2.

Differences among the entries and the controls for DI were significant ($P<0.0001$) and differences among the entries for DI2 were significant ($P<0.0001$). Separation of means using LSD ($P = 0.05$) for DI2 (Table 1) showed that there were significant differences among the entries and given that the resistant control value was 100, none of the entries were better than the mean of the *Rz2* resistant controls. Dunnett's test to compare the entries to the three different controls (Table 1) for DI2 indicated that both the *Rz2* and *Rz1+Rz2* controls were significantly better than the Rz1 control, thus indicating that the virus in this field does partially defeat Rz1. The average actual DI score for *Rz*1 gene (Beta4430R), *Rz*2 gene (GO17R), *Rz1+Rz2* genes (Angelina) and no resistance to rhizomania (Beta6600) controls were 31.1, 24.0, 24.4 and 60.2, respectively. The actual PR scores were 50.9, 78.0, 77.0 and 50.9 for these controls, respectively. The percent resistant beets were negatively correlated with disease index (DI2 and PR2 $r_s = -0.903$, $P<0.0001$ and DI and PR $r_s = -0.972$, $P<0.001$), which was expected. Interestingly, while there was a significant moderate positive correlation between curly top rating and DI ($r_s = 0.508$, $P<0.0001$) there was no significant correlation between the curly top rating and DI2 ($r_s = 0.169$, $p = 0.060$). The ranking of the entries based on DI or DI2 was correlated ($r_s = 0.910$, $P<0.0001$) and the same top four entries would have been selected using either method of scoring. However, using Local Controls did change the ranking for a few entries. The largest rank shift was entry 126 which moved (not counting controls) down from 9 (DI) to 22 (DI2). Conversely line 115 moved from 18 (DI) to 11 (DI2) when the index was used to account for local variation.

Entry information	Entry code	Curly top[z]	BtDI [y]	TrDI[x]	Controls			DI2[v]	
					Rz1 [w]	*Rz2*	*Rz1* + *Rz2*		
4921.....	130	3.6	22.70	0.2099	*	ns	ns	0.1005	a-c
GO17R (*Rz2*).....	1	4.1	23.50	0.2063	**	control	ns	n.a.	
P429 (CP04).....	123	3.9	23.59	0.2059	*	ns	ns	0.0996	a-d
Angelina (*Rz1*+*Rz2*).....	2	4.3	23.82	0.2049	**	ns	control	n.a.	
4842-ISO (C842).....	132	4.4	24.19	0.2033	*	ns	ns	0.1022	a
P431CT (CP09).....	122	4.1	25.38	0.1985	ns	ns	ns	0.1006	ab
R340(C79-C).....	111	3.9	25.59	0.1977	ns	ns	ns	0.0943	b-g
R926 (C26).....	117	4.4	26.65	0.1937	ns	ns	ns	0.0917	e-i
R927 (C27).....	118	5.0	27.18	0.1918	ns	ns	ns	0.0947	a-f
Y371 (C72).....	116	4.1	27.35	0.1912	ns	ns	ns	0.0956	a-e
P407/8 (CP07).....	126	4.4	28.11	0.1886	ns	ns	ns	0.0873	f-j
R378(Sp) (C78/3).....	101	4.4	28.17	0.1884	ns	ns	ns	0.0926	d-h
R421.....	119	5.3	28.29	0.188	ns	ns	ns	0.0915	e-j
R424/5 (C79-2/3).....	112	4.5	28.35	0.1878	ns	ns	ns	0.0897	e-j
Y393.....	107	4.5	28.51	0.1873	ns	ns	ns	0.0928	c-h
P430 (CP06).....	124	4.5	28.51	0.1873	ns	ns	ns	0.0942	b-g
R336 (C79-8).....	110	4.0	28.78	0.1864	ns	*	ns	0.0905	e-j
Y369(C69/2).....	102	5.9	28.81	0.1863	ns	*	ns	0.0892	e-j
Y390.....	103	4.8	28.97	0.1858	ns	*	ns	0.0898	e-j
R437 (C79-9).....	115	3.9	29.35	0.1846	ns	*	*	0.0919	d-i
4931 (C931).....	127	5.5	29.57	0.1839	ns	*	*	0.0904	e-j
Beta4430R (*Rz1*).....	3	4.7	30.02	0.1825	control	**	**	n.a.	
Y477.....	121	4.6	30.19	0.182	ns	*	*	0.0893	e-j
R039 (C39R).....	104	4.9	30.46	0.1812	ns	*	*	0.0883	e-j
N412iso (CN12).....	128	4.6	30.76	0.1803	ns	*	*	0.0867	g-k
R425 (C79-3).....	114	4.6	32.10	0.1765	ns	**	*	0.0846	i-k
R424 (C79-2).....	113	3.6	32.43	0.1756	ns	**	**	0.0866	g-k
Y492.....	106	4.4	32.73	0.1748	ns	**	**	0.0857	h-k
Y391.....	105	4.8	33.22	0.1735	ns	**	**	0.0893	e-j
P418-6 (CP08).....	125	4.0	33.26	0.1734	ns	**	**	0.0848	i-k
Y367 (C67).....	108	5.3	33.37	0.1731	ns	**	**	0.0838	jk
N472iso (CN72).....	129	4.6	33.49	0.1728	ns	**	**	0.0859	h-k
Y475.....	120	3.5	34.77	0.1696	ns	**	**	0.0794	kl
04-C37.....	109	5.5	42.22	0.1539	*	**	**	0.0759	l
Beta6600 (Sus. Check).	4	6.7	56.53	0.133	**	**	**	n.a.	
SP7322-0.....	131	6.3	62.20	0.1268	**	**	**	0.0638	m

[z] Mean curly top rating using scale from 0 = healthy to 9 = dead plant.

[y] BrDI is the back-transformed TrDI value.

[x] TrDI is the disease index value transformed using the inverse square-root and estimated using PROC MIXED - SAS .

[w] Comparison of DI for entries to a control using Dunnett's test, NS = non-significant, * = significance ($P \leq 0.05$), ** = significance ($P \leq 0.0001$).

[v] DI2 = (disease index entry /disease index Local Control). Means within the same columns followed by the same letter(s) are not significantly different (P=0.05) as determined by Fisher's protected LSD.