

Mungbean trial 2024 Minnesota

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Visual assessments

Visual plot assessments were taken on July 16 2024 by Jesse.

Of the 409 entries/plots, 387 were scored (the remaining were missed due to a navigation error during scoring the trial).

Of the 387 plots scores, 349 were genotypes/breeding lines and the remainder were the two check varieties (Albert Lea and OK2000)

Table 1: Visual assessment observation counts

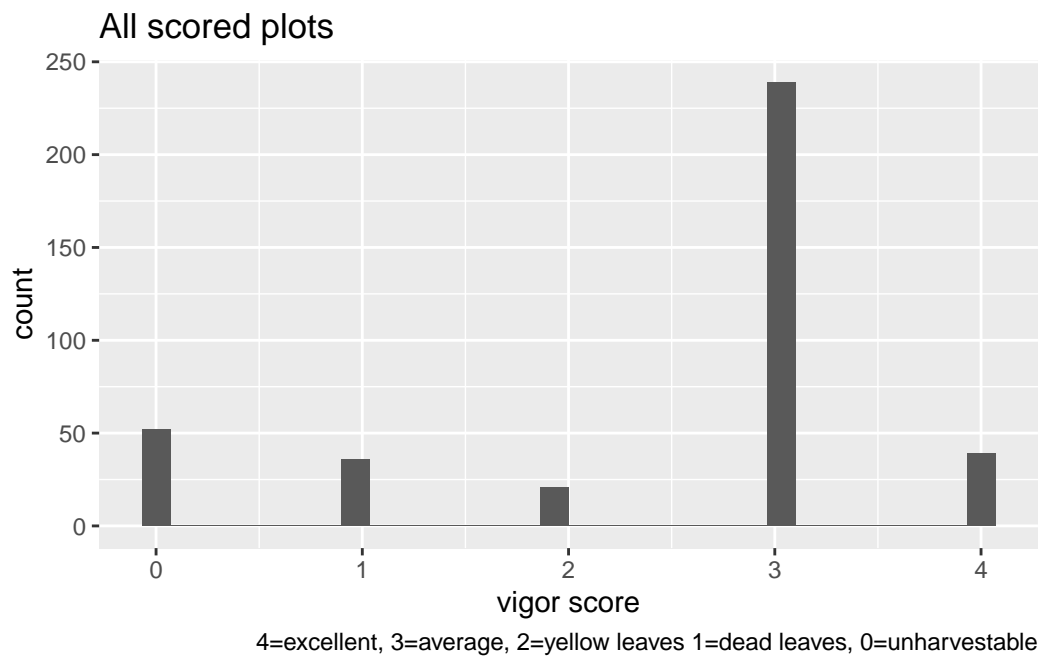
type	n
Albert Lea	19
OK2000	19
Breeding lines	349

Each line only had one rep, but two check varieties were diagonally replicated throughout the trial.

Of the 387 scored plots

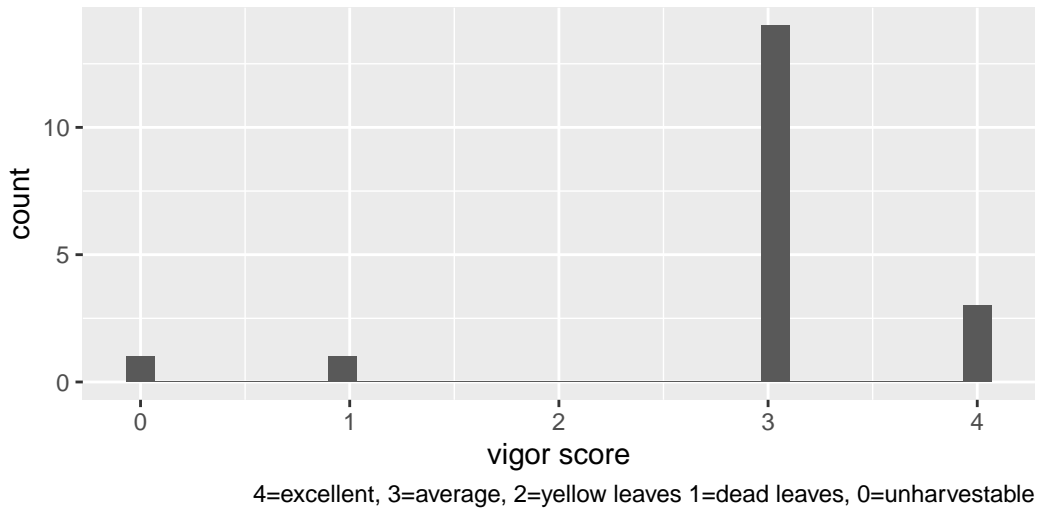
- 33 were notable for exceptionally good vigor.
- 21 genotypes had notable yellow leaves
- 35 had notably dead leaves
- 47 were deemed unharvestable due to poor population and stature.
- 63% of plots had sufficient population for a whole plot combine harvest and many were likely adjacent to a plot with insufficient population, resulting in border effect which would overestimate yield potential

Vigor scores

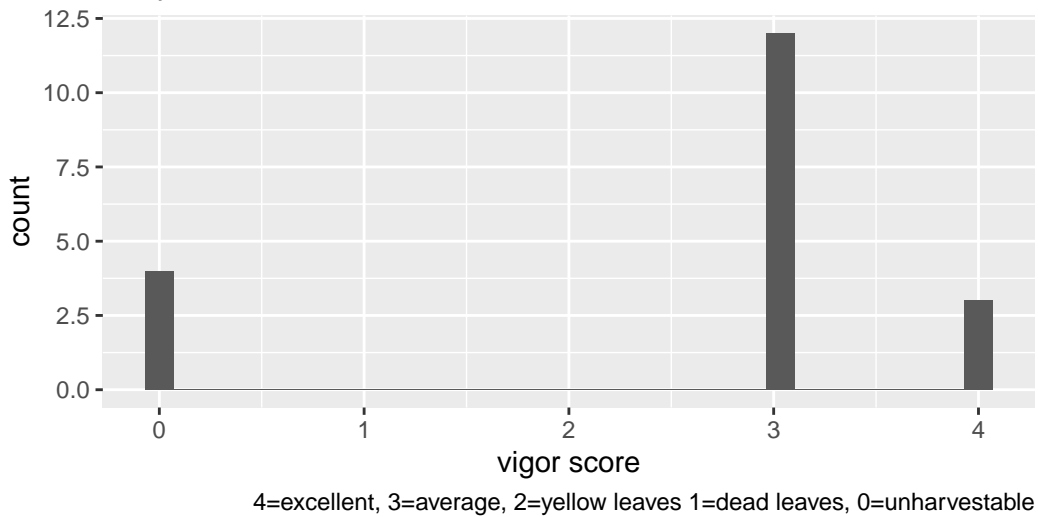


- 239 of the 387 scored plots, or 62% were scored as average vigor.

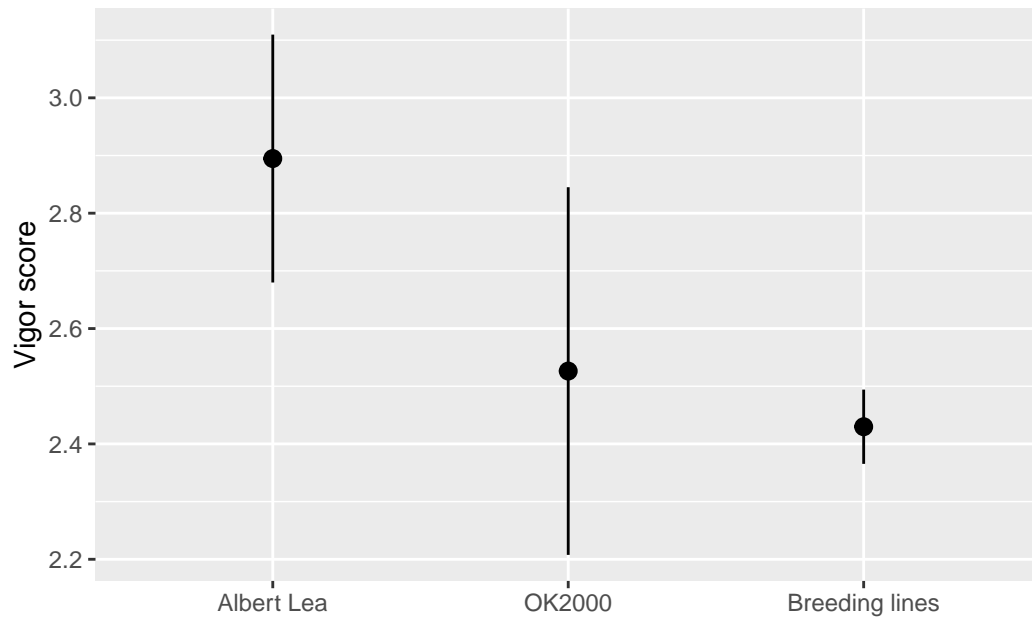
Only a commercial variety from Albert Lea Seeds



Only OK2000



- check plots were the only germplasm with replication throughout the trial. We expect their vigor to be similar and average around 3, but some plots were scored as unharvestable and others scored as exceptionally good vigor
- This could be due to true variation or data collection/entry error.



- On average, the two check varieties averaged better vigor than the breeding lines

Table 2: genotypes with exceptionally good vigor, scoring a vigor score of 4 on 16Jul2024

rowid	genotype	PLOT
1	PI 425586	5
2	PI 363341	8
3	PI 363514	38
4	PI 364225	39
5	PI 425503	111
6	PI 385297	130
7	PI 363678	131
8	PI 363699	132
9	PI 364123	185
10	PI 377304	207
11	PI 425842	222
12	PI 364205	227
13	PI 425085	255
14	PI 377259	263
15	PI 363358	273
16	PI 363974	274
17	PI 425425	275
18	PI 425822	276
19	PI 425481	283
20	PI 183458	284
21	PI 425840	296
22	PI 368332	304
23	PI 363988	320
24	PI 377039	330
25	PI 425811	333
26	PI 425219	334
27	PI 425582	335
28	PI 363222	350
29	PI 425456	357
30	PI 425136	373
31	PI 425580	380
32	PI 425587	387
33	PI 425533	397

The average vigor score was 2.46.

Table 3: lines with yellow leaves, scoring a vigor score of 2 on 16Jul2024

rowid	genotype	PLOT
1	PI 363565	23
2	PI 377239	31
3	PI 425487	37
4	PI 377296	49
5	PI 425388	51
6	PI 377208	60
7	PI 425862	86
8	PI 363485	113
9	PI 363823	148
10	PI 377256	165
11	PI 377202	239
12	PI 362327	244
13	PI 425552	250
14	PI 426058	262
15	PI 425577	286
16	PI 427024	345
17	PI 377342	359
18	PI 425554	391
19	PI 377207	395
20	PI 377268	404
21	PI 425240	405

Table 4: genotypes with dying leaves, scoring a vigor score of 1 on 16Jul2024

rowid	genotype	PLOT
1	PI 425575	82
2	PI 363779	92
3	PI 377283	95
4	PI 426042	102
5	PI 164726	104
6	PI 425399	114
7	PI 363591	117
8	PI 364230	149
9	PI 363645	170
10	PI 264686	183
11	PI 425435	237
12	PI 425592	256
13	PI 426029	257
14	PI 425418	258
15	PI 369795	259
16	PI 425264	271
17	PI 425766	280
18	PI 363592	281
19	PI 362307	302
20	PI 363271	303
21	PI 377313	310
22	PI 377223	315
23	PI 425261	326
24	PI 377349	331
25	PI 425507	332
26	PI 364214	344
27	PI 426118	349
28	PI 425483	351
29	PI 364049	353
30	PI 377338	354
31	PI 425557	358
32	PI 377312	369
33	PI 363419	378
34	PI 425546	379
35	PI 368305	402

Table 5: genotypes deemed unharvestable, scoring a vigor score of 0 on 16Jul2024. This could be due to insufficient population in the stand

rowid	genotype	PLOT
1	PI 363778	2
2	PI 376989	3
3	PI 364028	33
4	PI 377242	41
5	PI 376850	43
6	PI 425259	56
7	PI 368285	58
8	PI 377288	72
9	PI 364047	78
10	PI 377022	83
11	PI 363147	99
12	PI 376951	100
13	PI 425816	115
14	PI 363517	152
15	PI 425610	155
16	PI 363475	156
17	PI 377147	157
18	PI 425512	166
19	PI 426109	175
20	PI 425594	187
21	PI 425229	189
22	PI 164770	214
23	PI 377258	215
24	PI 363362	220
25	PI 426026	221
26	PI 363153	231
27	PI 363333	242
28	PI 368329	243
29	PI 363657	253
30	PI 425771	270
31	PI 363152	277
32	PI 425583	278
33	PI 363346	289
34	PI 363360	293
35	PI 363668	295
36	PI 364167	297
37	PI 425770	301
38	PI 377354	309

rowid	genotype	PLOT
39	PI 425509	311
40	PI 363615	312
41	PI 377275	317
42	PI 377272	347
43	PI 363359	362
44	PI 377138	363
45	PI 368302	366
46	PI 363301	368
47	PI 346315	370

Population scores

One of the key assumptions of the trial design we selected was they each plot or entry (2 ft x 10 ft) would have 2 rows of mungbeans at a sufficient population to form a canopied row. If this occurs, then all plots experience the same row spacing and can be combine harvested without any border effect from alleys.

Unfortunately, many plots did not score a “2” during the July visual assessment, meaning they did not have 2 rows with sufficient population. At this point, you cannot take a combine harvest of the plot because the seed yield of that plot will not represent the yield potential of the genotype but rather the effect of insufficient population on yield.

When there is insufficient population, this also impacts adjacent plots. If a genotype is next to a plot that has a lower population, it will experience less competition and perform better. So many plots that scored a “2” were also compromised because they were adjacent to plots that were not a “2”. I now realize this is another advantage of border or quadrat harvests within plots because it shelters the plot from the effects of the adjacent plot.

Overall, *we expected like 95% of plots scoring a “2”, in reality, this was 63%*

Table 6: population scores where a 2 is a sufficient population

rowcode	n	percent of total (%)
0	61	16
1	82	21
2	244	63

- 244 of the 387 scored plots, or 63% had sufficient population for a combine harvest
- Many of these plots likely also experienced border effect from adjacent plots with insufficient population

Table 7: population scores of the n=19 Check 1 (Albert Lea)

rowcode	n	percent of total (%)
0	1	5
1	4	21
2	14	74

Table 8: population scores of the n=19 Check 2 (OK2000)

rowcode	n	percent of total (%)
0	4	21
1	2	11
2	13	68

- There was no obvious difference between check varieties (which we'd expect to have a sufficient population to form a canopied row) and the breeding lines. Insufficient population seems to be randomly distributed throughout the trial, possibly due to in-field variability, planter performance, how we planted the trial or a data entry error when taking these visual scores