Use of Heritability Adjusted Relative Values (HARV) in Variety Trial Summary

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The current method

1. Relative Value at each site
   - A way to remove the environment main effect, which is not pertinent to variety evaluation

2. A CV% bar
   - Useful to treat good and bad tests differently

However, some improvements are needed…

Sample Data with hypothesized heritability

Relative yield Genotypes	ON1	ON2	ON3	ON4	NB	PEI	QC1	QC2	QC3
1028-32	91	73	106	105	97	91	101	102	127
1029-23	83	78	91	112	104	95	102	99	105
1042-8	84	97	99	103	90	95	92	95	89
1045-23	101	92	109	90	112	104	112	98	86
1058-4	107	85	106	77	98	107	105	114	114
1063-8	87	101	95	84	116	113	106	112	137
1069-11	65	97	97	111	101	100	96	96	126
1069-7	82	83	110	111	91	93	95	97	120
1069-9	82	75	106	92	106	95	96	93	122
1077-2	111	95	98	109	93	91	89	94	105
1079-1	123	127	113	96	107	98	97	88	117
1081-6	89	90	95	92	101	94	96	85	109
1127-5	93	105	105	90	117	87	108	105	118
1130-1	90	80	80	106	104	107	115	122	81
1139-1	101	81	97	93	97	109	114	104	117
1141-1	98	110	101	105	88	93	97	98	80
1143-1	103	115	101	97	94	96	96	97	98
1149-1	118	109	107	115	102	104	106	106	95
1158-1	104	120	100	97	99	95	98	94	78
1168-3	118	143	110	115	86	103	99	102	49
1169-4	102	130	103	116	94	102	86	95	102
1174-3	118	133	111	99	103	98	94	96	94
1175-11	127	158	107	110	104	97	95	95	60
1175-3	116	107	101	97	107	108	101	103	101
1175-4	117	118	97	95	101	100	89	90	96
1176-12	117	108	98	91	92	87	82	95	71
1179-3	91	85	90	90	94	96	82	86	80
Real values									
Reps	4	4	4	4	3	3	3	3	3
Mean	4719	2289	4507	4303	2713	3395	5963	6425	4055
SD	730	484	334	441	216	232	525	544	877
Hypothetical values									
CV = SE/Mean	3.1	18.9	9.4	15.9	12.3	11.2	14.5	1.5	35.5
SE	146	433	422	684	335	381	863	94	1442
Heritability	0.99	0.80	0.60	0.40	0.20	0.10	0.10	0.99	0.10
SD	723	388	200	177	43	23	53	539	88

Results using existing method

- Exclude high CV (>15%) trials
  - Why 15%?
- Treat other trials equally reliable

Genotypes	Relative yield ON1	ON3	NB	PEI	QC1	QC2	Mean
1028-32	91	106	97	91	101	102	98
1029-23	83	91	104	95	102	99	95
1042-8	84	99	90	95	92	95	93
1045-23	101	109	112	104	112	98	106
1058-4	107	106	98	107	105	114	106
1063-8	87	95	116	113	106	112	105
1069-11	65	97	101	100	96	96	92
1069-7	82	110	91	93	95	97	95
1069-9	82	106	106	95	96	93	96
1077-2	111	98	93	91	89	94	96
1079-1	123	113	107	98	97	88	104
1081-6	89	95	101	94	96	85	93
1127-5	93	105	117	87	108	105	103
1130-1	90	80	104	107	115	122	103
1139-1	101	97	97	109	114	104	104
1141-1	98	101	88	93	97	98	96
1143-1	103	101	94	96	96	97	98
1149-1	118	107	102	104	106	106	107
1158-1	104	100	99	95	98	94	98
1168-3	118	110	86	103	99	102	103
1169-4	102	103	94	102	86	95	97
1174-3	118	111	103	98	94	96	103
1175-11	127	107	104	97	95	95	104
1175-3	116	101	107	108	101	103	106
1175-4	117	97	101	100	89	90	99
1176-12	117	98	92	87	82	95	95
1179-3	91	90	94	96	82	86	90

Results using HARV

- No trial is excluded
- Trials are weighted by their heritability (H)

Genotypes	Heritability adjusted relative yield									Mean
	ON1	ON2	ON3	ON4	NB	PEI	QC1	QC2	QC3	
1028-32	92	78	104	102	99	99	100	102	103	98
1029-23	83	83	94	105	101	99	100	99	101	96
1042-8	84	97	99	101	98	100	99	95	99	97
1045-23	101	93	105	96	102	100	101	98	99	100
1058-4	107	88	104	91	100	101	100	113	101	101
1063-8	87	101	97	94	103	101	101	111	104	100
1069-11	65	98	98	104	100	100	100	96	103	96
1069-7	83	87	106	104	98	99	100	97	102	97
1069-9	82	80	104	97	101	100	100	93	102	95
1077-2	111	96	99	104	99	99	99	94	100	100
1079-1	123	121	108	98	101	100	100	88	102	105
1081-6	89	92	97	97	100	99	100	85	101	95
1127-5	93	104	103	96	103	99	101	105	102	101
1130-1	91	84	88	102	101	101	101	122	98	99
1139-1	101	84	98	97	99	101	101	104	102	99
1141-1	98	108	100	102	98	99	100	98	98	100
1143-1	103	112	100	99	99	100	100	97	100	101
1149-1	118	107	104	106	100	100	101	106	99	105
1158-1	104	116	100	99	100	99	100	95	98	101
1168-3	118	135	106	106	97	100	100	102	95	107
1169-4	102	124	102	106	99	100	99	95	100	103
1174-3	118	127	107	100	101	100	99	96	99	105
1175-11	127	146	104	104	101	100	100	95	96	108
1175-3	116	106	101	99	101	101	100	103	100	103
1175-4	116	115	98	98	100	100	99	90	100	102
1176-12	117	106	99	96	98	99	98	95	97	101
1179-3	91	88	94	96	99	100	98	87	98	94

Comparison between RV and HARV
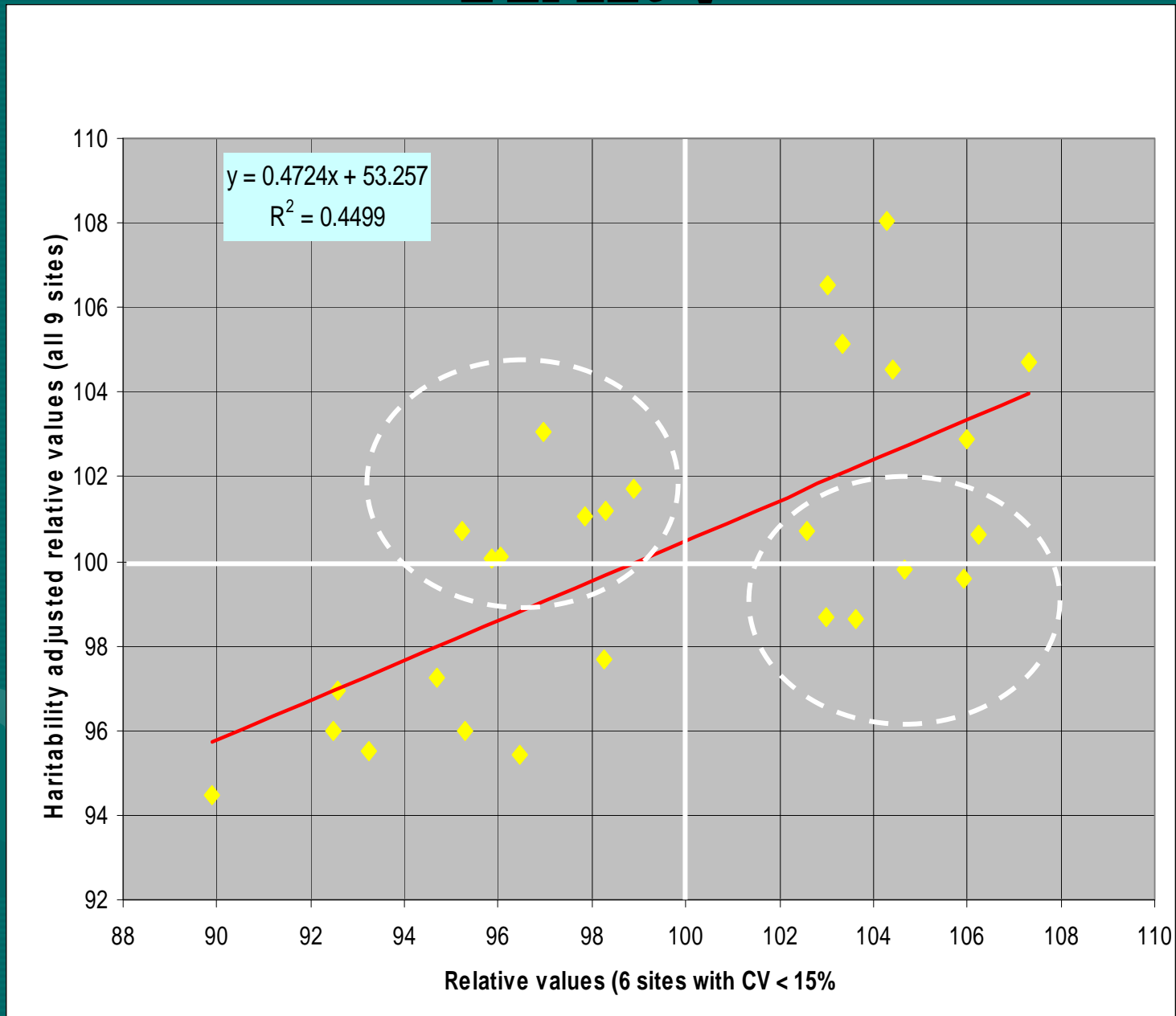
H

- H: "heritability" or "repeatability"
- [0,1]
- SE: standard error in the trial, needed to calculate both CV and H
- SD: standard deviation of means in the trial
- r: number of replications in the trial

$$H = 1 - (SE / SD)^2 / r$$

HARV

- RV = relative value in % of the trial mean
- HARV: Heritability adjusted relative value
- H is used as a shrinkage factor
  - When H = 1, HARV = RV
  - When H = 0, HARV = 1 (all varieties are the same as the average)

$$HARV = 1 - H(1 - RV)$$

Advantages of using HARV in variety summary

- Use all the data; no trials are excluded
  - No hassle in setting an artificial bar
- Use more information:
  - High CV tests are not completely useless
  - Low CV tests are not equally useful

Consequences

- Not much
- The variety rank should be generally the same if the CV or Heritability are in a reasonable range
- There could be rank changes otherwise