

A JSL script for the Analysis of Experimental Data in the Prognostic Breeding Methodology



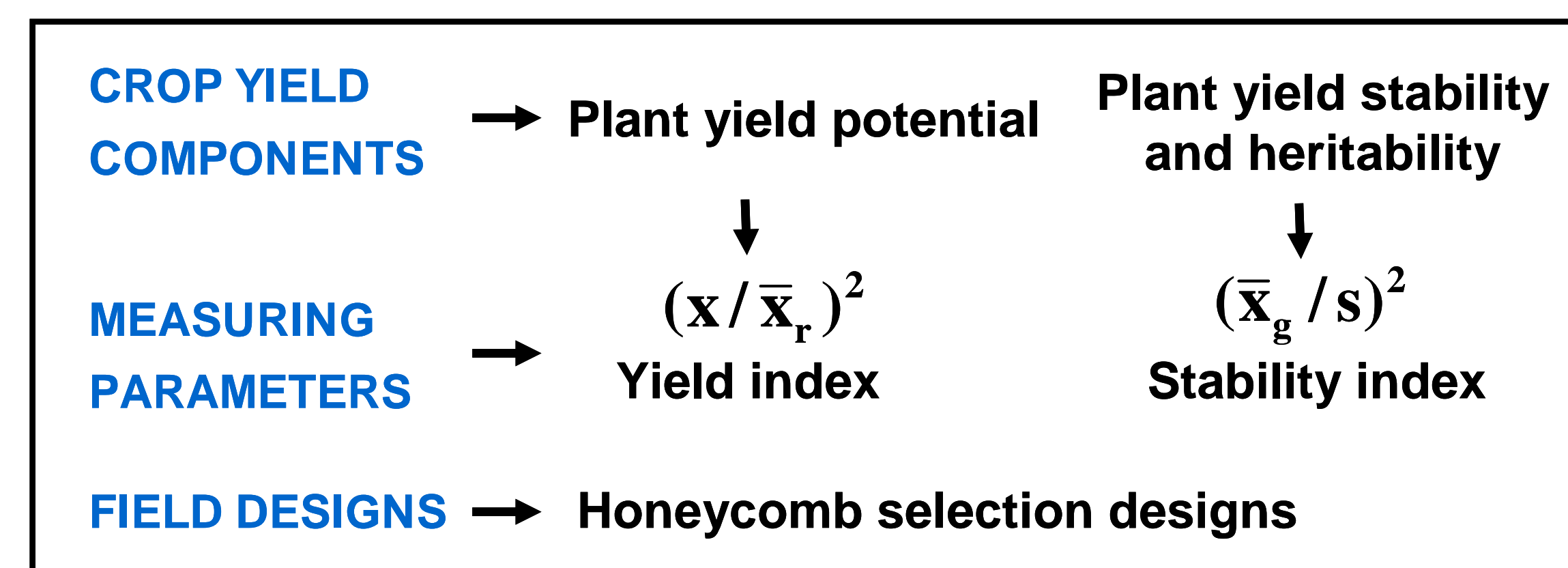
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Introduction

Prognostic breeding is an integrated crop improvement methodology founded on the principle that the unit of evaluation and selection is the individual plant grown in the absence of competition. Individual plants are evaluated for two parameters that constitute the components of the crop yield potential (Fasoula and Fasoula 2000; Fasoula 2013). The first parameter is the plant yield potential and the second is the plant yield stability and heritability. The product of the two parameters is the crop yield prognostic equation (Fasoula 2006, 2013), the elaboration of which is closely linked with the development of the honeycomb selection designs (Fasoulas and Fasoula 1995)

PROGNOSTIC BREEDING



$$pPE = (\bar{x} / \bar{x}_r)^2 \cdot (\bar{x}_g / s)^2$$

Prognostic Equation measures the crop yield potential of single plants

Features of the Honeycomb Designs

- 1 - Accurate single-plant phenotypic evaluation and selection at ultra-low plant density
- 2 - Use of any no. of entries (3 to >250) and large no. replications (>30)
- 3 - Moving replicates to minimize the effects of soil heterogeneity on single-plant yields
- 4 - Moving triangular grids to sample efficiently soil heterogeneity

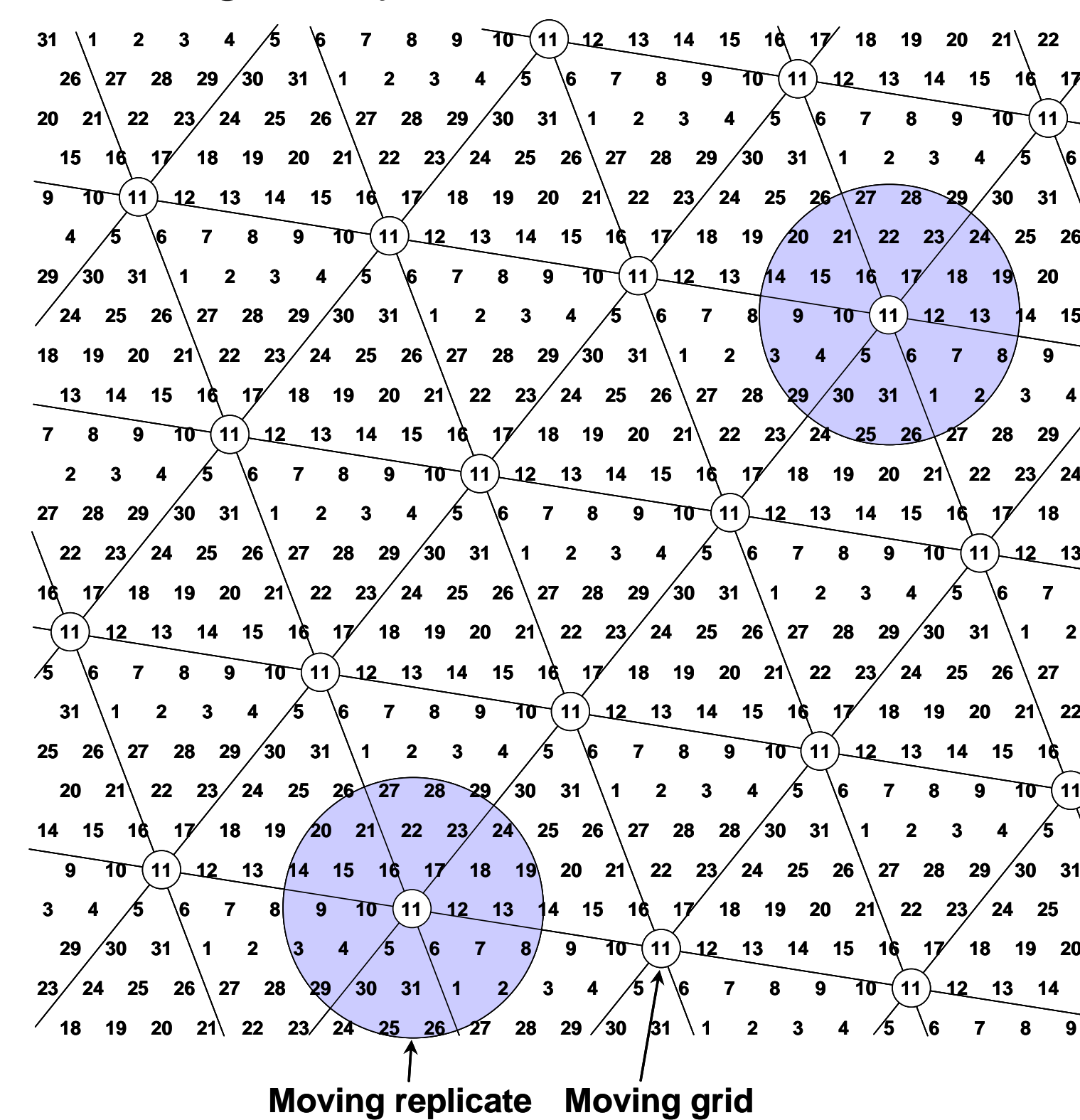
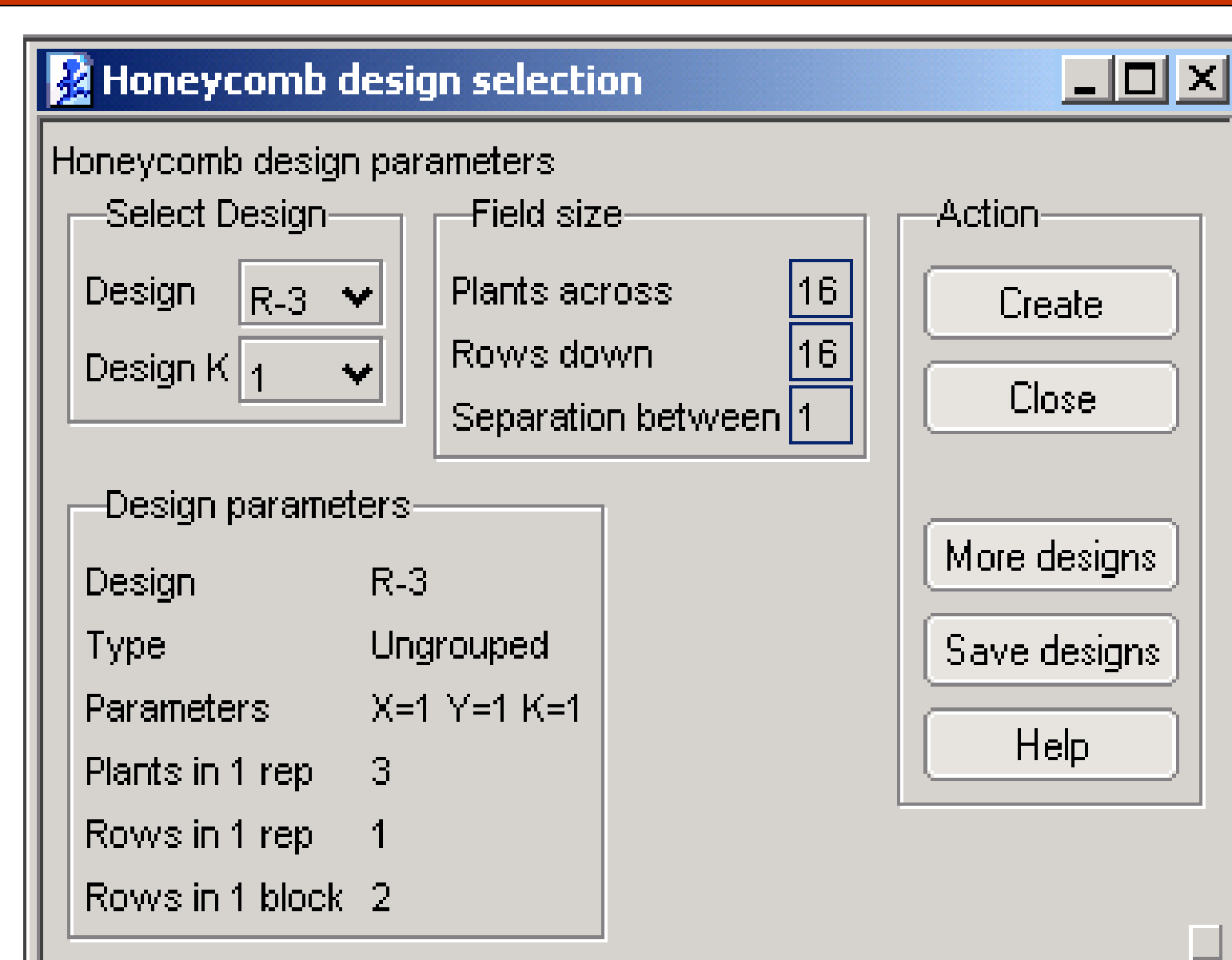


Fig. 1. The replicated-31 honeycomb design evaluates plants of 31 lines. Each plant is placed in the center of a moving complete replicate (purple circles). Plants of each line are placed in the corners of moving triangular grids (shown for line no. 11). The picture shows a soybean honeycomb trial in the field

The JSL script for the construction of honeycomb designs



The JMP program can construct all the different honeycomb designs and analyze the data according to the prognostic breeding methodology. When the user starts the program, the **Honeycomb design selection** window is displayed. Click on the **Design** and the **Field size** list-box to specify the no. of entries, the no. of plants and the no. of rows. The **Create** button will generate the specified honeycomb design



Fig. 2. Example of the construction of the replicated-57 honeycomb design using the JMP program. This design evaluates 57 entries and 14-16 plants per entry. As shown in the Overlay Plot, there are 22 horizontal field rows and 40 plants in each row for a total of 880 plants.

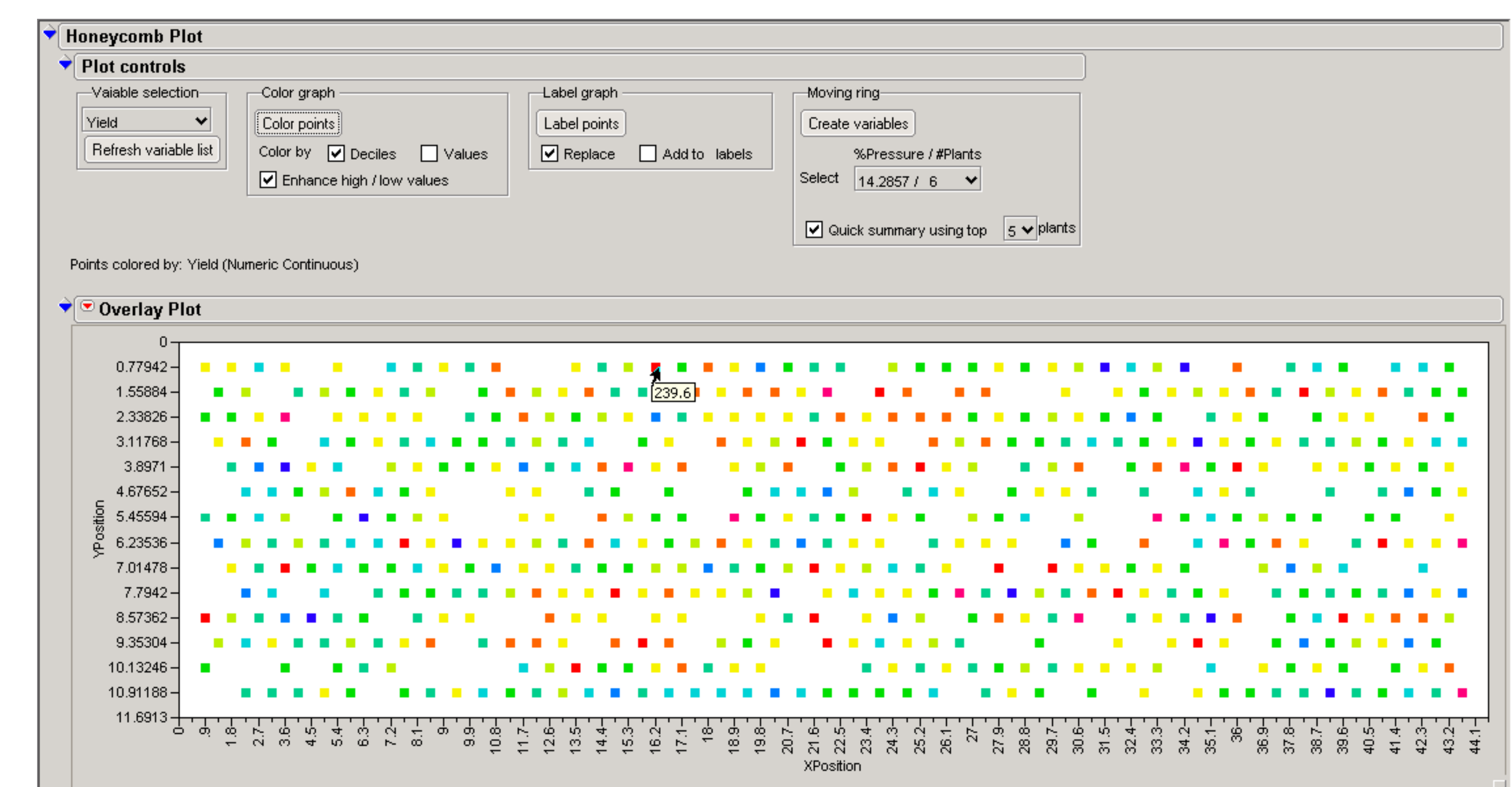


Fig. 3. The JMP program can display a field map with the axes adjusted to emphasize the triangular pattern of plants. The **Color points** button colors the graph points by the variable listed in **Variable selection** list-box (yield in this case). Lighter spots in the graph represent higher yield than darker spots. Missing plants are easily visualized. As shown, the soybean plant no. 18 in the 1st row has the high seed yield of 239.6g

Data summary analysis: Selection of the top 20 soybean plants for high crop yield potential using the plant prognostic equation

Line no.	Plant ID	Seed yield (g)	PYI	SI	pPE
18	808	254	2.54	40.0	101
18	1101	250	2.45	40.0	98
9	1029	301	2.90	33.8	98
12	802	181	1.34	70.5	94
12	1304	174	1.31	70.5	93
10	1448	255	2.08	42.3	88
9	904	239	2.58	33.8	88
12	1137	202	1.21	70.5	85
12	238	183	1.16	70.5	82
14	721	285	2.71	29.4	80
12	907	164	1.11	70.6	78
13	845	239	2.48	31.0	77
10	215	233	1.80	42.3	76
7	839	261	2.33	32.6	76
9	737	265	2.24	33.8	76
12	134	183	1.02	70.5	72
12	1241	170	1.01	70.5	71
9	1238	254	2.09	33.8	71
12	1032	180	0.97	70.5	69
10	821	214	1.58	42.3	67

Data are from a replicated-21 soybean trial that evaluated 21 sibling lines and a total of 670 plants

PYI and SI are the plant yield index and stability index respectively (both are unitless values)

$pPE = PYI \cdot SI = (\bar{x} / \bar{x}_r)^2 \cdot (\bar{x}_g / s)^2$ is the plant prognostic equation measuring the crop yield potential of each plant

References

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