

FIELD EXPERIMENT DESIGN WITH 30 SOYBEAN GENOTYPES FOR THE ASSESSMENT OF DROUGHT ADAPTATION UNDER FIELD CONDITIONS

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Abstract. Reliable evaluation of soybean genotypes for drought adaptation requires proper field-experiment design, balanced placement of genotypes across replications, and integrated recording of physiological, biochemical, and yield-related traits. This study describes a field experiment conducted at the experimental field of the Scientific Research Institute of Oilseed and Fiber Crops, where 30 soybean genotypes were arranged in three replications. Each replication consisted of six blocks, with five genotypes per block, resulting in a total of 90 experimental plots. The experiment included the cultivar Orzu and 29 breeding lines. The order of genotypes was changed among replications to reduce the influence of field microenvironmental heterogeneity. This design provides a methodological basis for the integrated assessment of phenological, morphological, physiological-biochemical, yield, and seed-quality traits, and for identifying promising drought-adapted soybean genotypes.

Keywords: soybean, Glycine max, genotype, field experiment, replication, block, drought, yield, protein, breeding.

Introduction

Soybean (*Glycine max* (L.) Merr.) is an important crop with high protein and oil content, while water deficit can substantially affect vegetative growth, flowering, pod formation, and seed filling. Field trials involving multiple genotypes are therefore essential, alongside laboratory assessments, for identifying drought-adapted germplasm. Field environments reveal the actual agroecological adaptability of a genotype; however, soil fertility, moisture distribution, microrelief, and plant competition can introduce additional variation. Consequently, the use of several replications and block-based placement increases experimental precision and statistical reliability.

Drought adaptation cannot be assessed solely by final yield. Water deficit can alter phenological development, leaf water status, the photosynthetic apparatus, osmotic adjustment, and oxidative-stress responses. Therefore, field experiments should integrate phenological stages, plant height, pod formation, and seed yield with traits such as chlorophyll status, relative water content, proline, malondialdehyde, and seed protein content. Such an integrated approach provides a more complete characterization of breeding material.

The aim of this study was to systematize the planting sequence of 30 soybean genotypes in a three-replication field experiment, present their block-wise arrangement, and define the main observation and analytical approaches for assessing drought adaptation under field conditions.



Figure 1. General view of soybean genotypes in the experimental field (Scientific Research Institute of Oilseed and Fiber Crops).

Materials and Methods

The experiment comprised 30 soybean genotypes. According to the electronic field-record layout, each genotype was planted in three replications. Each replication contained 30 plots divided into six blocks, with five genotypes in each block. Thus, the experiment consisted of 90 plots in total. The planting order of genotypes was changed among replications, which helps reduce systematic effects associated with spatial differences in soil moisture, fertility, and other microenvironmental factors.

Table 1. Thirty soybean genotypes included in the field experiment

No.	Genotype	No.	Genotype	No.	Genotype
1	Orzu	11	L-159	21	L-30
2	L-3	12	L-182	22	L-11
3	L-4	13	L-140	23	L-17
4	L-5	14	L-204	24	L-101
5	L-10	15	L-194	25	L-103
6	L-15	16	L-10195	26	L-106
7	L-16	17	L-196	27	L-114
8	L-19	18	L-27	28	L-115
9	L-116	19	L-28	29	L-7
10	L-195	20	L-29	30	L-1030

The field-record structure was designed for consistent registration of phenological and agronomic traits. It includes columns for planting date, emergence, branching, budding, flowering, pod formation, maturity, duration of the growing period, plant height, height of the lowest pod above the soil surface, numbers of one-, two-, and

three-seeded pods per plant, total pods and seeds, 1000-seed weight, seed yield per plant, plot yield, yield per hectare, and seed protein content.

Planting Sequence by Replication and Block

Each replication consisted of six blocks. Five genotypes were placed consecutively within each block. The position of the same genotype was changed in subsequent replications, allowing each genotype to be evaluated in different parts of the field. This approach reduces the risk of associating a genotype's performance with only one local field condition.

Table 2. Arrangement of 30 soybean genotypes across three replications and six blocks

Replication	Block	Plot 1	Plot 2	Plot 3	Plot 4	Plot 5
1	1	Orzu	L-16	L-140	L-28	L-103
1	2	L-3	L-19	L-204	L-29	L-106
1	3	L-4	L-116	L-194	L-30	L-114
1	4	L-5	L-195	L-10195	L-11	L-115
1	5	L-10	L-159	L-196	L-17	L-7
1	6	L-15	L-182	L-27	L-101	L-1030
2	1	Orzu	L-19	L-10195	L-30	L-7
2	2	L-3	L-116	L-196	L-11	L-1030
2	3	L-4	L-195	L-27	L-17	L-103
2	4	L-5	L-159	L-140	L-101	L-106
2	5	L-10	L-182	L-204	L-28	L-114
2	6	L-15	L-16	L-194	L-29	L-115
3	1	Orzu	L-182	L-194	L-11	L-106
3	2	L-3	L-16	L-10195	L-17	L-114
3	3	L-4	L-19	L-196	L-101	L-115
3	4	L-5	L-116	L-27	L-28	L-7
3	5	L-10	L-195	L-140	L-29	L-1030
3	6	L-15	L-159	L-204	L-30	L-103

Field Observations and Sampling Procedure

Phenological observations should be conducted in all plots using the same criteria. The dates of emergence, branching, budding, flowering, pod formation, and maturity should be recorded, followed by calculation of the number of days from planting to each developmental stage. These data make it possible to identify early- and late-maturing genotypes and to interpret the developmental stage at which each genotype encounters drought.

Morphological and yield components should be measured from sample plants selected according to the same procedure in each plot. Plant height, height of the lowest pod, number of pods and seeds, 1000-seed weight, and yield per plant describe important yield-structure traits. Plot yield should be converted to a per-hectare basis and used as one of the principal criteria for comparing the breeding value of genotypes.

For physiological and biochemical analyses, leaf sampling should be standardized by phenological stage and time of day. Relative leaf water content, chlorophyll/SPAD, photosynthesis or chlorophyll fluorescence, proline, and malondialdehyde (MDA) can be measured using a uniform protocol to compare genotype-specific stress responses. After seed maturity, protein and oil contents can be determined to assess whether physiological tolerance is also reflected in final product quality.

Integrated Assessment of Drought Adaptation

In an integrated assessment, different groups of traits complement each other. Phenological data indicate whether a genotype avoids or coincides with the most drought-prone period, whereas plant water status and photosynthetic traits describe the immediate physiological effect of stress. Proline accumulation is associated with osmotic adjustment, while MDA reflects membrane lipid peroxidation and oxidative injury. Yield and seed-quality traits represent the practical outcome of these protective responses.

Table 3. Main assessment groups recommended for the field experiment

Assessment group	Main traits	Breeding relevance
Phenology	Emergence, flowering, pod formation, maturity, growing period	Timing relative to stress and earliness
Morphology	Plant height, lowest pod height, pod and seed number	Plant architecture and yield structure
Physiology	RWC, SPAD/chlorophyll, photosynthesis, fluorescence	Water status and photosynthetic stability
Biochemistry	Proline, MDA, antioxidant enzymes	Osmotic and oxidative-stress response
Yield and quality	1000-seed weight, yield, protein, oil	Practical breeding and technological value

Statistical Analysis

For a three-replication experiment, mean values and measures of dispersion should be calculated for each genotype, followed by analysis of variance to assess the effects of genotype and replication. If the trial is conducted in parallel under well-watered and water-deficit treatments, the genotype $\times$ water-regime interaction should also be tested. This helps distinguish true genotype-specific drought response from simple differences in yield.

When many traits are recorded, correlation analysis, principal component analysis (PCA), and cluster analysis can be used for integrated grouping of genotypes. If yield data are available under both control and stress conditions, stress tolerance index (STI),

geometric mean productivity (GMP), and yield stability index (YSI) can be calculated to identify genotypes that maintain high productivity under both favorable and drought-stressed conditions.

Scientific and Practical Significance

The experimental design allows 30 genotypes to be tested under the same field conditions in three independent replications. Such a structure is suitable for selecting promising parental material from genebank and breeding collections, identifying lines that maintain yield and seed quality, and choosing contrasting genotypes for subsequent physiological, biochemical, or molecular-genetic studies. Combining field performance with seed protein and oil traits increases the probability of selecting genotypes that are not only drought-adapted but also valuable for practical production.

Prospects for the Use of Research Results

Multitrait data obtained from the field experiment can be used to generate a comprehensive profile for each genotype. Lines that maintain relatively high yield, have a suitable growing period, and possess a favorable height of the lowest pod for mechanized harvesting can be advanced to subsequent breeding stages. If these genotypes also maintain leaf water status and photosynthetic stability, show limited MDA accumulation, and retain high seed protein and oil levels, their breeding value for drought adaptation can be supported more reliably.

Promising and sensitive contrasting genotypes can subsequently be subjected to molecular-genetic analyses. Expression of drought-responsive genes, genetic markers, or other modern approaches can then be linked with the field phenotype. Initial field-based selection of contrasting genotypes helps optimize the number of materials used in molecular analyses and focuses research costs on the most informative samples.

If the experiment is repeated in subsequent years under different water regimes or agroecological conditions, genotype stability and genotype $\times$ environment interactions can be assessed. This is important for identifying lines that maintain stable yield and quality across environments rather than performing well only in a single year or location. Such material can be used in breeding, primary seed production, and the development of new soybean cultivars.

Conclusion

The placement of 30 soybean genotypes in three replications, with six blocks per replication and five genotypes per block, creates a systematic 90-plot field-experiment design at the Scientific Research Institute of Oilseed and Fiber Crops. Changing genotype order among replications is useful for reducing the influence of local field heterogeneity and for estimating genotype differences more reliably. Integrated analysis of phenological stages, morphological and yield traits, physiological-

biochemical responses, and seed-quality parameters provides a sound basis for selecting drought-adapted, high-yielding soybean genotypes with stable quality.

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