**Identifying High Yielding, Stable Chickpea Genotypes for Spring Sowing;**

**Specific Adaptation to Locations and Sowing Seasons in the Mediterranean Region**

Muhammad Imtiaz\*,1, Rajinder Singh Malhotra, Murari Singh and Suhaila Arslan

International Center for Agricultural Research in the Dry Areas (ICARDA)

PO Box 5466, Aleppo, Syria.

Tel. +963 21 2691 2262 (office); Fax +963 21 221 3490

**\*** Corresponding author

Email: m.imtiaz@cgiar.org

1Current address: International Maize and Wheat Improvement Centre (CIMMYT)

Pakistan Office, NARC, Park Road, Islamabad 44000, Pakistan

**Identifying High Yielding, Stable Chickpea Genotypes for Spring Sowing;**

**Specific Adaptation to Locations and Sowing Seasons in the Mediterranean Region**

# Abstract

Superior genotypes are needed to give farmers a choice of chickpea improved cultivars suitable for traditional spring sowing, . These can be used in a hybridization program to develop high yielding, spring-type genotypes or for direct release as cultivars. From 1997 to 2010, 68 experiments comprising 404 elite chickpea lines were conducted for two seasons per year (spring and winter) at two locations – Tel Hadya, Syria (TH) and Terbol, Lebanon (TR). Analyses of variance showed that genotypic differences were significant (*P* < 0.05) in 65 of 68 experiments. Partitioning the environments into components showed that genotype x season interaction was more important than genotype x location. The predicted means in the two seasons were significantly correlated, implying the possibility of undertaking the preliminary/advanced yield trials testing in only one of the seasons, such as at TH. However, at TR selection has to be season specific because of low predictability. Stability analyses of the lines over time showed that line S95082 (FLIP95-78C), with a predicted yield of 1725 kg ha-1, was the top yielding genotype at the TH spring sowing – temporal stability rank 14. The line S95419 ranked second for yield (1633 kg ha-1), followed by S95335 (FLIP95-147C) with a spring yield at TH of 1583 kg ha-1. GGE (genotype main effect (G) plus genotype x environment (GE) interaction) biplot analyses showed that the FLIP95-78C and S95335 genotypes were high yielding at TH, while FLIP98-91C and FLIP98-162C did better at TR in both seasons. Three lines, FLIP01-06C, FLIP01-30C, and FLIP01-49C, having high yields across locations and seasons and tolerant to drought, were identified for dual season sowing. The findings show the potential to improve chickpea for spring sowing. The ICARDA breeding program is enriching the germplasm base with elite chickpea genotypes benefiting regional and international chickpea improvement programs.

Chickpea (*Cicer arietinum* L.) is one of the world’s most important food legumes and is a source of protein grown in developing and developed countries around the world. Rainfall in Mediterranean environments mainly occurs in the winter months and chickpea is traditionally grown in the spring using conserved soil moisture. Studies conducted at the International Center for Agricultural Research in the Dry Areas (ICARDA) have demonstrated that the seed yield of chickpea can be substantially increased by changing the planting season in the Central and West Asia and North Africa (CWANA) region from the traditional spring to winter (Singh et al., 1997; Iliadis 2001;). Therefore, ICARDA has been working with the national programs of CWANA to develop chickpea cultivars suitable for winter cultivation (Malhotra et al., 2007). However, the winter cultivars should possess Ascochyta blight resistance and cold tolerance. The management of weed infestation, favorable conditions for Ascochyta blight infection, the occurrence of cold during winter, and the non-availability of seed of improved cultivars for winter planting contributed to the slow adoption of winter chickpea technology.

Therefore, despite yield advantage of winter sown chickpea, a large number of farmers still prefer to plant chickpea in the spring to avoid Ascochyta blight disease and weed infestations and achieve a large seed size, which fetches a high market price. However, spring sown chickpea yields are very low (almost half the yield of winter sown chickpea) in most of the countries in the CWANA region (Silim and Saxena, 1993a,b; Tawaha et al., 2005; FAO, 2010). The main reasons for the low yields of spring sown cultivars are their inherent low yield potential, the short season leads to less vegetative growth and susceptibility to natural vagaries in environment (drought, cold, Ascochyta blight susceptibility at seedling stage, and unsuitability for mechanized harvesting), but farmers continue to grow local landraces with very low productivity. Thus, it is equally important to develop high yielding cultivars suitable for spring sowing or dual season sowing so that farmers have the choice of selecting suitable cultivars for the spring or winter seasons as per their local environmental/agro-climatic conditions. To improve the productivity of spring sown chickpea, ICARDA distributes a Chickpea International Elite Nursery for Spring (CIEN-S). The nursery comprises high yielding, advance breeding lines (F7-F8 generation) to facilitate the introduction and selection of improved cultivars across the regions for spring sown conditions.

Genotype x environment interaction plays an important role in identifying the genotypes suitable for a specific (or broad) adaptation, and stability over the years. Breeders are always eager to release a genotype as a cultivar which has stable performance across environments (Berger et al., 2004; Berger et al., 2006; Yadav et al., 2010). To identify stable chickpea genotypes adapted to specific environments in relatively low rainfall locations (like TH – 334 mm annual average rainfall) and high rainfall locations (like TR – 519 mm annual average rainfall), 404 genotypes were planted in the spring and winter seasons at two locations. The four objectives of the field trials were to:

* Identify high yielding and stable genotypes for spring sowing.
* Clarify genotype x environment (G x E) interaction and the contributions of location and sowing season to the interaction.
* Compare genotypic variability among individual trials in the contrasting locations (TH versus TR) and
* Identify locations with the least genotype x year interaction.

# Materials and Methods

**Experimental materials**

The chickpea breeding program at ICARDA has been developing genetic materials suitable for spring (high yielding, drought and Fusarium wilt tolerant, large-seeded) and winter (cold tolerant, Ascochyta blight resistant, Fusarium wilt tolerant, large-seeded) sowing. The genetic materials (CIEN-S) developed for spring sowing were evaluated in each of the two seasons –winter and spring – and at each of the two locations –TH, at 36o 01 N, 36o56 E, 284 m above sea level, average annual precipitation 334 mm and TR, at 33o 49 N, 35o 59 E, 950 m above sea level, average annual precipitation 519 mm. Thus, there were four environments in total and the experiments were conducted in these environments for 14 years (from 1997 to 2010) using the same genetic material in a given year across all the four environments (location-season combinations). However, the genetic material over successive years had a variable number of common genotypes. In each year, all the genotypes were evaluated as a single set, i.e. in a single experimental design, except in 2000 and 2001 when relatively much larger numbers of genotypes were available. Hence these genotypes were grouped into three sets in 2000 and two sets in 2001 (Table - 1). Thus over 14 years, there were a total of 12 x 4 + 3 x 4 + 2 x 4 = 68 layouts or experiments.

**Experimental designs**

The experimental designs were incomplete blocks, either as square lattices or alpha-designs, with variable number of replications (Table -1). Each genotype was planted in 4 m long 2-row plots with a distance between rows of 30 cm and 8 cm between plants. The winter sowing was done between 15 December and 10 January, and harvested between 10 and 25 June. The spring sowing was carried out between 10 and 20 February, and harvested between 20 and 30 June. Seed yields were recorded on a plot basis (2.4 m2) and converted to kg ha-1 for statistical analyses.

**Statistical methods**

Individual trials were analyzed by fitting the mixed model, and incorporating the incomplete block design factors, to evaluate experimental error variability, efficiency of the incomplete blocks over complete blocks, significance of genotypic differences, and heritability (under assumed random effects of the genotypes). The best linear- unbiased predictor estimates and their standard errors were obtained for a standard analysis of multi-environment trials. Genotype responsiveness was estimated as the slope across the environments using Finlay and Wilkinson (1963). Since there are only four environments – location-season combinations, which can be justified as fixed – we used GGE biplot to indicate any possible specific adaptations of genotypes to these environments instead of evaluating the slopes. Furthermore, for each location-season combination, there were some genotypes which were evaluated over two years and these provided the scope for evaluating stability over time, the random component of environment. The temporal stability (i.e. Type 4 stability) of a genotype quantifies the variation of the genotype’s response with time. Lin and Binns (1988) measured temporal stability using the variance (mean square) of the yields over the years within the locations. We have noted a small limitation of this measure which can be explained as follows. Since the scale of variability in response to relatively higher values is likely to be higher than those for relatively lower values, the use of the Type 4 stability measure will penalize the genotypes with higher yields. To address this aspect, we used the coefficient of variation (CV) computed from the mean squares over time at a given location-season. These CVs were averaged over the location-season combinations to provide another measure of temporal stability, the temporal coefficient of variation (TCV). The association between the genotype means over the environments and stability over the years was assessed using simple correlation.

G x E interaction was partitioned in terms of location, season, and location x season and various components of variance were estimated from the plot data. To fit the mixed models and estimate the variance components, we used the residual maximum likelihood method algorithm of GenStat (Payne 2009).

The stable genotypes were further reviewed to identify high yielding genotypes for spring sowing at specific locations simply by selecting the top entries with 30% selection intensity. It was expected that those selected entries which were common to the winter and spring seasons would be useful for dual season use.

# Results and Discussion

**Genotypic variability in individual trials**

In two of the 68 experiments conducted, a large number of observations were missing so the data from these were excluded from the analysis. Analyses of variance for the remaining 66 experiments revealed that genotypic differences were statistically highly significant (*P* < 0.001) in 57 experiments, significant (*P* < 0.05) in six experiments and not significant (*P >* 0.05) in one experiment. The non-discriminating environment was excluded from the analysis to identify the stable and high yielding genotypes. The summary statistics on the trial/experiment – trial means over all genotypes and adjusted for incomplete blocks, experimental error (CV expressed as a percent) to measure the field heterogeneity, effectiveness of using incomplete blocks in terms of efficiency (%) over complete blocks, and heritability of yield estimated at these trials – are given in Table –2.

The overall mean yield in winter was higher than that from the spring sowing at each location, and the yield at TR (high rainfall) was higher than that at TH (low rainfall site) for each sowing season. This was expected, as winter sowing gives higher yields than spring sowing because of greater water use efficiency and the longer growth period (Singh et al., 1997; Silim and Saxena, 1993b). The CV varied from 7% at TR in winter to 66% at TH in spring. The high CV (66%) at TH-S could be attributed to the lower availability of moisture, which led to uneven crop establishment and a poor harvest..

The incomplete block designs showed a variable efficiency (up to 198% for TR-S), with an overall mean of 114%. In 68% of the trials (41 of 66 cases) incomplete blocks showed higher efficiency over randomized complete blocks. The heritability varied between 5% at TR-W and 90% at TH-W, with an overall mean of 61%. Some of the trials were affected by frequently occurring soil borne fungi and nematodes such as *Fusarium oxysporum f.sp. ciceris*and *Heterodera ciceri* in localized patches in the test locations. It seems that trials conducted under heterogeneous field conditions resulted in lower heritability estimates as compared to those conducted under homogenous condition (Malhotra and Singh, 1991). Similar findings were also reported for lentil (Sarker et al., 2010) and other crops (Singh et al., 2003) in homogenous trials.

**G x E interaction**

Partitioning the environments into locations and seasons showed significant genotype x season x location interaction and genotype x season interaction (Table –3), while genotype x location interaction was not significant. This means that genotype x season interaction is more important than genotype x location; which could be true because of the two distinct sowing times with different photoperiods, temperatures, and rainfall regimes, as previously reported for chickpea (Malhotra et al., 2007; Berger et al., 2011). The variance component estimates presented in Table –3, when compared to their standard errors, showed that G x E interaction was significant (*P* < 0.001). This significance was expected given the diverse nature of the genotypes tested in the different seasons under environments characterized by different photoperiods, rainfall and temperatures, the important adaptation cues in chickpea (Malhotra and Singh, 1991; Malhotra et al., 2007; Berger et al., 2006, 2011).

**Selection of high yielding and stable genotypes for spring sowing**

Stability of the lines over time was evaluated as the mean squared values over time within the four environments (Lin and Binns, 1988). The adaptability to the environments created by the two locations and seasons was evaluated by the slope (Finlay and Wilkinson, 1963). Correlations between genotype predicted means and the various indices were determined as -0.22 (from the slope), 0.17 (from mean squares over time, Type 4 stability), and -0.15 (with TCV), and each was highly significant (*P <* 0.001). However, with predictability of the mean performance in terms of the stability being very low, this provided scope for the selection of the lines for stable performance and high yield.

Of the 404 genotypes (including checks), 158 lines (excluding checks) were present in the trials for at least two years and hence enabled an estimation of stability over time. At TH, which is ICARDA’s main research station and variety testing/selection site, with a view to screening genotypic material suitable for spring sowing, 48 (30% of the 158) entries were selected for yield (Table – 4).

The top yielding line in the TH spring sowing, S95082, had a predicted yield of 1725 kg ha-1, and ranked 14th for temporal stability (based on the CV). The most stable line, S95419, (based on CV) ranked second for yield (1633 kg ha-1). This was followed by S95335 with a yield of 1583 kg ha-1 yield (Table – 4). With only four location-season combinations, the adaptability slope (Finlay and Wilkinson, 1963) had high standard errors and, therefore, we did not use these for the selection of lines. We used the GGE biplot (Yan, 2011; Fig. 1) option within the GenStat software to visualize ‘which won where’. This allowed us to group test environments based on crossover interactions among the best selected genotypes. To reduce the clutter of points and to exclude low yielding genotypes, we applied a 10% cull in each environment. The vertex genotypes that form the polygon in Fig. 2 were G273, G311, G321, G335, and G371 (Table – 4). The four test environments were cut into two groups by the superimposed lines – TH-W and TH-S as one group and TR-W and TR-S as another group. G311 (FLIP98-91C) and G273 (FLIP98-162C) are the vertex genotypes in the sector where TR-W and TR-S are placed and are, therefore, the winners at this location in both seasons. Similarly, the G335 (S95082) and G371 (S95335) genotypes are the winners at TH in both spring and winter. The fact that no environment fell into the G321 (FLIP99-23C) sector indicates that this genotype is not a winner in any of the environments and most likely will provide the poorest yield in all environments. Atta and Shah (2009) reported similar crossover interactions for chickpea.

The GGE biplot, based on the best selected genotypes, revealed a great deal of diversity among genotypes and among environments (Fig. 1). The value for both the principal components (PCs) was 84% (PC1 = 59%; PC2 = 25%), which represents a better goodness of fit of the biplot. Based on the average environment axis line and the stability line (Fig. 1), the best genotypes in the spring in TH could be ranked according to their mean yields as G355, G392, G354, G158, G378, and G371 (Table – 4; Fig. 1). Genotypes, like G321, were the least stable and yielded poorly in all environments.

The elite lines included in CIEN-S and tested across location-seasons include genotypes with comparatively good yield and tolerance to drought and Fusarium wilt disease. The three lines S95082, S95419, and S95335, identified for spring planting, also have a reasonable seed size – 32, 37, and 38 g per 100 seeds, respectively. These lines were given the FLIP numbers FLIP95-78C (S95082), FLIP95-147C (S95335), and FLIP95-176C (S95419). These lines have been kept for long term storage in the ICARDA gene bank and are also available for distribution to partner national agricultural research systems.

**The genotype means relationships between locations and between seasons**

The objective of each breeding program was to screen a large number of lines efficiently, using cost effective methods, and thus reduce the number of testing sites without compromising on the selection process or discarding desirable genotypes. Therefore, to see if both seasons are needed for evaluation at both locations, the correlations between the four location-season combinations were calculated from genotype predicted means in these environments. The predicted means in the two seasons are significantly correlated (r = 0.25 at TR and r =0.80 at TH; *P* < 0.001). At TH, the predictability of genotype performance in one season in terms of the response in the other is high. This means that one of the two seasons would serve the purpose for genotype selection. Therefore, it would be possible to eliminate testing of preliminary/advance yield trials in the spring season at TH and divert resources to other important experiments in the program. However, at TR, selection has to be done specifically for a season because of the low predictability (although this was significant). Correlations between predicted means at the two locations were -0.21 (*P <* 0.001) for spring and -0.095 (*P* < 0.05) for winter. The low level of association indicated that testing of elite lines at both locations in each season was justified in order to develop both winter and spring adapted cultivars. Similar findings were reported previously for chickpea (Malhotra et al., 2007), where the extent and nature of G x E interaction on yield was examined and genotypes that could produce high yields in both seasons were identified.

**Identification of stable, specifically adapted, and dual season genotypes**

Since the main selection site is TH, the lines were ranked for spring season yields at TH and then TR. The common genotypes, which were found within 30% of the top ranks (1 – 48) at the two locations, are listed in Table – 5. A selection intensity of 30% for each of the two seasons/locations was used and results in a more rigorous intensity level of 0.3 × 0.3 = 0.09, i.e. 9%, when selecting jointly for both the seasons/locations. There were 10 FLIP lines with predicted yields in the range 1042 to 1570 kg ha-1 at TH, where the local check yielded 986 kg ha-1. At TR the yield range was 1504 to 1884 kg ha-1, and the local check yield was 1314 kg ha-1. FLIP 01-56C was identified as the best line suitable for spring planting at TH. However, there were lines which performed better in spring in TR (Table – 5). This could be attributed to the better response of some genotypes to water availability at TR (TR rainfall being higher that that at TH). FLIP 01-56C probably did not respond well to the available moisture and other lines surpassed it at the TR location. However, the results provided an opportunity to select genotypes for various moisture levels, ranging from low to high. FLIP 01-56C also possesses resistance to Fusarium wilt and to drought and has moderate resistance to Ascochyta blight, a foliar disease of chickpea.

Similarly, we compared the results for TH spring (TH-S) with TH winter (TH-W) and TR spring (TR-S) with TR winter (TR-W). At TH there were 40 lines which could serve the purpose for both seasons with predicted means in the range 1048 to 1725 kg ha-1 (local check yield, 968 kg ha-1) during spring and in the range 1576 to 2858 kg ha-1 (local check yield, 1305 kg ha-1) in winter. Of these lines, 25 had significantly higher yields than the local check (Table – 6). The line S95082 maintained its top yielding position in both seasons while the yield of S95335 was within the top 4. There are 18 genotypes which can be recommended for both seasons at TR (a wetter site), with yields in the range 1526 to 1884 kg ha-1 (local check yield, 1314 kg ha-1) in spring and in the range 2235 to 2658 kg ha-1 (local check yield, 2019 kg ha-1) in winter. Among these lines there were just 10 which were significantly higher in seed yield in both seasons than the local checks (Table – 4).

When we compared the two locations, TH retained a greater number of genotypes suitable for both seasons (25 lines significantly superior to the local check). At TR, however, there weremuch stronger genotype x season interactions compared to those at TH, which may be the reason for the selection of relatively fewer numbers of genotypes for dual season purposes at this location (10 lines significantly superior to the local check). This could also result from a more favorable environment at TR, where genotypes that responded better were selected.

If the breeding program objective was to select lines for both seasons and different locations (representing an annual rainfall pattern of between 334 and 520 mm), then the three lines, FLIP01-06C, FLIP01-30C and FLIP01-49C, were found common to each of the four environments within a narrow range of yield (Table – 6). These could be recommended for both spring and winter sowing in areas with an annual rainfall of from 300 to 500 mm. Our stress evaluation studies at ICARDA have shown that these lines, FLIP01-06C, FLIP01- 30C, and FLIP 01-49C are also tolerant to drought and Fusarium wilt disease. Though the study has been conducted at two locations, the relevance of these location to the Mediterranean region has been documented earlier as a number of cultivars developed as a results of selection at these locations have been released as varieties for winter planting in the countries with Mediterranean type environments like Turkey, Iran, Morcocco, Australia, Tunisia, Portugal, Spain, Iran, and Algeria (Sabaghpour et al., 2006; Kusumenoglu et al., 2006; Siddique et al., 2007). The lines identified (FLIP01-06C, FLIP01- 30C, and FLIP 01-49C ) in this study are available for use in the chickpea breeding programs upon request.

**References**

Atta, B.M. and T.M. Shah. 2009. Stability analysis of elite chickpea genotypes tested under diverse environments. Aust. J. Crop Sci. 3:249-256.

Berger, J.D., M. Ali, P.S. Basu, B.D. Chaudhary, S.K. Chaturvedi, P.S. Deshmukh, et al. 2006. Genotype by environment studies demonstrate the critical role of phenology in adaptation of chickpea (*Cicer arietinum* L.) to high and low yielding environments of India. Field Crops Res. 98: 230-244.

Berger, J.D., N.C. Turner, K.H.M. Siddique, E.J. Knights, R.B. Brinsmead, I. Mock, et al. 2004. Genotype by environment studies across Australia reveal the importance of phenology for chickpea (*Cicer arietinum* L.) improvement. Aust. J. Agric. Res. 55:1-14.

Berger., J.D., S.P. Milroy, N.C. Turner, K.H. M. Siddique, M. Imtiaz, R. Malhotra. 2011. Chickpea evolution has selected for contrasting phonological mechanisms among different habitats. Euphytica 180:1-15.

FAO, 2010. Statistical database. www.fao.org. (accessed 10/05/2012)

Finlay, K.W. and G.N. Wilkinson. 1963. Analysis of adaptation in a plant breeding programme. Aust. J. Agric. Res. 14:742-754.

Iliadis, C. 2001. Evaluation of six chickpea varieties for seed yield under autumn and spring sowing. J. Agric. Sci. 137:439-444.

Lin, C.S. and M.R. Binns. 1988. A method of analyzing cultivar x location x year experiments: a new stability parameter. Theo. Appl. Genet. 76:425-430.

Malhotra, R.S. and K.B. Singh 1991. Classification of chickpea growing environments to control genotype by environment interaction. Euphytica 58:5-12.

Malhotra, R.S., M. Singh, and W. Erskine. 2007. Genotype x environment interaction and identification of dual-season cultivars in chickpea. Euphytica 158:119-127.

Payne. R.W. 2009. The guide to GenStat® release 12 Part 2: statistics. Lawes Agricultural Trust, Rothamsted Experimental Station, Harpenden, Herts.

Sabaghpour, S.H., Mahmodi, A.A., Saeed, A., Kamel, M., and Malhotra, R.S. 2006. Study on chickpea drought tolerance lines under dryland condition of Iran. Indian J. Crop Science, 1(1-2): 70-73.

Sarker, A., M. Singh, S. Rajaram, and W. Erskine. 2010. Adaptation of small-seeded red lentil (*Lens culinaris* Medik. subsp. culinaris) to diverse environments. Crop Sci. 50:1250-1259.

Siddique, K.H.M., Regan, K.I., and Malhotra, R.S. 2007. Registration of ‘Almaz’ Kabuli Chickpea Cultivar. Crop Science 47:436-437.

Silim, S.N. and M.C. Saxena. 1993a. Adaptation of spring sown chickpea to Mediterranean basin. I. Response to moisture supply. Field Crops Res. 34:121-136.

Silim, S.N. and M.C. Saxena.1993b. Adaptation of spring sown chickpea to Mediterranean basin. II. Factors influencing yield under drought. Field Crops Res. 34:137-146.

Singh, K.B., R.S. Malhotra, and M.C. Saxena. 1997. Superiority of winter sowing over traditional spring sowing of chickpea in the Mediterranean region. Agro. J. 89:112-118.

Singh, M., R.S. Malhotra, S. Ceccarelli, A. Sarker, S. Grando, and W. Erskine. 2003. Spatial variability models to improve dryland field trials. Exp. Agri39:151-160.

Tawaha, A.R.M., M.A. Turk, and K.D. Lee. 2005. Adaptation of chickpea to cultural practices in a Mediterranean type environment. Res. J. Agric. Biolog. Sci. 1:152-157.

Yadav, S.S., A.K. Verma, A.H. Rizvi, D. Singh, J. Kumar, and M. Andrews. 2010. Impact of genotype x environment interactions on the relative performance of diverse groups of chickpea (*Cicer arietinum* L.) varieties. Archi. Agron. Soil Sci. 56:49-64.

Yan, W. 2011.GGE Biplot vs. AMMI graphs for Genotype-by-Environment Data analysis, J. Indian Soc. Agric. Statist. 65:181-193.

Table –1. Number of genotypes tested each year under the Chickpea International Elite Nursery- Spring (CIEN-S) using experimental designs at Tel Hadya and Terbol in the winter and spring seasons

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name of trial† | Year | Experimental Design | Number of genotypes | Block size |
| CIEN-S | 1997 | Lattice design | 64 | 8 |
| CIEN-S | 1998 | Lattice design | 49 | 7 |
| CIEN-S | 1999 | Lattice design | 64 | 8 |
| CIEN-S | 2000 | Alpha design | 72 | 9 |
| CIEN-S | 2000 | Lattice design | 49 | 7 |
| CIEN-S | 2000 | Lattice design | 49 | 7 |
| CIEN-S | 2001 | Lattice design | 36 | 6 |
| CIEN-S | 2001 | Lattice design | 36 | 6 |
| CIEN-S | 2002 | Lattice design | 36 | 6 |
| CIEN-S | 2003 | Lattice design | 36 | 6 |
| CIEN-S | 2004 | Lattice design | 36 | 6 |
| CIEN-S | 2005 | Lattice design | 36 | 6 |
| CIEN-S | 2006 | Lattice design | 49 | 7 |
| CIEN-S | 2007 | Lattice design | 36 |  6 |
| CIEN-S | 2008 | Lattice design | 36 | 6 |
| CIEN-S | 2009 | Lattice design | 36 | 6 |
| CIEN-S | 2010 | Alpha design | 45 | 9 |

† CIEN-S – Chickpea International Elite Nursery-Spring

Table –2. Trial name, number, location, means overall genotypes, coefficient of variation (CV), design efficiency and heritability

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Location | TR-S | TR-W | TH-S | TH-W |
|  | No. trials | 17 | 17 | 16 | 16 |
| Yield (kg ha-1) | Mean | 1215 | 2095 | 759 | 1340 |
|  | Minimum | 608.5 | 1431 | 106.9 | 501.9 |
|  | Maximum | 1864 | 2612 | 1551 | 2580 |
| CV (%) | Mean | 16.6 | 12.05 | 23.3 | 13.57 |
|  | Minimum | 9.758 | 6.912 | 8.907 | 7.807 |
|  | Maximum | 31.9 | 19.75 | 66.16 | 27.24 |
| Efficiency (%)  | Mean | 110.5 | 112.7 | 109.8 | 120.3 |
|  | Minimum | 100 | 100 | 97.92 | 100 |
|  | Maximum | 197.8 | 187 | 162 | 180.6 |
| Heritability (%) | Mean | 68 | 61 | 58 | 59 |
|  | Minimum | 19 | 5 | 24 | 20 |
|  | Maximum | 87 | 82 | 86 | 90 |

TR-S – Terbol, spring; TR-W – Terbol, winter; TH-S – Tel Hadya, spring; TH-W – Tel Hadya, winter

Table –3. Estimates of variance components for genotype, genotype x environment interactions and genotype x location x season for yield in kg ha-1

|  |  |  |  |
| --- | --- | --- | --- |
| Random term | Variance component estimate | Estimated standard error | Phenotypic variance (%) |
| Genotype | 18,631\*\*\* | 2,461 | 23% |
| Genotype x location-season | 24,883\*\*\* | 2,340 | 30% |
| Error | 39,148 | 1,169 | 47% |
| Genotype x location | 566 | 2,433 | 2% |
| Genotype x season | 14,987\*\*\* | 3,031 | 44% |
| Genotype x location x season | 18,168\*\*\* | 2,758 | 54% |

\*\*\* Significant at the 0.001 probability level.

Table – 4. Best linear unbiased predictor estimates of genotypes, estimated Type 4 stability parameter and temporal coefficient of variation and rank of genotypes for the top 30% of genotypes selected at Tel Hadya in spring†

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Genotype | Tel Hadya† | Terbol† | Mean | Type 4 stability | Temporal CV |
| SN | Entry No. | Name | Spring | Winter | Spring | Winter |  | MSYrLoc | Rank | TCV | Rank |
|  |  |  | (kg ha-1) |  |  |  |  |
| 3 | 378 | S 95419 | **1,633** | **2,566** | 1,082 | 1,847 | 1,642 | 162 | 1 | 0.29 | 1 |
| 4 | 371 | S 95335 | **1,583** | **2,756** | 1,102 | 1,716 | 1,652 | 800 | 2 | 0.64 | 2 |
| 43 | 383 | S 95439 | 1,104 | **2,548** | 1,070 | 1,260 | 1,410 | 2,592 | 3 | 1.19 | 3 |
| 24 | 364 | S 95304 | **1,229** | **2,623** | 968 | 1,752 | 1,508 | 7,200 | 7 | 2.19 | 4 |
| 13 | 158 | FLIP 94-52C | **1,314** | **2,468** | 994 | 1,809 | 1,516 | 10,224 | 9 | 2.54 | 5 |
| 15 | 359 | S 95277 | **1,302** | **2,738** | 869 | 1,751 | 1,506 | 13,122 | 10 | 3.3 | 6 |
| 38 | 355 | S 95247 | 1,144 | **2,513** | 996 | 1,987 | 1,527 | 18,240 | 11 | 3.39 | 7 |
| 27 | 344 | S 95196 | **1,214** | **2,512** | 1,054 | 1,536 | 1,474 | 57,460 | 30 | 5.68 | 8 |
| 10 | 360 | S 95280 | **1,356** | **2,778** | 860 | 1,627 | 1,496 | 43,218 | 23 | 6.04 | 9 |
| 36 | 354 | S 95246 | 1,172 | **2,587** | 978 | 1,604 | 1,464 | 58,140 | 31 | 6.17 | 10 |
| 42 | 351 | S 95235 | 1,111 | **2,502** | 895 | 2,100 | 1,501 | 49,298 | 25 | 6.2 | 11 |
| 26 | 367 | S 95321 | **1,217** | **2,821** | 1,020 | 1,925 | 1,601 | 75,660 | 42 | 6.74 | 12 |
| 2 | 335 | S 95082 | **1,725** | **2,858** | 1,222 | 1,969 | 1,799 | 189,112 | 89 | 8.9 | 14 |
| 45 | 365 | S 95307 | 1,072 | **2,553** | 1,070 | 2,076 | 1,568 | 189,728 | 90 | 10.18 | 16 |
| 37 | 352 | S 95236 | 1,157 | **2,513** | 968 | 2,057 | 1,533 | 161,880 | 84 | 10.39 | 17 |
| 9 | 311 | FLIP 98-91C | **1,359.5** | **1,910** | 1,702 | 2,658 | 1,907 | 64,986 | 35 | 11.16 | 19 |
| 20 | 34 | FLIP 01-49C | **1,254** | **1,800** | 1,802 | 2,286 | 1,785 | 76,047 | 43 | 14.91 | 25 |
| 23 | 21 | FLIP 01-06C | **1,232.5** | **1,704** | 1,732 | 2,305 | 1,743 | 73,822 | 41 | 16.19 | 27 |
| 22 | 25 | FLIP 01-30C | **1,237** | **1,877** | 1,884 | 2,235 | 1,808 | 109,390 | 61 | 16.96 | 30 |
| 1 | 82 | FLIP 04-05C | NA | 1,053 | 1,622 | 1,972 | 1,549 | 110,946 | 63 | 17.41 | 31 |
| 32 | 10 | FLIP 00-20C | 1,181 | **1,636** | 1,538 | 2,075 | 1,608 | 106,477 | 59 | 18.23 | 36 |
| 5 | 38 | FLIP 01-56C | **1,570** | **1,306** | 1,504 | 2,162 | 1,645 | 246,389 | 102 | 18.55 | 38 |
| 8 | 247 | FLIP 98-106C | **1,360** | **1,806** | 1,536 | 2,192 | 1,723 | 133,716 | 72 | 18.59 | 40 |
| 7 | 221 | FLIP 97-50C | **1,389.5** | **1,659** | 1,,162 | 1,852 | 1,516 | 135,032 | 73 | 19.09 | 43 |
| 18 | 331 | FLIP 99-61C | **1,259.5** | **1,802** | 1,408 | 1,772 | 1,560 | 126,658 | 70 | 19.62 | 44 |
| 16 | 309 | FLIP 98-79C | **1,272.7** | **1,716** | 1,313 | 1,935 | 1,559 | 120,428 | 67 | 19.73 | 45 |
| 6 | 284 | FLIP 98-200C | **1,514** | **2,082** | 916 | 2,452 | 1,741 | 89,833 | 51 | 20.51 | 49 |
| 17 | 277 | FLIP 98-174C | **1,272** | **1,950** | 1,061 | 1,830 | 1,528 | 160,890 | 83 | 23.18 | 57 |
| 29 | 323 | FLIP 99-37C | **1,197.5** | **1,650** | 1,114 | 1,834 | 1,449 | 131,334 | 71 | 24.34 | 61 |
| 28 | 276 | FLIP 98-16C | **1,202.5** | **1,650** | 1,104 | 1,912 | 1,467 | 138,066 | 74 | 24.7 | 65 |
| 33 | 321 | FLIP 99-23C | 1,181 | **1,736** | 1,015 | 1,660 | 1,398 | 149,951 | 81 | 25.11 | 68 |
| 34 | 8 | FLIP 00-18C | 1,177.3 | **1,674** | 1,637 | 2,112 | 1,650 | 227,835 | 98 | 25.86 | 72 |
| 46 | 33 | FLIP 01-43C | 1,062 | 1,335 | 1,625 | 2,088 | 1,559 | 138,146 | 75 | 26.11 | 75 |
| 21 | 202 | FLIP 97-219C | **1,249.7** | **1,748** | 672 | 1,830 | 1,375 | 182,973 | 87 | 27.94 | 79 |
| 35 | 259 | FLIP 98-129C | 1,175.4 | **1,672** | 1,050 | 1,813 | 1,428 | 196,904 | 92 | 29.77 | 87 |
| 14 | 303 | FLIP 98-55C | **1,305** | **1,868** | 1,420 | 1,818 | 1,603 | 280,558 | 111 | 29.78 | 88 |
| 48 | 26 | FLIP 01-32C | 1,042 | 1,490 | 1,655 | 2,206 | 1,598 | 186,707 | 88 | 29.85 | 89 |
| 12 | 328 | FLIP 99-47C | **1,325.5** | **1,892** | 1,036 | 1,671 | 1,481 | 211,495 | 94 | 30.42 | 92 |
| 19 | 333 | FLIP 99-69C | **1,254.5** | **1,712** | 1,431 | 1,635 | 1,508 | 232,182 | 99 | 30.48 | 93 |
| 31 | 251 | FLIP 98-113C | 1,188.7 | **1,684** | 1,435 | 2,318 | 1,656 | 256,648 | 103 | 30.51 | 94 |
| 30 | 302 | FLIP 98-53C | **1,189.2** | **1,694** | 1,063 | 2,121 | 1,517 | 259,716 | 104 | 31.16 | 96 |
| 11 | 7 | FLIP 00-17C | **1,351** | 1,468 | 1,397 | 1,216 | 1,358 | 277,416 | 109 | 35.85 | 103 |
| 25 | 307 | FLIP 98-68C | **1,221** | 1,240 | 700 | 2,212 | 1,361 | 504,744 | 139 | 37.67 | 109 |
| 39 | 255 | FLIP 98-121C | 1,129 | **1,748** | 1,440 | 2,710 | 1,756 | 532,249 | 141 | 41 | 114 |
| 40 | 254 | FLIP 98-120C | 1,126.5 | **1,655** | 1,312 | 2,668 | 1,690 | 596,811 | 147 | 42.14 | 118 |
| 47 | 177 | FLIP 97-120C | 1,047.5 | **1,576** | 884 | 2,091 | 1,400 | 339,469 | 123 | 45.07 | 123 |
| 41 | 273 | FLIP 98-162C | 1,126 | **1,708** | 1,440 | 2,819 | 1,773 | 793,729 | 158 | 46.61 | 127 |
| 44 | 269 | FLIP 98-158C | 1,087 | 1,192 | 1,412 | 2,596 | 1,572 | 694,252 | 153 | 58.19 | 150 |
|  |  | Local check | 986 | 1,305 | 1,314 | 2,019 |  |  |  |  |  |
|  |  | Av. SE (mean) | 73.2 | 94.7 | 126.7 | 153.6 |  |  |  |  |  |
|  |  | Av. LSD (5%) | 203 | 263 | 351 | 426 |  |  |  |  |  |

† Underlined text indicates significantly superior to the local check at *P* < 5%.

NA– missing, Av. – average, SE – standard error, LSD – least significant difference at 5%, MSYrLoc – Mean square yield

Table –5. Predicted means of high yielding genotypes/lines that were common within the top 30% selection intensity at both the locations seasons-wise

|  |  |  |  |
| --- | --- | --- | --- |
|  | Genotype | Predicted mean yield (kg ha-1) (rank) in spring  | Predicted mean yield (kg ha-1) (rank) in winter |
| Entry no. | Name | Tel Hadya | Terbol | Tel Hadya | Terbol |
| 38 | FLIP 01-56C | 1,570 (4)† | 1,504 (45) |  |  |
| 247 | FLIP 98-106C | 1,360 (7) | 1,536 (38) |  |  |
| 311 | FLIP 98-91C | 1,360 (8) | 1,702 (8) | 1,910 (18) | 2,658 (5) |
| 34 | FLIP 01-49C | 1,254 (19) | 1,802 (2) |  |  |
| 25 | FLIP 01-30C | 1,237 (21) | 1,884 (1) | 1,877 (20) | 2,235 (47) |
| 21 | FLIP 01-06C | 1,233 (22) | 1,732 (5) | 1,704 (32) | 2,305 (33) |
| 10 | FLIP 00-20C | 1,181 (31) | 1,538 (37) |  |  |
| 8 | FLIP 00-18C | 1,177.3 (33) | 1,637 (19) |  |  |
| 33 | FLIP 01-43C | 1,062 (45) | 1,625 (20) |  |  |
| 26 | FLIP 01-32C | 1,042 (47) | 1,655 (17) |  |  |
|  | Local check | 986 | 1,314 | 1,305 | 2,019 |
|  | Av. SE  | 73.2 | 94.7 | 126.7 | 153.6 |

† underline indicates significantly superior to the local check at *P* < 5%.

Av.SE = Average standard error.

**Table**–6. Predicted means of high yielding genotypes/lines that were common within the top 30% selection intensity at each locations in different seasons

|  |  |  |  |
| --- | --- | --- | --- |
|  | Genotype† | Predicted mean yield (kg ha-1) (rank) in spring | Predicted mean yield (kg ha-1) (rank) in winter |
| Entry no. | Name | Tel Hadya | Terbol | Tel Hadya | Terbol |
| 25 | FLIP 01-30C | 1,237 (21) | 1,884 (1) | 1,877 (20) | 2,235 (47) |
| 34 | FLIP 01-49C | 1,254 (19) | 1,802 (2) | 1,800 (25) | 2,286 (38) |
| 21 | FLIP 01-06C | 1,233 (22) | 1,732 (5) | 1,704 (32) | 2,305 (33) |
|  | Local check | 986 | 1314 | 1305 | 2019 |
|  | Av. SE | 73.2 | 94.7 | 126.7 | 153.6 |

†The above three lines yielded significantly more than the respective local checks at *P* < 5%, except at Terbol in winter.

Av.SE = Average standard error.



Figure 1. GGE biplot (scatter plot) for genotypes and environment using lowest 10% of genotypes culled from each environment. Plots are environment scaled/focused and without normalization of GGE data. TH-S – Tel Hadya, spring; TH-W – Tel Hadya, winter; TR-S – Terbol, spring; TR-W ­ Terbol, winter. The genotype labels - G8 = FLIP 00-18C, G10 = FLIP 00-20C, G21 = FLIP 01-06C, G25 = FLIP 01-30C, G34 = FLIP 01-49C, G158 = FLIP 94-52C, G221 = FLIP 97-50C, G247 = FLIP 98-106C, G251 = FLIP 98-113C, G254 = FLIP 98-120C, G255 = FLIP 98-121C, G259 = FLIP 98-129C, G273 = FLIP 98-162C, G276 = FLIP 98-16C, G277 = FLIP 98-174C, G284 = FLIP 98-200C, G302 = FLIP 98-53C, G303 = FLIP 98-55C, G309 = FLIP 98-79C, G311 = FLIP 98-91C, G321 = FLIP 99-23C, G328 = FLIP 99-47C, G331 = FLIP 99-61C, G333 = FLIP 99-69C, G352 = S 95236, G364 = S 95304, G365 = S 95307, G367 = S 95321, G371 = S 95335, G378 = S 95419



Figure 2. GGE biplot for comparing genotypes using lowest 10% of genotypes culled from each environment. Plots are environment scaled/focused and without normalization of GGE data. TH-S – Tel Hadya, spring; TH-W – Tel Hadya, winter; TR-S – Terbol, spring; TR-W – Terbol, winter. The genotype labels are same as given in the caption of Figure 1.