Breeding Progress for Yield in Winter Wheat Genotypes Targeted to Irrigated Environments of the CWANA region

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Abstract

The international winter wheat improvement program (IWWIP), an alliance between Turkey-CIMMYT-ICARDA, has distributed improved germplasm to different National Agricultural Research Systems (NARS) partners through international nurseries and yield trials for the last 13 years. This study was carried out in order to determine the rate of breeding progress for yield and yield related traits at IWWIP using data of the international winter wheat yield trials (IWWYT) , IWWYT 1 – 13, collected from 1997 - 2010 in irrigated environments across different countries. The relative grain yield of the best line (BL) expressed as percent of the best check (Kinaci-97), widely grown cultivar (Bezostaya) and trial mean (TM) increased at a rate of 0.6, 1.6 and 0.2% /year, each non-significant ($P>0.05$), respectively. Regression analysis indicated that TM has increased at a rate of 91.9 kg/ha/year ($P=0.007$). The net realized breeding progress was estimated by accounting the variability due to management and weather conditions using surrogate variables such as integrated biological indices taken as means of common checks. The net realized gain for the BL was 66.2 ± 19.7 kg/ha/year ($P=0.01$). Success rate of the BL, per cent of sites where the BL exceeds the local check in grain yield, ranged from 50 to 87% across trials. To date, more than 40 varieties of IWWIP origin have been released in 10 countries of Central and West Asia including Afghanistan, Turkey, Iran, Uzbekistan and Tajikistan. Some varieties, such as Solh and Kinaci-97, have been released under different names in different countries indicating their broad adaptation. Cluster analysis of IWWYT sites indicated that IWWIP sites in Turkey and Syria are associated with most of the testing sites in Central and West Asia and North Africa (CWANA) region. The recently identified high yielding genotypes are recommended for direct release and/or parental purposes by the respective NARS.

Key words: genetic gain, biological index, time trend, winter wheat, yield

Introduction

37 Wheat is the most widely grown cereal crop in the world and one of the central pillars of global
38 food security. About 651 million tons of wheat was produced on 217 million hectares in 2010
39 with average yield of 3t/ha⁻¹ (FAO 2012). Winter and facultative wheats are grown on an
40 estimated 80 million ha of the 226 million ha devoted to wheat worldwide. Out of this area, the
41 Central and West Asia and North Africa (CWANA) region accounts for about 18 million hectares.
42 Though wheat is the dominant crop in this region, its productivity is very low (1-2.5 t/ha) and
43 highly variable due to abiotic stresses (drought, cold, heat, salinity) and biotic stresses such as
44 yellow rust (*Puccinia striiformis*), leaf rust (*Puccinia recondita*), stem rust (*Puccinia graminis*),
45 root rots (*Fusarium culmorum*), Russian Wheat Aphid (*Diuraphis noxia*), Sunn pest (*Eurygaster*
46 *integriceps*), and Hessian Fly (*Mayetiola destructor*) (Braun et al. 1998; Morgounov et al. 2012;
47 Sharma et al. 2010).

48
49 Genetic gain studies for yield and other agronomic traits are important for any crop breeding
50 program in order to evaluate its strength and weakness, demonstrate to the general public about
51 its potential contributions and design priorities and strategies for future breeding activities.
52 Genetic gain or relative contribution of plant breeding to yield improvement in a given cropping
53 region can be estimated by comparing commercial cultivars released during a period of time
54 grown in common environments using progress evaluation trials or multi-environment trials
55 (METs) that are routinely conducted as part of the breeding programs (Fufa et al. 2005;
56 Graybosch and Peterson 2010; Mackay et al. 2010; Reynolds et al. 2007; Slafer and Andrade
57 1989; Trethowan et al. 2002; Xio et al. 2012). Analysis of the large data sets obtained from
58 METs over time gives the opportunity to expand the size of genotypes and environments; to
59 estimate the performance of genotypes within and across the group of environments for which
60 they were bred; and to exploit the genotype x environment (G x E) interactions and
61 rationalization of environments for testing in future.

62
63 The international winter wheat improvement program (IWWIP), an alliance between Turkey-
64 CIMMYT (International Center for Maize and Wheat Improvement) – ICARDA (International
65 Center for Agricultural Research in the Dry Areas), was formed in 1991 to develop high yielding
66 and disease and insect resistant wheat genotypes with acceptable grain quality for the world in
67 general and the CWANA in particular. It has distributed improved germplasm to different

68 National Agricultural Research Systems (NARS) partners through international nurseries and yield
69 trials for the last 13 years. However, the genetic gains for yield and other traits were not analyzed
70 to-date. This study is, therefore, carried out to determine the rate of wheat breeding progress for
71 grain yield and other traits at IWWIP using IWWYT 1 - 13 data collected from 1997-2010 across
72 different countries.

73

74 **Materials and methods**

75

76 Locations, genotypes and experimental designs

77 Hallmark cultivars grown dominantly in the CWANA region, landraces, spring wheat mega
78 cultivars, synthetic wheats and elite breeding lines are routinely used to compose crossing blocks.
79 Annually about 500-1000 simple, top and backcrosses are developed. Mostly, winter x spring simple
80 crosses are made and backcrossed/ top crossed with winter wheat genotypes at Izmir and Eskisehir
81 in Turkey and Tel Hadya in Syria. Evaluation and selection of segregating populations and advanced
82 lines were carried out at six different locations: Edirne, Konya, Eskisehir, Diyarbakır, Adapazari and
83 Ankara in Turkey and at Tel Hadya in Syria using selected bulk/modified pedigree selection
84 methods under supplemental irrigation systems.

85 Selected genotypes under such rigorous processes are distributed annually to NARS through
86 international nurseries and yield trials. For this study, we have used 12 trials, IWWYT 1-IWWYT 13
87 (1997-2010, except IWWYT6 in 2003) which are principally developed for high yield potential and
88 irrigated environments. The test locations and IWWYT numbers carried out at each location are
89 indicated in Table 1. A total of 310 genotypes and 114 environments were used for this study from
90 1997-2010. Each IWWYT were composed of mostly 25 genotypes including three common check
91 cultivars (Beszostaya, Katia, Kinagi-97) and a local check cultivar. In IWWYTs 12 and 13, a total of
92 20 and 40 genotypes, respectively were tested. The genotypes in each trial were planted using alpha
93 lattice design (Patterson and Williams 1976; Payne 2009) in two replications in a plot size of 2.5 m
94 length, six rows with 0.2m spacing between rows. The 4 central rows (net plot size of 3m²) were
95 harvested at maturity. Standard agronomic practices were applied as per the recommendation of each
96 location in each country. Data were mostly recorded for days to heading, days to maturity, diseases,
97 plant height (cm), 1000 grain weight (g), and grain yield (kg/ha).

98

Insert Table 1 here

99 **Statistical analysis**

100 Estimation of Breeding Progress

101 Evaluation of genotypes in a given trial comprised of multi-location testing and the adjusted
102 mean values of genotypes were obtained as a first step by analyzing the data using the
103 experimental design factors in the model following restricted maximum likelihood (REML)
104 method for the incomplete block design. The adjusted grain yield of each genotype at each
105 location was obtained as the best linear unbiased prediction (BLUP) for the incomplete block
106 differences of the alpha design used. The table of genotype x location (GxL) mean values was
107 further modeled using AMMI (Additive Main effects and Multiplicative Interaction) model. The
108 significant multiplicative terms were retained to represent the pattern in the GxL interaction and,
109 therefore, for predicting the genotypes performance in a given location. Such a predicted value
110 thus becomes free from the noise that may arise due to interrelationship between the interaction
111 components and experimental errors. The details on AMMI methodology is indicated in Gauch
112 et al. (2008).

113 The progress for grain yield was estimated by regressing the relative yield of the best line (BL)
114 in each trial across years. Relative yield of BL is yield of BL expressed as percentage of the yield
115 of Kinaci-97, Bezostaya and TM each. Kinaci- 97 is the best performing check cultivar and
116 Bezostaya is the most widely grown cultivar in the CWANA region (Sharma et al. 2010). The
117 net realized breeding progress was determined by the change in the yield of the BL after
118 adjusting for the variation due to the management and weather factors following the methods of
119 Finlay and Wilkinson (1963). Mean of the common check cultivars across trials stands for a
120 biological indicator or an integrated index of the general performance of the environment. While
121 the mean of common checks could be used to measure the trial performance overall the
122 locations, the mean of local checks can be justified to account for any specific differences
123 assigned to the locations. Thus, the progress made in the breeding process could be evaluated
124 using multiple linear regression of the yield of the BL on mean of common checks (CC), local
125 checks (LC) and time variable (i.e. year number), as represented by: $BL = a + b CC + c LC + d$
126 Year; where the constants: a is intercept, b and c are environmental effect comprised as slopes of
127 CC and LC, while d is the 'net progress' made due to breeding and selection per year. We also
128 examined the question if there is any real progress made in each of the common checks (Kinaci-

97, Bezostaya and Katia), using the above approach. We have also determined the success rate (SR) of the BL in each trial as % of sites where the BL was yielding higher than the local check (Tadesse et al. 2010).

Clustering of Testing Sites

With a view to rationalize the locations that were carried forward during the course of multi-year testing and retained during 2010 (the latest year of testing, IWWYT13), we applied a hierarchical clustering method on 40 genotypes predicted means at 15 locations. The similarity index values between two environments were computed using Euclidean squared distance and the average linkage method of clustering, also known as UPGMA (unweighted pair group method with arithmetic mean), was used to generate the clusters under the Genstat software (Payne 2009).

Results

Progress in grain yield

The performance of the BL in each trial is indicated in Table 2. Mean grain yield of the BL ranged from 4391kg/ha in entry number 25 (HYS/7C//KRC(ES84-16)/3/SERI) of Trial 2 to 6658 kg/ha in entry number 9818 (VORONA//MILAN/SHA7/3/MV17) of Trial 11.

Insert Table 2 here

The performance of Bezostaya, Kinaci-97, Katia and the local check is indicated in Fig.1. The performance of these check cultivars varied from season to season with the highest in the 11th IWWYT (2008/9 season) and the lowest in the 3rd IWWYT (1999 season).

Insert Fig 1 here

Simple regression of relative grain yield of BL in each trial across years is indicated in Fig. 2a, b & c. The relative grain yield of the BL expressed in per cent of Kinaci-97 (Fig 2a), Bezostaya (Fig 2b) and TM (Fig 2c) increased at a rate of 0.6, 1.6 and 0.2% per year, respectively. However, there was no significant linear increase of relative grain yield of BL to Kinaci-97 nor to Bezostaya as the correlation between time and the relative yields of BL were 0.41 (p =0.19) and 0.55 (p=0.064), respectively.

Insert Fig 2 here

160
161 When the effect of management and weather conditions over years were ignored, then grain
162 yield of the BL increased at a rate of 110 kg/ha/year ($R^2 = 0.66$; $P = 0.001$), while the trial mean
163 (TM) increased at a rate of 91.9 kg/ha/year ($R^2 = 0.53$; $P = 0.007$) (Fig 3).

164
165 **Insert Fig 3 here**

166 Accounting for the management and weather conditions, the net realized breeding progress of the BL increased at
167 the rate of 66.2 ± 19.7 kg/ha/year ($P=0.01$). As indicated in Table 3, each of the equations showed a highly
168 satisfactory fit to the data ($P<0.001$ and percentage variance accounted exceeded 85%). The
169 coefficient 'd' measuring progress over years was found significant ($P=0.01$) only for the BL but
170 not for any of the checks ($P>0.05$). The yields of checks exhibited a marginal linear trend with
171 time as shown by positive correlations: 0.604 ($P=0.038$) for Kinaci97, 0.501 ($P=0.097$) for
172 Bezostaya and 0.465 ($P=0.128$) for Katia. As expected, there was no significant progress made in
173 the grain yield of check cultivars when accounted for the year effects.

174
175 **Insert Table 3 here**

176 The SR of the BL remained constant with time as the correlation was 0.20 ($p=0.53$). The linear regression of
177 SR on year was: $SR = 55.67 (\pm 7.15) + 0.476(\pm 0.73)$ (Year -1995) with residual variance exceeding total
178 variance ($R^2 = 0.041$; $P=0.53$). In this case, the 95% confidence limit for average SR (%) was
179 (39.7, 71.6). The observed range for SR was 50 – 87% with mean of 60% indicating that in each trial the BL
180 performs better than the local check in more than 50% of the locations (Fig 4).

181
182 **Insert Fig 4 here**

183
184
185 **Clustering of testing sites**

186 Cluster analysis based on mean grain yield performance of the locations across trials has grouped
187 the locations into four major clusters at 95% similarity level (Fig 5). Clusters, I to IV may be
188 assigned to the groups of locations from the top to the bottom in the dendrogram. Thus the
189 cluster on the top, Cluster I consists of locations AFG22 (Bamyan, Afghanistan), UKR01
190 (Odessa, Ukraine), IRN01 (Karaj, Iran), TAJ01 (Hisar, Tajikistan), and TUR03 (Sakarya,

Turkey). Cluster II (below Cluster I) had majority of test locations. Cluster III consists of BUL01(Novisad, Bulgaria) and SRB01(Dobroudja, Serbia). Two locations, KYR01 (Bishkek, Kyrgyzstan) and KAZ02 (Saryagashsky, Kazakhstan), were grouped in cluster IV. The genotypes response pattern to the locations in this cluster (IV) are very different from the other locations to the extent that cluster IV did not merge with other clusters even at 50% level of similarity. The main IWWIP breeding sites such as TUR09 (Eskisehir), TUR13 (Konya), TUR07 (Edirne), and SYR01 (Aleppo) are grouped in cluster II.

Insert Fig 5 here

Discussion

Development and identification of high yielding genotypes with wide adaptation and resistance to biotic and abiotic stresses remain the top priorities of the IWWIP program. There are different approaches of determining the breeding progress or the rate of genetic gain for grain yield and other traits. Some studies use yield of historical genotypes grown in the same environment (Fischer and Wall 1976; McCaig and DePauw 1995; Sayre et al. 1997; Sadras and Lawson, 2011) while others have used mean yield to examine progress over time in highly productive environments (Calderini et al. 1995; Kulshrestha and Jain 1982). Trethowan et al. (2002) have used regression analysis using the mean of the five highest yielding entries expressed as per cent of the trial mean across years to determine the rate of breeding progress in elite spring wheat yield trial (ESWYT) and semi-arid wheat yield trial (SAWYT). Tadesse et al. (2010) have used success rate analysis of best lines in the high rain fall wheat yield trials (HRWYT) to demonstrate yield gains over years or trials.

In this study, we have estimated breeding progress in IWWIP using some of the stated approaches. The grain yield performance of check cultivars showed an increasing trend except in some years such as 2010 in which there was an epidemic of yellow rust in the whole of the CWANA region (Hodson and Nazari 2010; Morgounov et al. 2012; Ziyaev et al. 2011). Similarly, wheat yield in the region has increased significantly for which crop management must

have played an important role indicating that productivity of wheat is not only associated with genetic gains but also with the prevailing conditions such as management, drought and diseases. The relative grain yield of the BL in per cent of Bezostaya has increased at a rate of 1.6%/year while its relative grain yield in per cent of Kinaci-97 and the TM was at a rate of 0.6 and 0.2 %/year which is relatively low. Similar genetic gains have been reported in different countries (Abbate et al. 1998; Austin et al. 1980, 1989; Brancourt-Hulmel et al. 2003, Cox et al. 1988, Donmez et al. 2001; Sayre et al. 1997; Waddington et al. 1986). Recently, using historical data sets, Mackay et al. (2010) have reported that at least 88% of the improvement in yield of cereals and oil seed crops in the United Kingdom is attributable to genetic improvement. The net realized breeding progress of the BL was estimated in terms of the coefficient of time after accounting for the variation due to management and weather variables in terms of the means of the common checks as a biological measure of the environment (Finlay and Wilkinson 1963) and also to account for any location specific differences in terms of the local check mean. The BL showed statistically significant breeding progress. An effective assessment of environment can be enhanced by increasing the number of common genotypes across locations/environments.

Another alternative was the use of TM to describe the environments but this also suffers from the facts that its genotype-base varies with year due to exclusion and inclusion of lines in the trial and also the BL mean is part of the trial mean. Using the TM as a biological measure of the change in the environment, the yield progress of the BL in each trials across years was estimated by the linear regression: $Y = 928(\pm 823) + 1.096 (\pm 0.200)TM + 29.1(\pm 24.3) (\text{Year}-1995)$; percentage variance accounted for was 96.7 (DF=9), $P < 0.001$ (for multiple regression) and $P = 0.026$ for the Year. In this case too, the breeding progress was significant and the increase per year was 29.1kg/ha/year. Using TM as indicator for the environments, there was no significant trend with time for each of the check cultivars indicating that genetic gain is only for the breeding lines.

Based on the SR analysis, entry number 9810 of IWWYT 3, entry number 9819 of IWWYT 10 and entry number 34 of IWWYT 13 showed the highest SR levels of 87, 70 and 68%, respectively. Those genotypes with the highest SR have high yield potential with wide adaptation as they exceeded the performance of the local check in many locations. It is expected that these genotypes would be released by the respective national programs. To date, more than 40 wheat varieties of IWWIP origin have been released in 10 countries of Central and West Asia including

253 Afghanistan, Iran and Turkey. Most of the dominantly grown varieties in the winter wheat
254 production areas of the CWANA region are facultative types. Some varieties, such as Solh
255 (OK82282//BOW/NKT) and Kinaci-97 (YMH/TOB//MCD/3/LIRA), have been released under
256 different names in different countries indicating their broad adaptation. The former is released in
257 Afghanistan and Kyrgyzstan while the later has been released in Turkey, Afghanistan and
258 Uzbekistan. Recently, a high yielding and yellow rust resistant genotype named MURAJ
259 (DORADE-5//KS82117/MLT) has been submitted for release in Uzbekistan and Syria.
260 The high yielding genotypes identified in IWWYT 1 through 13 are recommended for direct
261 release by the respective NARS.

262
263 Cluster analysis of IWWYT sites based on mean grain yield performance indicated that the
264 IWWIP breeding sites in Turkey and Syria are associated with most of the wheat testing sites in
265 the CWANA region. Such finding could help analyse the possibility of reducing the number of
266 IWWIP breeding sites currently being used in Turkey. In such a decision, however, it is
267 important to consider representativeness, high yield potential and high heritability (Allen et al.
268 1978; Braun et al. 1992; Lillemo et al. 2004; Tadesse et al. 2010), where maximum efficiency
269 would be achieved both in resource utilization and breeding gain. With a view to examine
270 whether rationalization of test locations can be carried out in terms of climatic variables,
271 hierarchical cluster analysis was performed using altitude data. The cluster formation was done
272 at 95% similarity levels which resulted in four clusters. It was found that the two sets of clusters
273 of the locations are not significantly associated (the data not shown). This implies that the
274 similarity of the test locations based on yields differ significantly from those based on the
275 climatic parameters. These results are consistent with the findings of Sarker et al. (2007, 2010) in
276 lentils where the yield based clusters differed significantly from the agro-ecological zones using
277 climatic variables.

Commented [R1]: I think since this point is not a finding or part of objective, we keep it in the Discussion section only. I have added those two references also.

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