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Interpreting genotype × environment interactions for grain yield of rainfed durum wheat in Iran



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ABSTRACT

Clustering genotype × environment (GE) interactions and understanding the causes of GE interactions are among the most important tasks in crop breeding programs. Pattern analysis (cluster and ordination techniques) was applied to analyze GE interactions for grain yield of 24 durum wheat (*Triticum turgidum* L. var. *durum*) genotypes (breeding lines and old and new cultivars) along with a popular bread wheat (*Triticum aestivum*) cultivar grown in 21 different rainfed environments during the 2010–2013 cropping seasons. To investigate the causes of GE interaction, several genotypic and environmental covariables were used. In a combined ANOVA, environment was the predominant source of variation, accounting for 81.2% of the total sum of squares (TSS), and the remaining TSS due to the GE interaction effect was almost seven times that of the genetic effect. Cluster analysis separated the environments into four groups with similar discriminating ability among genotypes, and genotypes into five groups with similar patterns in yield performance. Pattern analysis confirmed two major environmental clusters (cold and warm), and allowed the discrimination and characterization of genotype adaptation. Within the cold-environment cluster, several subclusters were identified. The breeding lines were most adapted to moderate and warm environments, whereas the old varieties were adapted to cold environments. The results indicated that winter rainfall and plant height were among the environmental and genotypic covariables, respectively, that contributed most to GE interaction for grain yield in rainfed durum wheat.

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1. Introduction

Durum wheat accounts for a small part of the world wheat industry, representing approximately 5% of acreage and 10% of total wheat production. World durum wheat production in

recent years has been approximately 30 million tons, with the European Union, Canada, and the United States accounting for nearly 60% of total production. Durum wheat is one of the most important crops in the Mediterranean areas, mainly in the Central and West Asia and North Africa (CWANA) region

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[1]. This region produces about 13 million tons annually, with Turkey, Syria, Morocco, Tunisia, Algeria, and Iran accounting for 84% of that production [1]. Rainfall and temperature in Mediterranean dryland areas show large and unpredictable fluctuations within and among cropping seasons. Durum wheat in Iran is cultivated across diverse environments, ranging from warm lowlands to cold highlands. The improvement of a crop's productivity under stress conditions requires genotypes with stress tolerance and yield stability [2].

To ensure valid genotype recommendation, a common practice among breeders is to repeat yield trials over years to validate recommendations. With this approach, crossover-type genotype \times environment (GE) interactions are frequently observed [3], limiting the adaptation of new varieties to only certain environments. In durum wheat, as in many other crops, insufficient yield stability has been recognized as one of the main factors responsible for the gap between yield potential and actual yield, particularly in drought-prone environments [4,5].

The GE interaction, defined as the variation in relative performance of genotypes in different environments [6], is challenging to plant breeders because it complicates the selection of superior genotypes, thereby reducing genetic progress [7]. If GE interactions are present, breeders need to identify stable genotypes with relatively consistent performance across a range of environments.

Several statistical methods have been proposed to investigate GE interactions. These range from univariate parametric models to multivariate models. Joint regression is the most popular of the univariate methods because of its simplicity of calculation and application [8]. Among the multivariate methods, pattern analysis has been successfully applied to analyzing GE interactions in multi-environment trials (MET) [9–12]. Pattern analysis consists of the complementary procedures of classification (clustering) and ordination [13,14]. GE interaction data obtained from regional yield trials can be investigated by pattern analysis [14–16] to identify genotypes with similar responses across environments and to identify environments that produce similar discriminations among the genotypes growing in them. Cluster analysis summarizes the complexity of the data while retaining most of its information by permitting the description of responses with relatively few genotype clusters, environment clusters, or both [17]. Biplot analysis summarizes the data by representing the patterns of the data in a small number of dimensions.

Numerous methods have been used in the search for understanding of the causes of GE interaction [18]. These methods can be categorized into two major strategies. The first involves factorial regression analysis of the GE matrix upon environmental factors, genotypic traits, or combinations of both [19]. The second involves correlation or regression analysis in which the environmental and/or genotypic interaction principal component (PC) scores of the GE matrix are related to environmental and/or genotypic covariables [20,21]. By relating the PC1 and PC2 scores to environmental conditions and genotypic traits, an understanding of the environmental and genotypic basis of the non-crossover and crossover GE interactions can be achieved [22].

The main objectives of this study were to (i) classify the GE interactions for grain yield of 25 wheat genotypes grown in 21

different rainfed environments and (ii) investigate the causes of GE interactions in durum wheat yield trials in Iran.

2. Materials and methods

2.1. Plant material and climatic data

Twenty four durum wheat genotypes (Table 1) including 21 breeding lines (G1–G21), one new (G22) and two old cultivars (G23, G24), along with one popular old bread wheat cultivar (G25) were tested in seven rainfed research stations representative of the major rainfed durum wheat-growing areas in Iran, during three cropping seasons (2010–2013), resulting in 21 environments (combinations of location and year). The seven stations were Maragheh (M11, M12, and M13 representing the 2011, 2012, and 2013 seasons), Qamloo (Q11, Q12, Q13), Shirvan (S11, S12, S13), Uromieh (U11, U12, U13), Ardebil (A11, A12, A13) (cold locations); Kermanshah (K11, K12, K13) (moderately cold location); and Ilam (I11, I12, I13) (warm location) (Table 2). In each environment, the experimental layout was a randomized complete block design with three replications. Plot size was 7.2 m² (6 rows, 6 m long, with 20-cm row spacing). Management practices recommended for each location were followed in all yield trials. The grain yields were measured on a plot basis and converted to kg ha⁻¹ for the statistical analyses.

In addition to grain yield, drought adaptive traits including days to heading (DTH), days to maturity (DTM), plant height (PLH), and 1000-kernel weight (TKW) were measured for the genotypes in each environment. These traits were used as genotypic covariables. Climatic variables including monthly rainfall, minimum and maximum temperature, average temperature, freezing days, relative humidity, and evaporation were obtained from climatological stations established at the research stations and used as environmental covariables.

2.2. Data analysis

Combined analysis of variance (ANOVA) for grain yield data was performed to determine the effects of genotype (G), environment (E), and GE interaction effects. Pattern analysis was performed using the IRRISTAT statistical program on the basis of standardized mean data for each environment, following Fox and Rosielle [23]. Hierarchical agglomerative clustering [9] was applied to the GE interaction data matrix with incremental sums of squares [24] as the fusion criterion. In other words, in any part of the dendrogram, members or groups were joined to minimize the new within-group sums of squares. Dendrograms were constructed on the basis of fusion levels using the Ward method [24] to examine similarities in pattern of traits of interest among genotypes (in response to environments) and environments (in discriminating among genotypes). Classification efficacy was determined by the sum of squares retained in the reduced GE interaction data matrix. Ordination was performed on the environment standardized mean yield data using the singular-value decomposition (SVD) algorithm with results represented by a biplot [25,26]. The data were modeled in two dimensions, and the efficacy of the model was determined by the proportion of the sum of squares accounted for by each

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