Heat stress and yield stability of wheat genotypes under different sowing dates across agro-ecosystems in India

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ABSTRACT

Among the most significant impacts of climate change is the potential increase of food insecurity. The predicted impact of temperature rise due to climate change on the crop production and productivity can be mediated through different crop management adaptations such as shifted sowing dates. We investigated the effects of sowing dates on yield stability of wheat across agro-ecosystems and years using multi-environment trials. The objectives of the study were as follows: (i) to evaluate the genotype × environment × management (G × E × M) for wheat genotypes, (ii) to predict yield performance and identify high stable wheat genotypes in different management practices, and (iii) to make genotype-specific management and high performing genotype recommendations within and across agro-ecological regions. A diverse set of twenty-one genotypes was evaluated over three years (2012–2014) under ten levels of crop management practices (ten different dates of sowing: D01-D10) across three agro-ecological regions (BR, MP and PB) of India in replicated trials. Data were analyzed with SASG × E and RG × E programs using SAS and R programming languages, respectively. Results revealed that the impact of shifted sowing dates on yield stability was unevenly spread across management practices. Across locations, the genotype 'CSW 18' (G03), 'DPW 621-50' (G05), 'BAZ' (G01) were the best performer and high stable in early, normal and later sowing dates, respectively. Across and within an individual location(s), the pattern of predicted yield suggests that the low performing genotypes during early sowing dates tend to became high performer during late sowing dates. Similarly, high predictive yield and high stable genotypes from early planting tend to have variable predicted yield with low stability during normal and late sowing dates for across and within an individual location(s). Low predictive yield and low stable genotypes had disease resistant genes and, thus, can be served as parent for future breeding, where trait value low is desired.

1. Introduction

Climate change threatens to exacerbate existing threats to food security and livelihoods due to a combination of factors that include the increasing frequency and intensity of climate hazards, diminishing agricultural yields and reduced production in vulnerable regions, rising health and sanitation risks, increasing water scarcity, and intensifying conflicts over scarce resources, which would lead to new humanitarian crises as well as increasing displacement (IPCC, 2007). Understanding the specific impacts of climate change on food security is challenging because vulnerabilities are unevenly spread across the world. Even remote changes in climatic conditions can affect food security elsewhere. For examples, temperature changes affect the timing of runoff in Ganges catchments, causing an increase in peak flow during the monsoon period, but dry season river-flow is still very low (Stern, 2007). One of the most significant long-term climate change is temperature rise. Global average temperature is expected to rise as a result of climate change, and the spatial pattern of this rise is such that all areas will see an increase in temperature. By the 2050 s the global average temperature is projected to have risen between 2 and 4 °C above the pre-industrial climate. Empirical evidence suggests that increases in temperature in the period 1980–2008 have already resulted in average global maize and wheat yield reductions of 3.8% and 5.5% respectively, compared to a non-climate scenario (Lobell et al., 2011). Yield is a complex quantitative trait and greatly influenced by external environment, which results in scale or rank shift in its performance (Dia, 2012; Dia et al., 2016a). This relative shift of genotype performance from one environment (location × year combination) to another is known as genotype × environment interaction (G × E) (Dia et al., 2012a; Dia et al., 2012b).

Increases in local temperatures can generate devastating agricultural losses, and can be critical if they coincide with key stages of crop development (Wollenweber et al., 2003). The yields of many cereal crops can be drastically reduced by temperatures above 32 °C during the flowering stage: for instance, rice grain sterility occurs in temperatures in the mid–30s (Porter and Gawith, 1999; Wheeler et al., 2000; VaraPrasad et al., 2003; Hatfield et al., 2011). Empirical studies using historical crop-trial data have predicted that adverse impact of heat stress on crop yield can be mitigated by shifting sowing dates (Dhillon and Ortiz-Monasterio, 1993). Substantial studies have been conducted to identify high yielding and consistent performing genotypes (also known as stable genotypes). However, most of the high stable genotypes are less predictable across shifted sowing dates (crop management practices) since plant breeders often perform analysis of two-way data (genotype × site or G × E) for several consecutive years to detect stable genotypes without taking crop management practices into account (Dia, 2005; Dia et al., 2009; Gathala et al., 2011; Jat et al., 2009; Jat et al., 2013; Sapkota et al., 2017; Weindorf et al., 2008a; Weindorf et al., 2008b). Approximately one-sixth of the world's population currently lives in glacier-fed river basins where temperatures are projected to increase, particularly in areas such as the Indo-Gangetic Plain; these elevated temperature pressures will result in greater stress on crop yield and stability (Stern, 2007). Although little research has been carried out on the impacts of heat stress on crop yield, it is important to assess the potential effects, particularly in the context of yield stability. In this paper, we propose to identify high yielding and high stable wheat genotypes across Indo-Gangetic Plain (environments) and over ten different sowing dates (crop management practices).

The impenetrable interaction of a crop bio-system with the soil, the atmosphere, and the environment that a plant lives in introduces challenges when making breeding decisions because it complicates the demonstration of superiority of any genotype across environments. Genotype × environment interaction may result in low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This reduction leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll,

1963; Alghamdi, 2004; Kumar et al., 2013a). Several strategies have been proposed to deal with G × E, and the most powerful strategy is to exploit G × E either to develop locally adapted material or to use G × E to better characterize the genotypes (DeLacy et al., 1996; Mathews et al., 2008). Genotype × environment interaction can be characterized using statistical methods ranging from univariate to multivariate models. The univariate models include regression slope, deviation from regression, environmental variance, and Kang's yield-stability; multivariate models include genotype main effects plus genotype by environment interaction (GGE) biplot, and additive main effects and multiplicative interaction (AMMI) (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Shukla, 1972; Yan, 2001; Kang, 1993; Yan and Kang, 2003; Gauch, 2006). Multivariate models could be graphically represented through biplots where genotypes and environments are plotted in a single graph. Recently, hierarchical Bayesian and mixed models were introduced to model heterogeneous variance among environments and different correlation structures among environments (Jat and Serre, 2016; Jarquín et al., 2016; Li et al., 2010; Malosetti et al., 2004; Mathews et al., 2008). Mixed models allow more flexibility to model unbalanced data using restricted maximum likelihood estimates (REML). Each statistical method reflects different aspects of the G × E, and no single method adequately explains genotype performance across environments (Dia et al., 2016a). Stability statistics are best used in combination with trait performance (mean or BLUP: Best Linear Unbiased Predictor is an estimate of random effect) and have successfully been used in plant breeding.

In this study, we were interested in understanding differential sensitivity of certain wheat genotypes to different agro-ecological environments in India under shifted sowing dates for enhancing the selection of superior and stable genotypes. The objectives of the study were as follows: (i) to evaluate the genotype × environment × management interaction (G × E × M) for wheat genotypes, (ii) to predict yield performance and identify high stable wheat genotypes in different management practices, and (iii) to make genotype-specific management and high performing genotype recommendations within and across agro-ecological regions.

2. Materials and methods

2.1. Germplasm, location and management

Twenty-one genotypes of wheat were evaluated across three years (2012–2014) and three locations ranging from western to eastern Indo-Gangetic plains under ten different dates of sowing (management practices). Locations were chosen to represent the major wheat growing agro-ecological conditions for major wheat production regions in India: Pusa (25° 57′ 08″ N; 85° 40′ 13″ E), Bihar (BR), Jabalpur (23° 10′ 7.6″ N; 79° 55′ 55″ E), Madhya Pradesh (MP), and Ludhiana (30° 59′ 28″ N; 75° 44′ 11″ E), Punjab (PB) (Supplemental Figs. 1 and 2). The soils of the experimental plots at three locations, PB, MP and BR, were sandy loam, clay loam and silty loam, respectively. Twenty-one genotypes were semi-dwarf spring wheat chosen to represent new vs. old release; stress resistant vs. susceptible; rust resistant vs. susceptible; eastern vs. northern adapted; tall vs. short stature; early vs. late maturity; low vs. high yield; and varied 1000 kernel weight, protein content, spikelets ear^{-1} and seeds spike^{-1}. These genotypes are advanced breeding lines or officially released cultivars. Here after the word 'genotype' is used to indicate cultigen, cultivar, variety or genotype. Genotypes were considered to be random and representative samples of a wide range of genetic and phenotypic diversity in the wheat germplasm population (Table 1). Wheat genotypes were evaluated at ten levels of crop management: date of sowing (D01 to D10). Ten dates of sowing were evenly spaced at 7 days apart with D01 (first date of sowing) and D10 (last date of sowing) scheduled for October 15 and December 17, respectively, for all three years (2012–2014). In Indo-Gangetic plains, the wheat sowing times are broadly classified into three categories: early (October),