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Effect of genotype × environment × management interactions on chickpea phenotypic stability

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Abstract. Crop varieties interact with the environment, which affects their performance. It is imperative to know how the environment affects these crop varieties in order to choose carefully the optimal environment for growth. Chickpea (*Cicer arietinum* L.) is grown in varying environmental conditions including conventional and no-tillage under both irrigated and rainfed farming systems. Hence, genotype × environment × management interactions can affect yield stability. An experiment was conducted in north-western New South Wales, Australia, to investigate these interactions and to determine possible environment types to help focus crop improvement. Eight environments were considered and genotype plus genotype × environment interaction (GGE) biplots were generated to assess genotype stability and interactions with environment. Genotype and environment main effects and genotype × environment interactions (GEI) accounted for 12.6%, 66% and 12% of the total variation in yield, respectively. The most productive and stable environments were not tilled, irrespective of moisture status. The most stable and productive genotype was Sonali, closely followed by PBA Slasher and ICCV 96853. The eight test environments grouped into two environment types that differentiated on the basis of tillage regime. Moisture was not a determinant of site grouping.

Additional keywords: chickpea genotypes, conventional tillage, genotype-by-environment interaction, genotype-by-environment-by-management, GGE biplots, no-till, phenotypic stability.

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Introduction

The main chickpea (*Cicer arietinum* L.) growing regions of Australia are in north-western New South Wales and Queensland, which have a subtropical climate, and Victoria, which is characterised by a temperate climate (Stern and Ernst 2000). Narrabri, in north-western New South Wales, has summer-dominant rainfall with median annual rainfall ranging from 600 to 800 mm (Dang *et al*. 2015). Chickpea in this area is sown in autumn and frequently exposed to high temperatures in spring, and low and variable in-season rainfall (Freebairn *et al*. 1991). However, yield stability can be improved by using various management options including no-till practices and supplementary irrigation. No-till systems are beneficial because they improve soil structure (Page *et al*. 2013), increase soil aggregate stability (Chan and Mead 1988; Li *et al*. 2007), and improve water storage as a result of increased infiltration rates and reduced water evaporation (Radford *et al*. 1995). The increase in infiltration rate can be attributed to earthworm activity and plant roots from the previous crop, which creates continuity of macropores.

Genotypes vary in their adaptability to environments, with some showing broad and others specific adaptation. The mean performance of a genotype denotes its average performance, whereas stability is a measure of variability across several environments (Yan *et al*. 2001). Lack of yield stability is directly related to higher genotype × environment interaction (GEI) (Fox and Geiger 1986). This interaction complicates the selection of genotypes in a breeding program by offsetting expected responses and reducing heritability (Gauch and Zobel 1997; Pande *et al*. 2013). To complicate matters further, not all stable genotypes are high yielding across a wide range of environments; thus, they may be highly stable but have low yield potential. Hence, stability alone is not an effective selection goal.

Multi-environment trial (MET) data are imperative to understanding GEI (Annicchiarico 2002). Analysis of such data provides an estimate of GEI and site correlations that can be used to group environments for better targeting of breeding and selection.

The subdivision of the breeding target into smaller homogeneous units (or zones of specific adaptation) allows the plant breeder to manage GEI and develop germplasm with the suite of traits required for different environment types (Gauch and Zobel 1997; Yan *et al*. 2001). The alternative is to develop broadly adapted genotypes that show a high level of phenotypic stability and yield potential (Kanouni *et al*. 2015). However, these cultivars are rare, and yield across a target region may be compromised in the search for broad adaptation (Gauch *et al*. 1996). The genotype main effect and genotype × environment interaction (GGE) biplot provides a visual representation of genotypes with high stable yield across multiple environments and can be used to match genotype performance to environment types (Yan *et al*. 2001). The ideal genotypes in a biplot should exhibit high scores of the first principal component (PC1), which denote high yield, and low PC2 scores, which represent high stability (Hamayoon *et al*. 2011). The ideal environment discriminates genotypes on the basis of genetic differences, thus improving the effectiveness of selection (Gauch and Zobel 1997). The genotype and GEI are the main sources of variation in the biplot, whereas the environment is not relevant (Gauch and Zobel 1997; Yan and Tinker 2006). Thus, the environmental and residual effects are excluded.

Although the genotype stability of crop species has been studied extensively (Lin *et al*. 1986), little attention has been given to yield stability of chickpea and the factors that might improve yield and yield stability.

Therefore, the aim of this study was to assess yield and yield stability of chickpea by: (*i*) estimating the extent of GEI in chickpea grown under varying environmental conditions, (*ii*) delineating the target environment into sub-environments or zones of specific adaptation, and (*iii*) identifying genotypes with high yield and yield stability both within and across environment types.

Materials and methods

A field experiment was conducted at the IA Watson Grains Research Centre near Narrabri, in north-western New South Wales, during 2014 and 2015. Thirty-six genotypes (Appendix 1) were arranged in randomised complete block designs with two replications under two tillage regimes at two irrigation levels in both years. The tillage treatments were no-tillage (NT, denoted N in environment codes, see Table 1) and conventional tillage (CT, denoted C in environment codes), and the irrigation treatments were with irrigation (IR) and without irrigation (rainfed, RF). The experiments were arranged in a quadrant with tillage regimes running in one direction and irrigation treatments established perpendicular to the tillage treatments. Tillage and irrigation treatments were not duplicated; thus, four separate environments were generated each year (representing each combination of tillage and irrigation), resulting in eight environments across both years (Table 1). The NT treatments were established in 2006 and followed a field pea–wheat–barley rotation without tillage until the site was utilised for experiments in 2014 and 2015.

Table 1. Field environments with different tillage and moisture regimes for analysis of chickpea phenotypic stability

Environment	Code	Management regime
1	IRC14	Irrigation, tillage, 2014 season
2	IRC15	Irrigation, tillage, 2015 season
3	IRN14	Irrigation, no-till, 2014 season
4	IRN15	Irrigation, no-till, 2015 season
5	RFC14	Rainfed, tillage, 2014 season
6	RFC15	Rainfed, tillage, 2015 season
7	RFN14	Rainfed, no-till, 2014 season
8	RFN15	Rainfed, no-till, 2015 season

Data were analysed by using the analysis of variance function of Genstat 18th Edition (VSN International, Hemel Hempstead, UK) to determine GEI for the eight environments and the 36 genotypes. Further analysis was performed to estimate the extent of GEI for each tillage–moisture combination, whereby GGE biplots were constructed using the GGE function in Genstat. Mean weather data (temperature, rainfall and rainfall distribution) were estimated for each genotype at the vegetative, flowering and podding phenophases.

Results

Climate data and experimental site

There were significant differences among genotypes ($P < 0.05$) for all climate parameters estimated in 2014 and 2015, with the exception of minimum temperature at flowering (Table 2). Mean minimum temperature was lower in 2014 than 2015, and a similar trend was observed for mean maximum temperature. Rainfall in 2014 during the vegetative phase was close to half that received in 2015, with a higher frequency of rainfall events in 2015 than 2014. Mean minimum temperature at flowering was similar in both years, whereas the mean maximum temperature at the same phenophase was almost 5°C lower in 2014 than 2015. Rainfall in 2014 at flowering was more than double that received in 2015. The mean minimum temperature at podding was >3°C lower in 2014 than 2015, and the same trend was observed for mean maximum temperature. In general, the 2015 season was hotter with higher rainfall than the 2014 season. Two irrigations were applied in both seasons by using a lateral-move sprinkler irrigation system. In 2014, 35 mm was applied at each of flowering and early podding, whereas in 2015, 36 mm was applied at flowering and 26 mm at late podding.

Grain yield in different environments

Chickpea mean grain yield was higher in 2014 than 2015. In general, NT environments produced higher yield than CT, and irrigated more than rainfed environments. The highest yielding environment was IRN14 (mean 2148 kg ha^{-1}) followed by IRC14 at 1999 kg ha^{-1} (Fig. 1). RFC14 and RFN14 environments had similar grain yields. The environment with the lowest yield was RFC15 (1145 kg ha^{-1}). The environments were ranked for yield in the order: IRN14 > IRC14 > RFN14 > RFC14 > IRN15 > RFN15 > IRC15 > RFC15. There was more grain yield variability in 2014 than in 2015, and IRC15 and IRN15 produced very similar yield.

Table 2. Mean weather conditions for each environment for different stages of chickpea development

MinT, Mean minimum temperature; MaxT, mean maximum temperature; RD, rainfall distribution. Environment codes are as listed in Table 1. Within a row, year means followed by the same letter are not significantly different at $P = 0.05$

Weather variable	IRN14	RFN14	IRC14	RFC14	IRN15	RFN15	IRC15	RFC15	2014 mean	2015 mean
					Vegetative stage					
MinT	4.7	4.7	4.7	4.6	5.5	5.2	5.5	5.2	4.7a	5.3b
MaxT	17.2	17.2	17.2	17.2	19.7	19.3	19.7	19.2	17.2a	19.4b
Rainfall	79.1	73.7	75.4	70.6	141.8	140.2	141.4	140.2	74.7a	140.9b
RD	23.4	22.3	22.5	21.6	28.5	28.0	28.4	28.0	22.4a	28.2b
					Flowering stage					
MinT	7.7	7.4	7.7	7.3	8.1	7.2	7.8	7.0	7.5a	7.5a
MaxT	21.0	20.5	20.9	20.3	25.9	25.0	25.5	24.6	20.7a	25.3b
Rainfall	78.6	50.0	81.9	53.1	43.0	7.6	46.7	10.5	65.9a	27.0b
RD	12.5	13.2	13.5	13.9	2.9	1.5	3.2	2.0	13.2a	2.4b
					Podding stage					
MinT	11.5	11.0	11.5	11.1	15.0	14.3	14.8	14.2	11.3a	14.6b
MaxT	25.9	24.8	25.7	25.0	30.1	30.3	30.2	30.4	25.3a	30.2b
Rainfall	47.3	11.0	47.1	9.9	46.6	17.1	43.2	16.1	28.8a	30.7b
RD	4.5	2.1	4.3	2.0	5.9	4.0	5.4	3.4	3.2a	4.7b

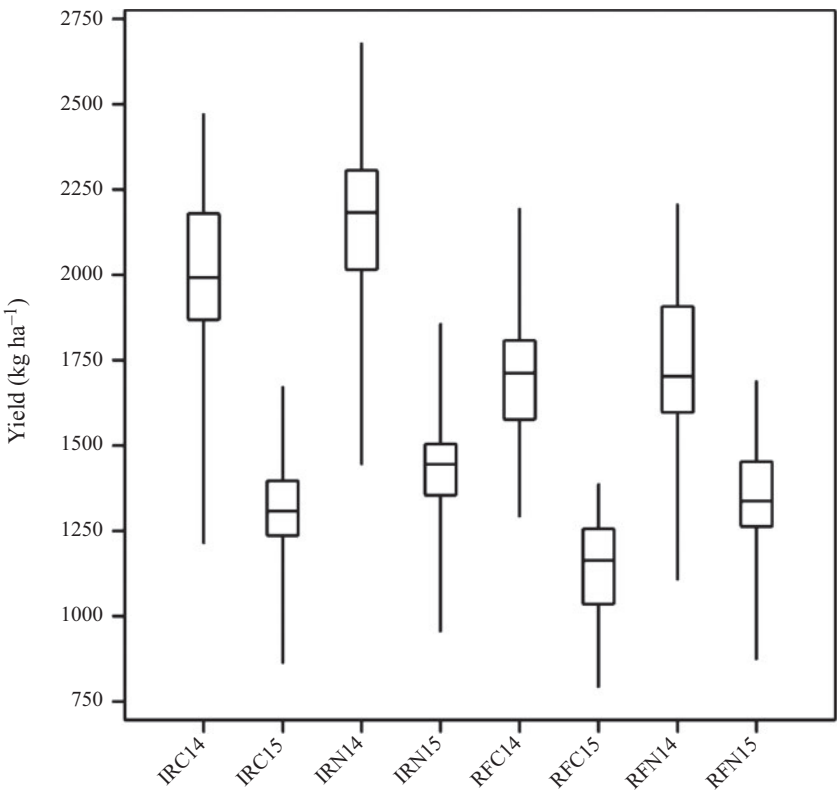

Fig. 1. Box plot for chickpea grain yield for different tillage and moisture regimes over two years (2014 and 2015). The box range denotes the interquartile range with the line in the middle of the box denoting the median. Both whiskers denote a quarter of the sample each. IR, Irrigation; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment.

Table 3. Combined analysis of variance for genotype and environment effects on mean chickpea grain yields
d.f., Degrees of freedom; SS, sums of squares; MS, mean sums of squares; VR, variance ratio; *F*-pr, Fischer test probability; TSS, total sums of squares

Source of variation	d.f.	SS	MS	VR	*F*-pr.	%TSS
Rep. stratum	1	16 641	16 641	0.54		
Genotype	35	11 992 315	342 638	11.11	<0.001	12.6
Environment	7	62 672 976	8 953 282	290.37	<0.001	66.0
Genotype × environment	245	11 412 558	46 582	1.51	<0.001	12.0
Residual	286	8 818 513	30 834			9.3
Total	574	94 909 369				

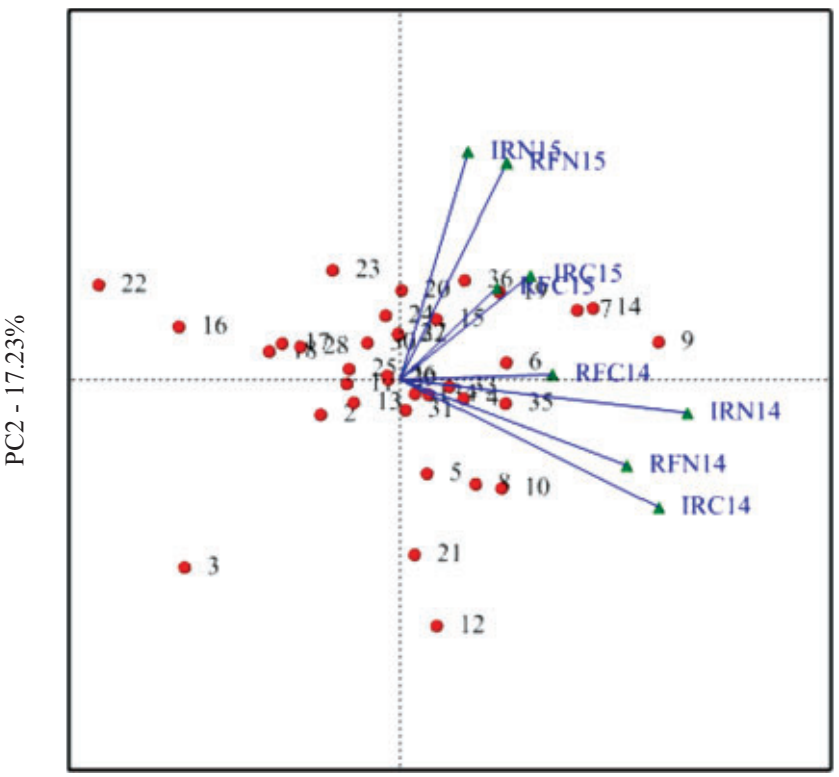

Fig. 2. GGE biplot of chickpea yield in different environments. Numbered circles indicate genotypes (see Appendix 1 for genotype codes) and lines/triangles indicate environments: IR, irrigated; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment.

Genotype, environment and genotype × environment interaction

When pooled across years, significant differences ($P < 0.001$) among genotypes were observed, which accounted for 12.6% of the total variation (Table 3). The environments were significantly different and accounted for 66% of the total variation in grain yield. The GEI was significant, indicating that genotypes had different yield rankings in the different environments. Genotype and GEI together accounted for 24.6% of the total variation observed in grain yield.

Environments

The first PC accounted for 59% of the total variation in yield and PC2 17%, together accounting for 76% of the total variation in yield (Fig. 2). The 2014 environments were positively correlated,

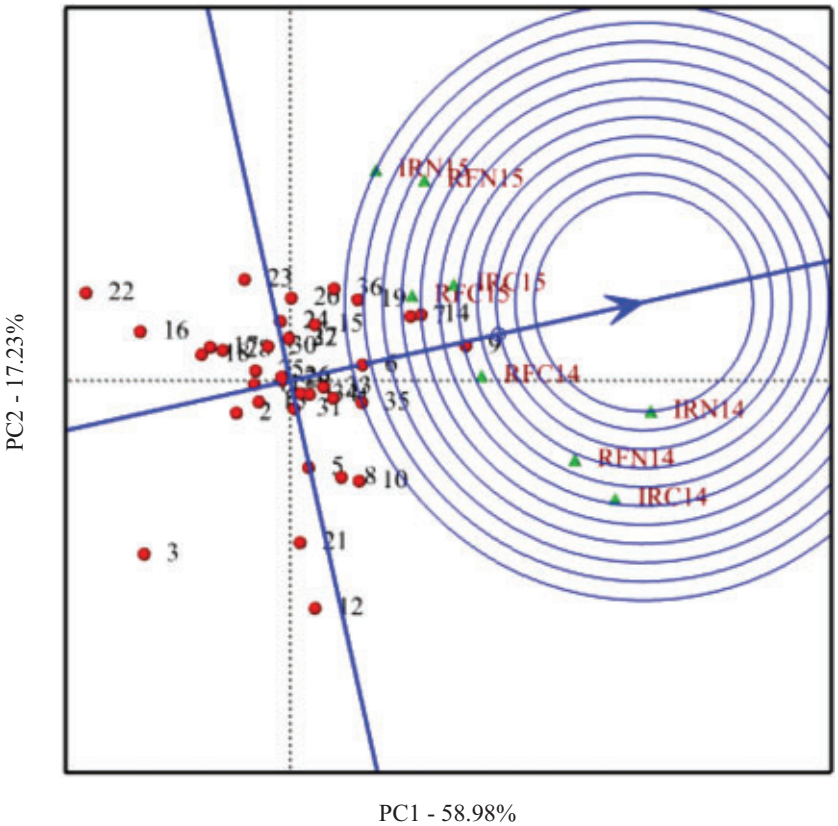

Fig. 3. GGE biplot for evaluating genotype and environment interactions on chickpea yield. Numbered circles indicate genotypes (see Appendix 1 for genotype codes) and triangles indicate environments: IR, irrigated; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment. The arrow in the middle of the concentric rings denotes the ideal environment.

with IRC14 and RFN14 the most similar and IRC14 and RFC14 the least. However, in 2015 environments correlated more on the basis of tillage practice than moisture. The highest level of similarity in 2015 was observed between IRC15 and RFC15.

The ideal environment

The most discriminating environments for grain yield were IRC14 and IRN14, and the least were RFC14, RFC15 and IRC15 (Fig. 3). The most representative environments were RFC15, IRC15 and RFC14 and the least were IRN15 and RFN15. However, an ideal environment should be both discriminating and representative. Thus, IRN14 was considered the ideal environment because it was both discriminating and representative and located near the centre of the concentric circles in Fig. 3. This environment was irrigated, so moisture stress was unlikely to be a differentiating factor; however, at flowering, it was cooler than 2015. The other environments close to the ideal were RFN14 and RFC14, indicating that 2014 was generally a better growing season than 2015. By contrast, IRN15 and RFN15 were discriminating but not representative and could be useful for selecting specifically adapted genotypes.

Mean grain yield and stability

Genotypic stability, measured by the length of the perpendicular line to the average environment axis and the proximity of the genotype to the average environment coordinate, is presented in Fig. 4. The most stable genotypes, although not the highest yielding, were PBA HatTrick (no. 6), Jimbour (no. 19) and ICCV 98801 (no. 15). By contrast, Sonali (no. 9) was less stable with higher GEI but had higher yield potential. The most unstable and low-yielding genotype was ICCV 05308 (no. 22).

The ideal genotype

The ideal genotype is that located as close as possible to the middle of the concentric circles in Fig. 5. Thus, the ideal genotype was Sonali (no. 9) followed by PBA Slasher (no. 7) and ICCV 96853 (no. 14).

Identification of environment types

The genotypes in the environment type (ET) plot fell into seven sections, each delineated by the perpendicular lines from the origin, and the environments differentiated into two sections

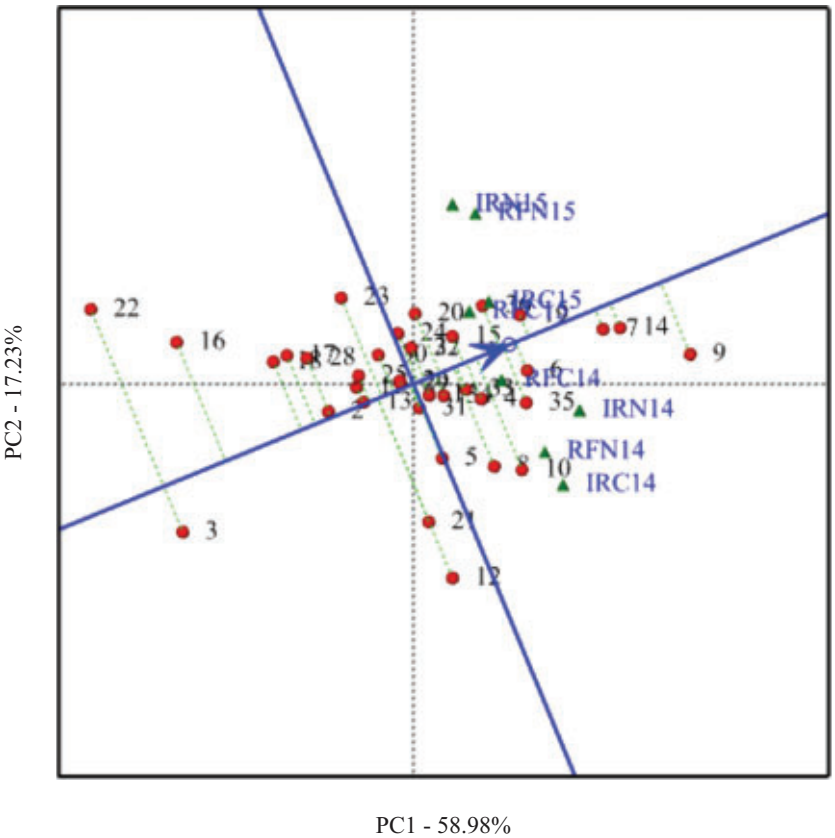

Fig. 4. Principal component analysis of grain yield and stability in chickpea genotypes. Numbered circles indicate genotypes (see Appendix 1 for genotype codes) and triangles indicate environments: IR, irrigated; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment.

(Fig. 6). Six environments grouped into one ET (IRC15, RFC15, RFC14, RFN14, IRN14 and IRC14) and were defined as ET1. The remaining two environments (IRN15 and RFN15) formed ET2. The CT regimes (RFC14, RFC15, IRC14, IRC15) clustered in ET1, indicating a degree of repeatability, based on tillage practice. The vertex genotypes, located furthest in each sector, were joined by equality lines to form a polygon such that all the other genotypes were inside the polygon (Yan and Tinker 2006). These vertex genotypes were to be the most responsive in each section of the plot. Sonali (no. 9) was a vertex genotype in ET1 and therefore the best performer. The equality line in ET1 connects Sonali, ICCV 96853 (no. 14), PBA Slasher (no. 7) and Jimbour (no. 19). Thus, the ranking in ET1 is Sonali > ICCV 96853 > PBA Slasher > Jimbour. There were no specific high-yielding genotypes in ET2 owing to a lack of vertex genotypes.

Discussion

Rainfall and distribution of rainfall produced significant differences at various chickpea phenophases. Although there was less vegetative-phase rainfall in 2014, yields were higher, indicating that other factors contributed to yield pre-anthesis. However, rainfall distribution during the critical flowering phenophase was higher and better distributed in 2014 than 2015. Year was the largest contributor to variation in yield in other studies (Haigh *et al*. 2005), and these differences were attributable to differences in rainfall and temperature between years. Temperature is important in determining chickpea yield, with temperatures <10°C (Chaturvedi *et al*. 2009) and >30°C (Summerfield *et al*. 1984) causing a reduction in grain yield. Minimum mean temperature differences were not large during the vegetative and flowering phases in 2014 and 2015. However, the higher mean maximum temperature at both flowering and podding stages in 2015 (with podding-stage temperatures >30°C) will have contributed to the lower observed yield in 2015.

The most discriminating and representative environments were IRN14 and RFN14. Both were characterised by NT practice, suggesting that the benefits of NT, including improved soil aggregate stability (Chan and Mead 1988), better soil structure (Page *et al*. 2013) and increased water storage (Radford *et al*. 1995) were important considerations for differentiating genotype responses. Other benefits of NT include reduced soil and water erosion (Verhulst *et al*. 2010), improved microbial activity (Balota *et al*. 2014) and improved soil-surface chemical properties (Busari *et al*. 2015). In general, the NT environments (IRN14, RFN14, IRN15 and RFN15) were more discriminating than the CT environments (RFC14, RFC15

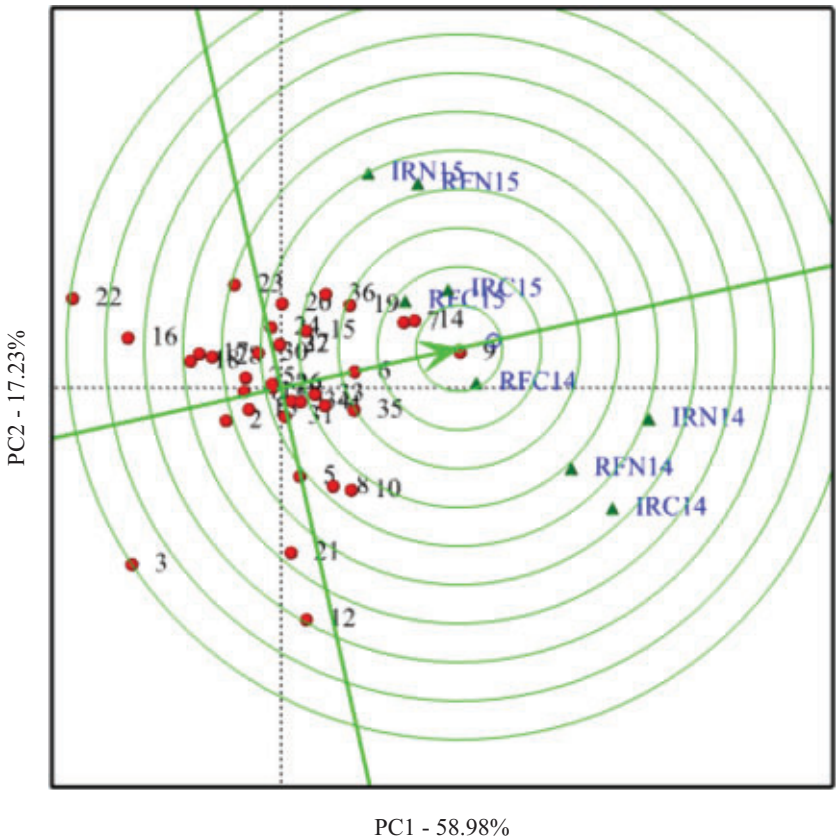

Fig. 5. Scatter plot from GGE biplot for evaluating the ideal chickpea genotype. Numbered circles indicate genotypes (see Appendix 1 for genotype codes) and triangles indicate environments: IR, irrigated; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment. The arrow in the middle of the concentric circles denotes the ideal genotype – the genotype closest to the arrow head is the ideal genotype.

and IRC15) with the exception of IRC14. The discrimination and representativeness of the NT environments may be attributed to the above-mentioned benefits.

Genotype stability is only effective if it is accompanied by high yields. Genotypes with both high yield and high yield stability were identified (PBA Slasher and ICCV 96853). However, although the highest yielding genotype, Sonali, was less stable, it still represents a suitable genotype for crossing and selection. Such genotypes could be selected for specific environment types, whereas genotypes with low yield and high stability would generally be discarded (Yan and Wu 2008).

Breeding programs strive to reduce costs by limiting the number of testing sites. It is therefore important to identify sites that are both highly discriminating and representative. This strategy allows the plant breeder to reduce cost and improve selection accuracy (Imtiaz *et al*. 2013). In the present study, two environment types were identified. ET1 was dominated by full-tillage environments, indicating that tillage produces a degree of environment specificity. Because both rainfed and irrigated sites are included in ET1, it is unlikely that better moisture retention, often associated with reduced tillage, was a factor. The different soil aggregates and finer structure associated with full tillage may have influenced root development and therefore adaptation. The analyses of the eight environments generated in this study indicate that just two are required to represent all the eight MET effectively. These are CT and NT. Moisture did not appear to be a significant differentiating factor in this experiment. Although more than one site of each ET would be required to represent the target environment properly, the target could comprise a series of locations with differential tillage treatments. Thus selection based on each ET could better focus selection and cultivar development (Yan *et al*. 2001).

Conclusions

Significant GEI was observed when chickpea genotypes were grown under varying conditions of tillage and moisture. Temperature, rainfall and irrigation all contributed to the significant GEI, particularly between seasons.

The ideal environment for selection and ideal genotypes were identified, and two primary environment types, based on similarities in tillage, were identified. The genotypes Sonali, PBA Slasher and ICCV 96853 were identified as suitable for cultivation across moisture and tillage regimes.

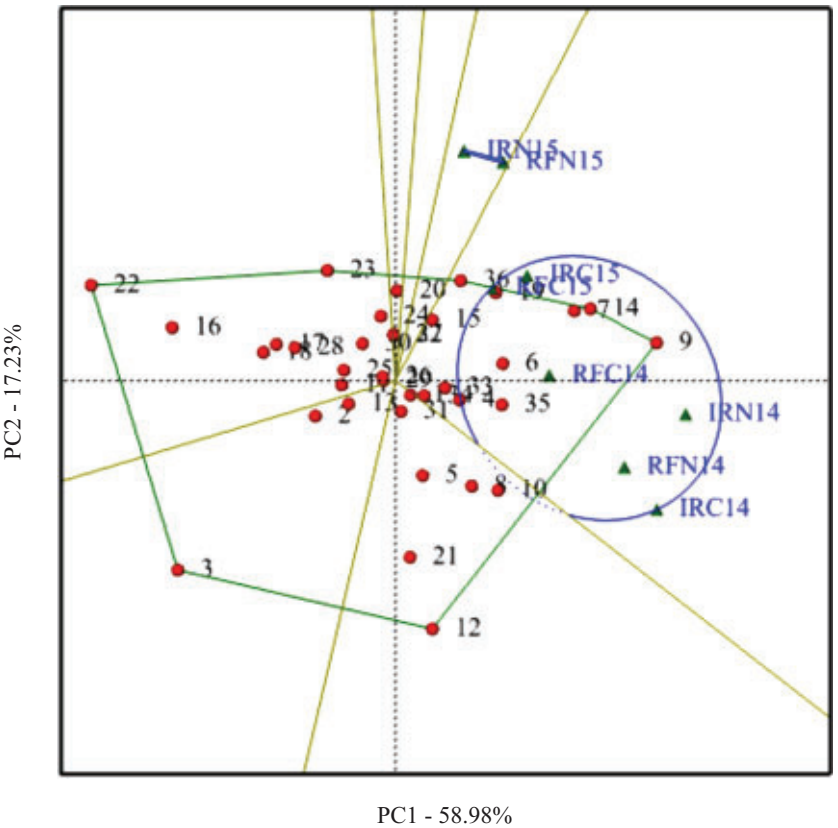

Fig. 6. GGE environment types for chickpea yield. Numbered circles indicate genotypes (see Appendix 1 for genotype codes) and triangles indicate environments: IR, irrigated; RF, rainfed; C, conventional tillage; N, no-tillage; 14 and 15 indicate the year of each experiment. The polygon represents the equality line for joining vertex genotypes. Environments of the same type are grouped.

These findings are specific to north-western New South Wales. Given that conservation agricultural practices tend to dominate in this agricultural system, it is likely that soil moisture is the primary differentiating factor across locations that implement these practices. However, conservation agriculture is not common practice in many other cropping systems globally and these results could have broader implications.

Conflicts of interest

The authors declare no conflicts of interest.

Acknowledgements

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Appendix 1. List of chickpea genotypes used for the experiment

No.	Name	Type	No.	Name	Type
1	Amethyst	Desi	19	Jimbour	Desi
2	Flipper	Desi	20	Jimbour #1	Desi
3	Genesis Kalkee	Kabuli	21	Flip 079C	Kabuli
4	Howzat	Desi	22	ICCV 05308	Kabuli
5	Kyabra	Desi	23	Austin	Desi
6	PBA HatTrick	Desi	24	Doolin	Desi
7	PBA Slasher	Desi	25	Howard	Desi
8	PBA Striker	Desi	26	Lyle	Desi
9	Sonali	Desi	27	Lyons	Desi
10	Tyson	Desi	28	Sal	Desi
11	Yorker	Desi	29	Sim	Desi
12	Genesis 079	Kabuli	30	Thomas	Desi
13	Genesis 090	Kabuli	31	Mix 1 (Yorker/Jimbour)	Desi
14	ICCV 96853	Desi	32	Mix 2 (Howzat/Flipper)	Desi
15	ICCV 98801	Desi	33	Mix 3 (Flipper/Jimbour)	Desi
16	ICCV 98813	Desi	34	Mix 4 (Yorker/Howzat)	Desi
17	ICCV 98816	Desi	35	Mix 5 (Howzat/Jimbour)	Desi
18	ICCV 98818	Desi	36	Mix 6 (Howzat/98813)	Desi