



Changes in yield determinants and quality traits in wheat after 12 cycles of recurrent selection

R. H. Maich¹ · G. A. Manera¹ · W. H. Londero¹ · L. S. Vanzetti^{2,3} · M. Helguera² · J. A. Di Rienzo¹

Received: 3 January 2020 / Accepted: 15 June 2020 / Published online: 8 July 2020
© Akadémiai Kiadó Zrt. 2020

Abstract

The objective of this study was to test the genetic response to 12 cycles of a recurrent selection program for grain yield and related traits. During two seasons the 39 S-derived families (three/C₀–C₁₂ populations) were evaluated under conventional (CT) and non-tillage (NT) systems. Grain and biomass yield were determined. The grain number per square meter and harvest index were also estimated. Flour protein content, sodium dodecyl sulphate sedimentation, and lactic acid solvent retention capacity were considered as end-use quality predictive tests. High molecular weight glutenin subunits (HMW-GS) variation was also analyzed. A significant increase in grain yield per selection cycle, estimated in 3.25 g m⁻² (1.3%) per year, was found under NT, but there was a not significant genetic progress under CT. The decrease in the percentage of protein in the most advanced selection cycles (11.0% vs. 9.7%) did not negatively affect its quality. HMW-GS variation analysis showed the erosion of extreme subunits related to gluten strength. After 24 years of recurrent selection, the grain yield was improved without affecting its industrial quality.

Keywords Wheat · Recurrent selection · Grain yield · Grain protein · HMW-GS

Abbreviations

| | |
|----------|------------------------------------------------------------|
| CT | Conventional tillage |
| NT | Non-tillage |
| SDS | Sodium dodecyl sulphate sedimentation |
| SRC | Solvent retention capacity |
| HMW-GS | High molecular weight glutenin subunits |
| LMW-GS | Low molecular weight glutenins subunits |
| SDS-PAGE | Sodium dodecyl sulphate polyacrylamide gel electrophoresis |
| RS | Recurrent selection |

Introduction

While some negative effects of non-tillage (NT) soil management can be seen (Herrera et al. 2013; Bankina et al. 2015), grain yields in conventional tillage (CT) and NT systems are comparable (Fernández et al. 2007; Tang et al. 2013). Lower yields under NT have led to the adoption of occasional strategic tillage in continuous NT farming systems; however, the impact in the long-term may be negligible or negative (Dang et al. 2015). These considerations agree with what was stated by Herrera et al. (2013), that many NT treatments had only some characteristics of well-established NT environments, that, according to Toliver et al. (2012) occurs after 10 years of NT. Maich and Di Rienzo (2014), comparing CT versus NT soil management, showed that only under CT a significant genetic progress was obtained. The grain yield obtained in the wheat crop cultivated under a newly implemented (6 year) NT soil management was 50% lower than those achieved in CT; this lower grain yield may have negatively affected the substantiation of a significant genetic progress in NT.

The increase in potential yields in wheat brought with it a decrease in the protein content of the grains. Moreover, a negative association has been observed between the SDS test (predictive test of the industrial quality of the flour) and the

Communicated by M. Taylor.

✉ R. H. Maich
rimaich@agro.unc.edu.ar

¹ Facultad de Ciencias Agropecuarias, Universidad Nacional de Córdoba, 5000 Córdoba, Argentina

² INTA EEA Marcos Juárez, Ruta 12 S/N, 2580 Marcos Juárez, Argentina

³ CONICET, Buenos Aires, Argentina

grain yield (Oelofse et al. 2010). However, the decrease in the amount of protein and the content of wet gluten could be compensated by an improvement in protein quality (Hristov et al. 2010). In this sense, the lactic acid solvent retention capacity (SRC) test is associated with the formation of the glutenin framework during baking and the strength of the gluten; therefore, it is useful to predict the breadmaking quality of wheat flour (Colombo et al. 2008).

Protein quality in wheat is mostly explained by allelic variation of the storage proteins glutenins and gliadins. Based on electrophoretic migration, glutenins are defined as high molecular weight glutenin subunits (HMW-GS) encoded at the *Glu-1* loci and low molecular weight glutenins subunits (LMW-GS) principally encoded by *Glu-3* loci. Allelic variation in loci encoding HMW-GS can be easily distinguished by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE). This simplicity has facilitated the identification of specific HMW-GS and their contribution to breadmaking quality. This information, combined with the presence of the 1BL/1RS rye translocation, was used to create a *Glu-1* quality score which is widely used for breadmaking selection and germplasm characterization in breeding programs (Bonafede et al. 2015).

The objectives of this study were to determine (1) genetic gain for grain yield and other agronomic traits after 12 cycles of recurrent selection, (2) the indirect effects on grain protein concentration, and (3) the genetic variation of HMW-GS.

Materials and methods

The recurrent selection program

The recurrent selection (RS) program was conducted in Campo Escuela de la Facultad de Ciencias Agropecuarias (Universidad Nacional de Córdoba), Córdoba (31° 29' S; 64° 00' W) in the central semiarid region of Argentina. The RS started in 1985 with an initial population (C_0) generated by crossing sixteen commercial varieties of bread wheat (*Triticum aestivum* L.) to obtain eighty-three F1 hybrid combinations. In each cycle of recurrent selection (each cycle is 2 years long because of evaluation and recombination), the selected material, in number no less than ten, out of a total of forty to fifty S_0 evaluated progenies, was crossed according to a complete diallel scheme. Throughout the 12 cycles of recurrent selection, the grain yield of the S_0 progenies became the main selection criteria. S_0 progenies were grown in single-row plots of 1.3 m long and 0.2 m row spacing, at a seeding rate of 100 grains per square meter, without replications and with regular controls. Check varieties were included at regular intervals for visual reference. The breeding program was conducted under rain-fed conditions,

without fertilization, and under CT until the ninth cycle of RS, from the tenth cycle of RS, NT conditions was used. Seed bulks of the selected progenies per cycle (C_0 – C_{12}) were created and multiplied annually. Plants from these seed mixtures were grown at regular spaces in both dimensions (20 cm by 20 cm) during 2013. Three plants per cycle with satisfactory grain production for further plot evaluation were retained.

The genetic progress measurement

Experiments were established during two successive seasons (2015 and 2016). Sowing was done on 5th and 4th of May 2015 and 2016, respectively. Heading occurred in September and maturity at the end of October. The 39 S-derived families (no less than three generations of selfing) were evaluated under CT and NT systems in two fields, next to each other, located in the same site of the selection program. Single row plots 5 m long with row spacing of 0.20 m, at a seeding rate of 250 viable seeds by square meter were used. Because of restrictions to randomization, imposed by the tillage practices, two replicates in complete blocks were allocated within each field. Complete weed control was done by hand weeding.

At the plot level, grain and biomass yield (g m^{-2}) were determined. The grain number per square meter and harvest index (%) were also calculated. For each trait, a linear mixed model (regression) was fitted to the experimental data. The fixed terms of the model included the tillage factor (conventional tillage–non-tillage), the number of recurrent selection cycles as a covariable, and the interaction between them. This way of specifying the fixed part of the model allows the fitting of two regression lines: one for each tillage practice. The random part of the model included the effects of: year, blocks within year-tillage practice, family, and the random interactions among year, and fixed terms of the model. A significance level of 5% was used in order to interpret results.

Climatic condition

Residual soil moisture stress is the most common type of water stress experienced by rain-fed wheat in this zone, leading to post-heading water stress. The first year (2015) was characterized by a low total rainfall (73 mm), with a strong water deficit occurring at heading. The second year (2016), by contrast, was wetter (150.4 mm).

Quality testing

Three experimental lines per cycle were analyzed. The cycles evaluated were: C_0 , C_4 , C_8 and C_{12} . The methods of AACC 44-19 and 46-13, respectively, were used to

determine the moisture and protein content in the flour. The quality of the flour was determined by the method of AACCI 56-11 (Lactic Acid SRC) and the sedimentation index in sodium dodecyl sulfate or SDS approved method 56–70 (AACCI 2000). Data from cycles of RS were analyzed using ANOVA using Di Rienzo, Guzmán y Casanoves test (DGC) as the pair-wise comparison method. Significance level was 0.05. All data were analyzed using a statistical software package InfoStat (Di Rienzo et al. 2018).

HMW glutenin subunits scoring

SDS-PAGE analysis was used to identify HMW-GS constitution in experimental lines. Briefly, gliadins were extracted with 1.5 M dimethylformamide from wholemeal flour (single seed, two extractions per family). After a brief centrifugation, the glutenin pellets were solubilized to be separated by SDS-PAGE as before (Moiraghi et al. 2013). HMW-GS were designated as previously described (Payne and Lawrence 1983). The presence of the highly expressed Bx7 subunit for Glu-B1 locus was tested in lines scored as 7 + 8 by SDS-PAGE using PCR markers according to Butow et al. (2004).

Results

Grain yield and related traits

Table 1 summarizes the *p* values for the hypothesis of null slopes under CT and NT (first two columns). *p* values for the hypothesis of non-difference between intercepts under CT and NT are shown in the third column. A summary of linear regression lines fitted to each trait are shown in Fig. 1. Regarding the slopes, under NT they were significantly greater than zero for grain yield, harvest index and seeds

Table 1 Summary of *p* values for the hypothesis of null slopes and for the differences between intercepts of regression lines fitted on the number of recurrent selection cycles under conventional tillage and non-tillage

| Trait | CT-slope <i>p</i> value | NT-slope <i>p</i> value | Intercept diff.(CT- NT) <i>p</i> value |
|-------------------------------------|----------------------------|----------------------------|-------------------------------------------------|
| Grain yield (g m ⁻²) | 0.110832 | 0.000805 | 0.169036 |
| Aerial biomass (g m ⁻²) | 0.706761 | 0.356418 | 0.878521 |
| Harvest index (%) | 0.000711 | 0.000000 | 0.081514 |
| Grains per square meter | 0.366139 | 0.001025 | 0.056932 |

CT Conventional tillage, NT non-tillage

p values for the hypothesis of null slopes: first two columns. *p* values for the hypothesis of non-difference between intercepts: third column

per square meter (Table 1—2nd column). Under CT, the trait that showed a slope significantly greater than zero was the harvest index (Table 1—1st column). A significant increase of grain yield under NT, around 3.25 g m⁻² (1.3%) per year, was observed. On the other hand, under CT the estimated increase per year was about 1.54 g m⁻² (0.7%) which was nonsignificantly different from zero (Table 1, Fig. 1a).

Grain quality traits

Table 2 shows the mean values corresponding to the quantitative and qualitative variables analyzed. Statistically significant differences between means were found for grain yield and protein percentage. While a significant positive trend, for grain yield was found, as more cycles of recurrent selection were achieved, on the other hand, the percentage of proteins in the flour decreased. The two predictive quality tests (SDS and the lactic acid SRC) did not show a significant trend after 12 cycles of RS.

High molecular weight glutenin subunits

A reduction in the allelic frequencies of the HMW-GS was observed. Six subunits were observed in C₀, five subunits in C₄, five subunits in C₈ and three subunits (17 + 18 and 7 + 8 segregating in line 12-3) in C₁₂ (Table 3). Taking into consideration the original allelic variation observed in the parents used in our study (Table 4), 2 + 12 (Klein Atlas, Marcos Juárez INTA, Leones INTA and Diamante INTA) was the first subunit eroded by RS followed by 7 + 9, 17 + 18, 7oe+8 and 2*. The final fixed HMW-GS combination was 1, 7 + 8, 5 + 10 discarding extreme HMW-GS associated with very strong (7oe+8) or weak (2 + 12, 7 + 9) gluten.

Discussion

Grain yield and related traits

During the evaluation of ten cycles of recurrent selection (Maich and Di Rienzo 2014), 6 years after replacing CT by NT (2005), only under CT the wheat showed a significant genetic gain for grain yield. In measuring the response to 12 cycles of recurrent selection, 10 years after replacing CT by NT, it was the NT soil management in which a significant change was in evidence. These results could be due to what was stated by Herrera et al. (2013), where many NT treatments had only some characteristics of well-established NT environments, which according to Toliver et al. (2012) occurs after 10 years of NT.

Considering that the largest contribution to the increased yield potential of modern wheat varieties came from the increase in harvest index (Zhang et al. 2012; Bustos et al.

Fig. 1 Regression lines on the number of recurrent selection cycles (NRSC), through conventional tillage (“c”—solid line) and non-tillage (“n”—dot dash line)

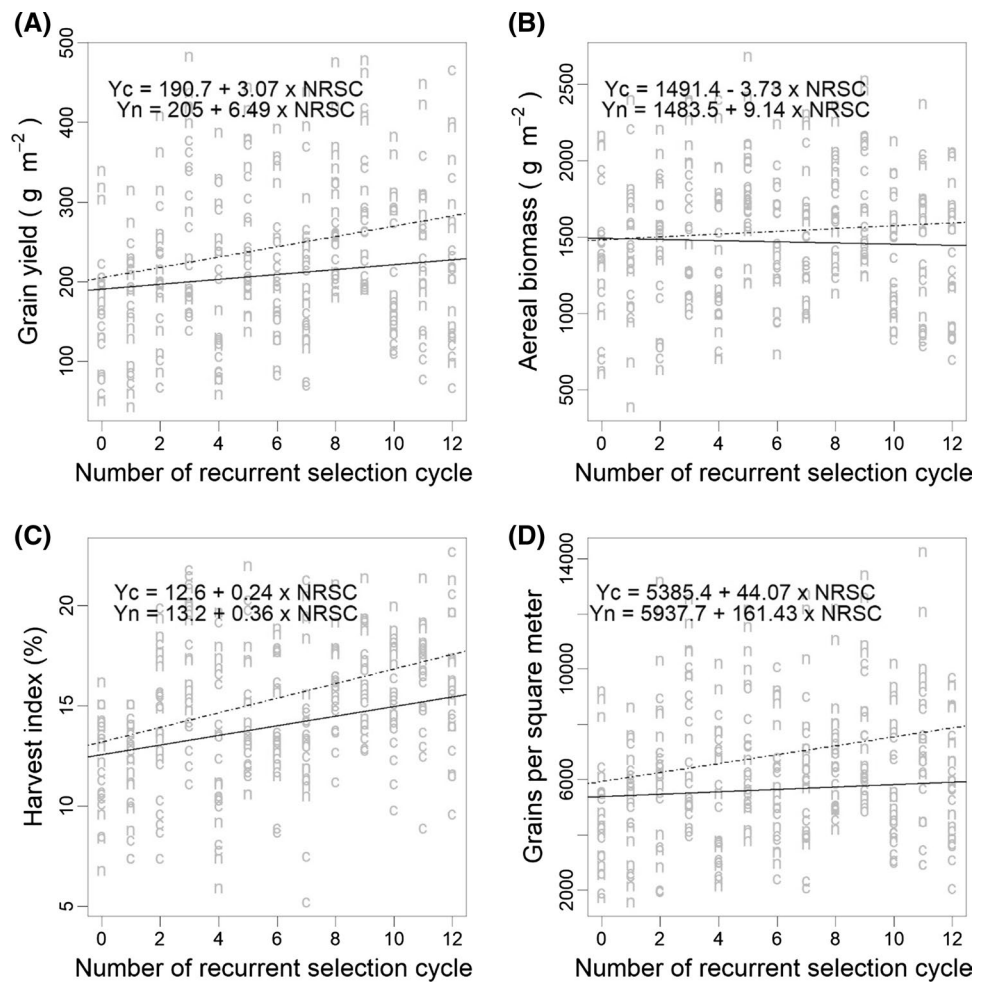


Table 2 Means values corresponding to grain yield and three variables associated with the gain quality after 12 cycles of recurrent selection in wheat averaged over conventional and non-tillage soil management

| Cycle | Grain yield (g m ⁻²) | Protein (%) | SDS (ml) | Lactic acid SRC (%) |
|----------------|----------------------------------|-------------|----------|---------------------|
| 0 | 171.7c | 11.0a | 12.4 | 111.7 |
| 4 | 183.3c | 10.2a | 12.0 | 112.5 |
| 8 | 277.6a | 9.2b | 11.1 | 113.8 |
| 12 | 226.1b | 9.7b | 10.8 | 110.1 |
| <i>p</i> value | 0.0001 | 0.0006 | 0.0625 | 0.6306 |

Means with a common letter are not significantly different ($p \leq 0.05$)

2013); our results under both, CT and NT soil management (Table 1, Fig. 1c), are coincident and were associated with the RS cycles attained, regardless of the environmental context in which the genetic progress was measured. On the other hand, our results did not show a significant trend in biomass production as dependent on the number of RS cycles (Table 1, Fig. 1b). Similarly to the conclusions of Royo et al. (2007), the genetic progress was due to changes

Table 3 HMW-GS composition observed in wheat genotypes considering different times in the recurrent selection program

| Genotype | <i>Glu-A1</i> | <i>Glu-B1</i> | <i>Glu-D1</i> |
|-------------------|---------------|---------------|---------------|
| C ₀₋₁ | 2* | 7+9 | 5+10 |
| C ₀₋₂ | 1 | 17+18 | 5+10 |
| C ₀₋₃ | 1 | 7oe+8 | 5+10 |
| C ₄₋₃ | 1 | 7oe+8 | 5+10 |
| C ₄₋₁ | 1 | 7+8 | 5+10 |
| C ₄₋₂ | 2* | 7+8 | 5+10 |
| C ₈₋₁ | 2* | 7+8 | 5+10 |
| C ₈₋₂ | 1 | 7+8 | 5+10 |
| C ₈₋₃ | 1 | 7oe+8 | 5+10 |
| C ₁₂₋₁ | 1 | 7+8 | 5+10 |
| C ₁₂₋₂ | 1 | 7+8 | 5+10 |
| C ₁₂₋₃ | 1 | 17+18/7+8 | 5+10 |

in photosynthate partitioning within the plant (harvest index) rather than biological carbon sequestration as a whole. Similar to other results (Guarda et al. 2004; Shearman et al. 2005), under the NT soil management the number of grains

Table 4 HMW-GS composition observed in wheat genotypes used as parents ordered according to release year

| Variety | Year of release | Pedigree | HMW-GS composition ^a |
|----------------------|-----------------|-------------------------------------------------------|---------------------------------|
| ‘Olaeta Artillero’ | 1954 | FLORENCE/APULIA//RELIANCE | 2* 7* + 9 5 + 10 |
| ‘Klein Atlas’ | 1963 | KLLU/KL157//KLRE | 1 7oe + 8 2 + 12 |
| ‘Marcos Juárez INTA’ | 1971 | SON64/KLRE | 5 + 10 ^b |
| ‘Klein Fortín’ | 1971 | KLAT’S’/KLIM’S | 2* 7oe + 8 5 + 10 |
| ‘Buck Namuncurá’ | 1971 | RMAG/BPAM//BAGE/GRAL.ROCA | 2* 7 + 8 5 + 10 |
| ‘Leones INTA’ | 1974 | SON64/TZPP//NAI60 = JAR’S’ | 1 7oe + 8 2 + 12 |
| ‘Buck Cencerro’ | 1974 | EUFCS/BQQ//BARU/3//BBOL/4//BMAN/3//BARU/ BQQ//RMAG | 2* 7* + 9 5 + 10 |
| ‘Dekalb Tala’ | 1974 | SON64/KLRE//MASSAUX5 | 1 7* + 9 5 + 10 |
| ‘Diamante INTA’ | 1975 | SON64/TZPP//NAI/3//NAR59 | 1 7 + 8 2 + 12 |
| ‘Cargill Trigal 700’ | 1977 | CNO’S’//JAR’S’ | 2 + 12 ⁽²⁾ |
| ‘Victoria INTA’ | 1978 | JAR’S’//BB/CNO | 1 7oe + 8 5 + 10 |
| ‘Norking Pan 70’ | 1978 | CNO/NAD//CHR | 1 17 + 18 5 + 10 |
| ‘Chasicó INTA’ | 1980 | BMAN/3//SON64A//SKE/ANE | 2* 7 + 8 5 + 10 |
| ‘Buck Pucará’ | 1980 | BCIM/3//CAL//TOB//BB//CC | 1 7oe + 8 5 + 10 |
| ‘Cargill Trigal 800’ | 1981 | SCOUT*5//AGENT//NAD//CO652643 | 5 + 10 ⁽²⁾ |
| ‘Las Rosas INTA’ | 1983 | KLAT//INIA//BB/4//NP876/Pj62//CAL/3//BB | 1 17 + 18 5 + 10 |

^aAccording to Gianibelli et al. (2002)

^bPartial information in this study. In italic BB, is the variety ‘Bobwhite’ carrying 1BL/1RS rye translocation

per unit land area contributed to the genetic gain of grain yield.

Grain quality traits

After 12 cycles of RS the highest grain yield achieved was accompanied by a decrease in the protein percentage. Similar results were obtained by Maich et al. (2017) after ten cycles of RS. The long-recognized negative relation between yield and protein content was fully substantiated. The absence of association between the predictive tests and the genetic progress achieved for grain yield questions the view that the amount and quality of the proteins necessarily go hand in hand.

High molecular weight glutenin subunits

A simple explanation of HMW-GS subunits fixation in the case of Ax1 and Dx5 + Dy10 subunits could be found in the higher frequency of these subunits in original panel of genotypes used in this recurrent selection program: 50% for Ax1 and 75% for Dx5 + Dy10. The situation is different for the fixed *Glu-B1* subunits combination 7 + 8 with an original frequency of 19% (varieties ‘Buck Namuncurá’, ‘Chasicó INTA’ and ‘Diamante INTA’). A possible explanation could be the co-selection of an alternative locus linked to the *Glu-B1* 7 + 8 subunit favoring local adaptation and/or yield. A good candidate can be the 1BL.1RS rye translocation, highly appreciated among breeders because of the presence

of resistance genes to several diseases and pests (Rabinovich 1998; Vanzetti et al. 2011) combined with higher yield and better performance under abiotic stresses (Howell et al. 2014). Available pedigree data shows that even though varieties carrying subunits 7 + 8 do not carry the 1BL.1RS rye translocation, varieties ‘Victoria INTA’, ‘Buck Pucará’ and ‘Las Rosas INTA’ include ‘Bobwhite’ carrying ‘Aurora’ as 1BL.1RS donor (Rabinovich 1998). The genetic position of the *Glu-B1* locus at the central portion of 1BL chromosome arm would allow the occurrence of recombination events, creating chromosomes with the combination 1BL.1RS and *Glu-B1* subunits 7 + 8. Further studies scoring the 1BL.1RS rye translocation in selected recurrent selection lines will elucidate this hypothesis.

Conclusions

The genetic progress for grain yield under NT was mainly driven by improvement in the harvest index rather than aerial biomass production. The absence of association between the flour quality predictive tests and the genetic progress achieved for grain yield puts into question the association between quantity, and flour quality of proteins. A possible explanation of this result may come from the observed HMW-GS erosion of extreme subunits related to gluten strength. After 24 years of recurrent selection, the grain yield was improved without affecting its baking quality.

References

- AACC (2000) Approved methods of the American Association of cereal chemists. American Association of Cereal Chemists, St. Paul
- Bankina B, Ruža A, Paura L, Priekule I (2015) The effects of soil tillage and crop rotation on the development of winter wheat leaf diseases. *Žemdirbystė (Agriculture)* 102:67–72
- Bonafede MD, Tranquilli G, Pflüger LA, Pena RJ, Dubcovsky J (2015) Effect of allelic variation at the Glu-3/Gli-1 loci on breadmaking quality parameters in hexaploid wheat (*Triticum aestivum* L.). *J Cereal Sci* 62:143–150
- Bustos DV, Hasan AK, Reynolds MP, Calderini DF (2013) Combining high grain number and weight through a DH-population to improve grain yield potential of wheat in high-yielding environments. *Field Crops Res* 145:106–115
- Butow BJ, Gale KR, Ikea J, Juhasz A, Bedö Z, Tamas L, Gianibelli MC (2004) Dissemination of the highly expressed Bx7 glutenin subunit (Glu-B1a1 allele) in wheat as revealed by novel PCR markers and RP-HPLC. *Theor Appl Genet* 109:1525–1535
- Colombo A, Pérez GT, Ribotta PD, León AE (2008) A Comparative study of physicochemical tests for quality prediction of Argentine wheat flours used as corrector flours and for cookie production. *J Cereal Sci* 45:775–780
- Dang YP, Moody PW, Bell MJ, Seymour NP, Dalal RC, Freebairn DM, Walker SR (2015) Strategic tillage in no-till farming systems in Australia's northern grains-growing regions: II. Implications for agronomy, soil and environment. *Soil Till Res* 152:115–123
- Di Rienzo JA, Casanoves F, Balzarini MG, Gonzalez L, Tablada M, Robledo CW (2018) InfoStat version (2018) Centro de Transferencia InfoStat, FCA, Universidad Nacional de Córdoba, Argentina. <http://www.infostat.com.ar>. Accessed 6 July 2020
- Fernández RO, Fernández PG, Cervera JG, Torres FP (2007) Soil properties and crop yields after 21 years of direct drilling trials in southern Spain. *Soil Till Res* 94:47–54
- Gianibelli MC, Echaide M, Larroque OR, Carrillo JM, Dubcovsky J (2002) Biochemical and molecular characterization of Glu-1 loci in Argentinean wheat cultivars. *Euphytica* 128:61–73
- Guarda G, Padovan S, Delogu G (2004) Grain yield, nitrogen-use efficiency and baking quality of old and modern Italian bread-wheat cultivars grown at different nitrogen levels. *Eur J Agron* 21:181–192
- Herrera JM, Verhulst N, Trethowan RM, Stamp P, Govaerts B (2013) Insights into genotype × tillage interaction effects on the grain yield of wheat and maize. *Crop Sci* 53:1845–1859
- Howell T, Hale I, Jankuloski L, Bonafede M, Gilbert M, Dubcovsky J (2014) Mapping a region within the 1RS.1BL translocation in common wheat affecting grain yield and canopy water status. *Theor Appl Genet* 127:2695–2709
- Hristov N, Mladenov N, Djuric V, Kondic-Spika A, Marjanovic-Jeromela A (2010) Improvement of wheat quality in cultivars released in Serbia during the 20 century. *Cereal Res Commun* 38:111–121
- Maich R, Di Rienzo JA (2014) Genotype × tillage interaction in a recurrent selection program in wheat. *Cereal Res Commun* 42:525–533
- Maich RH, Steffolani ME, Di Rienzo JA, Leon AE (2017) Association between grain yield, grain quality and morpho-physiological traits along ten cycles of recurrent selection in bread wheat (*Triticum aestivum* L.). *Cereal Res Commun* 45:146–153
- Moiraghi M, Vanzetti L, Pflüger L, Helguera M, Pérez GT (2013) Effect of high molecular weight glutenins and rye translocations on soft wheat flour cookie quality. *J Cereal Sci* 58:424–430
- Oelofse RM, Labuschagne MT, van Deventer CS (2010) Influencing factors of sodium dodecyl sulfate sedimentation in bread wheat. *J Cereal Sci* 52:96–99
- Payne PI, Lawrence GJ (1983) Catalogue of alleles for the complex gene loci, Glu-A1, Glu-B1, and Glu-D1 which code for high-molecular-weight subunits of glutenin in hexaploid wheat. *Cereal Res Commun* 11:29–35
- Rabinovich SV (1998) Importance of wheat-rye translocation for breeding modern cultivars of *Triticum aestivum* L. *Euphytica* 100:323–340
- Royo C, Álvaro F, Martos V, Ramdani A, Isidro J, Villegas D, García del Moral LF (2007) Genetic changes in durum wheat yield components and associated traits in Italian and Spanish varieties during the 20th century. *Euphytica* 155:259–270
- Shearman VJ, Sylvester-Bradley R, Scott RK, Foulkes MJ (2005) Physiological processes associated with wheat yield progress in the UK. *Crop Sci* 45:175–185
- Tang Y, Wu X, Li C, Wu C, Ma X, Huang G (2013) Long-term effect of year-round tillage patterns on yield and grain quality of wheat. *Plant Prod Sci* 16:365–373
- Toliver DK, Larson JA, Roberts RK, English BC, De La Torre Ugarte DG, West TO (2012) Effects of no-till on yields as influenced by crop and environmental factors. *Agron J* 104:530–541
- Vanzetti LS, Campos P, Demichelis M, Lombardo LA, Aurelia PR, Vaschetto LM, Bainotti CT, Helguera M (2011) Identification of leaf rust resistance genes in selected Argentinean bread wheat cultivars by gene postulation and molecular markers. *Electron J Biotechnol* 14:1–17
- Zhang H, Turner NC, Poole ML (2012) Increasing the harvest index of wheat in the high rainfall zones of southern Australia. *Field Crops Res* 129:111–123