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Article

Evaluation of the Productive Potential of a World Collection of Chickpeas (*Cicer arietinum* L.) for the Initiation of Breeding Programs for Adaptation to Conservation Agriculture

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Abstract: Transitioning to conservation agriculture is proving to be a better alternative and could become the norm in the future. Morocco, geographically located in a hot spot, is much more vulnerable to the hazards of climate change and the advantages of conservation agriculture remain a good compromise to ensure sustainable agricultural production. However, the lack of sufficient knowledge about this agricultural technology could be a hindrance and thus create mistrust among farmers. Therefore, the objective of our study is to evaluate the performance of a collection of chickpeas in each tillage system to identify genotypes that can be integrated into breeding programs for adaptation to conservation agriculture. Our study shows no significant effect of tillage on grain yield. Chlorophyll content and pod number made the strongest direct and positive contributions to yield for conventional and no-till, respectively. Nine genotypes including two checks (C1 and C2) were selected in both systems through MGIDI (multi-trait genotype–ideotype distance index) analysis. These genotypes would be potential candidates for breeding programs for adaptation to no-till because of their plasticity to reproduce acceptable yields in both till systems.

Keywords: conservation agriculture; conventional tillage; no-till; till system; chickpea; selection

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1. Introduction

Despite its benefits, including residue burial, seedbed preparation, crop root development [1,2], and especially good control of weeds, conventional agriculture has a major impact on several physical, but also biological, characteristics of soil [3–5] by drastically reducing the synergy between the soil and its microbial composition [6]. In Morocco, conventional farming accentuates soil organic matter depletion through deep plowing [7]. As a result, soils are denuded and much more exposed to erosion [8]. In addition, plowing significantly and negatively affects nodule formation and, therefore, atmospheric nitrogen fixation in legumes in general and chickpea in particular [9–11]. The erosive aspect of conventional agriculture is undeniable and is much expressed in contrast to conservation agriculture [12]. Conventional agriculture thus leaves a much more alarming finding that in Morocco soil degradation, caused by agriculture, would concern a little over 5 million hectares [13,14]. It should be noted that population growth and land degradation mean that cultivable land is, in Morocco and almost everywhere else in the world, a constantly diminishing resource.

Thus, in the face of the current challenges related to climate change, strongly characterized by the scarcity of rainfall, the drying up of rivers, and high temperatures, the transition to conservation agriculture would probably be seen as a better alternative and thus impose itself in the future as the norm. Taking into account climate change scenarios, Morocco, located in the MENA (Middle East and North Africa) region, which is considered a hot spot due to climate change, is in this case much more vulnerable and exposed to the negative effects of extreme environmental conditions [15–17]. In this case, adopting other agricultural technologies such as conservation agriculture remains a necessity in order to maintain productive and sustainable agriculture. Indeed, in addition to the preservation of the soil and its ecosystems, conservation agriculture is undeniably economic through the limited use of machinery, but also the efficient use of soil water by crops [18–20]. As demonstrated by several studies, in this case the meta-analysis conducted by Pittelkow et al. [21] across several countries, direct seeding, along with the two other basic principles of conservation agriculture (the maintenance of crop residues and rotation), would be much more advantageous and would ensure the maintenance of the physical, chemical and biological properties of the soil to avoid soil degradation caused largely by intensive agriculture.

Agriculture remains the primary source of water resources in Morocco. Declining rainfall combined with rising temperatures suggests that Morocco will gradually move toward increasing aridity over the coming decades [22]. During the 2021/2022 agricultural season, Morocco, according to reports from the Ministry of the Environment, recorded the most severe drought it has experienced in the last decade. Faced with these constraints related to water availability, agricultural practices aimed at limiting soil water loss become more than a necessity to contain the adverse effects of drought on agricultural production [23]. Therefore, finding the balance between the productive potential of crops and the conservation of the production environment (land resources) is all the more worrying as it constitutes a contextual problem.

Practicing conservation agriculture with the same plant material selected for criteria of interest (high yield, early cycle, and high biomass) in a conventional farming system shows limitations, especially on crop performance responses that are sometimes confusing and variable depending on the species and the environment. Thus, researching to select genotypes more adapted to conservation agriculture would be one of the keys that could initiate the adoption of conservation agriculture by farmers. Evaluating a large collection will help to better identify genotypes with a particular adaptation to one system over another and also to carefully monitor the parameters studied in both systems to identify traits of interest to better target the selection of adaptations to conservation agriculture.

In addition to being advocated by the SDGs (Sustainable Development Goals), the adoption of regenerative agriculture would be a necessity and not a choice for responsible, sustainable, and especially resilient agriculture in the face of socioclimatic changes. Indeed, the transition to conservation agriculture would be a means for the integrated management of natural resources reconciling agricultural modernization, sustainable development, and biodiversity conservation. On a global scale, conservation agriculture is undergoing accelerated adoption and is now practiced in about 12% of cultivated areas [24]. In Morocco, where agriculture remains a lever of the economic sector [25], the challenge for conservation agriculture is twofold: to produce sustainably to ensure food security in a growing demographic context, and to reduce or even clearly stop soil degradation [26]. The weight of agriculture in the national economy is effectively pushing the authorities to rethink agriculture for its sustainability and productivity. The Moroccan "green generation" plan advocated for 2030 involves strategies to propel sustainable agriculture, and some of the axes aim to expand the area dedicated to conservation agriculture to just over one million hectares. The dissemination and transfer of technologies by research institutions in Morocco have, however, allowed for a rapid but less accelerated adoption. The observation shows that the transition to this sustainable agricultural production system is not effective today and is punctuated by the vagaries of the technical itinerary (the availability of suitable machinery, inputs, productive plant material, etc.).

In semiarid regions, the challenge of conservation agriculture is much greater, as water remains a non-negligible factor for production. As has been demonstrated in several studies, crop yields in areas where annual rainfall is below 200 mm can be increased through direct seeding [27,28]. Located largely in arid and semiarid regions, arable land in Morocco is mainly cultivated with cereals and legumes. Chickpea, the second most widely grown legume in the country, is usually grown in rainfed systems and receives an average of 250–350 mm of rainfall. As a result, it is more exposed to inequalities in rainfall distribution during crop years [29] and also to the remarkable decrease in rainfall during the last decade. In addition to being conditioned by climatic factors, precisely water availability, its yields are then dictated by soil fertility but also its physical properties.

In addition to expanding the knowledge base on conservation agriculture in Moroccan dryland areas, the main objective is to evaluate the performance of genotypes in each of the production systems (conventional tillage and no-till), to understand the existing interactions between genotypes and till system, and to identify relevant strong correlations between the studied traits concerning the two systems to select promising genotypes to be integrated into eventual breeding programs for adaptation to conservation agriculture.

2. Materials and Methods

2.1. Experimental Site Climatic Conditions

The experimental site of the National Institute of Agricultural Research (INRA-Morocco), where the trials were installed, was that of Sidi Aidi located 16 km north of Settat (331089 latitude, −7.63522 longitude). The soil of the site has a clayey texture and slightly silty shoots on the surface that crack during drying, and its apparent density increases with depth. This area is characterized by a semiarid climate with much hotter/drier summers and cold/wet winters. Over the past ten years, the site has experienced an average seasonal rainfall of 367 mm during crop years.

Trials were conducted during the 2020–2021 cropping season between late November and mid-May. During the growing season, we recorded significant inter-monthly rainfall variation and temperatures varied slightly (Figure 1). The cumulative rainfall recorded was 347.2 mm and the average temperature was 14.1 °C. January and March had the highest rainfall. Additionally, the lowest temperature was recorded in January while the highest was recorded in May (Figure 1). Compared to the precipitation that the experimental site received in recent years, it can be said that the year was wet. Both trials received the highest rainfall during the vegetative stage and there was not a single month (throughout the cycle) when there was no rainfall. Thus, it can be said that the distribution of rainfall between the months was much more advantageous. These data were automatically recorded using a meteorological measuring station (iMETOS IMT200, iMetos 3.3, Weiz, Austria) installed at the experimental site.

2.2. Plant Material, Trial Design, and Treatments

The experiment concerned two chickpea trials conducted on two different plots with plant material essentially composed of a part of the world collection of 156 chickpea accessions and 66 local genotypes (landraces), including 6 check varieties composed of 3 varieties (C6 (Moubarak), C5 (Bochra), and C4 (Arifi)), released by INRA Morocco in food legume selection programs for conventional sowing, and 3 local varieties (C3 (Local Zair), C2 (Local Gharb), and C1 (Local Chaouia)). The six local checks were selected for their high yields in conventional agriculture, their resistance to certain diseases (anthracnose, fusariosis. . .), their upright growth habit, their earliness, and, therefore, their tolerance to terminal drought. The remaining 60 were a combination of genotypes collected from farmers and some traditional genotypes supplied by INRA's gene bank. The entire collection comprised 153 Kabuli and 63 Desi genotypes. Among the local genotypes, there were only 4 Desi genotypes, more often used in crossbreeding blocks thanks to their disease resistance (rust, etc.) and drought tolerance. The genotypes in this collection come from 15 different countries. We have 66 genotypes from Morocco, 5 from Austria, 2 from Egypt, 15 from Spain, 12 from Ethiopia, 18 from India, 28 from Iran, 6 from Italy, 3 from Jordan, 14 from Mexico, 9 from Pakistan, 13 from Russia, 6 from Syria, 3 from Tunisia, and 22 from Turkey. This collection is essentially made up of genotypes with three biological statuses, in particular landraces, breeding lines, or varieties. Additional details on all genotypes are provided in the Supplementary Data (Table S1).

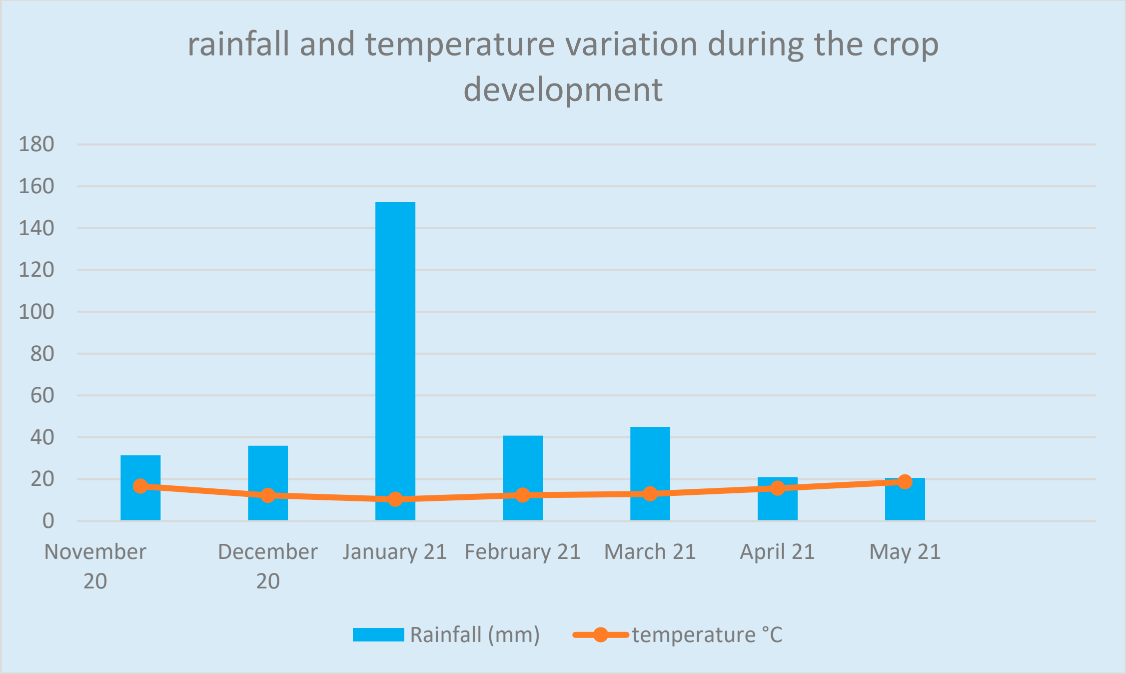


Figure 1. Cumulative rainfall (histogram) and average temperatures (curve) during the 2020/2021 cropping season.

Both trials were set up according to an augmented randomized complete block design (RCBD) with six blocks each consisting of 18 elementary plots. The six checks were replicated in each of the six blocks. Each trial consisted of 252 elementary plots and each of the elementary plots consisted of four 6 m rows with a spacing between the rows of 0.5 m, i.e., a total area of 15 m^2 for each elementary plot. The spacing between the elementary plots of the same block and between the blocks was one and two meters, respectively.

Each experimental treatment involved the genotype variable and the tillage factor (system). Both trials (no-till and conventional tillage) were conducted in plots where wheat was the preceding crop and the no-till plot was covered with crop residues. Both trials received a single fertilizer application (50 kg/ha of ammonium sulfate (21%)). The mineral (NO_3, P, and K) and organic matter contents of the soil in each of the two systems are reported in Supplementary Data (Table S2). Weeds were controlled, in both trials, either via an application of Gallant super (0.5 L/ha) or via manual and/or mechanical removal.

The no-till trial was conducted on soil that had not been disturbed by agricultural machinery, and residues from previous crops were removed manually or by a single pass of machinery if necessary. The removal of crop residues from the no-till area was carried out just before seeding. Conventional seeding was carried out on land previously prepared by tillage involving burying crop residues and preparing the seedbed 35 to 40 cm deep using a tractor-drawn disc plow. The seeding was finally carried out in November using a seeder adapted to direct seeding at a depth of about 5 to 8 cm and by hand in furrows 20 to 25 cm deep for the conventional seeding trial. For each genotype, the seeding rate was 25 grains per linear meter. Harvesting was performed manually on 26 May for both trials.

2.3. Evaluations and Measurements of the Parameters

Early vigor, estimated on a scale of 1–5 [30]; flowering and pod formation dates, noted when 50% of the plants had started to form flowers and pods, respectively [30]; and plant height, measured with a graduated ruler from the base to the top of the plant, were all evaluated directly on the elementary plot corresponding to each genotype. Chlorophyll content was measured using a Chlorophyll Meter Plus SPAD 502 (Konica Minolta Sensing, Tokyo, Japan) on well-developed leaves. Chlorophyll content, then, was the average value of four samples taken from different plants in each plot, following the method proposed by [31]. Relative water content was measured using the formula proposed by Barrs and Weatherley [32] on young leaves removed from the upper half of the plant. The number of primary and secondary branches, the number of pods and empty pods, and the number of grains were recorded by directly counting on a sample of 5 plants taken at random from each elementary plot. Hundred seed weight and biomass were measured using a precision balance. The total grain yield was measured on the entire 15 m^2 of the elementary plot in kg per plot to be converted into g/m^2.

2.4. Data Analysis

All the fifteen measured traits were subjected to analyses using the R v4.2.2 software. Note that due to non-germination, two genotypes were eliminated in both systems during the analyses. ANOVA analysis was performed on the combined data from both systems to assess the genotype × system interaction and the lme4 package [33] was used to build a linear mixed model. The statistical method of residual maximum likelihood was used with the model. The model considers genotype, system, and genotype × system interaction as fixed effects, and block, block × genotype interaction, and block × system interaction are random effects. ANOVA analysis and statistical significance ($p < 0.05$ for significant and $p < 0.001$ for highly significant) were given for the fixed effects. Tukey's multiple comparison tests were performed to see differences between genotype means and between the means of the two systems on all measured parameters. In addition, two other analyses of variance were performed. One is a split plot for only the checks using their data from both systems combined and the other is an analysis of the variance of each system separately in augmented-RCBD for all genotypes. Path analysis and correlation analysis were performed using the metan package [34] to identify the traits that contribute strongly to grain yield and the association between traits in each system. Using the standardized means of each genotype across all traits, principal component analysis was performed with the factoextra package [35] to get an idea of the variables that contribute to the high variability of responses observed in each system. Finally, the MGIDI (multi-trait genotype–ideotype distance index) analysis [36] was carried out in each system in order to be able to select for each system and have a precise idea of the ideal genotypes that would be promising in both systems at the same time. This analysis was carried out only on the grain yield and its components, namely the number of pods, the number of grains, the biomass, and the hundred grain weight. The metan package was used as proposed by Olivoto and Nardino [36] with weighting on grain yield and biomass with a selection intensity of about 14 to identify the thirty best genotypes in each till system.

3. Results

3.1. Effect of Till System, Genotype, and Their Interaction on All Measured Traits

The responses of the different parameters measured varied between genotypes of the same system and between the two systems taken independently. For all the measured traits, we found a highly significant effect of genotype and genotype × system interaction (Table 1). However, the system effect was not significant for some traits. The effect of till system was highly significant for two traits, namely hundred seed weight and relative water content. The till system factor had no significant effect on grain yield (Table 1). Parameters such as early vigor, flowering date, the number of main stems, the number of primary branches, and chlorophyll content also had no significant effect for till system. The significance of the effect of till system on days to pod formation, height, the number of seeds, and biomass was less significant (Table 1).

Table 1. Mean squares and significance levels of till system, genotype (Entry), and their interaction effects on grain yield and other traits according to ANOVA analysis.

	Meansq						
	EV	**DF**	**DPF**	**PH**	**NPB**	**NSB**	**NPd5P**
TillSystem	0.01703 ns	11.363 ns	27.585 *	43.429 *	0.20237 ns	33.330 ns	19,330.4 **
Entry	1.17538 ***	114.567 ***	36.382 ***	103.300 ***	0.30195 ***	16.132 ***	12,068.2 ***
TillSystem: Entry	1.00289 ***	67.453 ***	32.190 ***	52.918 ***	0.25761 ***	15.633 ***	7391.2 ***

	Meansq							
	NEPd5P	**NS5P**	**HSW**	**SW5P**	**BY5P**	**GY**	**RWC**	**Chl**
TillSystem	1645.09 **	4211.1 *	61.121 ***	414.26 ns	5328.6 *	97.62 ns	2491.27 ***	16.60 ns
Entry	182.77 ***	16,575.4 ***	224.362 ***	991.07 ***	5572.7 ***	1240.71 ***	59.90 ***	542.24 **
TillSystem: Entry	160.83 ***	9991.7 ***	16.783 ***	633.86 ***	4636.7 ***	1078.36 ***	49.48 ***	179.20 **

EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). Significance level: ns: $p > 0.05$; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

Analysis of variance for each system separately reveals a slightly different genotype effect between the two systems. Hundred seed weight and number of pods have a highly significant genotype effect in each system (Tables 2 and 3). On the other hand, there was no significant genotype effect on grain yield in either system (Tables 2 and 3). In direct seeding, the highly significant genotype effect is recorded on four traits, namely hundred-grain weight, number of pods, number of grains, and plant height (Table 2). In direct seeding, a highly significant genotype effect was also observed on four traits, namely hundred-seed weight, number of empty pods, number of pods, and relative water content (Table 3). In direct seeding, the majority of traits showed no significant genotype effect, unlike in conventional seeding.

Table 2. Analysis of variance of 15 agro-morphological traits measured in a population of 220 chickpea genotypes in an augmented randomized complete block design in conventional seeding.

Source	**Df**	**BY5P**	**Chl**	**DF**	**DPF**	**EV**	**GY**	**HSW**	**NEPd5P**
Genotypes (G)	219	5977.32 *	218.53 ns	42.92 ns	51.14 ns	0.59 *	1812.12 ns	127.55 **	272.56 *
Checks (C)	5	4495.63 ns	458.25 *	71.04 ns	50.53 ns	0.38 ns	8647.12 **	384.63 **	376.67 *
(G) versus (C)	214	6011.94 *	212.93 ns	42.26 ns	51.16 ns	0.6 *	1652.43 ns	121.54 **	270.12 *
Residuals	25	2814.79	175.51	32.27	40.4	0.34	1500.65	7.45	126.87
Source	Df	NPB	NPd5P	NS5P	NSB	PH	RWC	SW5P	
Genotypes (G)	219	0.31 *	12,811.74 **	17,397.51 **	17.89 *	71.17 **	58.57 ns	1238.4 ns	
Checks (C)	5	0.85 **	13,056.45 *	9442.83 ns	22.14 ns	54.01 ns	165.55 ns	921.27 ns	
(G) versus (C)	214	0.29 *	12,806.02 **	17,583.37 **	17.79 *	71.57 **	56.07 ns	1245.81 ns	
Residuals	25	0.16	4515.26	4760.52	9.36	29.2	79.3	964.67	

EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). ns: $p > 0.05$; * $p \leq 0.05$; ** $p \leq 0.01$.

Table 3. Analysis of variance of 15 agro-morphological traits measured in a population of 220 chickpea genotypes in an augmented randomized complete block design in no-till.

Source	**Df**	**BY5P**	**Chl**	**DF**	**DPF**	**EV**	**GY**	**HSW**	**NEPd5P**
Genotypes (G)	219	4252.91 ns	202.57 ns	139.38 ns	55.4 ns	1.59 ns	870.33 ns	112.96 **	74.49 **
Checks (C)	5	866.96 ns	730.75 **	248.64 *	66.51 ns	0.38 ns	5586.45 **	346 **	22.49 ns
(G) versus (C)	214	4332.02 ns	190.23 ns	136.83 ns	55.14 ns	1.62 ns	760.14 ns	107.52 **	75.7 **
Residuals	25	5659.78	171.47	91.42	48.14	1.28	1148.63	5.71	30.91
Source	Df	NPB	NPd5P	NS5P	NSB	PH	RWC	SW5P	
Genotypes (G)	219	0.25 ns	6628.57 **	9173.5 ns	13.88 ns	62.06 *	42.86 **	389.42 ns	
Checks (C)	5	0.17 ns	8907.53 *	6609.83 ns	36.17 *	117.25 *	8.93 ns	418.19 ns	
(G) versus (C)	214	0.25 ns	6575.32 **	9233.4 ns	13.36 ns	60.78 *	43.65 **	388.75 ns	
Residuals	25	0.35	2492.75	6695.09	10.11	32.14	11.61	443.69	

EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). ns: $p > 0.05$; * $p \leq 0.05$; ** $p \leq 0.01$.

3.2. Performance and Effect of Till System, Genotype, and Their Interaction for the Checks Varieties

In parallel with the analysis of variance of the combined data for all genotypes, an analysis of variance was performed on the six control genotypes only. Knowing that the six controls are repeated in each block and in each of the two systems, this allowed us to perform an analysis according to a split-plot design. In this case, the two tillage systems were considered as the main plot and the genotypes as the sub-plot. The genotype × system interaction was significant only on the number of empty pods ($p < 0.05$) (Supplementary Data, Table S3). Thus, additionally, we found that on all checks, conventional seeding produced significantly more empty pods than no-till. We noted that the effect of till system gave almost the same significance as that obtained by the majority of the traits in the combined data analysis of all genotypes. The effect of till system generated significant differences in checks through the number of days to pod formation, plant height, the number of pods, number of empty pods, relative water content, and hundred seed weight. Thus, till system was slightly significant for hundred seed weight with superiority in conventional seeding for most checks.

As in the analysis of the combined data for all genotypes, the till system had no significant effect on grain yield (Supplementary Data, Table S3). However, the effect of genotype, which was highly significant on all traits in the analysis of the combined data of all genotypes, was not significant in the analysis of the checks for some traits such as early vigor, grain number, biomass, and relative water content. In addition, although they were derived from conventional seeding programs, the cycle of the checks (via phenological dates) did not show significant differences between the two systems. The highest early vigor, number of secondary branches, number of pods, number of seeds, and grain yield were obtained by the C6 check followed by the C5 (except for early vigor) in the conventional seeding (Figure 2a,f,g,i,m). The same check, C6, had the highest chlorophyll content of the two systems in conventional seeding. Compared to the other checks in both systems, check C5 gave the highest values of biomass, plant height, and number of primary branches. Nevertheless, except for check C5, the other checks produced higher biomass values under no-till than under conventional seeding (Figure 2l). Of the fifteen traits measured on the checks in both systems, with significant or non-significant differences, conventional seeding outperformed no-till in twelve traits.

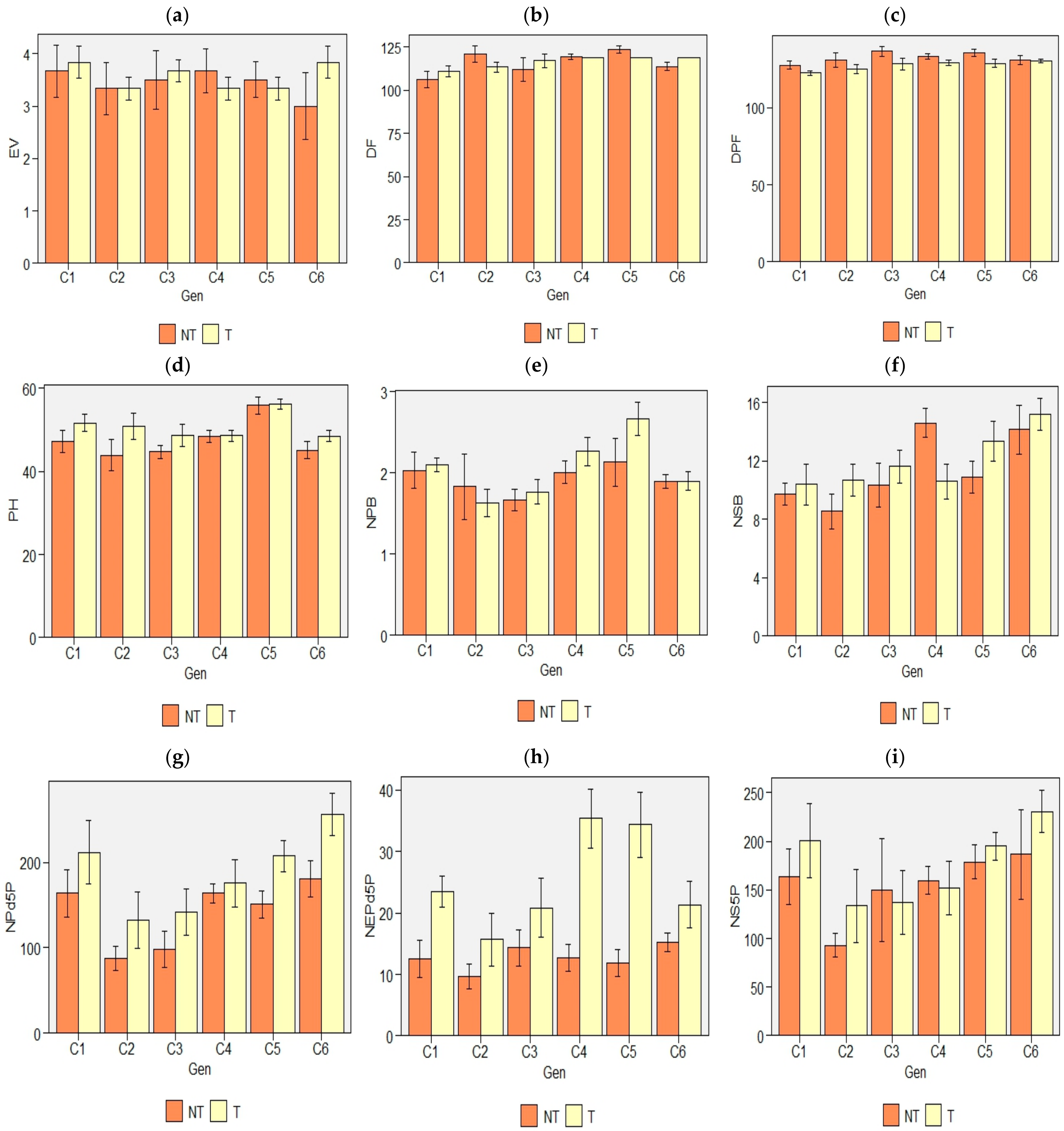


Figure 2. *Cont.*

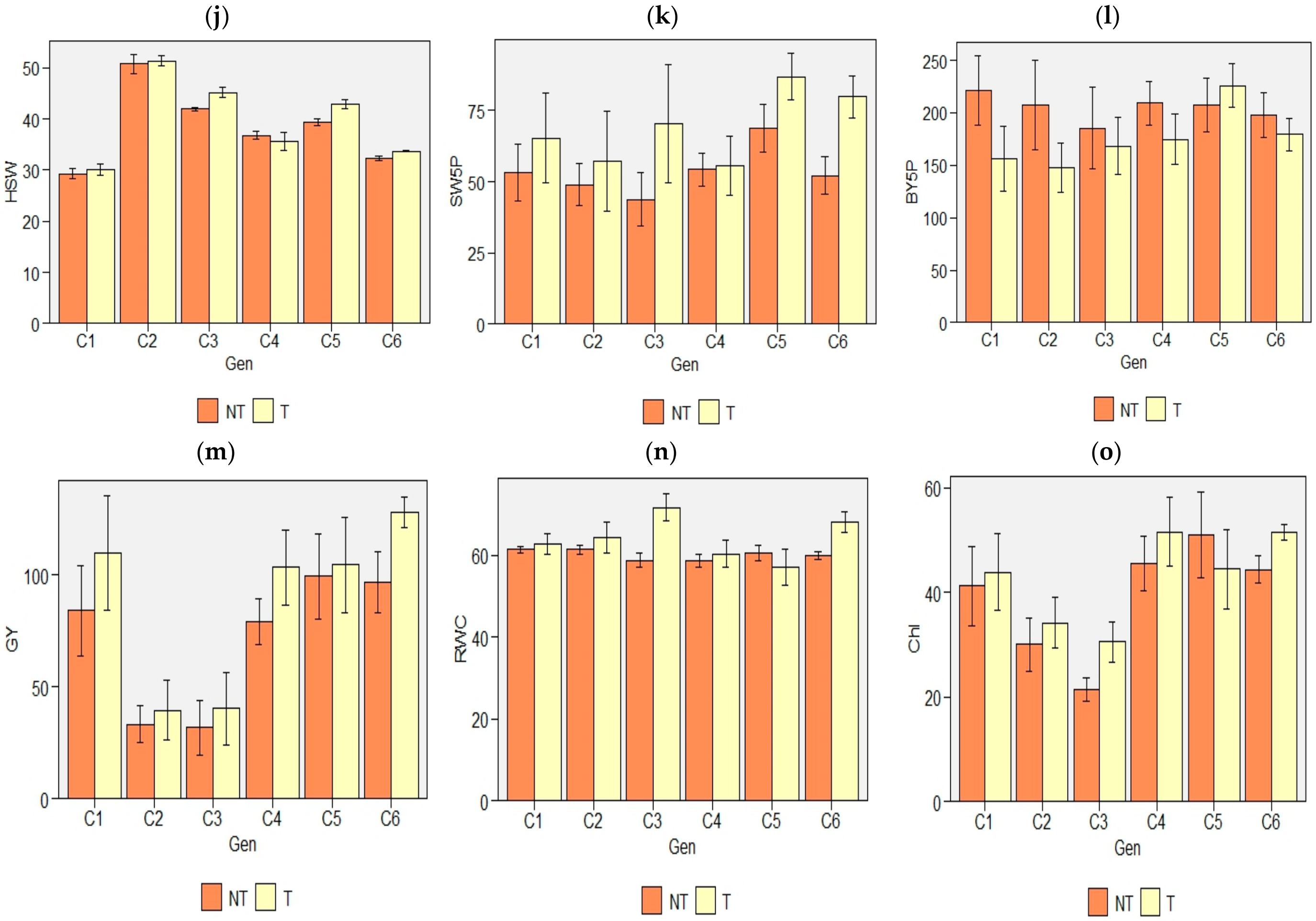


Figure 2. Performance of all traits on the six check chickpea genotypes in the two systems. (**a**): EV (early vigor), (**b**): DF (days to flowering), (**c**): DPF (days to pod formation), (**d**): PH (plant height), (**e**): NPB (number of primary branches), (**f**): NSB (number of secondary branches), (**g**): NPd5P (number of pods), (**h**): NEPd5P (number of empty pods), (**i**): NS5P (number of seeds), (**j**): HSW (hundred seed weight), (**k**): SW5P (seed weight), (**l**): BY5P (biomass), (**m**): GY (grain yield), (**n**): RWC (relative water content), (**o**): Chl (chlorophyll content), and NT: no-till, T: tillage.

3.3. Performance of Genotypes by Traits, Estimation of Phenotypic Variability, and Heritability on the Two Tillage Systems

The minimum, maximum, coefficient of variation, and heritability were calculated for both systems. The high variability of the mean, minimum, and maximum values obtained between the different traits is necessary for an improvement in quantitative traits and would imply that a selection of genotypes for no-till is possible.

The mean comparison test shows that conventional seeding exceeded direct seeding by significantly higher mean values for the number of primary branches, number of pods, number of grains, plant height, and hundred-grain weight (Table 4). On the other hand, we found that no-till produced a significantly higher average biomass than conventional seeding. We also found, as was the case for the checks, that no-till produced significantly fewer empty pods compared to conventional seeding. Grain yield, chlorophyll content, early vigor, the number of secondary branches, and days to flowering did not show significant differences in mean values between the two systems (Table 4). For the majority of the traits studied, with significant or no differences, conventional seeding gave higher mean values than no-till.

Table 4. Comparison of means, estimation of phenotypic variables, and heritability on the 15 chickpea traits in the two systems.

Trait	Till System	Mean	Std.Deviation	Min	Max	CV	CV.Category	hBS	hBS.Category
EV	NT	3.32 a	1.36	0.11	6.11	33.89	Medium	21.63	Low
	T	3.21 a	0.78	1.22	5.22	17.89	Low	43.68	Medium
DF	NT	116.3 a	12.33	83.56	140.22	8.22	Low	32.75	Medium
	T	118.96 a	6.51	86.89	135.06	4.79	Low	30.47	Medium
DPF	NT	137.56 a	8.17	116.44	164.94	5.06	Low	7.68	Low
	T	133.25 b	6.96	117.33	154.17	4.8	Low	26.02	Low
PH	NT	42.09 b	7.88	18.04	64.61	13.26	High	46.69	Medium
	T	44.23 a	10.19	20.59	67.13	12	Low	56.5	Medium
NPB	NT	1.76 a	0.58	0.6	3.23	33.13	Medium		
	T	1.93 b	0.56	0.86	7.86	20.85	Low	46.99	Medium
NSB	NT	12.55 a	3.83	4.52	24.72	25.62	Medium	30.16	Medium
	T	14.05 a	4.37	5.18	29.98	22.14	Low	45.82	Medium
NPd5P	NT	191.83 a	83.72	35.83	484.17	26.86	Medium	61.79	High
	T	247.45 b	115.45	19.25	595.42	27.93	Medium	66.03	High
NEPd5P	NT	16.2 a	9.01	0	42.86	35.19	Medium	58.39	Medium
	T	28.84 b	17.25	3	106.83	39.65	Low	55.62	Medium
NS5P	NT	198.47 a	98.27	3.47	554.14	42.36	Medium	29.93	Low
	T	240.89 b	133.86	0	648.69	29.58	Medium	73.35	High
HSW	NT	27.05 a	9.63	10.54	50.77	8.41	Low	93.69	High
	T	27.79 b	10.37	11.21	53.4	9.34	Low	92.91	High
SW5P	NT	48.98 a	21.1	0.12	112.17	42.48	Medium		
	T	64.36 a	37.43	0	228.01	47.96	High	25.09	Low
BY5P	NT	203.77 a	69.28	0	397.44	36.85	Medium		
	T	160.67 b	81.1	0	458.07	32.63	Medium	54.27	Medium
GY	NT	52.57 a	29.66	0	130.73	62.06	High		
	T	63.14 a	38.98	0	169.06	59.67	High	15.02	Low
RWC	NT	62.77 a	6.66	24.22	86.65	5.45	Low	73.68	High
	T	67.5 b	7.53	51.97	91.88	13.27	Low		
Chl	NT	35.27 a	14.1	5.61	78.81	36.65	Medium	15.69	Low
	T	38.44 a	15.08	0.25	86.23	34.01	Medium	22.94	Low

EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). Means followed by the same letter show no significant difference between the two systems.

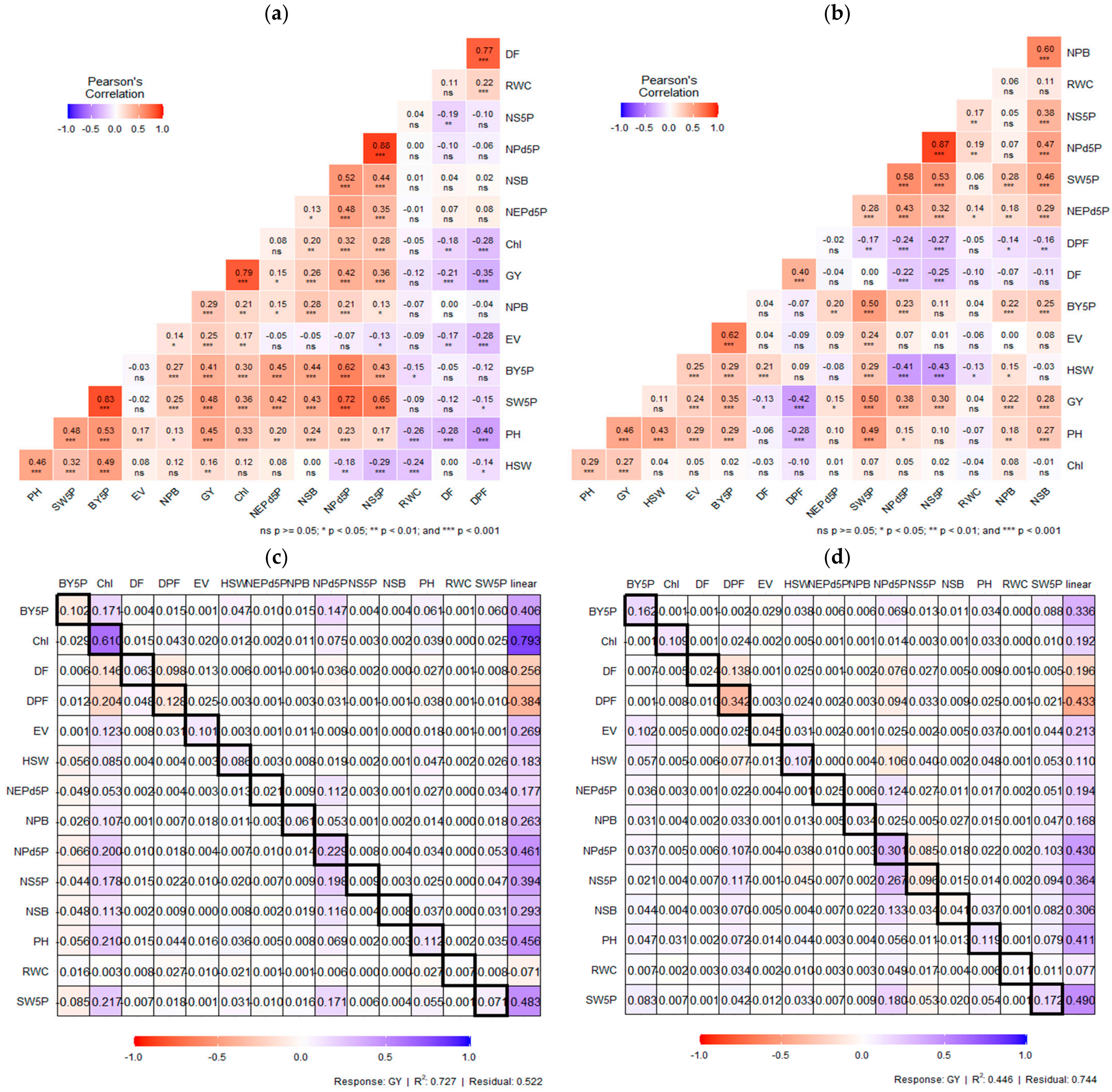
The grain yield ranged from 0 to 130.73 and from 0 to 169.06 g/m^2 in no-till and conventional seeding, respectively, and biomass ranged from 0 to 397.44 g/m^2 for no-till and from 0 to 458.07 g/m^2 for conventional seeding (Table 4). The coefficient of variation of grain yield was the highest of all traits in both systems, with 62.06 for conventional and 59.67 for no-till. This demonstrates the high variability that exists between genotypes in grain yield production in both systems. For all traits, the coefficient of variation ranged from 4.79 (for the flowering date in conventional seeding) to 62.06 (for yield in conventional seeding). The largest differences in the coefficient of variation of the same trait between the two systems were recorded on early vigor (33.89 for no-till and 17.89 for conventional), the number of primary branches (33.13 for no-till and 20.85 for conventional), and the number of grains (42.36 for direct seeding and 20.58 for conventional seeding) with mean values for direct seeding and conventional seeding of 3.32 and 3.21 for vigor, 1.76 and 1.93 for the number of primary branches, and 198.47 and 240.89 for number of grains (Table 4) respectively. These high variations can be explained by the heterogeneity of the responses of the different genotypes under the two systems.

Heritability had heterogeneous values between traits within the same system and between the same trait in both systems. Chlorophyll content and days to pod formation were the only traits that had low heritability in both systems at the same time. Heritability for some traits such as early vigor and the number of seeds was variable between systems. Days to flowering, plant height, the number of secondary branches, and the number of empty pods had moderate heritability in both systems. Hundred seed weight with a heritability of 93.69 and 92.91 and number of pods with a heritability of 61.79 and 66.03 in no-till and conventional seeding, respectively, both had the highest values of heritability for the same trait in both systems and this would imply that selection through these two traits in the systems would be effective.

3.4. Phenotypic Correlations between All Traits and the Contribution of Each Trait to Grain Yield in Each System

The Pearson correlation coefficient calculated in each system shows, for some traits, similar relationships in the two trials, while for other traits the relationships are opposed. Among the fifteen traits studied, the correlation matrix reveals significant and interesting relationships in both systems. Seven (in conventional seeding) and three (in no-till) strong positive correlations (exceeding 0.60) were found in both trials (Figure 3a,b). The highest correlation, between yield and a trait, was recorded in conventional seeding, between grain yield and chlorophyll content (0.79) (Figure 3a). This same correlation was less strong (0.27) but very significant in no-till (Figure 3b). The strongest positive and significant correlation between all traits in the two trials was observed between the number of grains and the number of pods, and it was 0.88 and 0.87 in conventional and no-till (Figure 3a,b), respectively. The hundred seed weight had a positive and significant correlation with grain yield in conventional seeding, while in no-till, their correlation was positive but remained non-significant. Plant height, biomass, the number of pods and grains, early vigor, and the number of primary and secondary branches all correlated positively and significantly with grain yield in both systems. Relative water content, which had a positive but non-significant correlation with yield in no-till, had a negative correlation with yield in conventional seeding that was still non-significant. On the other hand, the yield had three negative correlations in conventional seeding against two very significant negative correlations in no-till with the number of days to flowering and the number of days to pod formation. This result shows that regardless of the tillage system, early genotypes would have better productivity compared to late genotypes.

Understanding the contribution of each trait to grain yield in each system is crucial and would help in this sense to consider beforehand the traits of great interest to investigate them well in order to directly or indirectly improve the grain yield in no-till. It can be seen that most of the direct contributions in both systems are small or moderate. Thus, only one very high direct positive effect was obtained in both systems. Chlorophyll content, which had a strong positive correlation with grain yield in conventional seeding, also showed the highest positive direct effect (0.610) on yield in conventional seeding (Figure 3c). This same trait also contributed directly to grain yield in a moderately positive way in no-till (0.109) (Figure 3d). Pod number contributed moderately in both systems, with a contribution of 0.229 and 0.301 in conventional and no-till, respectively. Plant height and hundred seed weight also contributed positively and directly in a moderate way to yield in both systems. Biomass, which showed a direct positive effect on yield in no-till, however, made a direct but negative contribution to yield in conventional seeding (Figure 3c,d). A negative and moderate direct effect was identified on the number of days to pod formation in both systems. Indirect contributions, positive or negative, to yield remained low in both systems for most traits. However, we noted that in the conventional system, the indirect and positive contribution of the plant height, the number of pods and grains, the number of secondary branches, and the early vigor through the chlorophyll content was moderate (Figure 3c). There was also a positive indirect contribution from the number of pods via the number of grains in both systems (Figure 3c,d).



(**a**)

Pearson's Correlation

	PH	SW5P	BY5P	EV	NPB	GY	Chl	NEPd5P	NSB	NPd5P	NS5P	RWC	DF	DPF
DF														0.77 ***
RWC													0.11 ns	0.22 ***
NS5P												0.04 ns	-0.19 **	-0.10 ns
NPd5P											0.88 ***	0.00 ns	-0.10 ns	-0.06 ns
NSB										0.52 ***	0.44 ***	0.01 ns	0.04 ns	0.02 ns
NEPd5P									0.13 *	0.48 ***	0.35 ***	-0.01 ns	0.07 ns	0.08 ns
Chl								0.08 ns	0.20 **	0.32 ***	0.28 ***	-0.05 ns	-0.18 **	-0.28 ***
GY							0.79 ***	0.15 *	0.26 ***	0.42 ***	0.36 ***	-0.12 ns	-0.21 ***	-0.35 ***
NPB						0.29 ***	0.21 **	0.15 *	0.28 ***	0.21 ***	0.13 *	-0.07 ns	0.00 ns	-0.04 ns
EV					0.14 *	0.25 ***	0.17 **	-0.05 ns	-0.05 ns	-0.07 ns	-0.13 *	-0.09 ns	-0.17 **	-0.28 ***
BY5P				-0.03 ns	0.27 ***	0.41 ***	0.30 ***	0.45 ***	0.44 ***	0.62 ***	0.43 ***	-0.15 *	-0.05 ns	-0.12 ns
SW5P			0.83 ***	-0.02 ns	0.25 ***	0.48 ***	0.36 ***	0.42 ***	0.43 ***	0.72 ***	0.65 ***	-0.09 ns	-0.12 ns	-0.15 *
PH		0.48 ***	0.53 ***	0.17 **	0.13 *	0.45 ***	0.33 ***	0.20 **	0.24 ***	0.23 ***	0.17 **	-0.26 ***	-0.28 ***	-0.40 ***
HSW	0.46 ***	0.32 ***	0.49 ***	0.08 ns	0.12 ns	0.16 **	0.12 ns	0.08 ns	0.00 ns	-0.18 **	-0.29 ***	-0.24 ***	0.00 ns	-0.14 *

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

(**b**)

Pearson's Correlation

	PH	GY	HSW	EV	BY5P	DF	DPF	NEPd5P	SW5P	NPd5P	NS5P	RWC	NPB	NSB
NPB														0.60 ***
RWC													0.06 ns	0.11 ns
NS5P												0.17 **	0.05 ns	0.38 ***
NPd5P											0.87 ***	0.19 **	0.07 ns	0.47 ***
SW5P										0.58 ***	0.53 ***	0.06 ns	0.28 ***	0.46 ***
NEPd5P									0.28 ***	0.43 ***	0.32 ***	0.14 *	0.18 **	0.29 ***
DPF								-0.02 ns	-0.17 **	-0.24 ***	-0.27 ***	-0.05 ns	-0.14 *	-0.16 **
DF							0.40 ***	-0.04 ns	0.00 ns	-0.22 ***	-0.25 ***	-0.10 ns	-0.07 ns	-0.11 ns
BY5P						0.04 ns	-0.07 ns	0.20 **	0.50 ***	0.23 ***	0.11 ns	0.04 ns	0.22 ***	0.25 ***
EV					0.62 ***	0.04 ns	-0.09 ns	0.09 ns	0.24 ***	0.07 ns	0.01 ns	-0.06 ns	0.00 ns	0.08 ns
HSW				0.25 ***	0.29 ***	0.21 ***	0.09 ns	-0.08 ns	0.29 ***	-0.41 ***	-0.43 ***	-0.13 *	0.15 *	-0.03 ns
GY			0.11 ns	0.24 ***	0.35 ***	-0.13 *	-0.42 ***	0.15 *	0.50 ***	0.38 ***	0.30 ***	0.04 ns	0.22 ***	0.28 ***
PH		0.46 ***	0.43 ***	0.29 ***	0.29 ***	-0.06 ns	-0.28 ***	0.10 ns	0.49 ***	0.15 *	0.10 ns	-0.07 ns	0.18 **	0.27 ***
Chl	0.29 ***	0.27 ***	0.04 ns	0.05 ns	0.02 ns	-0.03 ns	-0.10 ns	0.01 ns	0.07 ns	0.05 ns	0.02 ns	-0.04 ns	0.08 ns	-0.01 ns

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

(**c**)

	BY5P	Chl	DF	DPF	EV	HSW	NEPd5P	NPB	NPd5P	NS5P	NSB	PH	RWC	SW5P	linear
BY5P	0.102	0.171	-0.004	0.015	-0.001	0.047	-0.010	0.015	0.147	0.004	0.004	0.061	-0.001	0.060	0.406
Chl	-0.029	0.610	0.015	0.043	0.020	0.012	-0.002	0.011	0.075	0.003	0.002	0.039	0.000	0.025	0.793
DF	0.006	-0.146	0.063	0.098	-0.013	0.006	-0.001	-0.001	-0.036	-0.002	0.000	-0.027	0.001	-0.008	-0.256
DPF	0.012	-0.204	0.048	0.128	0.025	-0.003	-0.001	-0.003	-0.031	-0.001	-0.001	-0.038	0.001	-0.010	-0.384
EV	0.001	0.123	-0.008	0.031	0.101	0.003	0.001	0.011	-0.009	-0.001	0.000	0.018	-0.001	-0.001	0.269
HSW	-0.056	0.085	0.004	0.004	0.003	0.086	0.003	0.008	-0.019	-0.002	0.001	0.047	-0.002	0.026	0.183
NEPd5P	-0.049	0.053	0.002	-0.004	0.003	0.013	0.021	0.009	0.112	0.003	0.001	0.027	0.000	0.034	0.177
NPB	-0.026	0.107	-0.001	0.007	0.018	0.011	-0.003	0.061	0.053	0.001	0.002	0.014	0.000	0.018	0.263
NPd5P	-0.066	0.200	-0.010	0.018	-0.004	-0.007	-0.010	0.014	0.229	0.008	0.004	0.034	0.000	0.053	0.461
NS5P	-0.044	0.178	-0.015	0.022	-0.010	-0.020	-0.007	0.009	0.198	0.009	0.003	0.025	0.000	0.047	0.394
NSB	-0.048	0.113	-0.002	0.009	0.000	0.008	-0.002	0.019	0.116	0.004	0.008	0.037	0.000	0.031	0.293
PH	-0.056	0.210	-0.015	0.044	0.016	0.036	-0.005	0.008	0.069	0.002	0.003	0.112	-0.002	0.035	0.456
RWC	0.016	-0.003	0.008	-0.027	-0.010	-0.021	0.001	-0.001	-0.006	0.000	0.000	-0.027	0.007	-0.008	-0.071
SW5P	-0.085	0.217	-0.007	0.018	-0.001	0.031	-0.010	0.016	0.171	0.006	0.004	0.055	-0.001	0.071	0.483

Response: GY | R^2: 0.727 | Residual: 0.522

(**d**)

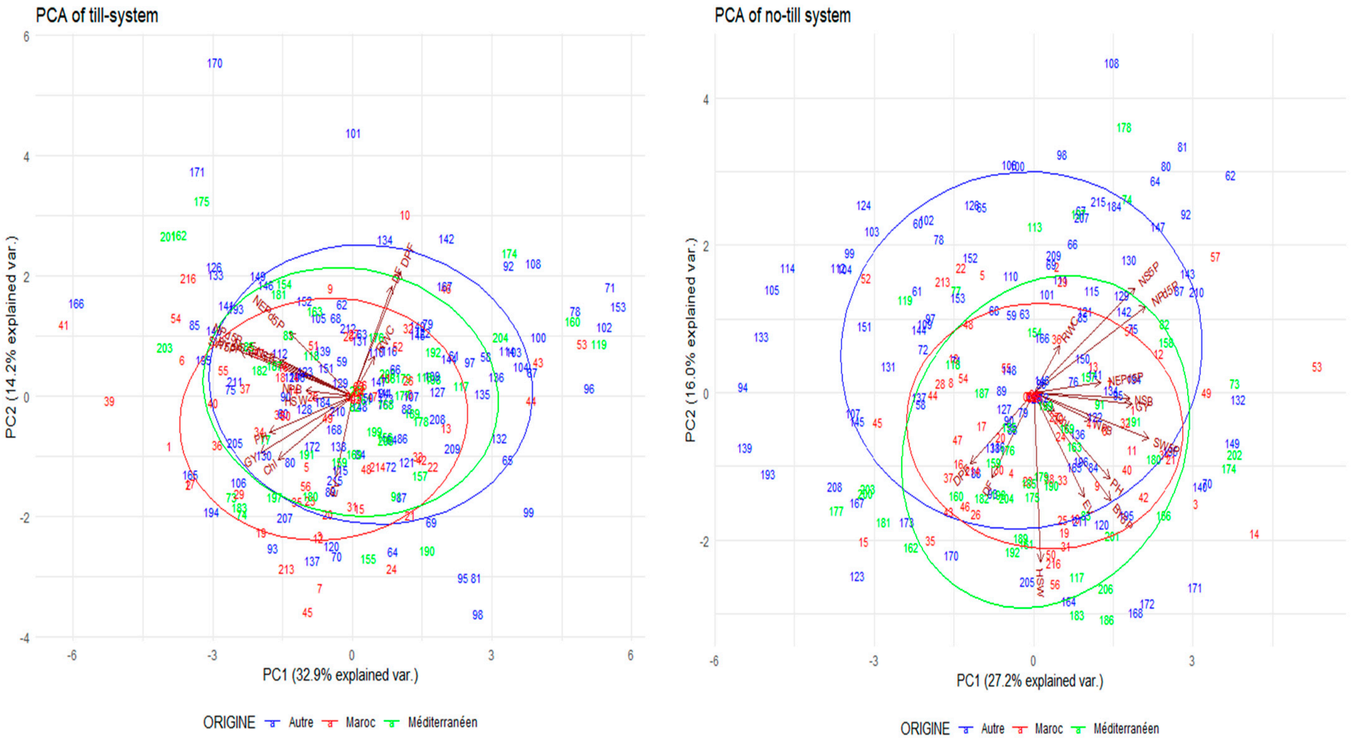
	BY5P	Chl	DF	DPF	EV	HSW	NEPd5P	NPB	NPd5P	NS5P	NSB	PH	RWC	SW5P	linear
BY5P	0.162	0.001	-0.001	-0.002	-0.029	0.038	-0.006	0.006	0.069	-0.013	-0.011	0.034	0.000	0.088	0.336
Chl	-0.001	0.109	0.001	0.024	-0.002	0.005	-0.001	0.001	0.014	-0.003	0.001	0.033	0.000	0.010	0.192
DF	0.007	-0.005	0.024	-0.138	-0.001	0.025	0.001	-0.002	-0.076	0.027	0.005	-0.009	-0.001	-0.005	-0.196
DPF	0.001	-0.008	-0.010	0.342	0.003	0.024	0.002	-0.003	-0.094	0.033	0.009	-0.025	-0.001	-0.021	-0.433
EV	0.102	0.005	0.000	0.025	0.045	0.031	-0.002	-0.001	0.025	-0.002	-0.005	0.037	-0.001	0.044	0.213
HSW	0.057	0.005	-0.006	-0.077	-0.013	0.107	0.000	0.004	-0.106	0.040	-0.002	0.048	-0.001	0.053	0.110
NEPd5P	0.036	0.003	0.001	0.022	-0.004	-0.001	0.025	0.006	0.124	-0.027	-0.011	0.017	0.002	0.051	0.194
NPB	0.031	0.004	0.002	0.033	0.001	0.013	-0.005	0.034	0.025	-0.005	-0.027	0.015	0.001	0.047	0.168
NPd5P	0.037	0.005	0.006	0.107	-0.004	-0.038	-0.010	0.003	0.301	-0.085	-0.018	0.022	0.002	0.103	0.430
NS5P	0.021	0.004	0.007	0.117	-0.001	-0.045	-0.007	0.002	0.267	0.096	-0.015	0.014	0.002	0.094	0.364
NSB	0.044	-0.004	0.003	0.070	-0.005	0.004	-0.007	0.022	0.133	-0.034	0.041	0.037	0.001	0.082	0.306
PH	0.047	0.031	0.002	0.072	-0.014	0.044	-0.003	0.004	0.056	-0.011	-0.013	0.119	0.001	0.079	0.411
RWC	0.007	-0.002	0.003	0.034	0.002	-0.010	-0.003	0.003	0.049	-0.017	-0.004	0.006	0.011	0.011	0.077
SW5P	0.083	0.007	0.001	0.042	-0.012	0.033	-0.007	0.009	0.180	-0.053	-0.020	0.054	0.001	0.172	0.490

Response: GY | R^2: 0.446 | Residual: 0.744

Figure 3. Phenotypic correlation and path analysis of each system. EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). Significance level: ns: $p > 0.05$; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. (**a**,**b**): Phenotypic correlation for conventional tillage and no-till respectively. (**c**,**d**): path analysis for conventional tillage and no-till respectively.

3.5. Variation in the Phenotypic Response of All Genotypes in the Two Tillage Systems

The principal component analysis highlighted the variations existing in the two systems according to the traits. In conventional tillage, the first two components captured 47.1% (PC1 = 32.9 and PC2 = 14.5) of the total phenotypic variance explained compared to 43.2% (PC1 = 27.2 and PC2 = 16) for the first two components of no-till (Figure 4a,b). Grain yield and its components, except hundred seed weight (having a low contribution in the first two principal components), had a consistent contribution of more than 10% of the variance explained by the first principal component in conventional seeding, and the number of days to flowering and pod formation contributed strongly (more than 20%) to the second component in conventional seeding. Thus, in conventional seeding, the first axis (PC1) was related to yield while the second was related to genotype phenology. This trend was not totally the same in no-till. That is, apart from biomass and hundred seed weight, which contributed strongly to the second principal component, the number of pods and grains, which still explained the variability captured by the first principal component. Thus, it can be said that genotypes correlated to the first principal component in both systems would have acceptable yields regardless of the system. And the second principal component in conventional seeding would separate early from late genotypes (Figure 4a).



(**a**) (**b**)

Figure 4. PCA biplots describing the variability of phenotypic responses and distribution of chickpea genotypes in each tillage system. EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). (**a**): PCA of conventional tillage. (**b**): PCA of no-till.

All of the plant material studied is placed into three groups according to their provenance to see if their responses would have any relationship to their geographical origins. For this purpose, the genotypes were classified into three distinct groups. One group was composed only of Moroccan genotypes, the second group included all Mediterranean genotypes, and the last group included all genotypes that were neither Moroccan nor Mediterranean. We noted that the distribution of genotypes in conventional seeding showed a tendency for Moroccan genotypes to converge towards the center, although the separation with Mediterranean and other accessions (from Asia, America, etc.) was not clear-cut enough. However, in direct seeding, there was a strong concentration of Moroccan genotypes in the center, which were more or less mixed with Mediterranean accessions, but which (these two groups) were distinguished from other genotypes.

This tendency to bring Moroccan genotypes closer to Mediterranean genotypes could be explained by similar responses between the genotypes of the two groups. In conventional seeding, the majority of Moroccan genotypes differed from the other two groups in their earliness, whereas in direct seeding, the distinction was seen in pod and grain production (Figure 4a,b).

The hierarchical cluster analysis performed on all the traits showed little difference in classification between the two systems according to the assignment of a genotype to a group, and in both systems, the genotypes were grouped in six distinct clusters (Figure 5a,b). However, the group of assignment of a genotype sometimes differed between the two systems, although the same genotypes were sometimes found in the same clusters in both systems. Although the same number of clusters was found in both tillage systems, the number of individuals forming a cluster was quite variable within the same system and between the two systems. Cluster C1 had the lowest number of genotypes in both systems. In cluster C1, there was only one local genotype in conventional seeding, whereas in direct seeding, there were two non-Mediterranean genotypes ("other"). In the case of the C2 cluster, we had a grouping of 30 genotypes, of which only 2 were Moroccan in conventional seeding and 43 genotypes in direct seeding, of which 8 were local genotypes. We noticed, then, that the C2 cluster had, in both systems, a weak representation of Moroccan and Mediterranean genotypes, contrary to Indian and Iranian genotypes, which were much better represented. Regarding cluster C3, it gathered the greatest number of genotypes in direct seeding, and in conventional seeding, it was the second. Cluster C3 had a total of 87 individuals in no-till, including 25 Moroccan genotypes, and 53 individuals in conventional seeding, including 26 Moroccan genotypes (Figure 5a,b). Cluster C3 was, then, the second-largest cluster in terms of local genotypes for all clusters formed in both systems. The six checks were found in cluster C4 in no-till and they were well separated from the other genotypes in a separate sub-cluster, and it was the same case in conventional seeding, except that this time, they were grouped in cluster C6. In contrast to conventional seeding, the checks in no-till were found close to a large number of local genotypes. The latter were less numerous in the C6 cluster in conventional seeding where we had the checks. Thus, in conventional seeding, the checks would have responses that distinguish them from a large number of local genotypes. As for cluster C5, in both tillage systems, it totaled a small number of genotypes with a very limited number of local genotypes. With 99 genotypes in conventional tillage, the C6 cluster had the highest number of genotypes of all the clusters constructed in both systems. At the same time, it was the cluster with the highest concentration of local genotypes in conventional seeding.

The C1 cluster genotype in conventional seeding is known for its upright habit, with a significant height of up to 50 cm. The two genotypes of cluster C1 in no-till were characterized by a lower chlorophyll content and a lower grain yield. In both systems, cluster C2 grouped genotypes with an early vigor that is around average with a rather important and average relative water content in conventional and no-till systems, respectively. This same group had a slightly later life cycle for most genotypes, with very low grain yield and biomass. The largest number of genotypes in cluster C3 in conventional seeding were distinguished by a relative water content around the average and a grain yield and biomass well above average. In no-till, the genotypes of cluster C3 were characterized by below-average biomass, average grain yield, and relative water content. Cluster C4 was characterized by genotypes with high biomass and an above-average grain yield. Most of them also had a plant height and a chlorophyll content that were around the average. The genotypes of cluster C5 for conventional seeding, although they produced a high number of pods and a high biomass, had a grain yield below average. In no-till, the C5 cluster genotypes had low hundred seed weight but average grain yield, relative water content, and chlorophyll content. In no-till, the C6 cluster showed genotypes whose most common traits were certainly the number of pods and grains that were largely high compared to the average. However, they had a low hundred seed weight and an average relative water content. The genotypes of cluster C6 from conventional seeding had a low variation in the number of days to flowering and pod formation. For most of these genotypes, grain yield and biomass were below average and hundred seed weight was about average.

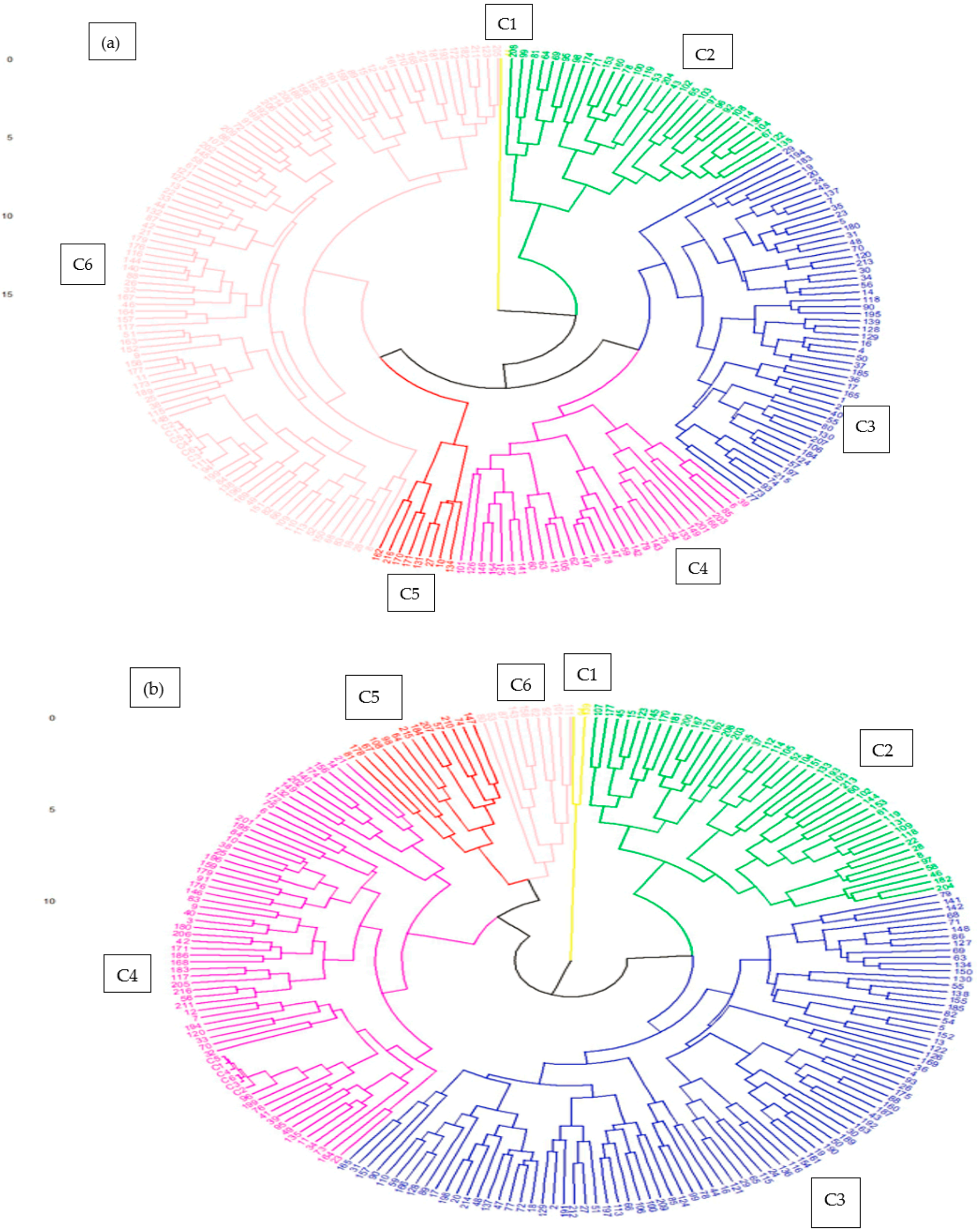


Figure 5. Hierarchical clustering of the two tillage systems ((**a**): conventional and (**b**): no-till) for the fifteen traits studied on all chickpea accessions. C (cluster).

3.6. Selection in the Two Tillage Systems with the MGIDI

The majority of traits, including grain yield, in both no-till and conventional seeding were concentrated in the FA2 group (Figure 6a,b). Only hundred seed weight was selected in the first group FA1 in both systems. The strengths and weaknesses of the genotypes identified at the same time in the two systems were different according to the contribution of the factors in each system. The FA2 factor (which gathers grain yield and biomass in both systems) showed, for the C6 and C1 checks and the 212 and 195 genotypes, a strong contribution to MGIDI in no-till, which was the opposite in conventional seeding. The opposite trend was observed for genotypes 19 and 40. Genotypes 40 and 180 had the two factors in conventional seeding exactly on the black dashed line that denotes the theoretical values if both factors contributed equally (Figure 6a). Genotypes such as 185, 25, and 9 have FA2, in both systems, inside the black dashed line. And it can be understood that they were selected in both systems due to their potential grain yield and high biomass. Among the genotypes identified in both systems, we can see that the C6 check and genotypes 9, 25, and 195 had the lowest gap between FA1 and FA2 in both systems. And it says that, in both systems, they had an almost equal inclination between hundred seed weight and grain yield.

The two factors obtained from the calculation of the MGIDI index did not show significant variability between the two systems in terms of matching a trait to the factors. Figure 6b,d show the genotypes selected for conventional and no-till, respectively. Of the six checks, four were selected (C1, C4, C5 and C6) in no-till and only two (C1 and C6) in conventional seeding. The checks C1 and C6 were located in both systems (Figure 7). Other genotypes such as 212, 185, 19, 25, 9, 40 and 195 were selected in both systems (Figure 7), which could be explained by their performance in both systems. Genotypes 1 and 128 were located in no-till and conventional seeding (Figure 6b,d), respectively, just after the red dots (designating the selected genotypes). This shows that these genotypes would also gather some interesting traits in each system where they were identified.

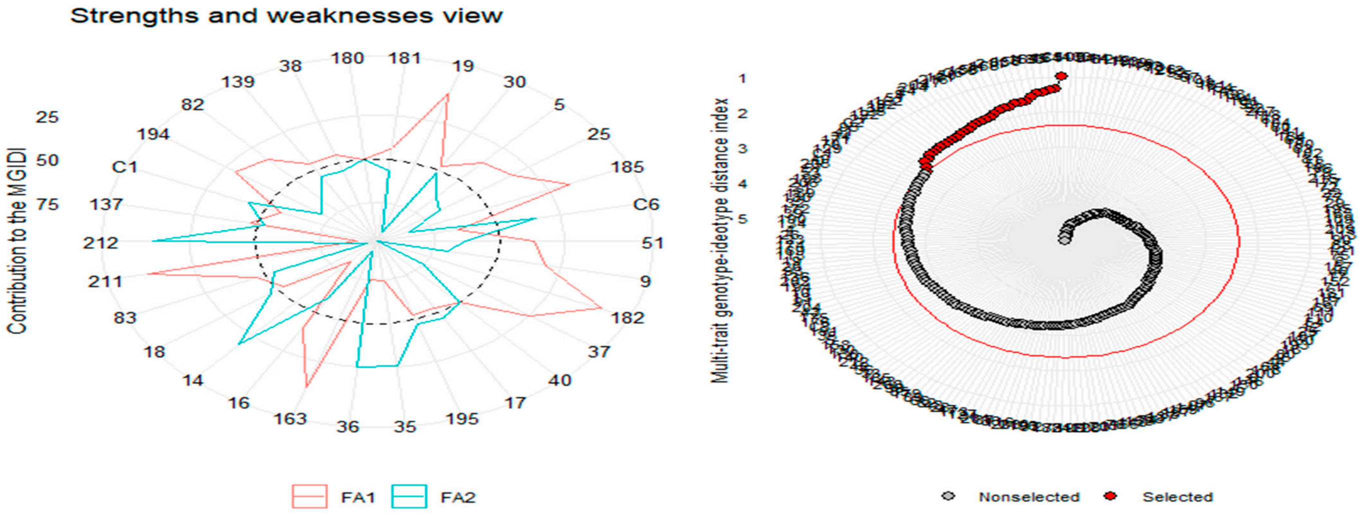

(**a**) (**b**)

Figure 6. *Cont.*

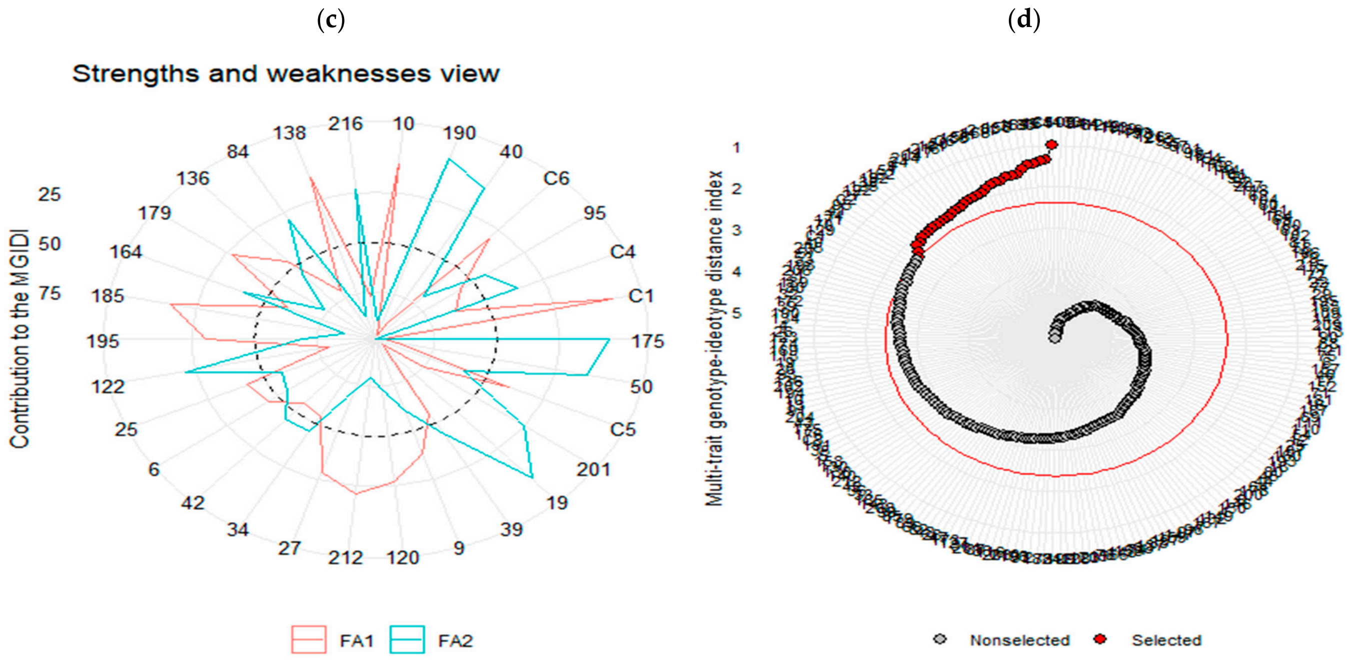

(**c**) (**d**)

Figure 6. View of strengths and weaknesses of selected genotypes in each system and ranking of genotypes based on MGIDI. FA1: HSW; FA2: GY, NPd5P, NS5P, SW5P, and BY5P. EV (early vigor), DF (days to flowering), DPF (days to pod formation), PH (plant height), NPB (number of primary branches), NSB (number of secondary branches), NPd5P (number of pods), NEPd5P (number of empty pods), NS5P (number of seeds) HSW (hundred seed weight), SW5P (seed weight), BY5P (biomass), GY (grain yield), RWC (relative water content), and Chl (chlorophyll content). (**a**,**c**): strengths and weaknesses of genotypes in conventional seeding and no-till respectively and (**b**,**d**): genotypes selection in conventional and direct seeding respectively.

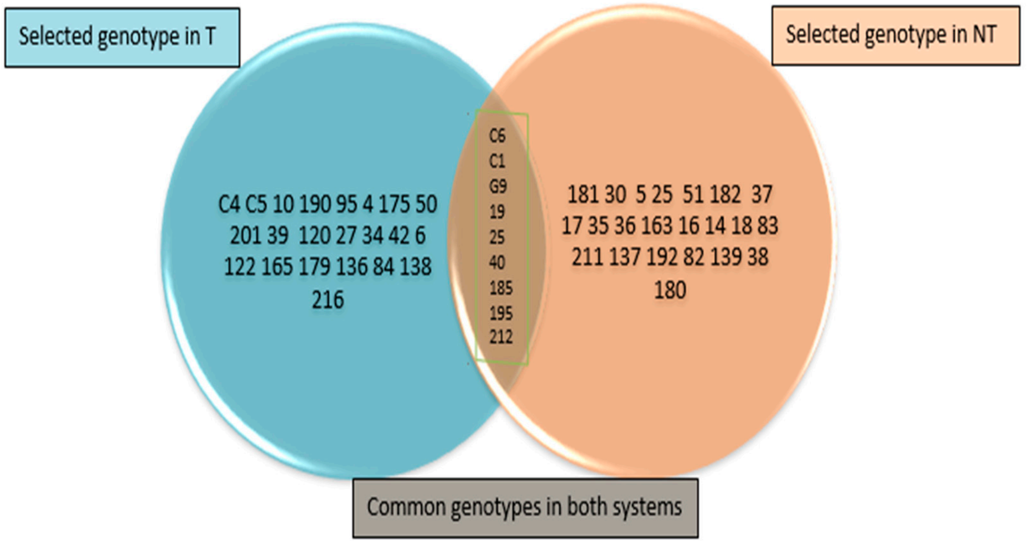


Figure 7. Visualization of the selected genotypes in the two tillage systems through a Venn diagram. T (tillage), NT (no-till).

We noticed that the two checks C1 and C6, although they were from the selection programs for conventional seeding, received a low contribution of FA2 in no-till compared to conventional seeding, which would indicate their high performance in grain yield and biomass in no-till compared to conventional seeding. The lowest contribution of FA1, for genotypes selected at the same time in both systems, was recorded in no-till for genotype 40, while the low contribution for FA2 was obtained in conventional seeding by genotype 19 and by the C1 check in no-till. In general, the genotypes selected in conventional seeding were strongly influenced by the FA2 group. Nevertheless, the two groups FA1 and FA2 had an almost equal influence on the genotypes selected in no-till. It should be noted that out of nine genotypes identified in both systems at the same time, six were local genotypes, only one was a Mediterranean genotype and the other two were neither Moroccan nor Mediterranean.

4. Discussion

The practice of conservation agriculture is attracting a lot of interest worldwide because of its benefits, and the area dedicated to it is increasing significantly [37].

In Morocco, the adoption of conservation agriculture is still in its infancy, and the state is trying through several projects to sensitize and convince farmers of the advantages of conservation agriculture. Thus, due to its strong dependence on environmental hazards (climatic region, soil, rainfall. . .) [38,39], research on conservation agriculture, especially on effective practices to adopt and suitable genotypes, would be a good asset to promote this agricultural management technology to farmers in order to encourage them to opt for conservation agriculture. The use, in conservation agriculture, of plant material previously selected in conventional agriculture programs shows limits in terms of genotype performance and reveals contrasting results on several traits [40], hence the need to carry out research and conduct programs that can reassure the farmer of the performance of the varieties that will be proposed for direct seeding. However, before conducting such programs for adaptation to conservation agriculture practices, it is crucial to first judge the need for such programs by having a clear idea of the traits that contribute strongly to grain yield, the strength of their heritability, and also to understand the degree of genotype × system interaction across traits.

4.1. Genotype × System Interaction and Effect of Genotype on All the Traits Studied

For most of the traits studied, we found highly significant results, especially on the genotype × system interaction. This is in agreement with the results reported on barley, wheat, chickpea, and lentil [41,42]. However, other research found the association between genotype and tillage system insignificant [43]. Thus, the existing interaction in our case can be explained by the high diversity that our plant material presents. This highly significant genotype × system interaction on the majority of the traits leaves us with a large possibility of a selection, in relation to till system, that would be effective. Thus, traits such as hundred-seed weight, relative water content, the number of pods and the number of empty pods need to be carefully monitored, as they could well help us in similar breeding programs for adaptation to conservation agriculture. Our study also shows an effect of genotype that is highly significant on all traits except chlorophyll content. This is quite obvious because our results sometimes showed huge differences between the performance of genotypes across the different traits measured.

4.2. Effect of Tillage on Grain Yield and All Other Traits

Grain yield could be translated as a variable whose final result is the sum of several influences such as crop management practices, in this case tillage. Research on the effect of tillage on yield and its components often results in findings pointing to a significant effect of tillage on the grain yield of chickpea and other crops [3,44], just as other studies prove the opposite [45]. This diversity of response sometimes finds explanation in the pedoclimatic context of the region in question, including the type of soil where tillage is practiced, the distribution of rainfall and thermal variations, and also in the genetic variability of the genotypes evaluated.

In our research, tillage did not have a significant effect on grain yield. The same is true for early vigor, days to flowering and pod formation, number of secondary branches, and chlorophyll content. Thus, given the low impact of tillage on grain yield and these traits (early vigor, days to flowering and pod formation, the number of secondary branches, and chlorophyll content), they did not show significant differences between the two tillage systems. Similar results, showing a non-significant effect of tillage on grain yield, were obtained in lentil by Devkota et al. [46], in barley in the Mediterranean region by Martinrueda et al. [47], and in chickpea by Rathore et al. [2] and Mishra et al. [48]. From fourteen years of studies on the effect of tillage on barley yield, Morell et al. [19] manage to conclude that in a favorable year in terms of rainfall, the difference between the two tillage systems on grain yield is not significant. This thesis was also supported by Muñoz-Romero et al. [1], showing that in good moisture conditions, both systems tend to produce almost the same yields. In Syria, Piggin et al. [42] also confirmed, after working on several sowing date combinations, that the two systems often produced close yields in most combinations.

Given that the plant material used was derived from conventional seeding breeding programs, the fact that there was no significant difference in grain yield between the two systems would indicate that breeding for no-till adaptation could increase the potential yield of chickpea in no-till. In fact, in the absence of selection for adaptation to conservation agriculture, the use in no-till of some genotypes previously selected for conventional seeding would cause less or no loss of genotype yield potential. Of all the genotypes tested, some were found to have the potential to reproduce acceptable yields in no-till despite being from conventional seeding breeding programs. That said, exploring this germplasm by further evaluating it under conservation agriculture conditions would provide farmers with varieties that can maintain better and stable yields in the systems. Such a parallel breeding approach to conservation agriculture and conventional seeding was proposed by Herrera et al. [49] to ensure the performance of genotypes in both systems simultaneously.

In agreement with some results recorded on chickpea and wheat, it was found that tillage would impact yield components and plant height [3,50]. Hundred seed weight was the yield component that recorded the most significant effect of tillage ($p < 0.001$). A significantly higher hundred seed weight was recorded in conventional tillage compared to no-till. This is in agreement with the results obtained in the Spanish Mediterranean region by Lopez-Bellido et al. [51] and in the Turkish arid sown area by Kayan et al. [52]. Pod number also had a highly significant tillage effect ($p < 0.01$). Contrary to Jan et al. [53], our results show a significant difference in the number of pods produced between the two systems. The effect of tillage on the number of pods was also significant but less important ($p < 0.05$). For the checks in this case, significant differences were observed for the number of grains, the number of primary and secondary branches, the plant height, and the relative water content, with a slight superiority in conventional seeding. Results showing superiority in conventional seeding were reported by Roohi et al. [43], and this would explain that these genotypes have a strong adaptation to conventional seeding through these traits.

As for biomass, a significant ($p < 0.05$) effect of tillage was found. Biomass was significantly higher in no-till than in conventional tillage, yet conventional tillage produced more grain. High dry biomass was also found in vetch by Sidiras et al. [54] and in chickpea by Horn et al. [55] in no-till compared to conventional seeding. In our study, we had a positive but not significant correlation between the number of grains and biomass in no-till, and this was not the case in conventional seeding, where their correlation was very significant. It can be said that genotypes under no-till adopt behavior that allows them to concentrate a large part of their organic matter towards the development of biomass, which sometimes penalizes the production of pods and grains. Lopez-Bellido et al. [51] found that the inefficient redistribution of soil N to different parts of the plant would cause variations in grain yield and biomass in chickpea. In Iranian arid seedland, Barzegar et al. [56] found that at chickpea maturity, biomass increased with reduced tillage.

4.3. Heritability and Potential of Improvement for Adaptation to Conservation Agriculture

The greater variability observed among the genotypes in our study leaves a wider opportunity to be able to improve genotypes for adaptation to conservation agriculture.

Beyond this variability, heritability serves as an input for chickpea breeding programs [57]. As such, in our case, the phenotypic values of the traits are quite important, but also knowing the genetic weight of the traits in the two tillage systems would help to better situate ourselves when selecting for adaptation to conservation agriculture. Hundred seed weight and the number of pods had high heritability in both systems. This provides good information on the reliability of their phenotypic values [58] and would indicate that selection for adaptation to conservation agriculture is possible through these traits. Fairly high heritability on hundred-seed weight and the number of pods has been reported in many chickpea studies [59–61]. Early vigor and grain number had low heritability in no-till and high in conventional seeding. It is assumed that the environment (tillage system) would have a great influence on these two traits, and selection via these traits for adaptation to conservation agriculture would have less chance of acquiring genetic gain [62]. In addition to this, the two traits with low heritability in both tillage systems, namely chlorophyll content and days to pod formation, would be less relevant to emphasize in breeding programs for adaptation to conservation agriculture.

4.4. Relationship between the Traits and Grouping of Genotypes for Selection

Our study identified relevant correlations and contributions between grain yield and some studied traits. The existing relationships between certain traits and grain yield could directly or indirectly be effective in selection for adaptation to conservation agriculture because it would help to better enhance yield in conservation agriculture. Till system could have an effect on the relationships between traits and vary their contribution and correlation depending on the tillage system.

Pod number and chlorophyll content were the two traits with the highest contribution to grain yield in no-till and conventional tillage, respectively. Other fairly significant contributions to grain yield were recorded in no-till, including biomass and chlorophyll content. Similar to what was revealed by Edalat et al. [63], Naderi et al. [45], and Lopez-Bellido et al. [51] in chickpea, a positive and significant correlation was found in both systems between grain yield and a number of traits, namely, the number of pods and grains, plant height, the number of primary and secondary branches, hundred grain weight and biomass.

Cluster C3 revealed by the hierarchical analysis turns out to be the one that groups the genotypes with a high yield potential in conventional seeding. It can be seen that the MGIDI analysis proposed by Olivoto and Nardino [36] selected the great majority of genotypes of cluster C3 in conventional seeding. In the case of no-till, cluster C4 is the one that gathers the genotypes with the most grain yield and biomass. Moreover, we noticed that most of the genotypes identified in this C4 cluster are also selected in the MGIDI analysis. The effectiveness of this index in selecting a superior ideotype has been reported in several studies [64,65].

5. Conclusions

The main objective of this study was to have a global idea of the performance of the genotypes studied in each system in order to examine the effectiveness of starting breeding programs for the adaptation of chickpea to conservation agriculture. This study, being the first to have conducted experiments in Morocco on a large enough diversity, could well serve to lay the foundations for future breeding programs for adaptation to conservation agriculture. In our study, we found that the genotype × system interaction is highly significant on grain yield and its components and other traits evaluated. This result leaves us the great possibility to initiate breeding programs for adaptation to conservation agriculture. In addition, tillage did not show a significant effect on grain yield. The fact that our study showed statistically similar grain yields between the two tillage systems is a relevant finding that serves as a strong argument to farmers. This demonstrates that the abandonment by farmers of conventional seeding in favor of conservation agriculture would entail less or no risk on yield drops and would contribute to the maintenance of good soil quality [66] by producing at drastically reduced costs [67,68].

Paying attention to certain traits, especially in relation to their correlation and contribution to grain yield, would be a serious avenue to be effective and efficient in breeding programs for conservation agriculture. Genotypes selected simultaneously in both tillage systems by MGIDI analysis, such as the local checks C1 and C6, would be potential candidates for breeding programs for adaptation to no-till because they would have the plasticity to reproduce acceptable yields regardless of the tillage system.

However, much research has yielded mixed and sometimes contradictory results regarding selection for adaptation to no-till. It is, therefore, important to be located in a breeding environment with well-known climatic and soil conditions and well-mastered farm management to be much more efficient. Therefore, as reported by several authors in several crops, in such studies, the effect of intra- and inter-annual rainfall and temperature variations are considerable and have a significant influence on the responses of genotypes to the two tillage systems [39,69]. So, it would be wise to conduct further experiments to fully observe and understand the environmental and year effects.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/su151511927/s1.

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