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Morphological, biological, productive and qualitative characterization of 68 guar (*Cyamopsis tetragonoloba* (L.) Taub.) genotypes

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Abstract

Guar (*Cyamopsis tetragonoloba (L.) Taub.*) is a valuable industrial crop, widely cultivated in India and Pakistan for the high galactomannan content of its endosperm. The present multi-trait characterization of 68 guar genotypes was conducted to identify an ideotype combining desirable traits suitable for cultivation in a Mediterranean climate and that allow an easy harvest. Plant height, branch number, stem diameter, length of crop cycle, number of cluster, number of pods per plant, number of seeds per pod, 1000 seeds weight, seed production per plant, galactomannan and protein content were measured. In addition, correlations between morphological and productive traits were applied, calculating the relationships between traits, and giving biological meaning to the ideotype. To select high performance genotypes under Mediterranean climate, we mainly took into consideration non-branching (easy harvestability, uniformity of maturation) and short crop cycle genotypes with valuable productive and qualitative traits. In this view, the results showed that 17 genotypes resulted non-branching, 11 genotypes showed a short crop cycle and seven genotypes were characterized by a seed production greater than 50 g plant^{-1}. Among them, four genotypes (PI 288757, PI 340263, NC70300525and PI 288745) combine all these desirable traits with good seed production and therefore should be selected as multi-trait high performance genotypes. As far as the galactomannan and protein contents are concerned, a lower coefficient of variation emerged when compared to those of the morphological or productive traits. Correlation analysis showed that plant production was related to cluster number, number of pods per plant, seeds per pod, number of branch

and length of crop cycle. Finally, a negative association between galactomannan and protein content was found.

Keywords: guar, characterization, genotypes, productive and qualitative traits, correlations.

1. Introduction

Guar (*Cyamopsis tetragonoloba (L.) Taub.*) or cluster bean, is an erect or bushy, herbaceous, summer legume. Being considered a minor crop, international official statistical data are unavailable for guar. Sharma (2010) reports that the 95% of the world production is in India and Pakistan, while minor cultivations are also reported for the USA, where it was introduced in 1903 (Hymowitz and Matlock 1963). Guar is self-pollinating plant with a very small percentage of cross-pollination (Stafford and Hymowitz 1980). Its origin is uncertain since it has not been found in the wild state. The most accepted theory reports it could be derived from *Cyamopsis senegalensis,* whose centre of origin is located in Africa (or in the Arabian Peninsula), and that it has been introduced as flotsam or as feed during horse trades by Arabs in India, where it was domesticated (Hymowitz 1972). This is known as *trans-domestication* theory.

Once cultivated for cattle feed and human food (green pods), guar is now considered an industrial crop due to the high galactomannan (long branching polymers of mannose and galactose) content of its endosperm, named guar gum. Guar gum has exceptionally high viscosity, outperforming many other hydrocolloids thanks to its ability to hydrate rapidly in cold water, which is not found in starches (Mathur, 2012; Mudgil et al., 2011). When dissolved in water it forms a gel used as stiffener, thickener, stabiliser and strengthener in a wide range of industries such as food, paper, explosives, textile, cosmetics, oil well drilling muds and ore flotation. In the past few years, the demand for guar gum increased greatly mainly for the oil and gas industry. Although several chemical companies are working on developing synthetic polymers whose properties might rival those of guar gum, no substitute, as effective as guar is for hydraulic fracturing, has yet been developed (Beckwith 2012). After gum extraction, the by-product, composed of seed coat and germ, is a highly valuable protein-rich feed supplement for ruminants (Chiofalo et al. in press; Gresta et al. 2017).

Guar is as heat tolerant and drought tolerant as any crop grown in the Mediterranean area. Guar, compared to other summer legumes, can be grown with few inputs (Gresta et al. 2014) and has a relatively low water requirement (Alexander et al. 1988). It is an inexpensive crop to grow. Guar is also considered an excellent soil improving crop, able to fit well into crop rotation systems of different areas of the world (Rao et al. 1995; Saxena et al. 1997). Guar thrives in sandy soil, but it also grows in clay soil if well ploughed and well drained, since it is very intolerant to waterlogging. It also tolerates low fertility and high salinity soils (Ashraf et al. 2005; Francois et al. 1990).

Previous researches have reported a wide variability for guar on many morphological, biological and productive traits (Manivannan et al. 2015; Mayank et al., 2016; Morris, 2010; Sultan et al., 2012). Guar genotypes, in fact, show very large variability: plant height ranges from 0.5 to 3.0 m; length of the crop cycle can range from 80 to 160 days or more, depending on the genotype and the environment; plant habit varies from single-stem to basal branching pattern. As a general rule, guar also exhibits indeterminate growth: it flowers and sets pods from a few weeks after seed emergence until the end of biological cycle with a consequent lack of uniformity in seed maturity. Some determinate growth varieties have been developed in the USA (Stafford and Ray, 1985).

The commercial market of varieties is limited to some varieties produced in USA and others in India and Pakistan. On this topic, a rapid visual method to evaluate seed traits has been reported by Gresta et al. (2016b). Adaptation of guar to the Mediterranean region has been proved (Sortino and Gresta 2007; Gresta et al. 2013; Gresta et al. 2016a), where its high drought and salinity tolerance well fits with the high temperature, poor erratic rainfall and elevated water salt content of the coastal areas. However, one of the main obstacles to the cultivation in the Mediterranean environment (and also in many other areas of the world) is the long crop cycle, since the crop is still in field when the rains of late summer season fall (end of September and beyond), causing problems with the combine harvest. Researches have also been addressed to the identification of genotypes with reduced temperature requirements for seed germination in order to potentially sow earlier (Gresta et al. submitted). However, very little research has been conducted to characterise and select appropriate genotypes for the Mediterranean environments together with high productive and qualitative traits. This notwithstanding, evaluate and characterize guar germplasm has a key importance for future scenarios of its applications and its cultivation all over the world. This present research investigated 68 guar genotypes from a morphological, biological, productive and qualitative point of view.

2. Material and methods

2.1 General information and morphological, biological and productive traits

The trial was carried out in Botricello, Calabria, southern Italy (CZ, 19 m a.s.l., 38° 56′ 19″ North, 16° 52′ 55″ East) in 2014, on a sand-silt soil, which main characteristics are reported in Table 1.

Sixty-eight genotypes were tested (Table 2): 63 accessions were provided by two different seed banks, the remaining five genotypes (placed at the end of the list) are registered varieties or genotypes owned by the Department of Agraria, University of Reggio Calabria, Italy.

A rotary hoeing was performed at the beginning of April to bury previous wheat residues. A 30-40 cm ploughing was executed at the end of April followed by a rotary harrowing. At the seedbed tillage, a fertilization using a total amount of 22 kg ha^{-1} N, 70 kg ha^{-1} P_2O_5 and 32 kg ha^{-1} K_2O was applied, using as fertilizer 11-22-16 plus simple super phosphate. As a consequence of the lack of nodulation observed during the crop cycle, 100 kg ha^{-1} of N as ammonium nitrate were added at the appearance of the eighth leaf.

Sowing was performed manually on the 10 May on rows 1.0 m long, adopting an intra-row distance of 0.10 m and an inter-row distance of 0.50 m, therefore it has been used a density of 20 plants m^2. Seed were placed at 2-3 cm depth. The rows were north-south oriented to allow the best radiation capture. A completely randomized design with three replications was adopted. The small amount of seed supplied by seed banks forced us to a small size of the plot area (1.5 x 1.0 m). Two guar rows were sowed around the experimental field to avoid any edge effect. Just after sowing, chemical weed management was applied, following the indication reported by Avola et al. (2008) to control weeds in grain legumes, using a mix of Stomp aqua (pendimethalin) and Afalon (linuron), at the dose of 2+1 l ha^{-1}, respectively. Subsequently, weeds were controlled by manual weeding. Immediately after sowing, the plots were irrigated with a sprinkling system to trigger the active chemical compounds of herbicides. A second irrigation with the same system was performed five days after the first one. Further irrigation was conducted with a drip system. Total irrigation was about 3000 m^3 ha^{-1} applied in five irrigations from the May to 25 July.

Harvest was carried out stepwise following the maturation of different genotypes, from 12 October to 21 November. Plants were considered mature when the 75% of the legume were brown and mature.

For each genotype, on 10 plants randomly selected, the following parameters were measured: plant height, branch number, stem diameter, length of the crop cycle, number of clusters per plant, number of pods per plant, number of seeds per pod (on 20 pods per plant), 1000 seed weight and seed production per plant.

2.2 Qualitative analysis

Seeds of the 3 replications of the 68 guar genotypes were milled separately in to guar flour using a laboratory mill (Retsch Model ZM100) with a sieve of 0.5 mm diameter. The dry weight of guar flour obtained after milling was determined in a IR drier at 110 °C. . The method for galactomannans determination was based on the quantitative hydrolysis of galactomannan to D-galactose and manno-oligosaccharides using a combination of β-mannanase and α-galactosidase as reported by McCleary (1981) and adapted by Megazyme method "Galactomannan assay procedure" (https://secure.megazyme.com/files/Booklet/K-GALM_DATA.pdf), with the following modifications: After elimination of the raffinose series oligosaccharides by repeated ethanol precipitation, the samples of guar seed flour were resuspended in 50 mM acetate buffer, pH 4.5, and incubated for 30 min at 95–100 °C with vigorous stirring on a vortex stirrer every 10 min and further incubated for another 30 min at 50 °C. This procedure is necessary to ensure complete solubilization of the galactomannans. The method with the modification is consolidated in the literature (Gresta et al., 2013; Gresta et al., 2016b).

Guar seeds were also analysed for their total nitrogen content (Kjeldahl method). Analyses were carried out in duplicate on each sample of seeds.

2.3 Data analysis

Mean, median, standard deviation and the coefficient of variation on morphological, biological, productive and qualitative traits were computed. To assess simultaneously all the variables studied and to identify any correlations among them, a Pearson correlation was performed. From correlation matrix, data were generated for the multivariate statistical techniques of principal component (PC) factor analysis using StatistiXL 2.0, a plug-in statistics tool for MS Excel (Roberts and Withers, Broadway —Nedlands, Western Australia). Varimax rotation was used for rotation of principal factors through the transformation of factors to maximizes the sum of the variances of the squared loadings (squared correlations between variables and factors) and approximate a simple structure. For this test, we used the eigenvalue greater than one as component retention criteria, and, according with MacCallum et al. (1999), a value greater than 0.6 as acceptable score.

2.4 Metereological data

The air temperature and rainfall data were recorded using a meteorological data logger located near the experimental field.

Rainfall in the whole year was 599 mm, mainly concentrated in the period between November and March (83%), typical amount for the Mediterranean environment. During the growing season, from May to October, the amount of rainfall was only 76 mm. Minimum and maximum daily temperatures increased gradually from May to the first ten day of August. The minimum temperature was recorded at the end of May (14.1°C) while the highest temperature was 36.3 °C at the beginning of August. After that, temperatures began to decline reaching average temperature around 20°C at harvest (Figure 1).

3. Results and Discussions

3.1 Biometric traits

Biometric traits were studied to find valuable genotypes able to reduce seed loss during mechanical harvest and improve productive performance.

Plant height showed an average of 59.6 cm, ranging from 34.0 cm for HF118 61104 to 97.3 cm for PI 547070, with a total CV of 20.9% (Table 3). The median was 59.5 cm, indicating that the sample was uniformly distributed.

The number of branches per plant showed a very wide CV (72.9%), related to a very large variability (from 0 to 11.7 branches per plant). Seventeen genotypes (PI 288762, PI 288757, PI 212986, PI 288745, PI 288742, PI 288738, PI 116034, PI 236479, PI 255928, PI 254368, PI 198297, PI 547070, NC70 300525, Q20023 95327, Monument, India 2, India 3) resulted non-branching, while the remaining genotypes ranged between 2 and 11.7 branches per plant (Table 4). The non-branching trait could represent one the most important characters that may affect the sowing density and improve the mechanized harvest, representing a valuable traits for breeding purposes looking for non-branching or fine-branching genotypes. In fact, even though branching genotypes show a higher seed yield per plant, single stem genotypes allow for a denser sowing rate, a better uniformity of maturation and minor loss of seed at harvest.

Morris (2010), studying 73 guar accessions, reports a higher plant height (from 50 to 220 cm) than observed in our trial, whereas Raghuprakash *et al.* (2008) obtained similar values in terms of number of branches (from 0 to 8.3).

The stem diameter was on average 7.9 mm (median 7.7 mm); the maximum value was detected in PI 288381 (12.5±0.0 mm) and the minimum value in PI 426635 (5.0±0.9 mm), with a CV of 21.5%.

3.2 Length of crop cycle

The studied genotypes completed the whole crop cycle between the middle of October and the beginning of November. The value of the median (190 days), compared to the mean (181.6 days), indicated that a large part of the genotypes (39) were late genotypes. Eleven genotypes (PI 288757,

PI 288759, PI 212986, PI 288745, PI 426639, PI 116034, PI 236479, PI 288758, PI 426633, PI 340263, NC70 300525) showed the shortest crop cycle between 155 and 163 days, 12 medium-early genotypes reached the end of the cycle between 163 and 175 days, and 6 medium-late genotypes between 175 and 184 days. . As previously reported, the excessive length of the crop cycle represents the main obstacle to the introduction of guar in the Mediterranean area. In fact, earliness is probably the most important trait in our experiment, allowing for an early harvest. Contrarily, a long crop cycle does not allow mechanized harvest, since the crop is still in field when the rains of late summer season fall (end of September and beyond).

3.3 Productive traits

The cluster number per plant was on average 22.4 (median 19.5) with values between 6.0 (s.d. ±1.0) and 60.0 (s.d. ± 17.4) (PI 288347 and Lewis, respectively) and with a CV of 51.8% (Table 5 and 6). Pods per plant resulted on average 122.5 (median 116.2) with and a total CV of 51.7% and values ranging between 19.7±10.0 (PI 288347 – n. 22) and 290.7±162.3 (PI 340253 – n. 4). Both traits showed a very high CV, indicating that a very large variability was present in the genotypes. The number of seeds per pod together with the 1000-seed weight were one of the studied traits with the lowest variability (CV 12.1% and 9.7%, respectively). Plants showed an average number of seeds per pod of 6.6, with a median of 6.7 indicating a normally distribution of the population. High number of seeds per pod was also recorded on NC70300525 (n. 51), PI288384 (n. 20), PI116034 (n. 24), HF11861104 (n. 58) and CP6661044 (n. 62). The 1000-seed weight resulted on average 40.1 g (median 40.0 g) with values included between 31.6±1.2 g (NC70 300525 – n. 51) and 48.3±1.5 g (PI 254368 – n. 34). High seed weight was also recorded on PI 255928 (n. 33) (47.7±1.9 g), PI 212986 (n. 14) (47.2±0.8 g), PI 288384 (n. 20) (47.1±1.0 g), PI 340253 (n. 4) (46.6±2.3 g), PI 288381 (n. 30) (46.3±1.5 g), PI 340263 (n. 42) (45.9±1.0 g), PI 340346 (n. 8) (45.5±1.8), PI 288758 (n. 27) (45.1±5.5 g) and PI 288762 (n. 3) (45.1 ±1.6 g).

Finally plant seed production was on average 29.0 g (median 27.0 g) with a wide variability among genotypes (CV 53.6%) starting from 3.6 ± 1.4 g (Pusa Mausmi300537 – n. 45) up to 73.7±42.5 g (PI 340253 – n. 4). Namely, seven genotypes exhibited a plant production greater than 50 g: PI 271646 (n. 29) (59.7 ± 34.3 g), Nawabshar300528 (n. 46) (55.5±36.1 g), PI 288749 (n. 32) (55.4 ± 37.1 g), Lewis (n. 66) (54.4 ± 27.2 g), Lasbella95042 (n. 47) (53.3 ± 37.8 g) and S-47-295069 (n. 55) (52.1 ± 51.4 g).

Raghuprakash et al. (2008) obtained a considerably lower number of pods per plant (from 17 to 87), but a similar number of seeds per pod (from 6.53 to 8.53) and of 1000-seed weight (from 28.9 to

44.5 g). Morris (2010) reports comparable values of seed weight (ranging from 23 to 48 g for thousand seed weight on 73 guar accessions), associated with a low coefficient of variation (15%). A significantly lower variability was found by Sultan et al. (2012) and Manivannan et al. (2015) for number of seeds per pod and seed weight compared to pods per plant. Namely, Sultan *et al*. (2012) in a research carried out in Pakistan on 101 genotypes, found a slightly higher number of seeds per pod (8.1 on average), with a lighter 1000-seed weight (30 g). Gresta et al. (2013), in a trial carried out in irrigated plots in a Mediterranean environment, found 1000-seed weight included between 28.2 g and 31.3 g and an average number of seeds per pod of 7.2. Obviously our results of seeds per plant must be related to the plant density adopted (20 plants m^{-2}) since a higher density would have favoured the single stem genotypes (with a lower amount of seeds per plant), while a lower density would have favoured branching genotypes (with a higher amount of seeds per plant).

3.4 Qualitative characterization

The seed collection previously studied for the morphological, phenological and productive traits, was also characterised from a qualitative point of view, taking into account the main traits useful for its desired outcome: galactomannans (for industrial use) and protein (for feed use of the by-product). As reported in the literature, the high protein content of guar seeds is one of the most important nutritional factors, which allows their use as excellent protein supplements for animal feeding (Bressani 1993).

Among the 68 genotypes, the galactomannan content ranged from 19.6% up to 32.3% with an average value of 26.5% (median 26.3%), while protein content ranged from 26.0% to 33.5% with an average value of 30.2% (median 30.4%) (Table 7). As expected, coefficient of variation for galactomannan and protein content was very low (9.9% and 4.9%, respectively), when compared to those of the morphological and productive traits, indicating that the qualitative parameters have a narrow range of variability upon which start a breeding program.

The genotype with the highest content of galactomannans was PI323302 (n. 1) (32.3±1.0%); a content of galactomannans higher than 30% was also recorded on PI255928 (n. 33) (31.1±2.0%), Monument (n. 65) (31.1±0.0), PI426635 (n. 37) (30.8±0.3%), PI426633 (n. 39) (30.8±0.8%), FSSRQ77999 (n. 57) (30.7±0.1), PI340253 (n. 4) (30.4±1.1) and Tari300529 (n. 50) (30.3±0.5) (Table 8). The genotypes with the highest content of protein were PI288385 (n. 31) (33.5±0.0%) and PI288347 (n. 22) (33.1±0.0%).

Our results are in agreement with Gresta et al. (2013) who, in a similar environment, obtained values of galactomannan content of 30.2% for Kinman and 28.8% for Lewis. Yadav et al. (2003) in India, in a sowing density trial (from 10 to 25 kg ha^{-1}), reported galactomannan values ranging from

29.9% to 31.2%. Compared to reports from Bhatti and Sial (1971) and Elsheikh et al. (1999), a greater seed protein content was measured in the present experiment. Similar protein content was also detected in guar by Jain et al. (1987). On average, the chemical composition of guar seeds showed similar values to those reported by Badr et al. (2014). Also Eldaw (1998) observed in three genotypes a similar content of crude protein (29.1%). On the other hand, Kays et al. (2006), in guar seeds of nine different accessions, reported a lower level of crude protein (26.4%).

3.5 Correlations

In the present study, interesting correlations emerged among morphological, productive and qualitative traits. Plant production was positively linked to the number of pods per plant (0.947), to the cluster number (0.647), to the seeds per pod (0.459) and to the number of branch (0.407) (Table 9). Obviously branching genotypes have a greater number of clusters, but at the same time a poorer harvestability. For this reason, in order to identify an ideotype with desirable traits, we did not take into consideration this parameter.

The cluster number was positively associated with branch number (0.480). Likewise, the number of pods per plant was higher in the branching genotypes (0.444) and increased with the increase of cluster number (0.657). The number of pods per plant was also significantly and positively related to the number of seeds per pod (0.348). The 1000-seed weight was negatively related with the number of seeds per pod (−0.307) and the number of cluster (-0.256).

In our trial, we assessed the number of clusters, number of pods per plant and number of seeds per pod as the main yield components related to plant seed yield, laying the foundations for future breeding works. Manivannan et al. (2015) in a study on 42 guar genotypes included clusters per plant and pods per plant among the main yield components positively related to seeds per plant. In previous studies (Sultan *et al*., 2012), the main yield components correlated to grain yield were individuated in the number of pods per plant and in the seed weight. Contrarily, Raghuprakash et al. (2009) and Ibrahim et al. (2012) in two different trials, affirmed that the main guar yield components were pods per plant and seeds per pod, indicating them as the main discriminant indicators to improve guar seed yield.

As far as the qualitative traits are concerned, a positive correlation was found between protein percentage and 1000-seed weight (0.469), indicating that bigger seeds have higher value of protein percentage. Protein content (%) resulted also negatively related to number of seeds per pod (-0.354). A negative association also emerged between protein and galactomannan content (-0.418), and it was documented here for the first time (Figure 2). From a physiological point of view, the negative relation between galactomannan and protein content suggests that seed galactomannans increase at the expense of protein content, causing competition of carbon source, as well as it has been demonstrated for carbohydrates and protein in faba bean (Gasim et al. 2015), for oil and protein in rapeseed (Grami et al. 1977; Kennedy et al. 2011) and in soybean (Wilcox and Shibles 2001; Charron et al. 2005).

3.6 PCA (Principal Component Analysis) of the 68 genotypes

To identify patterns in our dataset and to express the data in such a way to highlight its similarities and differences, we applied the multivariate statistical technique of the Principal Components Analysis. The eigenvalues, the percentage of variance and aggregation are shown in table 10. Only the three first principal components had eigenvalues higher than one, and thus, according to the Kaiser's criterion (Kaiser 1958), data may be condensed (dimensional reduction) in three factors, which account, as a whole, for 74% of the total data variability. This means that a quote of 26% of the variability has been lost in the simplification of the PCA. We used the Varimax procedure to find a factor rotation that maximizes the sum of the variances of the squared loadings. The first component, which explain 33.3% of the variation, was primarily a measure of productivity (pods per plant, plant production and clusters per plant). As each of these variables increase, so do the other two. Component two, responsible for 21.4% of the variation, was mainly represented by the branch number and the length of the crop cycle. Component three contributed for 19.3% of the variation and it is associated with plant height and 1000-seeds weight. The graphical representation of the relationships between genotypes and parameters shows a distinction among the genotypes (Figure 3). A group of seven genotypes clearly stands out for the highest values of PC1, corresponding to the genotypes with the highest number of clusters, of pods per plant and of seeds per pod and consequently with the most productive genotypes (>50 g plant^{-1}), even though with a late maturation (except the cv "Lewis" - n. 66 - which has a medium-short crop cycle). The remaining genotypes showing lower values of PC1, on the contrary, are characterized by low seed production per plant, partially justified by a shorter crop cycle and a lower branch number (negative values of PC2). At this regard, it is interesting to note, that the early non-branching genotype PI 288757 (n. 12) showed also a good productive performance (43.4 g plant^{-1}), followed by the genotypes PI 340263 (n. 42 – 32.7 g plant^{-1}), NC70 300525 (n. 51) and PI 288745 (n. 15) (31.0 and 30.6 g plant^{-1}, respectively).

4. Conclusions

The present research, focused on a multi-trait characterization of genotypes of guar, was driven by the individuation of desirable and valuable traits in an ideotype suitable for cultivation in Mediterranean climate with easy harvestability. For these reasons, to select high performance genotypes we mainly considered non-branching (easy harvestability, uniformity of maturation) and short crop cycle plants, together with high seed production. Results proved that 17 genotypes resulted non-branching, 11 genotypes showed a short crop cycle, 7 genotypes were characterized by a seed production greater than 50 g plant^{-1}.

Four of the studied genotypes emerged as they exhibit more than one desirable trait: PI 288757 (n. 12), PI 340263 (n. 42), NC70300525 (n. 51) and PI 288745 (n. 15) combine short crop cycle, medium-high seed production and fine branching. Moreover, Lewis (n. 66) must be mentioned for its very high seed production associated with medium-short crop cycle and few branching habitus.

As far as the qualitative traits are concerned, galactomannan and protein content, genotypes showed a lower coefficient of variation compared to those of the morphological or productive traits, indicating that the qualitative parameters have a narrow range of variability upon which start a breeding program; eight genotypes showed a galactomannan content greater than 30% with valuable protein content. Finally, an interesting association was found between galactomannan and protein content, with a highly significative negative relation. This association highlights that breeding process looking for guar genotypes improved for galactomannan content will have as a result seeds with a lower protein content.

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Highlights

- 17 guar genotypes resulted non-branching, 11 genotypes showed a short crop cycle
- 7 genotypes were characterized by a high seed production greater than 50 g plant^{-1}
- 4 genotypes combine many desirable traits including a good seed production.
- Plant production was related to pods per plant and seeds per pod.
- An interesting association was found between galactomannans and protein content.

Table 1. Chemical and physical properties of the soil (Botricello - RC, Southern Italy)

Property	Value
Skeleton (>0,2 mm) (g kg^{-1})	36
Sand (0,02-0,2 mm) (g kg^{-1})	780
Silt (0,002-0,02 mm) (g kg^{-1})	274
Clay (<0,002 mm) (g kg^{-1})	94
Total limestone ($CaCO_3$) (g kg^{-1})	89
Active limestone (CaCO3) (g kg^{-1})	14
Total nitrogen (N) (g kg^{-1})	0.5
Organic substance (g kg^{-1})	9.0
C/N	10.3
Phosphorus assimilable (P_2O_5) (mg kg^{-1})	31
Exchangeable potassium (K_2O) (mg kg^{-1})	208
pH	7.9
Conductivity (saturated extract) (dS m^{-1})	0.36
Cation exchange capacity (meq 100 g^{-1})	12.9
Exchangeable calcium (CaO) (mg kg^{-1})	3016
Exchangeable magnesium (MgO) (mg kg^{-1})	266
Exchangeable sodium (Na) (mg kg^{-1})	90

Table 2. Guar genotypes tested in this trial

ID	Accession	Origin	Seed Bank	ID	Accession	Origin	Seed Bank
1	PI 323302	India	A	35	PI 198297	India	A
2	PI 340509	India	A	36	PI 340601	India	A
3	PI 288762	India	A	37	PI 426635	Pakistan	A
4	PI 340253	India	A	38	PI 426631	Pakistan	A
5	PI 288760	India	A	39	PI 426633	Pakistan	A
6	PI 164420	India	A	40	PI 275322	India	A
7	PI 288392	India	A	41	PI 547070	Texas	A
8	PI 340346	India	A	42	PI 340263	India	A
9	PI 288377	India	A	43	HALL 78000	Australia	B
10	PI 268228	India	A	44	CP31 61055	Australia	B
11	PI 271542	India	A	45	PUSA MAUSMI 300537	Australia	B
12	PI 288757	India	A	46	NAWABSHAR 300528	Australia	B
13	PI 288759	India	A	47	LASBELLA 95042	Australia	B
14	PI 212986	India	A	48	BROOKS 77998	Australia	B
15	PI 288745	India	A	49	KATHSEL 300538	Australia	B
16	PI 288742	India	A	50	TARI 300529	Australia	B
17	PI 288738	India	A	51	NC70 300525	Australia	B
18	PI 288362	India	A	52	95078 (NA 444 X Texas)	Australia	B
19	PI 288435	India	A	53	Q20023 95327	Australia	B
20	PI 288384	India	A	54	FINE BRACHING1 95046	Australia	B
21	PI 288394	India	A	55	S - 47 - 2 95069	Australia	B
22	PI 288347	India	A	56	MA20SAN 68794	Australia	B
23	PI 426639	Pakistan	A	57	FSSRQ 77999	Australia	B
24	PI 116034	India	A	58	HF118 61104	Australia	B
25	PI 288763	India	A	59	PUSA MAUSMI 61043	Australia	B
26	PI 236479	India	A	60	IC9229/P3 62437	Australia	B
27	PI 288758	India	A	61	CP380 61051	Australia	B
28	PI 288748	India	A	62	CP66 61044	Australia	B
29	PI 271646	India	A	63	VADAVALLI 61050	Australia	B
30	PI 288381	India	A	64	KINMAN	Texas	C
31	PI 288385	India	A	65	MONUMENT	Texas	C
32	PI 288749	India	A	66	LEWIS	Texas	C
33	PI 255928	India	A	67	INDIA 2	India	C
34	PI 254368	India,	A	68	INDIA 3	India	C

Seed bank:
A = ARS-USDA, Georgia
B= Australian Grains Genebank, Canberra
C= University of Reggio Calabria

Table 3. Main biometric parameters and length of the crop cycle of the 68 guar genotypes

	Plant height (cm)	Branch number (n)	Stem diameter (mm)	Length of crop cycle (days)
Mean	59.6	5.3	7.9	181.6
Median	59.5	7.2	7.7	190.0
Std. Dev.	12.4	3.9	1.7	11.1
Std. Err.	1.5	0.5	0.2	1.3
Min	34.0	0.0	5.0	155.0
Max	97.3	11.7	12.5	195.0
CV (%)	20.9	72.9	21.5	6.1

Table 4. Biometric parameters and length of the crop cycle of each of the 68 guar genotypes ± standard deviation

ID	Accessions	Plant height			Branch number			Stem diameter			Length of crop cycle (days)
		cm		s.d.	n		s.d.	mm		s.d.	
1	PI 323302	45.7	±	4.5	10	±	4.6	5.3	±	0.3	175-184
2	PI 340509	60.3	±	8.5	7	±	2.6	6.7	±	0.6	188-195
3	PI 288762	72.0	±	8.2	0	±	0.5	8.0	±	1.0	188-195
4	PI 340253	62.3	±	9.3	11	±	5.1	7.8	±	1.0	188-195
5	PI 288760	71.2	±	6.7	2	±	0.6	8.7	±	0.6	175-184
6	PI 164420	53.7	±	3.2	10	±	3.1	6.3	±	0.6	188-195
7	PI 288392	57.0	±	3.6	8	±	1.0	9.8	±	0.3	175-184
8	PI 340346	49.3	±	6.0	7	±	0.0	7.0	±	0.0	163-170
9	PI 288377	52.0	±	2.6	9	±	4.6	6.8	±	1.3	188-195
10	PI 268228	53.3	±	6.5	10	±	3.5	7.0	±	0.0	188-195
11	PI 271542	54.0	±	10.1	8	±	2.5	6.2	±	1.2	188-195
12	PI 288757	70.3	±	2.5	0	±	0.6	8.5	±	0.0	155-163
13	PI 288759	41.3	±	19.5	1	±	1.0	5.5	±	0.5	155-163
14	PI 212986	65.3	±	5.7	0	±	0.0	6.7	±	0.3	155-163
15	PI 288745	71.0	±	14.7	0	±	0.6	8.3	±	2.9	155-163
16	PI 288742	72.2	±	6.1	0	±	0.6	7.9	±	0.3	188-195
17	PI 288738	77.7	±	5.5	0	±	0.0	9.7	±	0.3	163-175
18	PI 288362	44.3	±	2.5	9	±	0.6	8.0	±	0.0	188-195
19	PI 288435	59.0	±	2.6	9	±	1.0	6.8	±	0.8	188-195
20	PI 288384	58.3	±	7.6	8	±	3.0	12.2	±	0.6	188-195
21	PI 288394	62.3	±	6.8	9	±	1.5	10.3	±	0.6	188-195
22	PI 288347	58.7	±	8.1	7	±	2.1	11.5	±	0.0	188-195
23	PI 426639	55.0	±	4.4	8	±	0.6	6.2	±	0.3	155-163
24	PI 116034	56.7	±	1.2	0	±	0.0	6.7	±	0.6	155-163
25	PI 288763	45.3	±	5.0	10	±	2.0	5.7	±	0.3	188-195
26	PI 236479	65.0	±	15.1	0	±	0.0	7.5	±	0.9	155-163
27	PI 288758	41.3	±	5.1	2	±	3.5	6.0	±	0.9	155-163
28	PI 288748	67.7	±	4.0	1	±	2.3	7.5	±	0.0	175-184
29	PI 271646	57.3	±	2.5	9	±	2.6	7.0	±	0.9	188-195
30	PI 288381	63.3	±	5.8	8	±	1.5	12.5	±	0.0	188-195
31	PI 288385	60.3	±	4.5	9	±	1.7	11.0	±	0.0	188-195
32	PI 288749	68.0	±	19.3	4	±	5.5	8.3	±	0.6	188-195
33	PI 255928	65.3	±	7.0	0	±	0.0	7.0	±	0.9	163-175
34	PI 254368	76.3	±	4.3	0	±	0.0	7.8	±	0.8	163-175

Table 4 (bis). Biometric parameters and length of the crop cycle of each of the 68 guar genotypes ± standard deviation

ID	Accessions	Plant height			Branch number			Stem diameter			Length of crop cycle (days)
		cm		s.d.	n		s.d.	mm		s.d.	
35	PI 198297	54.0	±	3.5	0	±	0.6	9.3	±	0.3	188-195
36	PI 340601	46.7	±	2.5	7	±	1.5	7.3	±	1.2	188-195
37	PI 426635	40.7	±	4.0	5	±	1.7	5.0	±	0.9	175-184
38	PI 426631	45.0	±	6.2	8	±	2.1	6.7	±	0.6	163-175
39	PI 426633	41.0	±	3.6	6	±	0.6	5.3	±	0.6	155-163
40	PI 275322	41.3	±	3.1	6	±	1.2	6.0	±	0.0	188-195
41	PI 547070	97.3	±	6.8	0	±	0.6	9.0	±	1.0	188-195
42	PI 340263	85.3	±	3.8	1	±	0.6	9.5	±	0.0	155-163
43	HALL 78000	58.7	±	6.4	8	±	1.5	7.5	±	0.5	188-195
44	CP31 61055	64.7	±	4.7	8	±	1.6	8.7	±	0.6	188-195
45	PUSA MAUSMI 300537	74.0	±	8.7	1	±	0.6	11.3	±	1.2	188-195
46	NAWABSHAR 300528	70.0	±	2.0	9	±	2.1	8.7	±	0.6	188-195
47	LASBELLA 95042	47.3	±	3.5	10	±	2.1	7.3	±	0.3	175-184
48	BROOKS 77998	60.0	±	3.5	8	±	2.0	7.2	±	0.8	188-195
49	KATHSEL 300538	57.3	±	3.2	8	±	1.2	7.0	±	0.0	163-175
50	TARI 300529	53.0	±	5.6	9	±	1.5	7.3	±	0.6	188-195
51	NC70 300525	66.0	±	2.6	0	±	0.6	8.0	±	0.0	155-163
52	95078 (NA 444 X Texse)	64.7	±	4.5	8	±	0.6	7.2	±	0.3	188-195
53	Q20023 95327	77.7	±	1.6	0	±	0.0	8.5	±	0.9	163-175
54	FINE BRACHING	59.0	±	1.0	7	±	1.0	7.3	±	0.3	188-195
55	S - 47 - 2 95069	67.7	±	3.1	12	±	1.5	8.2	±	0.8	188-195
56	MA20SAN 68794	65.3	±	5.0	8	±	0.0	8.0	±	0.0	188-195
57	FSSRQ 77999	66.3	±	6.6	10	±	1.6	6.0	±	0.0	188-195
58	HF118 61104	34.0	±	1.0	8	±	1.2	7.2	±	0.6	163-175
59	PUSA MAUSMI 61043	45.0	±	5.0	9	±	3.2	7.7	±	0.3	188-195
60	IC9229/P3 62437	52.3	±	6.3	9	±	1.5	9.3	±	0.6	188-195
61	CP380 61051	55.3	±	14.5	2	±	2.3	10.0	±	1.7	188-195
62	CP66 61044	60.0	±	0.7	6	±	1.6	9.0	±	0.0	188-195
63	VADAVALLI 61050	67.7	±	10.0	2	±	1.5	11.7	±	0.8	188-195
64	KINMAN	37.7	±	3.8	5	±	0.6	5.3	±	0.6	188-195
65	MONUMENT	64.7	±	4.2	0	±	0	8.3	±	0.3	163-175
66	LEWIS	40.7	±	1.6	7	±	7.1	7.7	±	0.3	163-175
67	INDIA 2	77.3	±	2.5	0	±	0.0	9.7	±	1.2	163-175
68	INDIA 3	80.0	±	4.4	0	±	0.0	8.5	±	0.0	163-175

Table 5. Main productive traits

	Clusters per plant (n)	Pods per plant (n)	Seeds per pod (n)	1000 seed weight (g)	Seed per plant (g)
Mean	22.4	122.5	6.6	40.1	29.0
Median	19.5	116.2	6.7	40.0	27.0
Std. Dev.	11.6	63.4	8.0	3.9	15.5
Std. Err.	1.4	7.68	0.1	0.5	1.9
Min	6.0	19.7	3.5	31.6	3.6
Max	60.0	290.7	8.1	48.3	73.7
CV	51.8	51.7	12.1	9.7	53.6

Table 6. Productive traits of each of the 68 guar genotypes ± standard deviation

ID	Clusters per plant		Pods per plant		Seeds per pod		1000 seed weight		Seed per plant	
	n	s.d.	n	s.d.	n	s.d.	g	s.d.	g	s.d.
1	20.0	± 2.6	206.0	± 101.6	7.3	± 1.1	38.3	± 2.0	49.6	± 21.9
2	14.0	± 2.6	95.3	± 30.4	6.2	± 0.6	43.5	± 1.8	25.7	± 8.5
3	12.3	± 2.3	124.3	± 33.9	6.5	± 0.7	45.1	± 1.6	29.2	± 11.7
4	21.0	± 7.8	290.7	± 162.3	6.5	± 0.1	46.6	± 2.3	73.7	± 42.5
5	9.3	± 1.5	80.0	± 3.0	6.7	± 0.5	43.9	± 2.4	29.4	± 3.1
6	28.0	± 14.1	149.0	± 49.6	7.1	± 0.2	37.6	± 1.6	38.3	± 21.1
7	17.0	± 9.5	133.7	± 103.6	6.6	± 0.2	39.9	± 1.0	27.4	± 25.5
8	20.3	± 6.5	61.3	± 12.9	4.7	± 1.7	45.5	± 1.8	9.2	± 3.0
9	12.0	± 3.6	74.3	± 60.3	6.5	± 0.5	40.8	± 2.8	18.7	± 16.8
10	9.3	± 4.9	78.7	± 92.1	7.3	± 0.6	40.9	± 0.5	17.0	± 20.1
11	18.3	± 4.9	162.7	± 141.5	6.4	± 0.3	42.9	± 0.6	37.7	± 33.4
12	18.3	± 17.0	186.0	± 146.4	7.1	± 0.6	43.2	± 0.7	43.4	± 36.2
13	9.0	± 1.0	75.3	± 4.2	7.1	± 0.4	39.0	± 2.5	17.7	± 2.6
14	15.0	± 2.0	68.3	± 31.6	6.4	± 0.5	47.2	± 0.8	19.6	± 9.9
15	12.0	± 7.8	113.7	± 93.4	6.7	± 0.4	42.8	± 4.0	30.6	± 27.5
16	12.3	± 0.6	56.7	± 33.8	6.7	± 0.3	44.3	± 1.1	20.8	± 6.5
17	8.7	± 0.6	115.0	± 8.6	6.2	± 0.8	43.7	± 0.9	26.9	± 11.0
18	17.3	± 8.0	77.0	± 56.0	5.0	± 1.1	39.9	± 2.5	12.7	± 9.5
19	21.3	± 11.6	109.3	± 64.9	6.0	± 1.0	37.8	± 2.5	19.0	± 4.1
20	20.3	± 8.6	99.3	± 66.0	7.6	± 0.1	47.1	± 1.0	33.0	± 21.4
21	19.3	± 6.7	153.3	± 80.2	6.2	± 0.6	40.1	± 3.6	35.6	± 21.6
22	6.0	± 1.0	19.7	± 10.0	5.8	± 0.8	43.9	± 2.0	4.6	± 2.2
23	17.0	± 3.6	59.3	± 27.2	6.2	± 0.2	38.4	± 1.2	12.5	± 5.2
24	9.0	± 1.0	52.7	± 3.8	7.5	± 0.4	33.6	± 1.4	11.5	± 1.2
25	37.7	± 13.5	186.7	± 67.5	7.0	± 0.4	43.6	± 1.3	49.3	± 18.6
26	9.0	± 2.6	36.0	± 10.0	6.2	± 0.3	41.0	± 7.6	8.1	± 2.8
27	15.7	± 7.2	79.7	± 27.8	6.6	± 0.2	45.1	± 5.5	17.6	± 6.2
28	10.7	± 2.5	82.0	± 23.8	6.9	± 0.8	44.3	± 2.3	20.7	± 5.8
29	36.3	± 13.7	276.7	± 146.1	7.0	± 0.6	38.1	± 0.2	59.7	± 34.3
30	17.7	± 2.3	74.7	± 12.9	7.0	± 0.1	46.3	± 1.5	21.5	± 3.2
31	15.3	± 10.0	60.7	± 35.5	6.2	± 0.5	44.4	± 1.5	14.3	± 8.9
32	30.0	± 20.0	194.3	± 108.8	7.0	± 0.2	41.8	± 2.1	55.4	± 37.1
33	13.7	± 1.2	50.7	± 31.6	5.7	± 0.4	47.7	± 1.9	11.1	± 4.9
34	18.0	± 2.0	68.7	± 8.8	5.3	± 0.7	48.3	± 1.5	13.9	± 3.1

Table 6 (bis). Productive traits of each of the 68 guar genotypes ± standard deviation

ID	Clusters per plant			Pods per plant			Seeds per pod			1000 seed weight			Seed per plant		
	n		s.d.	n		s.d.	n		s.d.	g		s.d.	g		s.d.
35	13.7	±	2.3	110.3	±	24.4	6.7	±	0.8	39.9	±	4.8	27.1	±	12.7
36	32.7	±	2.5	127.7	±	15.4	7.0	±	0.4	36.2	±	2.8	30.1	±	3.9
37	16.3	±	4.0	31.7	±	0.1	6.8	±	0.5	37.5	±	2.0	7.7	±	2.7
38	18.7	±	4.5	41.3	±	6.3	7.3	±	0.9	36.3	±	1.4	10.4	±	4.4
39	19.7	±	4.7	49.3	±	6.0	6.2	±	0.9	41.8	±	2.9	11.9	±	5.4
40	29.0	±	10.6	134.3	±	70.0	5.5	±	0.4	43.4	±	1.7	24.2	±	13.0
41	21.0	±	1.7	89.0	±	2.2	6.0	±	0.2	39.0	±	0.1	16.0	±	3.1
42	11.0	±	1.0	109.0	±	25.6	7.1	±	0.7	45.9	±	1.0	32.7	±	11.0
43	28.0	±	4.0	140.0	±	55.6	6.5	±	0.8	36.3	±	1.1	25.9	±	5.6
44	24.0	±	2.6	95.7	±	1.0	7.1	±	0.7	37.4	±	0.1	20.2	±	8.7
45	11.3	±	3.2	32.7	±	2.6	4.7	±	1.0	35.6	±	2.3	3.6	±	1.4
46	45.0	±	3.0	178.7	±	196.2	6.8	±	0.2	39.5	±	3.3	55.5	±	36.1
47	58.3	±	25.7	178.3	±	85.3	6.7	±	0.6	40.6	±	1.6	53.3	±	37.8
48	24.3	±	13.6	180.0	±	120.0	7.1	±	0.3	36.0	±	0.9	42.1	±	29.0
49	32.3	±	11.0	97.7	±	8.2	8.1	±	0.1	39.4	±	1.9	24.6	±	11.4
50	24.3	±	18.6	167.0	±	214.1	6.5	±	0.1	40.1	±	1.8	34.5	±	43.3
51	16.0	±	5.3	148.0	±	56.5	7.9	±	0.3	31.6	±	1.2	31.0	±	12.8
52	32.7	±	8.0	139.0	±	53.6	6.9	±	0.6	36.4	±	0.5	34.2	±	15.8
53	18.7	±	1.2	124.7	±	9.3	6.8	±	0.5	36.7	±	0.4	23.6	±	2.6
54	25.3	±	6.7	188.0	±	77.1	7.2	±	1.1	38.4	±	0.5	45.4	±	19.4
55	40.0	±	20.0	278.7	±	280.7	6.6	±	0.4	37.6	±	0.5	52.1	±	51.4
56	34.0	±	8.2	117.3	±	25.6	6.3	±	1.0	38.4	±	5.6	25.6	±	15.1
57	20.0	±	13.7	185.0	±	120.3	6.4	±	1.2	36.5	±	0.8	39.0	±	28.0
58	39.3	±	10.0	140.0	±	81.5	7.5	±	0.6	41.1	±	1.8	35.3	±	24.6
59	37.7	±	22.4	143.3	±	57.8	6.9	±	0.8	39.9	±	3.3	30.4	±	14.2
60	24.7	±	5.1	186.3	±	125.3	5.6	±	1.2	37.6	±	1.1	49.7	±	36.4
61	29.7	±	11.7	160.0	±	119.1	8.1	±	0.4	38.6	±	0.4	46.3	±	38.6
62	50.0	±	8.0	206.3	±	35.8	7.5	±	1.0	38.8	±	1.0	48.6	±	8.3
63	20.3	±	5.5	139.7	±	49.4	7.2	±	0.7	44.0	±	6.3	38.2	±	12.4
64	33.7	±	12.1	126.0	±	30.1	6.7	±	0.5	39.1	±	0.1	36.0	±	21.2
65	12.3	±	0.6	89.0	±	4.7	7.4	±	0.1	32.4	±	0.6	23.6	±	1.0
66	60.0	±	17.4	287.7	±	138.4	6.8	±	0.5	35.3	±	1.4	54.4	±	27.2
67	25.0	±	4.4	67.0	±	8.2	6.0	±	0.4	48.1	±	2.1	15.9	±	4.9
68	14.0	±	1.0	34.7	±	0.1	3.5	±	0.4	44.0	±	2.0	4.3	±	0.9

Table 7. Main parameters of qualitative traits

	Galactomannan content %	Protein content %
Mean	26.5	30.2
Median	26.3	30.4
Std. Dev.	2.6	1.5
Std. Err.	0.3	0.2
Min	19.6	26.0
Max	32.3	33.5
CV	9.9	4.9

Table 8. Galactomannan and protein content of each of the 68 guar genotypes ± standard deviation

ID	Galactomannan content			Protein content			ID	Galactomannan content			Protein content		
	%		s.d.	%		s.d.		%		s.d.	%		s.d.
1	32.3	±	1.0	30.3	±	0.2	35	28.1	±	0.3	30.0	±	0.0
2	29.2	±	0.4	30.7	±	0.4	36	29.7	±	0.1	28.2	±	0.0
3	27.4	±	0.7	30.8	±	0.0	37	30.8	±	0.3	28.8	±	0.2
4	30.4	±	1.1	28.9	±	0.0	38	28.3	±	0.0	28.1	±	0.1
5	28.1	±	2.3	30.5	±	0.3	39	30.8	±	0.8	29.2	±	0.2
6	27.2	±	0.4	30.8	±	0.6	40	27.0	±	0.2	28.5	±	0.1
7	19.9	±	0.7	31.3	±	0.1	41	25.4	±	0.6	30.5	±	0.0
8	26.2	±	0.7	31.2	±	0.2	42	27.1	±	0.8	30.5	±	0.0
9	26.3	±	1.4	30.4	±	0.3	43	25.8	±	0.1	31.4	±	0.1
10	28.0	±	0.5	29.9	±	0.3	44	26.3	±	0.2	31.7	±	0.1
11	21.7	±	2.5	30.9	±	0.0	45	27.5	±	2.0	30.2	±	0.1
12	24.9	±	0.6	30.9	±	0.3	46	28.1	±	0.0	30.2	±	0.1
13	24.1	±	0.2	29.2	±	0.1	47	29.2	±	1.2	27.0	±	0.2
14	29.6	±	3.1	31.1	±	0.6	48	28.3	±	0.2	28.1	±	0.0
15	24.4	±	1.8	29.2	±	0.2	49	25.2	±	0.8	29.4	±	0.5
16	27.8	±	1.3	29.9	±	0.0	50	30.3	±	0.5	29.7	±	0.2
17	24.6	±	0.3	31.0	±	0.0	51	25.0	±	0.6	26.0	±	0.2
18	24.5	±	0.6	32.0	±	0.0	52	26.3	±	0.3	30.7	±	0.3
19	23.1	±	1.4	32.8	±	0.1	53	28.3	±	0.4	28.3	±	0.6
20	25.6	±	0.5	31.9	±	0.1	54	24.9	±	0.3	30.5	±	0.2
21	23.1	±	0.9	29.7	±	0.4	55	26.5	±	0.6	31.7	±	0.5
22	24.5	±	0.4	33.1	±	0.0	56	26.4	±	0.1	30.4	±	0.0
23	23.9	±	0.2	31.8	±	0.2	57	30.7	±	0.1	29.6	±	0.1
24	28.8	±	1.0	27.7	±	0.2	58	25.6	±	0.1	29.5	±	0.0
25	26.2	±	0.9	28.5	±	0.2	59	27.5	±	0.0	29.1	±	0.0
26	27.7	±	0.4	31.2	±	0.9	60	24.6	±	0.6	29.1	±	0.0
27	26.0	±	0.8	29.5	±	0.0	61	24.6	±	0.2	30.8	±	0.0
28	26.4	±	0.5	30.3	±	0.2	62	24.1	±	0.9	32.0	±	0.2
29	19.6	±	1.0	30.5	±	0.1	63	27.2	±	0.5	30.4	±	0.0
30	26.3	±	0.2	32.7	±	0.3	64	25.9	±	0.6	29.1	±	0.1
31	21.4	±	0.0	33.5	±	0.0	65	31.1	±	0.0	26.8	±	0.2
32	24.7	±	0.5	30.4	±	0.2	66	27.3	±	0.5	28.6	±	0.0
33	31.1	±	2.0	31.3	±	0.2	67	26.1	±	0.1	31.1	±	0.0
34	25.3	±	1.2	31.6	±	0.2	68	23.7	±	0.8	31.7	±	0.0

Table 9. Correlation analysis among studied factors

	Branch number	Plant height	Cluster number	Pods per plant	Seeds per pod	Seed weight	Seed per Plant	Crop cycle	Galactomannan	Protein
Branch number	-	-0.503 ***	0.480 ***	0.444 ***	0.095 ns	-0.206 ns	0.407 ***	0.545 ***	-0.083 ns	0.083 ns
Plant height		-	-0.302 *	-0.096 ns	-0.187 ns	0.219 ns	-0.087 ns	-0.039 ns	-0.073 ns	0.285 *
Cluster number			-	0.657 ***	0.228 ns	-0.256 *	0.647 ***	0.272 *	-0.059 ns	-0.188 ns
Pods per plant				-	0.348 **	-0.222 ns	0.947 ***	0.335 **	-0.076 ns	-0.210 ns
Seeds per pod					-	-0.307 *	0.459 ***	-0.007 ns	0.098 ns	-0.354 **
Seed weight						-	-0.116 ns	-0.094 ns	-0.058 ns	0.469 ***
Seed per plant							-	0.343 **	-0.026 ns	-0.236 ns
Lenght of crop cycle								-	-0.105 ns	0.222 ns
Galactomannans										0.418 ***
Protein									-	

Table 10. PCA table

Explained Variance (Eigenvalues)			
Value	**PC 1**	**PC 2**	**PC 3**
Eigenvalue	2.662	1.714	1.547
% of Variance	33.277	21.424	19.338
Cumulate %	33.277	54.701	74.039

Component Loadings	**PC 1**	**PC 2**	**PC 3**
Branch number	0.244	*0.786*	-0.400
Plant height	0.081	-0.337	*0.800*
Cluster number	*0.651*	0.369	-0.278
Pods per plant	*0.911*	0.264	-0.046
Seeds per pod	0.588	-0.374	-0.451
1000 seed weight	-0.210	0.089	*0.673*
Seed per plant	*0.945*	0.219	-0.012
Length of crop cycle	0.245	*0.762*	0.101

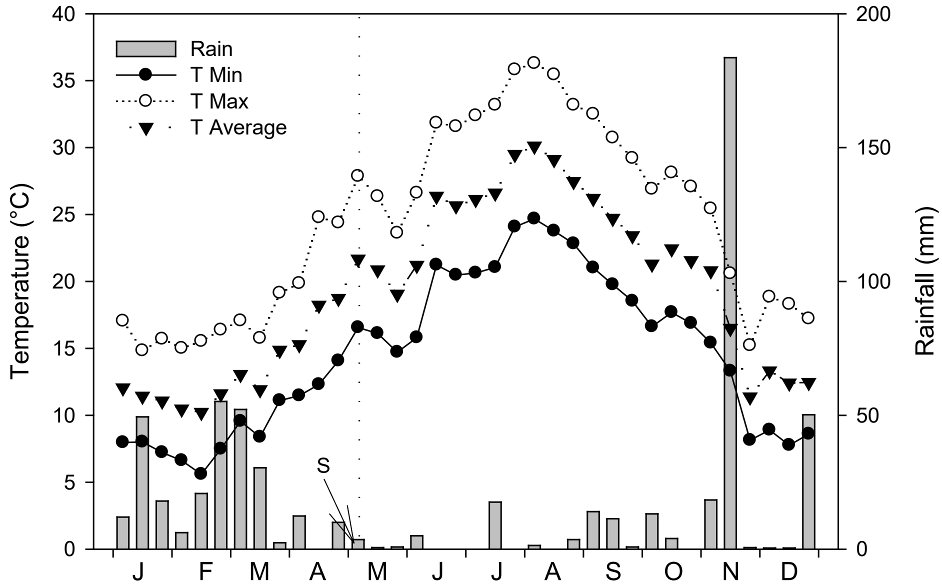

Figure 1. Thermopluviometric diagram during 2014 at the experimental field (Botricello, RC)

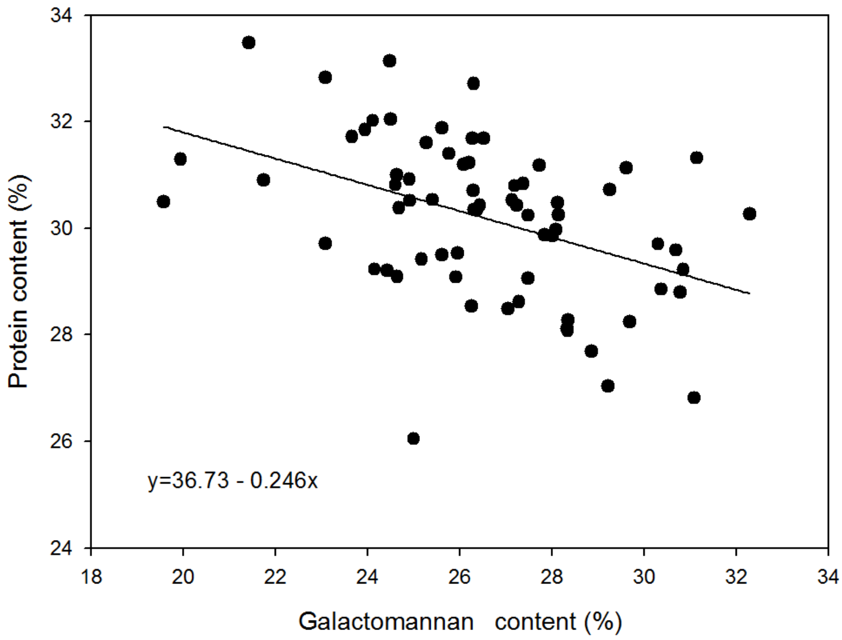

Figure 2. Relation between galactomannan and protein content (F test = 15.301, p≤0.001) in guar genotypes

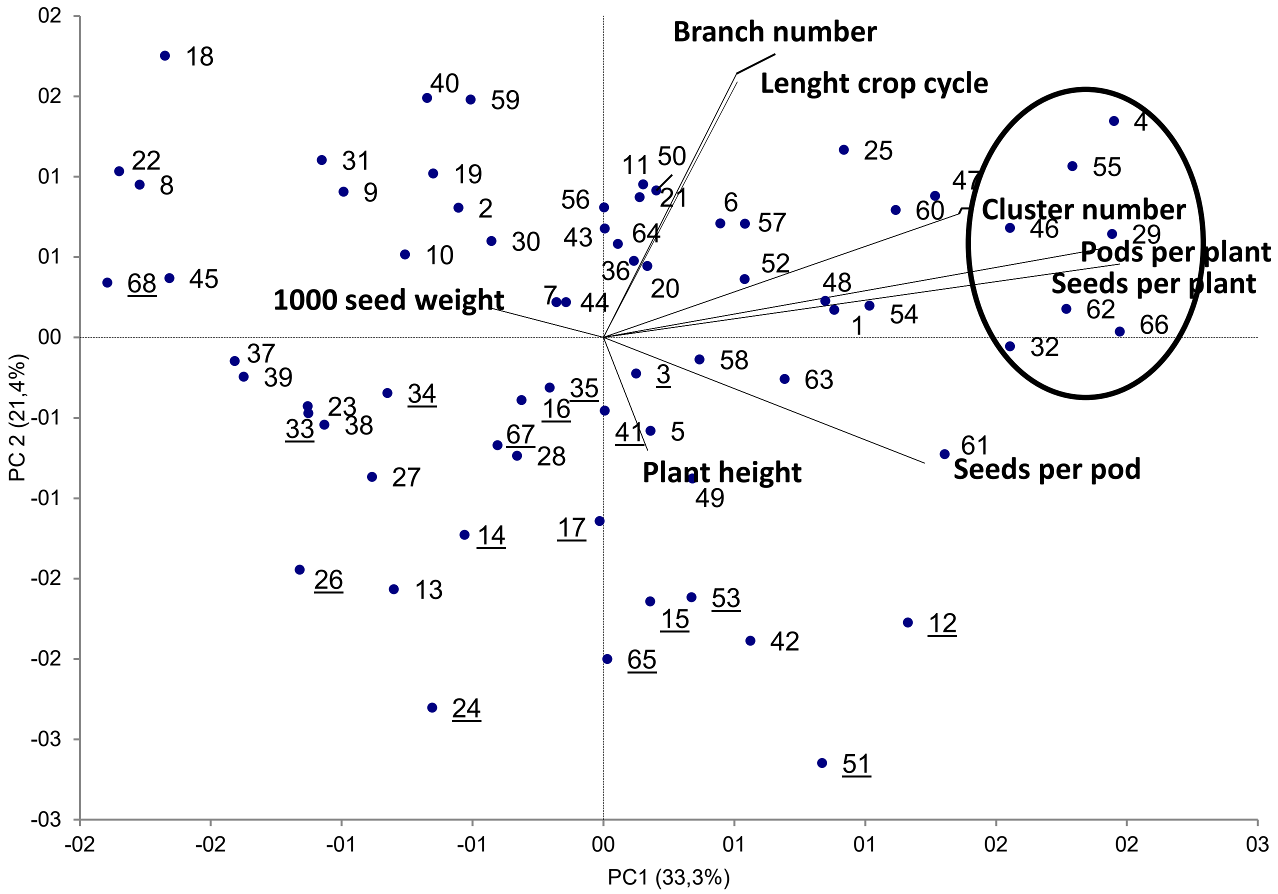

Figure 3. Biplot of the first two principal components. The rays connecting the traits are referred to as trait vectors. The vector length of a trait measures the magnitude of its effect (positive or negative). Point are the 64 genotypes. The underlined genotypes are non-branching genotypes.