CANONICAL CORRELATION AND AGRONOMIC PERFORMANCE OF QUINOA (*CHENOPODIUM QUINOA* WILLD)

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ABSTRACT – Quinoa culture expresses a high nutritional value in its grains, used both in human and animal food. Its nutritional characteristics are the result of the composition of proteins, amino acids and especially gluten-free grains. This work was aimed at evidencing the agronomic performance and linear and canonical associations of Quinoa crop grown Rio Grande do Sul state. The trials were carried out in the municipality of Pelotas - Rio Grande do Sul, Brazil. The experimental design was randomized blocks, with three Quinoa genotypes, being them Altiplano, Salcedo and BRS Piabiru, arranged in four replicates. The morphological differentiation of quinoa genotypes occurs through the number of teeth expressed by leaves. Quinoa seed yield is based on the joint action of mass of one thousand seeds, number of seeds per inflorescence and number of seeds per plant, being the Altiplano and Salcedo genotypes considered superior. Seed yield components of quinoa plants are potentialized by plant height, petiole length, leaf teeth number and flower length. The definition of agronomic performance, linear and canonical associations is a pioneer study for this species and may be used in future studies with pseudocereals focused on seed science and technology.

Keywords: descriptors, interrelation, morphological characters, multiple regression, yield components.

CORRELAÇÃO CANÔNICA E DESEMPENHO AGRONÔMICO DE QUINOA (CHENOPODIUM QUINOA WILLD)

RESUMO – A cultura da quinoa expressa um alto valor nutricional em seus grãos, usados tanto na alimentação humana quanto animal. Suas características nutricionais são resultantes da composição por proteínas, aminoácidos e principalmente os grãos isentos de glúten. Este trabalho teve por objetivo evidenciar o desemepenho agronômico, as associações lineares e canônicas de Quinoa cultivada no Rio Grande do Sul. O experimento foi realizado no município de Pelotas - Rio Grande do Sul, Brasil. O delineamento experimental utilizado foi de blocos ao acaso, utilizando três genótipos de Quinoa, sendo estes Altiplano, Salcedo e BRS Piabiru, dispostos em quatro repetições.A diferenciação morfologicamente dos genótipos de quinoa ocorre através do número de dentes expressos pelas folhas. A produtividade de sementes da quinoa é baseado na ação conjunta da massa de mil sementes, número de sementes por inflorescência e número de sementes por planta, sendo os genótipos Altiplano e Salcedo considerados superiores. Os componentes da produtividade de sementes são potecializados pela altura da planta, comprimento do pedúnculo, número de dentes da folha e comprimento da flor das plantas de quinoa. A definição do desempenho agronômico, associações lineares e canônicas apresenta-se pioneiro para esta espécie, e pode ser utilizado em futuros estudos com pseudocereais voltado a ciência e tecnologia de sementes.

Palavras chave: caracteres morfológicos, componentes do rendimento, descritores, inter-relação, regressão múltipla.

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INTRODUCTION

Quinoa (*Chenopodium quinoa*Willd) is characterized as a crop of annual cycle, belonging to the Amaranthaceae family (Fuentes-Bazan et al., 2012). This species was domesticated thousands of years ago by native folks of the Andes Mountains (Spehar et al., 2002). Even with organomineral composition close to cereals, quinoa is considered a "pseudocereal". The Amaranthaceae family presents about 170 genera and approximately 2000 species distributed throughout the globe, except for cold regions of the Northern Hemisphere, being preferentially found in arid or saline environments (Judd et al., 2009; Souza and Lorenzi, 2012). Quinoa produces edible grains of high nutritional value for human and animal diet, which are rich in protein, amino acids, iron, zinc, besides of being gluten-free (Spears, 2007; Strenske et al., 2017).

In Brazil, its grown has become attractive for biomass production and soil covering, an alternative for agricultural system diversification, tolerance to soil stressing conditions, and to reduce cultivation costs (Spehar and Santos, 2002). The study of correlation between morphological traits and yield components allows to infer which associations are fundamental to explain the crop productive potential (Szareski et al., 2018).

The linear and inter-group correlations between traits allow to identify which of them are determinant for achieving a superior genotype (Brum et al., 2011). Biometric analysis performed through canonical correlations reveals gains greater than those verified through linear associations. Furthermore, it allows to compare yield components to morphological attributes (Carvalho et al., 2015). Canonical correlation represents a multivariate statistical model that enables the calculation of linear relations between two orders, or two groups of traits (Protásio et al., 2012). The basic principle of this analysis is the development of a linear combination in each set of traits, which allows to maximize the correlation between intergroup attributes and simplifies the understanding of relationship between groups of traits of agronomic interest (Nascimento Filho et al., 2012).

In this context, the analysis of agronomic traits is considered a didactic method for understanding the factors involved and their associations, as well as to decompose the correlation of cause and effect, as well as the tendencies between groups of dependent and explainable traits (Zilio et al., 2011). Therefore, this work was aimed at evidencing the agronomic performance and linear and canonical associations of Quinoa crop grown Rio Grande do Sul state.

MATERIAL AND METHODS

The trials were carried out in the municipality of Pelotas - Rio Grande do Sul, Brazil, in the experimental station of the EmbrapaClimaTemperado, located in the coordinates: latitude 31°81'53"S and longitude 52°46"98'O, with altitude of 13.2 meters. The soil is classified as Argissolo Vermelho Distrófico com textura média a argilosa (Streck, 2008). The climate is considered Subtropical (Cfa), with averages ranging between 17ºC and 19ºC and average rainfall of 1500 mm per year (Köppen-Geiger, 2012).

The experimental design was randomized blocks, with three Quinoa genotypes, being them Altiplano, Salcedo and BRS Piabiru, arranged in four replicates. The experimental units consisted of five lines with six meters length spaced by 0.40 meters. The density used was 400,000 plants per ha^{-1}, being sown in two centimeters depth. In order to measure the traits of agronomic interest, 10 plants were randomly collected from the three central lines, excluding 0.5 meters of each plot extremity to minimize border effects in the experimental results. The agronomic traits were:

- Plant height (PH): measured from plant base to the apex using a ruler, results expressed in centimeters (cm).

- Number of ramifications (NR): measured by manual counting of the number of ramifications per plant, results expressed in units.

- Number of seeds per inflorescence (NSI): measured by manual counting of each inflorescence in the plant, results expressed in units.

- Number of seeds per plant (NSP): measured by manual counting of the total number of seeds in the plant, results expressed in units.

- Mass of one thousand seeds (MTS): obtained by manual counting of eight replicates of 100 seeds each, results expressed in grams (g).

- Petiole length (PL): measured using a caliper ruler, results expressed in cm.

- Leaf length (LL): measured with a ruler through the leaf extension, results expressed in cm.

- Leaf width (LW): measured with a ruler, results expressed in cm.

- Leaf teeth number(LTN): measured manually by counting the number of leaf cutouts, results expressed in units.

- Flower length (FL): measured with the aid of a digital caliper, results expressed in cm.

- Flower pedicel length (FPL): measured through a digital caliper, results expressed in cm.

- Plant seed yield (SY): obtained by weighing the total mass of seeds per plant, results expressed in kg/ha.

The data were submitted to analysis of variance in order to verify the assumptions of the model (Ramalho et al., 2012). Characters that presented significance were submitted to the Duncan test at 5% of probability. Likewise, the characters measured were submitted to linear correlation analysis with purpose of identifying the tendency of association and its significance based on the t test at 5% of significance. Afterwards, the matrix of linear associations was submitted to multicollinearity diagnosis through the matrix´s number of conditions (NC) (Cruz and Carneiro, 2003). The characters were subdivided into yield components (group I): SY, MTG, LTN and NSP, and morphological characters (group II) PH, NR, PL and LL. Thus, the canonical correlation analysis was performed, where the significance between groups of characters was obtained through the ratio (LRT) of the restricted maximum likelihood (Cruz and Regazzi, 1997).

For morphological description, 10 plants were collected per experimental unit. The measurements were performed for growth habit, stalk consistency, stalk shape, phyllotaxis, presence of petiole, hairiness, consistency, limb shape, leaf nerve, base, apex, leaf number, inflorescence, presence of pedicel, plant color, number of sepals, number of stamens, calyx attachment, stamen size, number of weaves, dehiscence of stamens, stamen insertion, number of stigmas, ovary position , number of locules, number of carpels, and number of eggs per locule.

RESULTS AND DISCUSSION

In order to identify the peculiarities expressed for each Quinoa genotype tested in Rio Grande do Sul state, were measured the characteristics growth habit, stalk consistency, stalk shape, phyllotaxis, presence of petiole, hairiness, consistency, limb shape, leaf nerve, base, apex, leaf number, inflorescence, presence of pedicel, plant color, number of sepals in the calyx, number of stamens, calyx attachment, stamen size, number of stamens weaves, stamens dehiscence, stamen insertion, ovary position , number of locules, number of carpels, and number of eggs per locule. These qualitative traits are presented in the Table 1, extractified for each genotype evaluated.

Table 1 - Qualitative description of Quinoa genotypes (Altiplano, Salcedo and Piabiru) grown in Rio Grande do Sul

Traits	Genotypes		
	Altiplano	**Salcedo**	**Piabiru**
Growth habit	Indeterminate	Indeterminate	Indeterminate
Stalk consistency	Herbaceous	Herbaceous	Herbaceous
Stalk shape	Cylindrical	Cylindrical	Cylindrical
Phyllotaxis	Alternatespiral	Alternatespiral	Alternatespiral
Presence of petiole	Yes	Yes	Yes
Hairiness	No	Glabrous	Glabrous
Consistency	Cartacea	Cartacea	Cartacea
Limbshape	Round	Round	Round
Venation	Parallel	Parallel	Parallel
Base	Truncate	Truncate	Truncate
Apex	Apiculate	Apiculate	Apiculate
Leafedge	Toothed	Toothed	Toothed
Inflorescence	Composed	Composed	Composed
Presence of pedicel	Subsessile	Subsessile	Subsessile
Plant color	Greenish	Greenish	Greenish
Number of sepals	5	5	5
Number of stamens	5	5	5
Calyx attachment	Gamosepalous	Gamosepalous	Gamosepalous
Stamen size	Isodynamous	Isodynamous	Isodynamous
Number of stamens weaves	2	2	2
Stamens dehiscence	Rimosa	Rimosa	Rimosa
Stamen insertion	Receptacle	Receptacle	Receptacle
Number of stigmas	2	2	2
Ovaryposition	Superior	Superior	Superior
Number of locules	1	1	1
Number of carpels	1	1	1
Number of eggs per locule	1	1	1

Variance analysis revealed significance at 5% of probability (Table 2) for the traits plant height (PH), number of ramifications (NR), number of seeds per inflorescence (NSI), number of seeds per plant (NSP), mass of one thousand seeds (MTS), petiole length (PL), leaf length (LL), leaf width (LW), leaf teeth number (LTN), flower length (FL), flower pedicel length (FPL) and seed yield (SY).

For the trait plant height (PH), superiority was evidenced for genotypes Altiplano and Salcedo genotype (Table 2). Regarding number of ramifications (NR), higher magnitudes were observed for genotype BRS Piabiru and Salcedo, as these genotypes present high phenotypic plasticity and advantageously respond to modifications imposed by the growing environment. Regarding number of seeds per inflorescence (NSI), number of seeds per plant (NSP), mass of one thousand seeds (MTS) and seed yield (SY), similar tendencies were observed for genotypes Salcedo and Altiplano. Although the mass of one thousand seeds is influenced by several environment factors, a fraction of it is determined by genetic factors intrinsic of a particular genotype (Szareski et al., 2015; Pandey and Torre, 1973).

Petiole length (PL) revealed higher magnitude to the genotype Altiplano. On the other hand, leaf length (LL), leaf width (LW) and leaf teeth number (LTN) were higher for Salcedo genotype, while pedicel length (PL) was higher for BRS Piabiru genotype (Table 2). Absence of significance was expressed for flower length (FL).

Table 2 - Analysis of variance and test of means by Duncan for 12 characters of Quinoa, being plant height (PH), number of ramifications (NR), number of seeds per inflorescence (NSI), number of seeds per plant (NSP), mass of one thousand seeds (MTS), petiole length (PL), leaf length (LL), leaf width (LW), leaf teeth number (LTN), flower length (FL), flower pedicel length (FPL) and seed yield (SY), for three quinoa genotypesgrown in Rio Grande do Sul state

Factorofvariation	Characters											
	Meansquares											
	PH	NR	NSI	NSP	MTS	PL	LL	LW	LTN	FL	FPL	GY
Genotyps	3062.9*	2347.6*	78663.2*	172100610.2*	0.8 *	181.3 *	2.5 *	6.2*	991.6 *	0.1*	7.1*	761.6 *
Blocks	229.8	781.1	3297	66855670.0	0.7	1.6	0.1	0.2	81.1	0.1	0.1	407.8
Complementar analyzes												
Genotyps	PH	NR	NSI	NSP	MTS	PL	LL	LW	LTN	FL	FPL	GY
Altiplano	157.8 a	35.4 b	155.3 a	5522 a	1.9 a	8.3 a	5.0 b	4.2 b	6.2 b	0.9 a	0.6 b	420 a
Salcedo	135.0 ab	50.5 ab	149.7 a	8118 a	1.8 a	0.9 b	5.8 a	5.3 a	22.1 a	1.1 a	0.5 b	672 a
BRS Piabiru	123.4 b	63.3 a	12.3 b	658 b	1.4 b	0.9 b	4.8 b	3.8 b	3.6 b	0.9 a	2.1 a	36 b

* means followed by the same letter in the column did not statistically differthrough Duncan test, at 5% of probability.

The linear correlation analysis (Table 3) was performed using the following characters: plant height (PH), number of ramifications (NR), number of seeds per inflorescence (NSI), number of seeds per plant (NSP), mass of one thousand seeds, (MTS), petiole length (PL), leaf length (LL), leaf teeth number (LTN), flower length (FL), flower pedicle length (FPL) and seed yield (SY) in order to verify which linear associations are significant and the tendencies between traits. Among the 66 correlations tested, only 18 were significant at 5% of probability by the t test.

In this context, the increment on number of seeds per plant (NSP) occurs when quinoa plants present higher seed formation per inflorescence (NSF). In contrast, it results in a decrease of flower pedicel size (FPL). For this crop, linear correlations show that seed yield components are closely related, as the increase of number of seeds per plant (NSP) is followed by an increment on mass of one thousand seeds (MTS) and seed yield per plant (SY).

Quinoa plants, when taller (PH), tend to present superiority for petiole length (PL). Similarly, it results on the increase of reproductive units which may elevate the number of seeds formed (NSF). However, when plants express superior stature, they tend to direct assimilates for morphological structures that are considered sources of photosynthetic products, for example, increasing leaf width (LW) and length (LL), as well as leaf teeth number (LTN) of round leaves. The increase of leaf dimensions (LL and LW) result in additions to leaf teeth number (LTN).

By increasing the number of ramifications (NR) it is possible to obtain reproductive structures with longer flower pedicel (FPL). However, it culminates in the reduction of leaf dimensions (LW and LTN), as well as the number of seeds formed (NSF) and seed yield per plant (SY). Seed yield of this species is closely correlated to the magnitude of seeds produced by inflorescence (NSI) and to mass of one thousand seeds (MTS). Therefore, these attributes are defined as the main seed yield components of quinoa.

The canonical correlation is based on the assumption that the characters do not present only a pair-to-pair linear tendency, being possible that not only a single trait influences on the main attributes of this species, but instead, two or more determinant characters. Due to the large number of characters measured in this study, and multiple interests on the associations, stratification was performed by groups of importance. Group I was defined as components of seed yield (SY, MTS, NSF and NSP), and group II was formed by secondary characters (PR, NR, PL, LL, LW, LTN, FL and FPL).

This multiple regression was subjected to significance of the association between groups through the restricted maximum likelihood ratio (LRT) at 5% of probability by the chi-square test. The inter-group correlation was evidenced elevated and significant (r = 0.87), being them dependent and explainable. Only the first canonical pair was necessary to explain, in a multivariate way, the interrelationships expressed, where high yielding quinoa plants with potentiated seed yield (SY), mass of one thousand seeds (MTS), number of seeds per inflorescence (NSF) and number of seeds per plant (NSP) are determined by situations where plant height (PH) is prioritized, as well as greater longitudinal (LL) and transversal (LW) leaves, higher number of leaf cutouts (LTN), petiole length (PL) and dimension of longitudinal reproductive structures (FL). However, these plants should express lower magnitude of ramifications (NR) and extension of flower pedicel (FPL). These structures are considered drains and costly to assimilates accumulation by the plant, resulting in unprofitable structures for seed yield of quinoa plants.

Table 3 - Pearson's linear correlation and canonical correlation significant for 12 agronomic characters:plant height (PH), number of ramifications (NR), number of seeds per inflorescence (NSI), number of seeds per plant (NSP), mass of one thousand seeds (MTS), petiole length (PL), leaf length (LL), leaf width (LW), leaf teeth number (LTN), flower length (FL), flower pedicel length (FPL) and seed yield (SY), measured in three quinoa genotypesgrown in Rio Grande do Sul state

Characters								
NSP*NSF	MTS*NSF	MTS*NSP	PL*PH	PL*NSI	LW*NSI	LW*LL	LTN*LL	LTF*LL
0.76*	0.56*	0.58*	0.42*	0.47*	0.41*	0.79*	0.46*	0.57*
FPL*NR	FPL*NSI	FPL*NSP	FPL*LW	FPL*LTN	SY*NSI	SY*NSP	SY*MTS	SY*FPL
0.40*	-0.61*	-0.50*	-0.43*	-0.37*	0.71*	0.98*	0.61*	-0.44*
Canonical correlations		Group I			Group II			
r	0.87	SY	0.13	x	PH	NR	PL	LL
		MTS	0.58		0.18	-0.71	0.52	0.01
LRT	0.0034*	NSI	0.58		LW	LTN	FL	FPL
		NSP	0.22		0.01	0.2	0.27	-0.43

For seed production, it is important to understand the existence of morphological differences among cultivars of the same species. In Brazil, the identification of cultivars is carried out, most of the times, through morphological descriptors (Bonow et al., 2007). This description aids to identify genetic and varietal contamination, therefore, the distinction between cultivars allows the separation of undesirable genetic materials within seed production fields, or in some cases, indicating the need for discard.

CONCLUSIONS

Quinoa seed yield is based on the joint action of mass of one thousand seeds, number of seeds per inflorescence and number of seeds per plant, being the Altiplano and Salcedo genotypes considered superior.

Seed yield components of quinoa plants are potentialized by plant height, petiole length, leaf teeth number and flower length.

The definition of agronomic performance, linear and canonical associations is a pioneer study for this species and may be used in future studies with pseudocereals focused on seed science and technology.

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