

Genetic Diversity in the Growth and Yield of Climate-Resilient Quinoa in Northern Vietnam's Conditions

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ABSTRACT— The quinoa crop is known as “the food for the future” and contains wide profits for human beings. Quinoa is a niche product with enlarged manufacturing, but it has the potential to be much more than just a food. It can produce the ecosystem switch from animal to plant-based protein diets and create a more sustainable food system. The study was implemented in the winter cropping season to evaluate the growth and yield characteristics of 25 selected quinoa genotypes. The criteria monitoring included: (i) growth criteria (growth duration, plant height, number of branches, number of leaves, stem diameter, and net assimilation rate), and (ii) grain yield criteria and its components (1000-seed weight, individual yield, and potential yield). The growth duration of the genotypes ranged from 73 to 119 days, potential yield ranged from 0.57 to 2.18 tons/ha. The high diversity of the quinoa collection was found and could be divided into four groups. As a result, based on the yield component criteria the 5 superlative genotypes were selected: Q5, 2 want, Chadmo, G26, and Sayana to assist in the research and selection of quinoa genotypes.

KEYWORDS: quinoa, climate-resilient, genetic diversity, growth

1. INTRODUCTION

Predictable disorders, conflict trends, and climate change significantly impact global food security. Food crop production has elevated to the top of national priorities simultaneously as dietary costs tend to rise. One of the countries that has been most severely impacted by climate change is Vietnam. With 42.7 million tons of rice produced, the nation ranks second in Southeast Asia and fifth in the globe [1]. The major explanations for the decrease in rice area within the agricultural sector structure are drought and contamination by saltwater. During the 2020/2021 dry season, the Mekong Delta's rice production area surpassed 210,000 hectares, and drought and saltwater intrusion impacted the agricultural output.

The scientific name for the quinoa plant is *Chenopodium quinoa*. It is an annual member of the amaranth family that originated in the Andes Mountains and is mostly cultivated in Ecuador, Bolivia, and Peru. For over 3,000 to 4,000 years, quinoa seeds have been utilized as a grain by the Andean people [2- 4]. The FAO decided to select quinoa as one of the crops to assist with ensuring food security in the coming century.

Different types of quinoa are capable of adapting in frigid highland regions as well as subtropical ones, and wide latitudes ranging from 21°30'S to 16°21'N, the range of average daily temperatures for the crop cycle was 9 to 22.1°C. A lesser variance was observed in the average daily photoperiods, ranging from 11.2 to 12.8 hours [5]. Many different quinoa landraces are available that can be adapted to diverse environments such as extreme aridity, low temperatures, and from above 4000m to nearly sea level. Where more traditional crops cannot be cultivated, stress-tolerant quinoa may be grown in marginal locations or harsher conditions [6]. Quinoa is therefore regarded as a worldwide crop. Quinoa is a grain that contains all the essential amino acids, is high in protein, high in calories, low in fatty oil, and most importantly, is free of gluten, which may lead to

considerable health problems in humans [7]. The protein ratio, calcium, iron, protein, and fiber content in quinoa is higher than all popular cereals today, so it is considered a food that assists in preventing cardiovascular diseases and improves health and bone health [4], [7], [8]. Quinoa is cultivated in several regions and cities around Vietnam. Quinoa plants have larger yields than in certain initial producing places due to adapting well to the natural conditions in our nation.

The quinoa HV1 variety was cultivated and developed in Vietnam between 1986 and 2000, producing 1.40 to 2.06 tons/ha in different provinces and cities throughout the country [9]. It claimed that Vietnam's climate is exceptionally suitable for quinoa. The productivity was even higher than in some of the original places [5]. Another field trial reported that two quinoa varieties, Red and Green, grew well in northern Vietnam in winter and spring cropping season and had the highest yield at a nitrogen dose of 90 kg N/ha [10]. Similarly, Atlas varieties achieved the highest yield at the same nitrogen dose in saline-affected soil conditions [11]. In the Highland Center under ferralsols and Acrisols soils, four quinoa varieties performed better under a nitrogen supplement of 150 kg N/ha [12]. Recent study results indicate that quinoa may be cultivated as a winter and spring crop in the northern delta [10], [13]. A diversity of 30 quinoa genotypes in response to drought stress was reported by [14]. It could be summarized that previous research on quinoa in Vietnam was mainly conducted with a limited number of varieties or in a short time under controlled greenhouse conditions. There was no research in evaluate growth and yield of large number of varieties under actual field conditions. Thus, this study evaluated the growth and yield of several quinoa genotypes to discover potential genotypes for quinoa production in Vietnam.

2. Materials and methods

2.1 Material

The research materials included 25 quinoa genotypes selected from the collection of 150 candidate genotypes by high germination rate as shown in Table 1.

Table 1: The investigated quinoa genotypes in the experiment

Name	Code	Origin	Name	Code	Origin
Sayana	G2	Bolivia	CT31	G15	Argentina
G18	G3	Argentina	Ahachuha	G16	Bolivia
Q1	G4	Argentina	Ru5	G20	United Kingdom
Sumari x ruy937	G5	United State	Atlas	G21	Netherland
Q3	G6	Argentina	Q4	G22	Argentina
42 test-1	G7	Chile x Bolivia	Q2	G25	Argentina
2BDJ	G8	Chile	G26	G23	Argentina
2 want	G9	Bolivia	Q5	G29	Argentina
42 test-2	G10	Chile x Bolivia	09	G30	Argentina
Atlas ND	G11	Netherland	Chadmo	G93	Chile
Ball Cayon	G12	Chile	G17	G111	Argentina
Riobamba	G13	Netherland	4K	G141	Chile
G23	G14	Argentina			

2.2 Experimental layout

In this study, we implemented observative and assessing investigated genotypes at the experimental field of the Faculty of Agronomy, Vietnam National University Agriculture, Gia Lam, Hanoi (latitude 20°60'N, longitude 105°56'W, altitude ~ 20 m.a.s.l) in the winter cropping season 2023 (October 2023 to January 2024). The experimental layout was a randomized complete block design with three replications. Before sowing, the

soil was plowed at 10 - 15 cm depth. The seeds were sown in rows with a row distance of 50 cm and a plant distance of 20 cm, 3 – 4 seeds/hill. Then, at 3 – 4 leaf stages, seedlings were thin to keep 1 seedling/hill for a plant density of 100,000 plants/ha. Each plot area was 7.5 m². The dose of fertilizers per hectare includes 10 tons of organic fertilizer, 400 - 500 kg of lime powder, 150 kg N, 90 kg P₂O₅, and 90 kg K₂O.

2.3 Criteria measurement

The growth duration indicators consist of time from sowing to emergence, inflorescence emergence, flowering, milky grain, thick grain, and ripe grain based on the BBCH scale that was determined by at least 50% of total plants on the plot have characteristics plants in the certain stages [15].

At harvest, the growth indicators encompass the number of leaves on the main stem, the number of primary branches, plant height, and the stem diameter at 2 cm from the above ground. Sample plants in each plot were randomly selected to determine leaf area by leaf area meter LI3100 (Licor, USA) and total dry weight after oven-drying at 80°C until constant weight at 30 days after sowing (t₁) and 60 days after sowing (t₂). The net assimilation rate (NAR) was calculated by following this formula:

$$\text{NAR (mg/m}^2\text{/day)} = \frac{\text{DW}_2 - \text{DW}_1}{t_2 - t_1} \times \frac{\log_e A_2 - \log_e A_1}{A_2 - A_1}$$

Where DW₁ and DW₂ are total dry weights at sampling times t₁ and t₂; log_eA₁ and log_eA₂ are the natural logs of leaf areas A₁ and A₂ at t₁ and t₂, respectively.

At harvest, the yield components were compost number of harvested plant/ha (PD), number of panicles/plant (NoP), number of seeds/panicle (NoSP), and the 1000-seed weight (P1000). After sun-drying the individual yield was calculated by the average seed weight of 10 sample plants/plot. The potential yield was calculated by the following formula:

$$\text{Potential yield (tons/ha)} = \text{P1000} \times \text{NoP} \times \text{NoS} \times \text{PD} \times 10^{-7}$$

2.4 Data analysis

The data were statistically processed by RStudio 2023.12.0 software and Microsoft Excel. The mean values of the treatments were compared by using the Least Significant Difference (LSD) at the probability level of 0.95 (α=0.05).

3. Results and discussion

3.1 The time duration of the quinoa genotypes throughout the growth stages

The quinoa genotypes took from 3 to 7 days from sowing to emergence (Table 2). G3 and G93 showed the longest emergence time (7 days), whereas other remaining genotypes took only 3 to 5 days for this stage.

Table 2: Time duration during the growth stages of quinoa genotypes (days)

Genotype	Emergence	Inflorescence emergence	Flowering	Milky grain	Thick grain	Ripe grain
G2	4	38	50	72	89	105
G3	7	29	35	45	56	73
G4	5	30	45	72	72	106
G5	4	32	49	56	82	102

G6	4	30	41	61	72	91
G7	4	30	41	60	70	85
G8	4	32	45	58	74	101
G9	4	35	49	56	80	106
G10	3	30	44	64	70	85
G11	4	30	55	73	90	110
G12	4	31	42	58	69	95
G13	4	30	42	54	62	78
G14	4	32	45	64	86	106
G15	4	30	48	67	85	100
G16	4	31	45	50	78	106
G20	5	30	41	56	72	96
G21	5	34	54	74	91	109
G22	4	31	43	61	73	92
G23	4	31	42	60	72	90
G25	4	31	59	79	92	110
G29	5	39	54	78	98	119
G30	3	38	49	63	72	93
G93	7	32	45	72	86	111
G111	5	34	48	73	85	107
G141	4	38	45	72	86	104

In the inflorescence emergence stage, the genotypes that had the longest time to emerge the flower were G29 (39 days), G2, G30, and G141 (38 days). In contrast, G3 was observed as the earliest inflorescence emergence genotype with only 29 days in length for this stage. The flowering stage is the sensitive period to environmental stresses of the quinoa, which influences future productivity. The earliest genotype to blossom was G3 (35 days after sowing), while the latest was G25 (59 days after sowing). The milk grain stage started from 45 to 79 days after sowing, where G3 was the earliest ripen genotype, it took only 45 days after sowing, while G25 and G29 were the latest ones starting at 79 and 78 days after sowing, respectively. Similarly, G3 took only 56 days after sowing to reach the thick grain stage, whereas the G29 took 98 days for this stage. The G29 had the longest time for ripening grain with 119 days followed by G93 (111 days), G25 and G11 (110 days). G3 and G13 were the ones that had the shortest time for ripening with only 73 and 78 days, respectively.

3.2 The growth characteristics of the quinoa genotypes

Plant heights of quinoa genotypes ranged from 74.8 to 111.1 cm, where G2 and G29 were the highest ones and G12 was the shortest one (Table 3). The range of leave numbers of the studied genotypes was from 35.0 to 47.8 leaves/main stem. G4, G21, G23, and G15 had the highest leave number on the main stem, while G13 had the lowest. The total number of branches of genotypes ranged from 16.3 to 25.4 branches/plant. The highest branch number belonged to G9 and G2, the lowest one was G13. The stem diameter fluctuated from 0.78 to 1.08 mm. The G6, G2, G9, G15, G16 and G30 were the large stem diameter genotypes (>1.0 mm); G13, G141 and G11 were the ones with the smallest stem diameter (≤ 0.8 mm). Due to the small stem diameter, the trellis had to be set up to prevent them from lodging.

Table 3: Growth indicators of quinoa genotypes

Genotype	Plant height (cm)	NoL (leaves/main stem)	NoB (branches/plant)	DS (cm)	NAR (mg/m ² /day)
G2	111.1	44.3	25.3	1.04	0.058
G3	90.1	43.5	21.4	0.85	0.482
G4	99.4	47.8	25.2	0.96	0.302
G5	94.6	41.5	19.0	0.88	0.047
G6	108.9	42.1	23.5	1.08	0.142
G7	88.1	38.6	19.7	0.82	0.583
G8	77.7	42.7	22.3	0.86	0.558
G9	98.5	40.1	25.4	1.03	0.059
G10	92.5	40.5	22.2	0.92	0.158
G11	77.2	35.1	16.4	0.80	0.149
G12	74.8	35.6	21.4	0.81	0.433
G13	97.8	35.0	16.3	0.78	0.462
G14	97.4	41.1	20.4	0.90	0.318
G15	103.5	44.7	23.7	1.00	0.790
G16	96.4	41.6	20.9	1.02	0.421
G20	96.1	41.6	22.7	0.90	0.595
G21	104.9	46.3	22.5	0.81	0.408
G22	88.3	37.7	23.7	0.84	0.045
G23	99.7	45.9	24.8	0.97	0.216
G25	101.1	44.4	18.9	0.83	0.047
G29	110.9	41.7	18.9	0.94	0.533
G30	103.6	39.7	24.6	1.02	0.488
G93	97.0	44.6	23.4	0.92	0.596
G111	94.9	43.0	22.4	0.90	0.265
G141	81.3	38.8	20.9	0.80	0.569
LSD_{0.05}	8.38	3.96	3.48	0.11	0.324

Note: NoL- the number of leaves on the main stem, NoB- the number of branches on the plant, DS- the diameter of the stem, NAR- net assimilation rate.

The NAR ranged from 0.047 to 0.790 mg/m²/day. The highest NAR was found in G15 followed by G93, whereas the lowest NAR was in G5 and G25 (0.047 mg/m²/day) and G9 (0.059 mg/m²/day).

3.3 The yield components of the quinoa genotypes

The 1000-seed weights (P1000) ranged from 2.87 to 4.96 g. G11 had the lowest seed weight, G2 (4.96 g) and G25 (4.74 g) displayed the highest seed weight. G7, G9, G10, G14, G29, G93 and G141 also had large seed size with a seed weight of over 4.00 g/1000 seeds (Table 4). There was a large variation in individual yield and potential yield of quinoa genotypes which ranged from 5.16 to 24.1 g/plant and from 0.52 to 2.18 tons/ha, respectively. G22 (5.16 g/plant) and G8 (7.35 g/plant) performed the lowest for individual yield. However, G4 showed the lowest potential yield with only 0.57 tons/ha, which was followed by G22 (0.65 tons/ha), G20 (0.79 tons/ha), and G6 (0.80 tons/ha). G29 (24.11 g/plant) and G3 (20.38 g/plant) were the genotypes having the best individual yield, but G93 and G9 were the best genotypes for potential yield performance with values of 2.14 and 2.18 tons/ha.

Table 4: Seed weight and yield of the quinoa genotypes

Genotype	P1000 (g)	Individual yield (g/plant)	Potential yield (tons/ha)
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G2	4.96	13.87	1.99
G3	3.86	20.38	1.45
G4	3.19	10.60	0.57
G6	3.18	12.41	0.80
G7	4.16	13.93	1.44
G8	3.99	7.35	1.03
G9	4.41	16.75	2.14
G10	4.02	16.49	1.50
G11	2.87	15.19	0.97
G12	4.05	13.03	1.38
G13	3.47	9.20	0.98
G14	4.00	8.43	1.16
G15	3.49	8.66	1.06
G16	3.75	14.34	1.31
G20	3.45	10.85	0.79
G21	3.89	9.46	1.04
G22	3.19	5.16	0.65
G23	3.71	15.33	1.66
G25	4.74	10.10	1.12
G29	4.50	24.11	1.54
G30	3.87	14.55	1.92
G93	4.47	17.36	2.18
G111	3.55	8.82	0.90
G141	4.23	15.30	1.47
LSD_{0.05}	0.89	9.83	0.97

Note: P1000- 1000 seed weight

3.4 Diversity analysis of quinoa genotypes for growth and yield performance

Principal Component Analysis (PCA), is a widely adopted technique in contemporary data analysis across numerous scientific fields. Its primary objective is to discover the most significant framework for re-expressing a specific dataset. By doing so, it aims to uncover concealed patterns within the data and eliminate unwanted noise. PCA has numerous practical uses, including dimensionality reduction, data condensation, feature extraction, and visual representation of information. PCA could assist us based on characteristics or many characteristics to predict another characteristic and also aids such correlation analysis, we could discover the rules of organisms, to be used to benefit humans [16]. Since analyzing the correlation between growth indicators and yield indicators supplies to breeders find rules and correlations between factors. PCA has been used in several studies recently to identify genetic diversity and categorize characteristics in quinoa. Individual yield, potential yield, weight of 1000 grains, plant height, number of leaves, number of branches, time from sowing to ripe grain stage, the diameter of stem, and net assimilation rate contributed mainly to the phenotypic variation of the experimental genotypes (Figure 1).

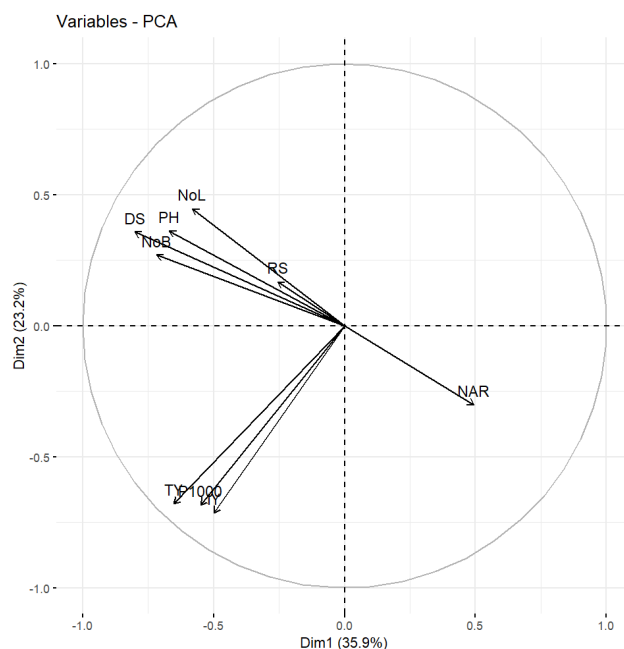


Figure 1 PCA of investigated quinoa genotypes

Note: Individual yield (IY), potential yield (PY), 1000-seed weight (P1000), plant height (PH), the number of leaves (NoL), the number of branches (NoB), time from sowing to ripe grain stage (RS), the stem diameter (DS), and net assimilation rate (NAR)

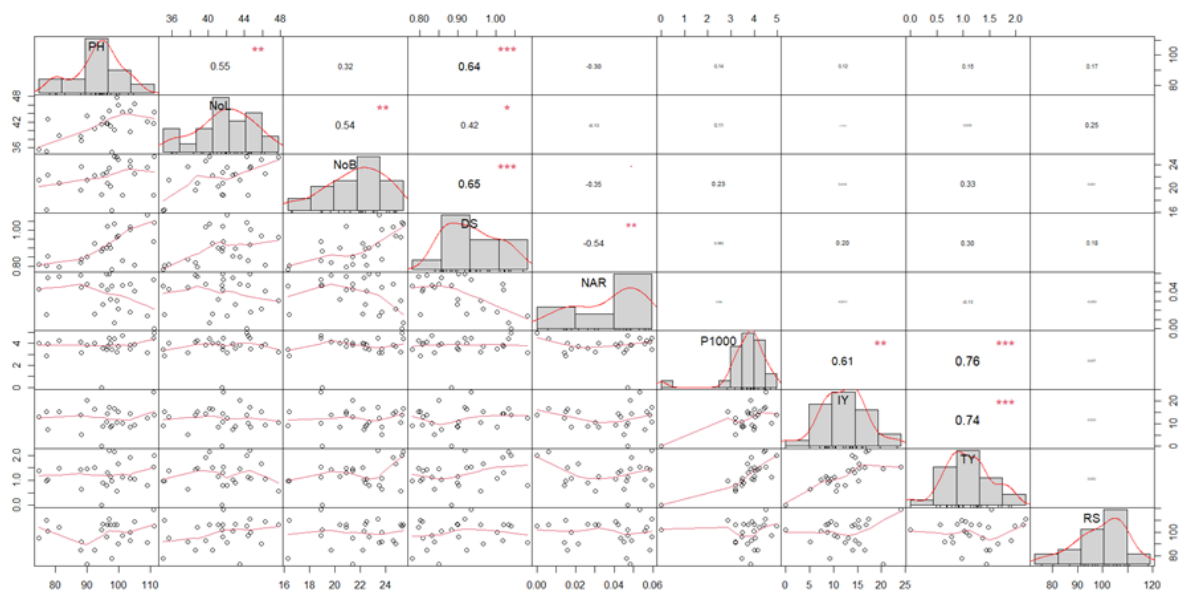


Figure 2 Correlation among growth and yield components of quinoa genotypes

Note: Individual yield (IY), potential yield (PY), 1000-seed weight (P1000), plant height (PH), the number of leaves (NoL), the number of branches (NoB), time from sowing to ripe grain stage (RS), the stem diameter (DS), and net assimilation rate (NAR)

The results of this experiment show that individual yield had a strong positive correlation with P1000, and potential yield, with correlation coefficients $r = 0.76$ and 0.74 , respectively; DS also had an average positive correlation with NoB and PH with correlation coefficients of $r = 0.65$ and 0.64 , respectively (Figure 2).

Through a cluster analysis of quinoa's genetic variation based on observable physical traits, researchers found that 25 genotypes were categorized into four primary groups (Figure 3). Group I, represented by G29 genotypes, differed significantly from the other clusters. Group II contains four genotypes (G13, G3, G7, G10), while Group III comprises four (G11, G12, G8, G141). Lastly, Group IV encompasses the remaining sixteen genotypes from the total twenty-five. The genetic differences among these groups can be utilized in quinoa breeding programs.

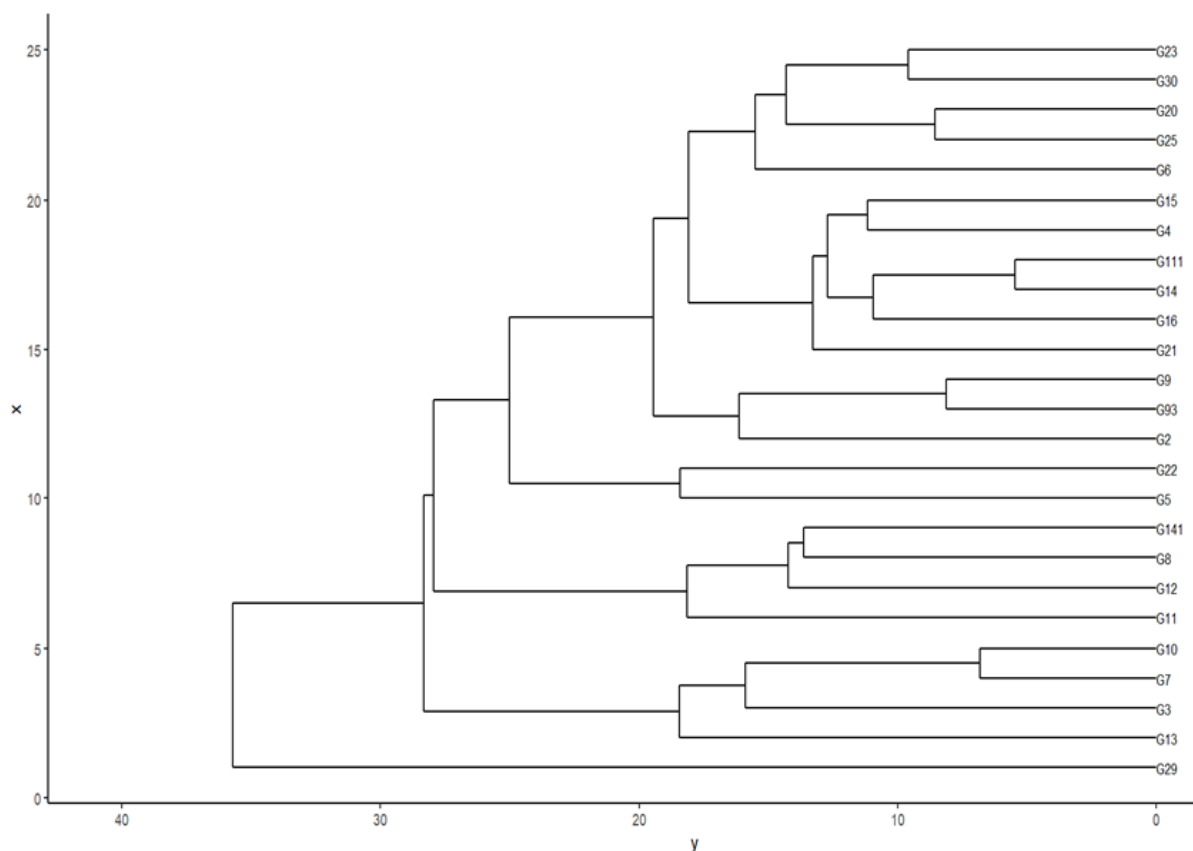


Figure 3 Dendrogram of genotypes based on phenotypic data

4. Conclusion

The result showed the large genetic diversity of 25 investigated quinoa genotypes for growth and yield indicators, which could be grouped into four groups. Q5 is located in a distinct group (group I). Group four consists of most of the genotypes (16 of a total of 25 genotypes). Quinoa grew well in Vietnam without disease and pest damage, among them, Q5, 2-want, Chadmo, G26, and Sayana had the best performance for growth and grain yield. These could assist in the breeding and development of quinoa production in Vietnam.

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