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CROP PRODUCTION

Phenological strategies and plant growth patterns in pea (*Pisum sativum* L.) to increase yield in the tropics

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ABSTRACT: *Pisum sativum* L., commonly known as pea, dry pea, green pea, or field pea, is a widely cultivated and economically important legume. It contains various nutritional and bioactive compounds that provide substantial health benefits. In tropical regions, peas are generally cultivated in highland environments due to their sensitivity to temperature, humidity, and rainfall. This study evaluated the growth responses of pea under medium-altitude tropical conditions by assessing the phenological variability and growth patterns of three genotypes namely TMG-8-2, BTG-1, and BW-44181(3)(1). Data analysis included analysis of variance (ANOVA), standard deviation, and plant growth analysis. The results showed significant differences in growth rates and developmental patterns among genotypes, with notable phenological variability in organ development rates. The TMG-8-2 genotype exhibited the fastest growth. Furthermore, growth analysis revealed that the BW-44181(3)(1) genotype presented the highest growth rate, while the BTG-1 genotype demonstrated an intermediate growth pattern.
Key words: growth analysis, tropical pea, phenology, tropical, yield.

Estratégias fenológicas e padrões de crescimento vegetal em ervilhas (*Pisum sativum* L.) visando o aumento da produtividade em regiões tropicais

RESUMO: *Pisum sativum* L., também conhecido como ervilha, ervilha seca, ervilha verde ou ervilha de campo, é uma leguminosa amplamente cultivada e de grande importância econômica. É rica em diversos compostos nutricionais e bioativos que oferecem inúmeros benefícios à saúde. Em regiões tropicais, essas culturas são geralmente cultivadas em áreas de altitude elevada devido à sua sensibilidade à temperatura, umidade e precipitação. Neste sentido, este estudo tem como objetivo avaliar a resposta do crescimento da ervilha às condições ambientais tropicais de altitude média, com foco na variabilidade fenológica e nos padrões de crescimento de três genótipos distintos, a saber: TMG-8-2, BTG-1 e BW-44181(3)(1). Para realizar o objetivo, a análise dos dados incluiu análise de variância (ANOVA), desvio padrão e avaliação do crescimento das plantas. Os resultados indicaram diferenças significativas nas taxas de crescimento e nos padrões de desenvolvimento entre os genótipos, com variabilidade fenológica observada na taxa de mudança dos órgãos. O genótipo TMG-8-2 apresentou o crescimento mais rápido. Além disso, a análise do crescimento revelou que o genótipo BW-44181(3)(1) apresentou a maior taxa de crescimento.
Palavras-chave: análise de crescimento, ervilha, fenologia, trópicos, produtividade.

INTRODUCTION

Pea (*Pisum sativum* L.) are legumes that play a significant role in various sectors, both nutritionally and economically. As a key commodity, peas are used not only for household consumption as vegetables and snacks but also in the food industry, in both fresh and processed forms. Nutritionally, peas are rich in protein (22-27%), complex carbohydrates (42.65%), sugars (4-10%), and fats (0.6-1.5%), as well as vitamins, minerals, fiber, and antioxidants that contribute to maintaining health and preventing various diseases (SMÝKAL et al., 2012). Additionally, pea has the potential to support the increasing global food demand, with sales projections expected to rise, reaching a value of $285 million from 2020 to 2026. In Indonesia, the importance of green pea is growing, as evidenced by the increase in imports from 33.82

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tons in 2021 to 1,508.69 tons in 2022. Similarly, imports of dry pea rose from 9,030.16 tons in 2021 to 10,875.46 tons in 2022 (FAOSTAT, 2024).

The increasing demand for pea underscores their significant market potential, both domestically and internationally, which can be met by boosting local production. However, a major challenge is that pea is primarily cultivated in subtropical regions, while production in tropical areas — especially in medium and lowland regions — remains very limited (ZANETTA et al., 2023). Environmental factors such as high temperatures, fluctuating humidity, and varying rainfall can adversely affect the growth and productivity of pea (DEVI et al., 2023; MOHAPATRA et al., 2020; PARIHAR et al., 2023; WANG et al., 2022; ZANETTA et al., 2024). Therefore, there is a need for superior and adaptive genotypes suited to these conditions. The variability of agronomic and morphological traits among local pea genotypes in Indonesia has been extensively documented, with moderate diversity observed in local genotypes (DAMARA et al., 2020; SARAGIH et al., 2018). Additionally, potential pea genotypes for medium and lowland cultivation were identified, including those collected from Karo, Garut, Semarang, Temanggung, Probolinggo, and Batu (WALUYO et al., 2019). Furthermore, significant genetic and phenotypic correlations between fresh and dry yields across various genotypes suggest the utility of these yield traits in breeding programs (CARGNELUTTI FILHO et al., 2024; PAMULATSIH & WALUYO, 2019; PANWAR et al., 2023; UHLARIK et al., 2022). Despite these findings, existing research primarily focuses on basic characterization, highlighting the need for further investigation into the growth of pea plants to specific environmental factors in tropical regions, particularly from a phenological and phenorhythmical perspective.

Plant phenology refers to the changes in the growth and development phases of plants over time, influenced by environmental factors such as temperature, humidity, rainfall, and photoperiod (PIAO et al., 2019; STUCKY et al., 2018; TANG et al., 2023). Observing plant phenophases, such as flowering and fruiting, provides valuable insights into plant adaptation to environmental conditions (CHEN et al., 2020; PEREIRA et al., 2024). In the context of tropical medium land legumes, a deeper understanding of plant phenology is essential for identifying the most promising genotypes for development. This knowledge can also aid in planning more effective cultivation strategies, predicting yields, and assisting in pest and disease management. Studies of pea phenology in subtropical environments indicate that variations in temperature and growing season can significantly affect aspects such as flowering time, pod mass, and total productivity per unit area (LAMBRECHT et al., 2023). Additionally, research has emphasized the role of temporal rhythms, such as circadian rhythms, in regulating physiological activities like leaf movement and flowering, highlighting the complex relationship between plants and their environment (WANG et al., 2022). As climate conditions continue to change due to global warming, further research into plant phenological responses under various environmental conditions is increasingly essential, with studies indicating that climate warming has led to a shift in flowering phenology, resulting in plants flowering earlier in response to rising temperatures (GEISSLER et al., 2023).

In addition to phenology, pea growth is profoundly influenced by biomass allocation and photosynthesis. Plant growth hinges on biomass accumulation, achieved through a delicate balance between carbon assimilation during photosynthesis and carbon loss through respiration (JANUŠKAITIENĖ & PETRAITYTĖ, 2017). Analyzing pea plant growth parameters, such as leaf area ratio (LAR), specific leaf area (SLA), and relative growth rate (RGR), provides valuable insights into plant adaptation to their environment. For example, the ratio of leaf area to leaf weight plays a crucial role in biomass allocation; subsequently, affecting growth rate and yield. Moreover, the use of RGR and net assimilation rate (NAR) is essential for understanding plant growth patterns, particularly in the context of environmental changes (WANG et al., 2022).

The importance of analyzing phenology and growth in plants is underscored by recent research, which highlights the role of the root system in influencing the phenotypic expression of above-ground plant characteristics (BEKTAS et al., 2023; QI et al., 2019; SLEIGHT et al., 2023; YOU et al., 2017). This research suggested that the shoot-root biomass ratio in legume plants is potentially related to high yields and other important agronomic traits (DU et al., 2019; POLANIA et al., 2017; SALIM et al., 2021). Increasing shoot-root biomass ratio has been shown to be associated with increasing yield and traits correlated yield in pea (MARTÍN-BRULL et al., 2024; MUBAROK et al., 2024; VOISIN et al., 2022). This phenomenon emphasized the importance of understanding the relationship between pea growth phases and tropical environmental conditions to optimize plant productivity. In this study, we focused

on observing the phenology and yield variability of pea grown in tropical areas which are known to have high temperatures and variable humidity. This research aimed to understand phenophase and phenorhythms as part of the phenology of local pea genotypes, which can be utilized to enhance pea production in the mid-altitude tropics. Phenophase and phenorhythm are crucial for determining the rate and timing of plant growth processes, ultimately contributing to more efficient cultivation strategies (KASHYAPI & BAHOT, 2012; PANFILOVA et al., 2021). Insights into plant yield characteristics are expected to play a significant role in plant breeding programs and the development of superior varieties capable of providing high yields in challenging tropical environments.

MATERIALS AND METHODS

The research was conducted from 2022 to 2023 at the experimental field of the Faculty of Agriculture, Brawijaya University, Malang (7°56'22"S 112°37'03"E; 507 m a.s.l). A randomized block design was employed to evaluate three pea genotypes: TMG-8-2 (G1), BTG-1 (G2), and BW-44181(3)(1) (G3). The genetic material utilized in this study was sourced from Plant Breeding Laboratory collection of Brawijaya University. Each genotype was replicated three times, with each replication consisting of 30 polybags measuring 30 x 30 cm. Each polybag was sown with a single seed. The experiment was carried out under tropical climate conditions (Table 1). Cultivation practices include the use of appropriate plant cultivation equipment and adherence to recommended maintenance guidelines for pea plants.

Phenological observations focused on phenophase (developmental events) and phenorhythm (intervals between stages), including germination, leaf and stem growth, root formation, flowering, pod development, seed maturation, and senescence. Data was collected every 10 days, except for germination and flowering, and calculated using standard growth analysis formulas with average and standard deviation.

Plant growth analysis

Plant growth was monitored using both destructive and non-destructive methods. Non-destructive observations included measurements of plant height, number of leaves, and leaf area, while destructive sampling involved the determination of total dry weight. Developmental traits such as days to flowering, days to harvest, and number of flowers were recorded, along with yield parameters including the number of pods and seeds per plant, pod and seed weight, and seed weight per pod. Observations were conducted every 10 days from 10 to 70 days after planting (DAP), following the methodology of (PANDEY et al., 2017).

Data analysis

Data analysis using software Microsoft Excel 2019, considering standard errors and 95% confidence interval. In addition, using the Statistical Tool of Agriculture Research (STAR) 2013 software. The level of significance for the analysis of variance uses 95% and if it is significantly different, it is continued with a further LSD test with a level of 5%.

RESULTS AND DISCUSSION

Phenorhythmic diversity of pea genotypes

All three genotypes displayed similar germination and early vegetative growth stages, with cotyledon emergence occurring around 3 dap and the appearance of true leaves shortly thereafter (Table 2). The duration of the vegetative and reproductive periods in peas is influenced by the interaction between temperature, humidity, and the specific genetic makeup of the plant (LAMBRECHT et al., 2023). Phenophase and phenorhythms from germination, vegetative growth, and root-shoot development in three genotypes exhibited similar early growth stages, with cotyledon emergence around 3 days after planting (dap) (Figure 1). High

Table 1 - Monthly temperature, humidity and rainfall data in Malang.

Month	--------Temperature (ºC)--------	----------Humidity (%)----------	----------Rainfall (mm)----------
November 2022	22.82	87.30	25.92
December 2022	24.00	83.98	7.83
January 2023	27.71	78.77	6.78

Table 2 - Different pea growth stage genotype.

Different pea genotypes (mean ± standard deviation) dap					
No.	Stages	Code	TMG-8-2	BW-44181-(3)-(1)	BTG-1
1	Root appears time	05	3 ± 0	3 ± 0	3 ± 0
2	Time to shoot	08	4 ± 0	3 ± 0	4 ± 0
3	The first true leaves open	11	9 ± 0	7 ± 0	8 ± 0
4	Number of leaves > 9	19	17 ± 4	21 ± 3	23 ± 3
5	Number of segments > 9	39	26 ± 3	23 ± 5	25 ± 3
6	Early flower buds appear	51	28 ± 2	31 ± 2	28 ± 3
7	The first flowers bloom	60	31 ± 3	34 ± 2	32 ± 3
8	Flowers bloom 50%	65	38 ± 0	43 ± 2	42 ± 3
9	End of flowering	69	43 ± 4	45 ± 3	48 ± 3
10	Pods emerge early	71	34 ± 3	37 ± 2	35 ± 3
11	50% pods developed/flat	75	38 ± 3	41 ± 2	38 ± 3
12	Fresh harvest time	79	44 ± 3	46 ± 2	46 ± 3
13	50% dry pods	80	51 ± 4	56 ± 2	56 ± 3
14	Dry harvest time	89	56 ± 4	61 ± 2	56 ± 3
15	Plant senescense	97	56 ± 5	64 ± 3	66 ± 3

temperatures at midaltitude tropical environment can significantly impact the phenology and phenorhythms of pea plants (WILLIAMS et al., 2022), leading to a reduction in the reproductive period, forced maturity, and negatively impacting seed development and quality. In the flowering phase, particularly at the 50% bloom stage, noticeable differences were observed among the three pea genotypes based on their mean flowering times. The TMG-8-2 genotype reached 50% flowering at 65 days, while BW-44181(3)(1) and BTG-1 reached the same stage at 38 ± 0 and 43 ± 2 days, respectively. The ANOVA results supported this observation, showing significant treatment effects on seed number per plant (NSP, MS = 819.53) and seed number per pod (NSPP, MS = 2.17). This indicated that the 50% flowering stage contributed more strongly to seed formation than pod formation (TASNIM et al., 2022). Additionally, high temperatures may negatively influence seed weight and germination rates, although heat-tolerant varieties tend to maintain better performance under such conditions. (LAMICHANEY et al., 2021; ZANETTA et al., 2023; 2024). Planting time which is related to changes in temperature, and genotypes affects the phenology and phenorhythms of pea plants during plant growth and development (SUMER, 2023).

Genotype (TMG-8-2) initiated flowering earlier than the other two genotypes, with flower bud emergence at 28 dap. BTG-1 and BW-44181(3)(1) began flowering at 26 dap and 30 dap, respectively. High temperatures during reproductive and seed-filling period decrease seed nitrogen amount in pea (LARMURE & MUNIER-JOLAIN, 2019) can severely reduce both seed yield and germination, early vegetative stage can lead to poor emergence, stunted growth, and impaired physiological functions in pea plants (DEVI et al., 2023; MOHAPATRA et al., 2020). TMG-8-2 and BW-44181(3)(1) exhibited synchronized senescence, with leaf and pod senescence occurring within a short timeframe (Figure 1). BTG-1 displayed a more prolonged senescence phase. Genetic variability among genotypes plays a crucial role in determining the timing and duration of different phenological stages (BOURGAULT et al., 2022; SEROVA et al., 2023).

Plant growth analysis

Genotypic variation impacts a broad spectrum of developmental traits, including phenophase timing and the progression of growth stages. Both genetic and environmental factors exert significant control over the developmental trajectory of plants (ALSUBHI & ALZAHRANI, 2024; BRATKOVIĆ et al., 2024). Plants with higher leaf area ratio have better light capture ability, providing a competitive advantage (HASSANPOUR-BOURKHEILI et al., 2020). The differences in leaf area ratio (LAR) values in the three genotypes (Figure 2A) are due to variations

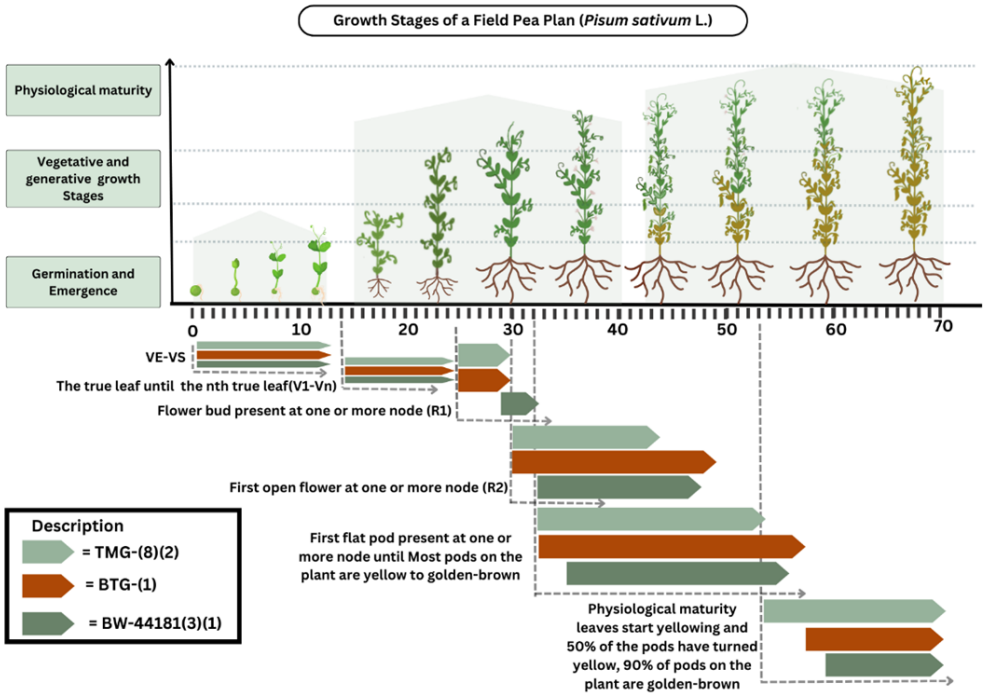


Figure 1 - The progression of vegetative organs and yields throughout the developmental and growth stages of the three pea genotypes.

in leaf area and number of leaves among the three genotypes. In previous studies, there were variations in leaf characteristics among different genotypes (COSMULESCU et al., 2020). The leaf weight ratio (LWR) (Figure 2B) during the vegetative phase when all plant organs are experiencing growth. This indicated that an increase in leaf weight ratio signifies a higher allocation of dry matter to leaves compared to the entire plant. In the early stages, plants focus on leaf organ formation and allocate all photosynthetic products to the leaves rather than the entire plant dry weight. Additionally, the efficiency of plant resource utilization, including water, can be determined by the genotype (GE et al., 2016).

Specific leaf area (SLA) values of the genotypes showed an increasing pattern in the growth phase, followed by a decrease when entering the generative phase (Figure 2C). Genetic, environmental, and plant age factors contribute to the SLA value, which is a key parameter in plastic morphology (KARAVIN, 2013; SAID et al., 2022). Plants exposed to higher light levels produced leaves with higher SLA values, indicating adaptation to light requirements. The increased relative growth rate (RGR) (Figure 2D) signifies a higher rate of standard growth across different plant components, allowing for comparative analysis of plant performance and serving as an indicator of plant viability (POMMERENING & MUSZTA, 2015). Net assimilation rate (NAR) (Figure 2E) quantifies the plant's efficiency in converting light energy into biomass within the assimilation area. While RGR is strongly correlated with increased plant height, genotypic differences in NAR and LAR responses explain variations in total dry mass accumulation (JI et al., 2021). The relationship between phenological variability and pea plant growth provides valuable insights for optimizing agronomic practices during critical phenological phases, such as flowering and harvesting.

Yield variability

The results showed that the field conditions (block effects) did not significantly ($\alpha < 0.05$) influence any of the measured traits (Table 3). However, significant differences were observed among the genotypes for two traits: seed number per plant (NSP) and seed number per pod (NSPP) at $\alpha < 0.05$. Further analysis using the least significant difference (LSD) test revealed that the genotype BW-44181(3)(1) significantly outperformed the other two genotypes, BTG-1 and TMG-8-2, in both seed

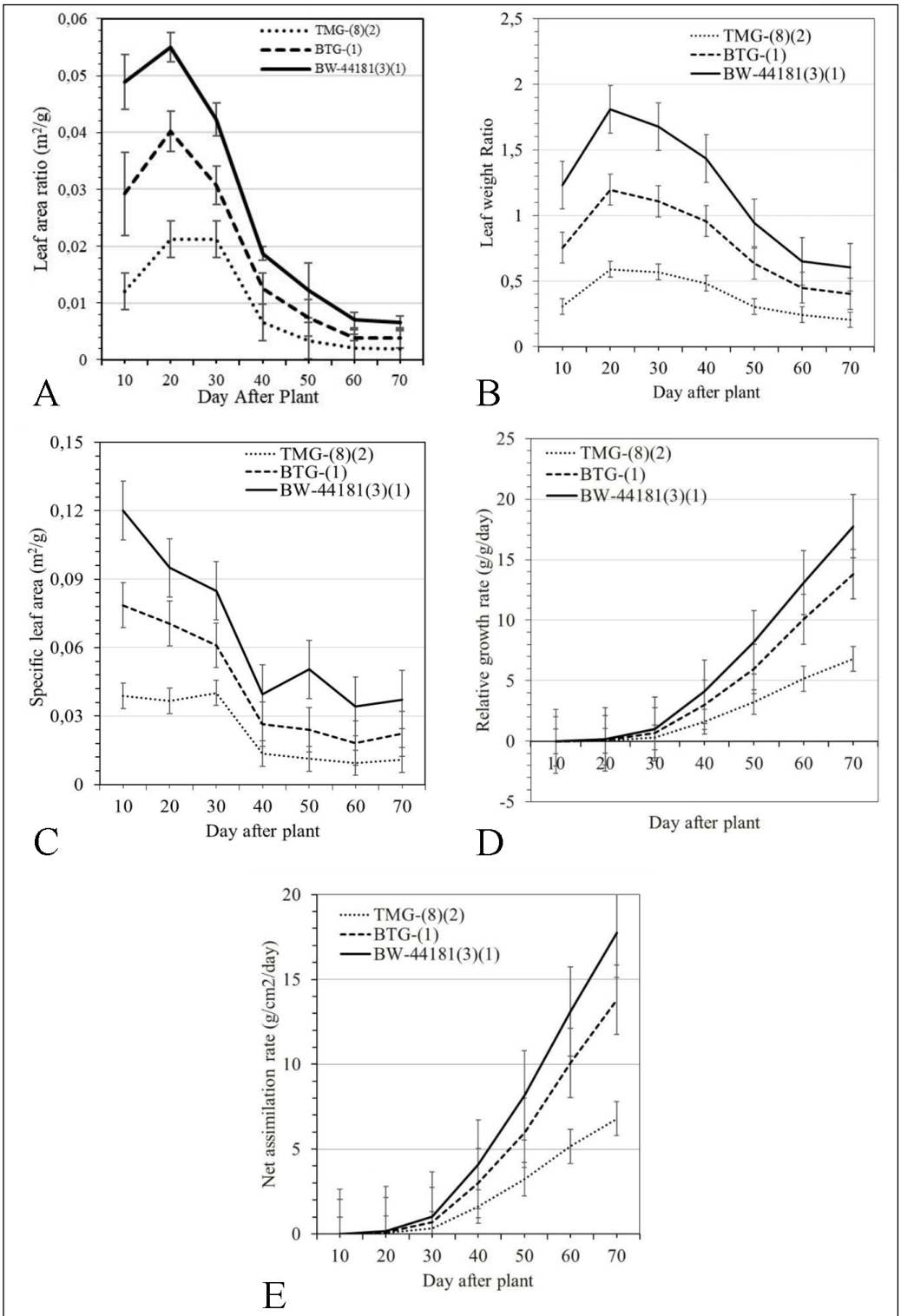


Figure 2 - Plant growth analysis of three pea genotypes — TMG-(8)(2), BTG-(1), and BW-44181(3)(1) — grown under mid-altitude tropical conditions. The panels show changes over time in five growth parameters: (A) Leaf Area Ratio (LAR); (B) Leaf Weight Ratio (LWR); (C) Specific Leaf Area (SLA); (D) Relative Growth Rate (RGR); and (E) Net Assimilation Rate (NAR), measured from 10 to 70 days after planting. Each point represents the mean value, and vertical bars indicate the standard error of the mean (± SE).

Table 3 - Analysis of variance of pea yield characteristics.

Source	df	----------Mean Square----------							
		NF (flowers number per plant)	NPP (pod number per plant)	NSP (seed number per plant)	100W (100 seeds weight)	PPW (pod weight per plant)	NSPP (seed number per pod)	SWP (seed weight per pod)	SWPP (seed weight per plant)
Block	2	7.132ns	14.57ns	212.95ns	3.21ns	0.009ns	0.004ns	0.002ns	7.04ns
Treatment	2	11.24ns	15.86ns	819.53*	8.41ns	0.01ns	2.17*	0.003ns	10.48ns
Error	4	4.72	7.57	53.58	1.58	0.005	0.13	0.002	2.61

Description: *significant F5%.

number traits. TMG-8-2 exhibited the lowest values for NSP and NSPP. While fertilization can influence seed numbers, selecting superior genotypes like BW-44181(3)(1) is a promising strategy to increase pea yield. The results of this further testing for the number of seeds per plant and the number of seeds per pod are presented in table 4. To maximize pea yield in tropics, a multifaceted approach is necessary. While fertilization can contribute to increasing the number of seeds per plant, the genetic potential of the cultivar plays a crucial role. The number of seeds per plant and number seed per pod are highly heritable trait, exhibiting significant variation among pea accessions (ZELEKE et al., 2024). By identifying and utilizing superior genotypes with high seed-setting potential, we can significantly improve overall yield (AYUPOV et al., 2019; OLLE et al., 2020; SAVAGE & BASSEL, 2016). Several studies have demonstrated significant variation in plant characteristics and yield among different pea genotypes (JAGADEESH et al., 2023; LUITEL et al., 2021; PATHAK et al., 2019).

CONCLUSION

This study revealed significant phenological diversity among the TMG-8-2, BW-44181-3-1, and BTG-1 pea genotypes, both in terms of phenorhythm and organ development rate. While TMG-8-2 exhibited the fastest phenorhythm, it displayed the slowest organ change rate. Yield diversity was primarily observed in the number of seeds per plant and number of seeds per pod. Several parameters, including plant height, leaf number, internode number, root nodule number, time to nine leaves, 50% flowering, fresh harvest, and senescence, significantly influenced plant growth and development. The three pea genotypes exhibited distinct growth patterns. BW-44181-3-1 demonstrated a higher growth rate compared to BTG-1 and TMG-8-2. As the plants progressed in times, their LAR, LWR, and SLA decreased, while SLW, NAR, and RGR increased. Genotypic differences were evident in growth and developmental stages, particularly during the generative and senescence phases.

Table 4 - Number of seed per plant and number of seed per pod three genotypes.

Genotypes	----------Number seed per plant----------	----------Number seed per pod----------
BW-44181-(3)-(1)	59.2a	5.4a
TMG-8-2	26.0b	3.9b
BTG-1	31.8b	3.5b

Means followed by the same lower case letter/s do not differ significantly at LSD 5%.

DATA AVAILABILITY STATEMENT

The raw data supporting the findings of this study are available from the corresponding author.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflicts of interest.

AUTHORS' CONTRIBUTIONS

All authors made substantial and equal contributions to the conception, design, and writing of the manuscript and approved the final version for publication.

DECLARATION OF USE OF ARTIFICIAL INTELLIGENCE

This study did not use artificial intelligence.

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