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Performance Evaluation of Potato (Solanum tuberosum L.) Varieties in the Hazara Region of Pakistan

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ABSTRACT

Potato (*Solanum tuberosum* L.) production in Pakistan is often limited by the use of poorly performing varieties and the prevalence of major diseases. In this study, fourteen genotypes were tested under the agro-ecological conditions of Hazara during the 2025 growing season using a randomized complete block design with three replications. The results showed statistically significant differences ($P \leq 0.01$) among genotypes for all recorded traits, reflecting considerable genetic variability. Among the yield components, tuber number was most strongly associated with yield ($r = 0.814$, $P < 0.01$), indicating its central role in productivity. In contrast, both early blight and common scab were negatively related to yield, suggesting that disease pressure substantially reduces performance. The genotype Gravity outperformed all others, producing the highest yield (16.97 kg plot^{-1}; approximately 30.2 t ha^{-1}), followed by ML-12-0801 and Kyra. The large variation observed for tuber number, coupled with minimal experimental error, points to strong genetic control of this trait. Overall, yield differences among genotypes were largely explained by their capacity to produce more tubers and maintain lower disease levels. While the findings are useful for identifying promising material under Hazara conditions, further evaluation across multiple locations and seasons is necessary before broader recommendations can be made.

1. Introduction

Potato (*Solanum tuberosum* L.) is one of the most important food crops globally, ranking third after rice and wheat in terms of human consumption and caloric contribution. Its importance has increased due to high productivity, short growth cycle, and adaptability across diverse agro-ecological environments. Global production reached approximately 383 million tonnes in 2023, cultivated over 16.8–18.1 million hectares with average yields ranging from 20 to 23 ha^{-1}, reflecting continuous gains through genetic improvement and agronomic advancements (Ojha et al., 2025). Asia dominates global production, with China and India contributing more than half of total output; however, yield variability across regions highlights the influence of management practices and environmental conditions on productivity (Zhao et al., 2024). In addition to its economic importance in supporting fresh and processing industries, potato plays a vital nutritional role by providing carbohydrates and essential micronutrients, contributing to both food and nutritional security (De Luca & Müller, 2025; Górska-Warsewicz et al., 2021).

In Pakistan, potato has emerged as a key crop with production reaching approximately 9.9 million tonnes in 2024–25, driven by expansion in cultivated area and increased adoption of improved varieties. Despite this progress, productivity remains constrained by limited access to quality seed, susceptibility to diseases such as early blight and common scab, and suboptimal agronomic practices, leading to reduced yield and tuber quality (Irfan et al., 2024). Although potato performs best under cool temperate conditions with optimal tuber bulking temperatures of 15–20°C, local production systems often fail to exploit this potential fully. These constraints emphasize the need for identifying high-performing and disease-tolerant genotypes suited to specific production environments.

The Hazara region of Pakistan, characterized by mid-altitude temperate conditions, represents a distinct agro-ecological zone where limited information is available on the performance of exotic potato germplasm. While previous studies have highlighted the importance of genotype environment interactions in determining yield performance, the lack of location-specific evaluations restricts effective varietal selection under farmer-relevant conditions. Therefore, systematic evaluation of introduced genotypes under local environments is essential to identify superior lines with improved yield potential and disease resistance.

In this context, the present study was conducted to: (i) evaluate the performance of fourteen potato genotypes under Hazara conditions; (ii) assess their response to major diseases, particularly early blight and common scab; and (iii) determine relationships among key agronomic traits and yield. The findings are expected to provide a scientific basis for genotype selection and contribute to breeding and seed system improvement efforts aimed at enhancing potato productivity in region-specific production systems.

2. Methodology (Materials & Methods)

Fourteen potato (*Solanum tuberosum* L.) genotypes, including thirteen exotic varieties and one locally adapted check (SM Kaghan), were evaluated for their adaptability at Hazara Agriculture Research station, Abbottabad (Latitude: 34.20° N & Longitude: 73.24° E) under Hazara agro-climatic conditions. The experimental site at Hazara Agriculture Research Station, Abbottabad is characterized by sandy loam soil with a pH of 6.5–6.8 under a temperate climate featuring mild summers, cool winters, and moderate seasonal rainfall.The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications to minimize environmental variability and enhance experimental precision (Gomez & Gomez, 1984). Each experimental plot consisted of five rows, maintaining a row-to-row spacing of 75 cm and plant-to-plant spacing of 25 cm. A total of 20 tubers were planted per row, resulting in 100 tubers per plot. Uniform, healthy, and disease-free seed tubers were used to ensure consistent crop establishment across all treatments.

The land was prepared using conventional tillage practices to achieve a fine seedbed suitable for potato cultivation. Basal fertilization was applied using urea, diammonium phosphate (DAP), and sulphate of potash (SOP) according to recommended regional agronomic practices. Nitrogen was applied in split doses to improve nutrient use efficiency, with top dressing carried out during the early vegetative growth stage. Standard agronomic practices, including irrigation, hoeing, earthing-up, and plant protection measures, were uniformly applied across all treatments to avoid management bias. These practices ensured that observed differences among genotypes were primarily due to genetic variability rather than environmental or management factors.

Data were recorded on phenological, growth, yield, and disease-related traits using standard and widely accepted methodologies. Days to 50% germination were recorded as the number of days from planting until half of the plants in each plot had emerged. Plant height was measured in centimeters from the soil surface to the apical tip of the plant at maturity, while the number of stems per plant was determined by counting the main stems per plant.

Yield-related parameters included the number of tubers per plant and the total tuber weight per plant, which were recorded at harvest to assess productivity. Disease assessment was conducted under natural field conditions, where early blight severity was evaluated using standard visual scoring scales based on symptom progression as described by Rotem (1994). Similarly, common scab incidence was calculated as the percentage of infected tubers per plot following established protocols (Andrade et al., 2019). These measurements provided a comprehensive evaluation of genotype performance in terms of growth, yield potential, and disease resistance.

Statistical Analysis

The collected data were subjected to analysis of variance (ANOVA) using the appropriate statistical model for a randomized complete block design (RCBD) to determine the significance of differences among genotypes at the 5% probability level ($\alpha = 0.05$) (Gomez & Gomez, 1984). Mean comparisons were performed using Fisher's Least Significant Difference (LSD) test at the 5% significance level to identify statistically distinct genotypes. The coefficient of variation (CV%) was calculated to assess the precision and reliability of the experiment. In addition, Pearson's correlation analysis was conducted to evaluate relationships among agronomic traits, yield components, and disease parameters, thereby identifying key factors influencing yield performance (Das et al., 2021). All statistical analyses were performed using R (version 4.1.2).

3. Results and Discussion

The analysis of variance (Table 1) revealed highly significant ($P \leq 0.001$) differences among genotypes for all evaluated agronomic and disease-related traits, indicating the presence of substantial genetic variability under the Hazara conditions. This high level of statistical significance across traits confirms that the evaluated genotypes responded differently under a uniform experimental environment, thereby providing a reliable basis for selection. The magnitude of F-values varied considerably among traits, ranging from 3.83 for plant height to an exceptionally high 2680.85 for tuber number. The extremely high F-value observed for tuber number is attributable to the combination of large genotypic mean differences and very low experimental error variance (MS = 1.13), which resulted in a substantial ratio of treatment variance to residual variance.

Table 1. Analysis of variance for the traits studied

Trait	Source of Variation	df	Mean Square (MS)	F-value	P-value	CV (%)
DTE	Genotypes	13	19.30	10.32	<0.001	3.82
	Replications	2	4.02	2.15	0.136	
	Error	26	1.87	—	—	
Plant Height (PH)	Genotypes	13	199.60	3.83	0.002	10.60
	Replications	2	79.20	1.52	0.237	
	Error	26	52.08	—	—	
Stem Number (NOS)	Genotypes	13	3.98	4.64	0.001	32.44
	Replications	2	1.50	1.75	0.194	
	Error	26	0.86	—	—	
Tuber Number (NT)	Genotypes	13	3017.67	2680.85	<0.001	1.70
	Replications	2	4.67	4.15	0.027	
	Error	26	1.13	—	—	
Tuber Weight (WOT)	Genotypes	13	59.40	14.71	<0.001	23.43
	Replications	2	3.49	0.86	0.433	
	Error	26	4.04	—	—	
Early Blight (EB)	Genotypes	13	1957.19	20.92	<0.001	17.15
	Replications	2	126.02	1.35	0.278	
	Error	26	93.56	—	—	
Common Scab (SCAB)	Genotypes	13	453.20	18.02	<0.001	18.41
	Replications	2	41.02	1.63	0.215	
	Error	26	25.15	—	—	

This indicates that tuber number is under strong genetic control and is less influenced by environmental fluctuations under the present experimental conditions. In contrast, comparatively lower F-values for traits such as plant height suggest moderate genetic influence and a relatively higher contribution of environmental factors to phenotypic expression. These findings collectively demonstrate that the observed variation among genotypes was primarily due to inherent genetic differences rather than experimental noise, thereby confirming the reliability and robustness of the experimental design and statistical analysis (Gomez & Gomez, 1984).

The coefficient of variation (CV%) ranged from 1.70% to 32.44%, reflecting an overall acceptable level of experimental precision across all measured traits. The very low CV values recorded for tuber number (1.70%) and days to emergence (3.82%) indicate minimal experimental error and highly uniform field conditions, which enhanced the accuracy of genotype comparisons. Such low variability, although relatively uncommon for count traits, can occur in well-managed field experiments where environmental heterogeneity is effectively minimized and planting material is uniform. The consistency in tuber number across replications suggests stable expression of this trait under the tested conditions. On the other hand, the relatively higher CV observed for stem number (32.44%) reflects greater biological variability, which may be attributed to differences in tuber physiological age, sprouting behavior, and apical dominance among genotypes (MacKerron, 2001). This variability indicates that stem number is more sensitive to both intrinsic physiological factors and micro-environmental variations within the field. Similar patterns of variation have been reported in potato studies, where vegetative traits often exhibit higher variability compared to yield components due to their dynamic response to environmental conditions (Haverkort & Struik, 2015; Docimo et al., 2023). Therefore, the combination of low CV for key yield traits and significant F-values across all parameters confirms that the experiment was conducted with high precision and that the results obtained are statistically reliable and biologically meaningful.

Trait-wise Performance
Days to Emergence (DTE)

Days to emergence exhibited significant variation among genotypes ($F = 10.32$; $P < 0.001$), indicating the presence of considerable genetic variability for early growth behavior. Emergence is largely influenced by physiological attributes of seed tubers, including dormancy status, carbohydrate reserves, and physiological age. Genotypes that emerged earlier generally showed a tendency toward higher tuber number and yield, which can be attributed to earlier canopy establishment and improved light interception, ultimately enhancing biomass production and assimilate availability (Singh & Sharma, 2018). Conversely, delayed emergence observed in some genotypes may be associated with suboptimal soil temperature and moisture conditions affecting sprout initiation and growth (Haverkort & Struik, 2015). The relatively low coefficient of variation for this trait further indicates that environmental variability was minimal, allowing reliable discrimination among genotypes.

Plant Height (PH)

Plant height differed significantly among genotypes ($F = 3.83$; $P = 0.002$), reflecting moderate genetic control over vegetative growth. Despite its importance as a growth parameter, plant height exhibited a weak to negative association with tuber yield, suggesting that excessive vegetative development may not necessarily translate into higher productivity. This phenomenon indicates inefficient assimilate partitioning, where photosynthates are preferentially allocated to shoot growth rather than tuber development. Optimal plant architecture, characterized by balanced canopy development rather than maximum height, is critical for efficient dry matter distribution (Das et al., 2021). Additionally, environmental factors such as nitrogen availability and temperature fluctuations are known to influence stem elongation and canopy structure, thereby affecting yield indirectly.

Stem Number per Plant (NOS)

Stem number showed significant variation ($F = 4.64$; $P = 0.001$), highlighting its importance as a yield-contributing trait. An increase in stem number enhances stolon formation, thereby increasing the number of potential tuber initiation sites. The positive association of stem number with both tuber number and tuber weight confirms its role as a critical determinant of yield formation. However, excessive stem density may lead to intra-plant competition for nutrients and assimilates, potentially limiting tuber growth. Stem number is strongly influenced by tuber physiological age and apical dominance, which regulate sprout development and subsequent stem emergence (MacKerron, 2001). Interestingly, a negative association between stem number and disease incidence was observed, suggesting that vigorous plants with well-developed canopies may suppress pathogen establishment through improved physiological resilience and microclimate modification.

Tuber Number (NT)

Tuber number exhibited highly significant variation with an exceptionally large F-value ($F = 2680.85$; $P < 0.001$), indicating strong genetic control of this trait. This high F-value is attributed to very low experimental error variance combined with substantial differences among genotype means, reflecting high experimental precision and uniform field conditions. Tuber number showed a strong positive association with tuber yield, confirming that yield under the present conditions was primarily driven by sink strength. Tuber initiation is regulated by environmental factors such as temperature, photoperiod, and assimilate availability, with optimal temperatures (15–20°C) favoring stolon differentiation and tuber formation (Haverkort & Struik, 2015).

Furthermore, tuber number exhibited strong negative associations with early blight and common scab, indicating that disease pressure significantly reduces tuber formation by impairing photosynthesis and limiting assimilate supply (Van der Waals et al., 2001). These findings emphasize that both genetic potential and disease resistance are critical for maximizing tuber production.

Tuber Weight (WOT)

Tuber weight varied significantly among genotypes ($F = 14.71$; $P < 0.001$), demonstrating its sensitivity to both genetic and environmental influences. The trait showed a strong dependence on tuber number, indicating that increased sink size contributes to overall yield. However, tuber weight was negatively associated with disease incidence, highlighting the detrimental effects of foliar and tuber diseases on assimilate translocation and starch accumulation. Environmental factors, particularly high temperatures during tuber bulking, can further reduce tuber size by limiting carbohydrate deposition (Haverkort & Struik, 2015). Thus, both physiological efficiency and disease management play key roles in determining final tuber weight.

Early Blight (EB)

Early blight showed significant variation among genotypes (F = 20.92; P < 0.001), indicating genetic differences in disease resistance. The disease reduces effective leaf area, thereby limiting photosynthetic capacity and reducing yield potential. Its development is strongly influenced by environmental conditions such as temperature, humidity, and leaf wetness duration (Van der Waals et al., 2001). The observed variability among genotypes suggests the presence of exploitable resistance, which can be utilized in breeding programs aimed at improving disease tolerance.

Common Scab (SCAB)

Common scab also exhibited significant variation (F = 18.02; P < 0.001), reflecting differential susceptibility among genotypes. Soil moisture and pH are key factors influencing disease severity, with drier conditions favoring infection (Lapaz et al., 2017). The negative association between scab incidence and yield confirms its economic importance, as it affects both yield and tuber quality. The identification of genotypes with lower scab incidence is therefore essential for sustainable production systems.

Overall Yield Performance

Substantial variability in yield performance was observed among genotypes (Figure 2), indicating strong genetic diversity under the tested conditions. The genotype Gravity produced the highest yield (16.97 kg plot^{-1}; ≈30.2 t ha^{-1}), followed by ML-12-0801 and Kyra, demonstrating superior performance under Hazara conditions. Moderate yields were recorded for Brianna and Rosline, whereas Lugano, Napoleon, and Palace exhibited poor performance, characterized by low tuber number and high disease incidence.

The wide yield range (2.29–16.97 kg plot^{-1}) clearly indicates that yield superiority was primarily associated with higher tuber number and reduced disease pressure. This is consistent with the correlation analysis, where tuber number showed a strong positive relationship with yield, while disease traits exhibited negative associations.

Integrated Interpretation of Genotypic Performance

The mean performance data (Table 2) revealed substantial variability among genotypes for all agronomic and disease-related traits, confirming the presence of significant genetic diversity. Gravity emerged as the best-performing genotype, combining high tuber number (131.9), maximum yield, and lowest disease incidence (early blight: 13.0%; scab: 6.3%). This indicates that superior productivity in potato is achieved through an optimal balance between sink capacity (tuber number) and disease resistance.

Similarly, ML-12-0801 and Kyra demonstrated high yield potential, supported by relatively high tuber numbers and moderate disease levels. In contrast, poorly performing genotypes such as Lugano exhibited low tuber number, reduced yield, and high disease susceptibility, indicating poor adaptation to the tested environment.

The observed variation among genotypes is primarily attributed to differences in genetic potential under uniform environmental conditions. The strong positive association between tuber number and yield confirms that tuber number is the principal determinant of productivity. Additionally, the inverse relationship between yield and disease severity highlights the importance of selecting disease-resistant genotypes for sustainable potato production systems.

These findings are consistent with previous reports that emphasize the dominant role of tuber number in determining yield and the significant impact of diseases such as early blight and common scab on reducing productivity (Bradshaw & Ramsay, 2020; Tsedaley, 2020).

Correlation Analysis

The correlation heatmap (Figure 1) provides a comprehensive overview of the relationships among agronomic and disease-related traits, offering valuable insights into the factors governing yield determination in potato genotypes. A strong positive correlation was observed between number of tubers (NT) and tuber weight (WOT), clearly indicating that yield under the present experimental conditions is primarily driven by increased tuber formation. This strong association highlights the importance of sink strength, where a greater number of tubers enhances the capacity for assimilating accumulation, ultimately leading to higher yield. Similarly, number of stems per plant (NOS) exhibited a positive association with both NT and WOT, suggesting that increased stem density promotes stolon formation and provides more sites for tuber initiation. This relationship underscores the indirect yet significant role of stem number in influencing yield through its effect on tuber production. Collectively, these findings reinforce the concept that yield improvement in potato is largely dependent on sink capacity, with tuber number serving as a key selection criterion in breeding programs aimed at enhancing productivity.

Table 2. Mean Performance of Potato Genotypes

Genotype	DTE (days)	PH (cm)	NOS	NT	Yield (kg plot^{-1})	Yield (t ha^{-1})	EB (%)	SCAB (%)
Gravity	34.67	67.72	5.33	131.90	16.97	30.20	13.00	6.33
ML-12-0801	34.67	69.05	4.67	102.50	14.64	26.05	19.00	9.00
TB-17-108	34.67	64.88	3.00	92.60	7.02	12.48	30.00	15.00
Kyra	34.67	57.29	4.00	78.20	14.55	25.87	32.33	15.67
Brianna	35.00	51.61	2.67	79.30	11.43	20.31	35.33	17.33
Rosline	44.00	59.09	2.67	55.60	9.15	16.27	61.33	30.33
Armedi	35.00	70.68	1.67	49.40	9.00	16.00	73.00	29.33
Lugano	37.67	76.39	2.00	17.30	2.29	4.07	93.67	44.00
Napoleon	36.33	72.45	2.33	28.70	4.50	8.01	85.00	40.67
Palace	36.67	68.92	2.00	32.80	5.10	9.07	82.33	38.00
Hermes	35.33	63.10	2.67	45.20	8.20	14.58	70.67	28.67
Desiree	36.00	66.50	3.00	60.10	10.50	18.66	55.33	25.00
Santé	35.67	62.80	3.33	70.40	12.30	21.87	40.00	20.67
Innovator	35.33	65.20	3.00	65.70	11.20	19.91	48.67	22.33

*(**LSD (0.05):** DTE = 3.43; PH = 12.11; NOS = 1.56; NT = 1.78; Yield = 3.37; EB = 16.23; SCAB = 8.42.)*

In contrast, early blight (EB) and common scab (SCAB) exhibited strong negative correlations with NT and WOT, demonstrating their substantial detrimental impact on yield formation. These negative associations indicate that disease pressure reduces both tuber initiation and tuber bulking by impairing photosynthetic efficiency and limiting assimilate translocation. The strong positive correlation observed between EB and SCAB further suggests that genotypes susceptible to one disease are likely to exhibit susceptibility to the other, possibly due to shared physiological weaknesses, compromised plant vigor, or underlying genetic factors affecting disease resistance. Additionally, days to emergence (DTE) showed weak negative correlations with yield-related traits, indicating that earlier-emerging genotypes tend to have a slight advantage in productivity. This advantage can be attributed to earlier canopy establishment, which enhances light interception, prolongs the photosynthetically active period, and improves overall biomass accumulation. Although plant height showed comparatively weaker associations with yield, its indirect effects through canopy architecture and resource allocation cannot be entirely disregarded.

Overall, the correlation analysis clearly demonstrates that yield variation among genotypes is primarily governed by tuber number and is significantly influenced by disease incidence. The combined effects of positive associations among yield components and negative associations with disease traits highlight the importance of selecting genotypes with both high tuber-producing ability and enhanced disease resistance. These findings are in close agreement with previous studies, which have consistently reported that tuber number is the most critical determinant of yield in potato, while disease severity particularly early blight and common scab plays a major role in reducing productivity by limiting photosynthesis and disrupting assimilate partitioning (Bradshaw & Ramsay, 2020; Tsedaley, 2020; Haverkort et al., 2023). Therefore, an integrated selection approach that simultaneously targets yield components and disease resistance is essential for achieving sustainable genetic improvement in potato.

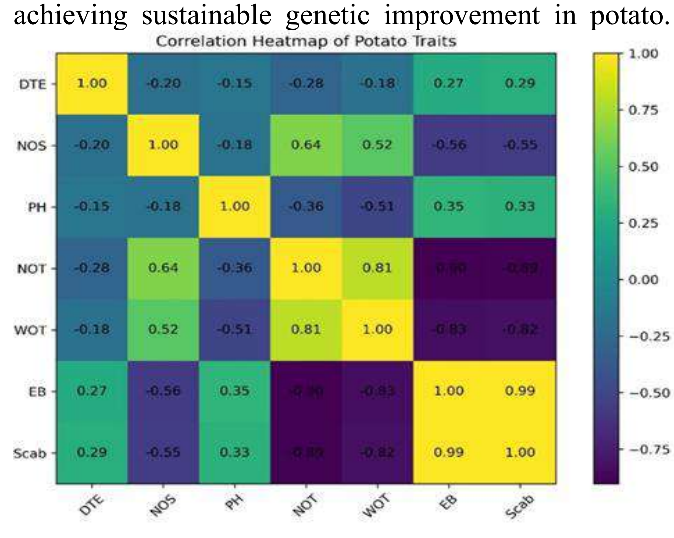

Figure 1: Correlation heatmap illustrating relationships among agronomic traits (DTE, PH, NOS, NT, WOT) and disease parameters (EB, SCAB) in potato genotypes

4. Conclusion

The present study revealed significant genetic variability among potato genotypes under Hazara conditions, enabling reliable identification of superior performers within a single-location evaluation framework. Yield variation was primarily governed by tuber number, confirming sink strength as the key determinant of productivity. In contrast, early blight and common scab exhibited negative associations with yield, highlighting the limiting effect of disease pressure on both tuber initiation and bulking. The low experimental error and strong genotype effects observed for key traits further indicate high precision and reliability of the results under uniform field conditions.

Among the evaluated genotypes, Gravity emerged as the top performer, combining high tuber number, superior yield, and lower disease incidence, followed by ML-12-0801 and Kyra, which also showed promising performance. These findings emphasize that simultaneous selection for enhanced tuber production and disease resistance is essential for improving potato productivity. However, since the study was conducted under a single environment, further validation through multi-location and multi-year trials is necessary before wider recommendation. Overall, the results provide a strong basis for varietal selection and breeding strategies aimed at improving yield stability and production efficiency in potato.

5. References

Andrade, M. H. M. L., Niederheitmann, M., de Paula Ribeiro, S. R. R., Oliveira, L. C., Pozza, E. A., & Pinto, C. A. B. P. (2019). Development and validation of a standard area diagram to assess common scab in potato tubers. *European Journal of Plant Pathology, 154*(3), 739–750. https://doi.org/10.1007/s10658-019-01728-5

Bradshaw, J. E., & Ramsay, G. (2020). Potato genetics and breeding. *Plant Breeding Reviews, 44*, 1–52.

Das, B., Sarker, U., & Azam, M. G. (2021). Correlation and path coefficient analysis in potato (*Solanum tuberosum* L.). *Heliyon, 7*(5), e07095. https://doi.org/10.1016/j.heliyon.2021.e07095

De Luca, A., & Müller, C. (2025). Global potato value chains and economic significance in developing and developed economies. *Agricultural Systems, 215*, 103879. https://doi.org/10.1016/j.agsy.2024.103879

Docimo, T., Scotti, N., Tamburino, R., Villano, C., Carputo, D., & D'Amelia, V. (2023). Potato nutraceuticals: Genomics and biotechnology for biofortification. In *Compendium of Crop Genome Designing for Nutraceuticals* (pp. 1–34). Springer.

Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research* (2nd ed.). John Wiley & Sons.

Górska-Warsewicz, H., Rejman, K., Kaczorowska, J., & Laskowski, W. (2021). Vegetables, potatoes and their products as sources of energy and nutrients in the average diet. *International Journal of Environmental Research and Public Health, 18*(6), 3217. https://doi.org/10.3390/ijerph18063217

Haverkort, A. J., & Struik, P. C. (2015). Yield levels of potato crops: Recent achievements and future prospects. *Field Crops Research, 182*, 76–85. https://doi.org/10.1016/j.fcr.2015.06.002

Haverkort, A. J., Struik, P. C., & van de Waart, M. (2023). Potato yield gaps and climate change. *Field Crops Research, 295*, 108865. https://doi.org/10.1016/j.fcr.2023.108865

Irfan, M., Fatima, S., Ali, A., & Haider, Z. (2024). Improving potato productivity in Pakistan through integrated disease management and improved seed systems. *Pakistan Journal of Agricultural Sciences, 61*(2), 245–256.

Lapaz, M., Huguet-Tapia, J. C., Siri, M. I., Verdier, E., Loria, R., & Pianzzola, M. J. (2017). Genotypic and phenotypic characterization of *Streptomyces* spp. causing potato common scab. *Plant Disease, 101*(8), 1362–1372. https://doi.org/10.1094/PDIS-09-16-1272-RE

MacKerron, D. K. L. (2001). Stem development and tuber formation in potato. *Annals of Applied Biology, 138*(2), 159–169.

Ojha, R., Karki, S., & Ali, M. (2025). Global trends in potato production, productivity, and sustainability. *Field Crops Research, 320*, 109678. https://doi.org/10.1016/j.fcr.2025.109678

Rotem, J. (1994). *The genus Alternaria: Biology, epidemiology, and pathogenicity*. APS Press.

Singh, B., & Sharma, S. (2018). Potato seed production systems Then and now. *Potato Journal, 45*(1), 45–60.

Tsedaley, B. (2020). Review on early blight (*Alternaria solani*) disease of potato. *Journal of Plant Pathology, 102*(1), 15–25. https://doi.org/10.1007/s42161-019-00366-8

Van der Waals, J. E., Korsten, L., & Aveling, T. A. S. (2001). A review of early blight of potato. *African Plant Protection, 7*(2), 91–102.

Zhao, L., Wang, Y., Chen, X., Liu, Z., & Zhang, H. (2024). Global yield trends and regional disparities in potato production systems. Agronomy Journal, 116(3), 1452–1465. https://doi.org/10.1002/agj2.21456.