

Comprehensive Evaluation and Selection on Integrated Resistance to Major Diseases and Desirable Agronomic Traits of 38 Sugar Beet (*Beta vulgaris* L.) Germplasm in Northeast China

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Abstract

Sugar beet (*Beta vulgaris* L.) is the cornerstone of global sugar production, but its yield is still seriously threatened bacterial wilt (*Rhizoctonia solani*), leaf spot (*Cercospora leaf spot*, CLS), root rot complex (*Fusarium spp.*) and other diseases. Traditional breeding struggles with yield-disease trade-offs and fragmented trait evaluation. This study establishes a multivariate framework integrating multi-disease resistance and agronomic traits for 38 germplasm accessions in Northeast China. Field trials quantified disease indices (DISB, BSDI, FRRCDI), yield parameters (root yield, sugar production), quality traits (sucrose, K⁺, Na⁺, α-N), and early vigor. Principal component analysis derived two core dimensions: Comprehensive Disease Resistance Value (CDRV, 48.7% variance) dominated by CLS resistance (loading = 0.82), and Comprehensive Agronomic Value (CAV, 31.2% variance) linked to sugar yield (0.89) and sucrose content (0.79). The selection index $D = \sqrt{(CDRV^2 + CAV^2)}$ ranked 780016A/1 ($D = 1.71$) and 8432/1 ($D = 1.70$) as elite performers, combining high root yield (54,233 kg·ha⁻¹), optimal sucrose (15.93–17.24%), and moderate multi-disease resistance (e.g., BSDI = 16.5–18.1). A variety of analyses were used to classify 38 germplasm resources into four functional groups, confirming synergistic trait combinations (Group I: elite accessions) and saline-adapted genotypes (Group IV: F85621 with 17.45% sucrose, 1.57 mmol/100g Na⁺). Key correlations included CLS severity-sugar yield anticorrelation ($r = -0.65$, $p < 0.001$) and Na⁺-sucrose trade-off ($r = -0.404$, $p < 0.05$). This framework overcomes single-trait limitations, providing validated germplasm and a data-driven strategy for breeding climate-resilient, high-yielding varieties.

Introduction

Crop germplasm resources constitute the genetic material inherited from parental lines to progeny, typically harbored within specific varieties[1, 2]. Maintaining germplasm diversity is essential for improving multiple traits and enhancing genetic gain. However, intensive modern agricultural practices have led to the widespread replacement of local crop varieties with a limited number of improved cultivars[3], resulting in diminished genetic diversity across most crops. This narrowing genetic base poses significant challenges for breeding new high-yielding, high-quality crop varieties[4].

Sugar beet (*B. vulgaris* L.) is a cornerstone of global sugar production, supplying 20–30% of the world's sucrose and serving as a vital rotation crop for sustainable agriculture[5, 6]. Its productivity faces persistent threats from soil- and foliar-borne pathogens, including damping-off (*Rhizoctonia solani*), CLS (*Cercospora beticola*), and root rot complex (primarily *Fusarium spp.* and *Aphanomyces cochlioides*) causing economically devastating losses[7, 8, 9]. In plants, damping-off significantly reduces seedling stands in nursery stages, severely impacting growth and yield not only in sugar beet[10] but also in rice[11], pepper[12], cotton[13], cucumber[14], and watermelon[15]. *Cercospora leaf spot* (CLS) progression involves initial necrotic spots on young leaves, leading to withering, defoliation, and nutrient redirection that depletes root sugar reserves, causing substantial losses in root weight and sugar content[17, 18]. *Fusarium* species are particularly dangerous root pathogens, reducing yield, sugar content, and juice purity[19], and causing diseases like *Fusarium culmorum*[20], root rot[21, 22], stem

rot[23], and storage root rot[24]. Quantitatively, sugar beet suffers severe productivity losses from key pathogens: damping-off (*Rhizoctonia solani*) reduces seedling stands by 30–50%[7], *Cercospora leaf spot* (CLS) causes 42% yield decline through defoliation and photosynthetic impairment[27], and root rot complex (*Fusarium spp.*) diminishes root biomass and sucrose extraction efficiency by up to 70%[9]. While chemical control via soil fumigants and fungicides remains prevalent[16, 25], it faces dual constraints: escalating concerns over ecosystem integrity, crop quality, and human health risks, coupled with declining efficacy due to pathogen resistance and climate variability[26]. Critically, non-chemical alternatives for sustainable disease management remain underdeveloped. Consequently, traditional breeding approaches targeting single-disease resistance are increasingly inadequate given climate-driven co-infection surges, necessitating germplasm with integrated multi-pathogen resilience that concurrently maintains yield and processing quality.

Current disease resistance evaluation paradigms exhibit critical limitations. Specifically, most studies prioritize single-disease screening under controlled conditions, largely neglecting field-based polyphasic pathogen pressures[28]. This fragmented approach risks unintended consequences; for example, selecting for *Cercospora* tolerance may inadvertently favor genotypes susceptible to root rot due to physiological resource allocation trade-offs[28]. Moreover, resistance assessments rarely incorporate holistic agronomic performance metrics[29], leading to commercially nonviable outcomes. Genotypes that resist damping-off but exhibit low sucrose yield or elevated detrimental impurities (e.g., α -amino nitrogen compromising sugar crystallizability) exemplify this disconnect. Empirical evidence confirms its prevalence: disease-resistant lines show 15% root yield reduction[30], while tolerant germplasm accumulates harmful sodium (> 4.0 mmol/100g)[31]. Consequently, such omissions perpetuate an adoption failure cycle where "resistant" varieties are abandoned due to latent agronomic deficiencies.

Crucially, synergistic evaluation of multi-disease resistance and end-use quality parameters remains underexplored. Existing indices like Disease Severity Index (DSI) or Area Under Disease Progress Curve (AUDPC) quantify pathogen burden but ignore consequential impacts on sucrose synthesis, storage stability, or processing efficiency[32, 33]. Key quality traits—brei alkalinity (linked to Na^+/K^+ ratio), α -N accumulation, and sucrose extraction yield—are seldom contextualized against disease scores. This gap is particularly acute for root rot, where infection alters root metabolism, elevating impurities that impede factory throughput[34]. Simultaneously, early vigor traits (e.g., cotyledon expansion, seedling biomass) may signal resilience to damping-off or resource mobilization capacity under biotic stress[35], yet their predictive value for late-season performance remains unvalidated in polygenic resistance models.

To bridge these gaps, this study aims to: 1) Establish a comprehensive evaluation system integrating phenotypic data on disease resistance indices (damping-off, *Cercospora* leaf spot, root rot severity), agronomic performance (root yield, sugar yield, sucrose content), process quality traits (K^+ , Na^+ , α -amino-N concentrations), and early-stage vigor (cotyledon area, seedling biomass, growth vigor); and 2) Identify elite germplasm exhibiting synergistic superiority in multi-disease resistance, yield potential, and processing quality using multivariate statistical approaches (PCA, cluster analysis, composite scoring). By correlating seedling vigor with adult disease resilience, we further aim to identify early-stage proxies

for field durability. The validated germplasm will directly accelerate breeding pipelines, delivering regionally adapted, multi-pathogen-resistant varieties with enhanced processing efficiency—thus addressing the urgent need of temperate sugar systems threatened by escalating pathogen co-emergence.

Materials and methods

Experimental materials

A total of 38 sugar beet (*B. vulgaris*) germplasm resources were evaluated in this study, including 17 N(Standard type), 6NZ(Standard high-sugar type), 3 NE(Standard-high yield type), 8 Z(High-sugar type), 2 E(High-yield type) and 2 LL(Low yield, low sugar type) economic types (Table 1). All the materials were developed by the New Variety Breeding Research Team at the Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS). This institute merged with Heilongjiang University in 2003.

Experimental design

This experiment was conducted at the sugar beet cultivation base of Heilongjiang University Hulan Campus (China Academy of Agricultural Sciences Sugar Beet Research Institute) experimental demonstration base (Fig. 1A). The study area is located in the northernmost part of Northeast China, where winters are long and cold, and summers are short and cool. The region has an annual average rainfall of 500–600 millimeters, mainly concentrated in the summer months. It has a continental monsoon climate and an altitude of 1000 meters. In 2023–2024, the total precipitation during the sugar beet growing season in June, July, and August was 311.7 mm, 12.3 mm, and 457.5 mm, respectively (Fig. 1B). The high temperatures in June, July, and August were 24°C, 29°C, and 28°C, respectively (Fig. 1C). The soil in the experimental area is black soil, and soybeans were planted the year before sowing (Supplementary materials table 1s).

Table 1

List of 38 sugar beet varieties and germplasm materials evaluated (N = Standard type, NZ = Standard high-sugar type, NE = Standard-high yield type, Z = High-sugar type, E = High-yield type, LL = Low yield, low sugar type).

Number	Name	Breeding Unit	Economic types
1	780016A/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NE
2	686 – 14/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
3	742+/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
4	7412/82/3–5/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	E
5	780024A/6/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
6	83461/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NE
7	780016B/1–1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
8	8432/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
9	780024B/12/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
10	86131/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
11	92011/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
12	92017/1–8/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
13	92012-2-1/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
14	92008+/1	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	E
15	7909	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
16	H1352	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
17	H133	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N

Number	Name	Breeding Unit	Economic types
18	F85621	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
19	D90M6	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
20	D90M8	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
21	H104	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
22	T4M47	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
23	7411	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
24	T-27	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	LL
25	7917M911	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	LL
26	KH-3	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NZ
27	J8671	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
28	J9451	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
29	7917/120	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
30	H0312	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
31	D90M9	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	NE
32	B8035	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
33	102AB	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
34	8216M15	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
35	8216M152	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z

Number	Name	Breeding Unit	Economic types
36	F86421	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z
37	1902	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	N
38	F8035	The Sugar Beet Research Institute of the Chinese Academy of Agricultural Sciences (CAAS)	Z

Morphological and Agronomic Measurements

Following seed sowing, representative plants from each plot were sampled 13 days post-emergence for seedling trait assessment. One hundred plants per accession were measured for cotyledon area (mm²), seedling biomass per 100 plants (g), and seedling vigor (scored on a standardized scale). At harvest maturity, three intact storage roots per plot were destructively sampled for quality trait analysis. From each root, 100-g tissue subsamples were homogenized to quantify potassium content (K⁺), sodium content (Na⁺), and α-amino nitrogen (α-N) (all expressed in mmol/100g fresh weight). Concurrently, plot-level agronomic traits were determined: total root fresh weight was converted to root yield (kg·ha⁻¹), brei refractometer readings provided brei sugar content (%), and sucrose content (%) was measured by polarimetry. Sugar yield (kg·ha⁻¹) was calculated as[37]:

$$\text{Sugar yield} = \frac{\text{Root yield} \times \text{Sucrose content}}{100}$$

The disease index (DI), Damping-off (Sheath Blight of Disease Index, DISB), Cercospora leaf spot (Brown Spot of Disease Index, BSDI) and Root rot diseases (Fusarium Root Rot Complex Disease Index, FRRCDI) of the test beet germplasm resources were calculated. A variety of methods were used to evaluate the disease resistance of the test materials comprehensively[38].

$$DI = 100 \times \frac{\sum (s_i n_i)}{iN} \quad (1)$$

DI represents the disease index, s_i is the number of disease levels, n_i is the number of beetles in the disease level, i is each level of disease classification, and N represents the total number of beetles surveyed. After calculating the disease index(DI) values of the three diseases according to Eq. (1).

$$\omega_i = \frac{P_i}{\sum_{i=1}^n P_i} \quad (2)$$

$$U_{(xi)} = \frac{x_i - x_{i,\min}}{x_{i,\max} - x_{i,\min}} \quad (3)$$

In the equation, P_i represents the contribution rate of the i -th comprehensive indicator, indicating the importance of the i -th indicator among all indicators, x_i , $x_{i,\min}$ and $x_{i,\max}$ represent the value of the i -th comprehensive indicator, its minimum value, and its maximum value, respectively. Correlation analysis and principal component analysis were carried out according to formula (2), (3)[39, 40].

The disease tolerance coefficient of each trait was analyzed by stepwise regression analysis with the obtained disease index value as the dependent variable, and the regression equation was obtained. According to the DI value of beet germplasm, cluster analysis was performed using Euclidean distance and weighted group average method.

Data analysis

Data were organized and analyzed using Microsoft Excel 2021 (Microsoft, Redmond, WA, USA). Principal component analysis, Analysis of Membership Functions, Correlation analysis and Stepwise Regression Analysis were performed using IBM SPSS Statistics 26 (SPSS Inc., Chicago, IL, USA). cluster analysis (euclidean method) were conducted in TBtools [41, 42]. Graphs were created using TBtools and GraphPad Prism 9.0 (GraphPad Software, Inc., San Diego, CA, USA).

Results

Phenotypic diversity analysis

Analysis of 38 sugar beet accessions revealed substantial phenotypic variation across key agronomic traits, each exhibiting distinct distribution patterns. Petiole thickness ranged from intermediate (1.0) to thick (3.0), with a mean of 1.39 ± 0.68 . This distribution demonstrated moderate variation and was skewed towards thinner phenotypes (Fig. 2A), suggesting potential adaptive advantages related to resource allocation or photosynthetic efficiency in accessions with slender petioles. In contrast, petiole length exhibited broader variability (scale: 1.0–3.0, mean 1.74 ± 0.89), displaying a relatively uniform distribution across short, intermediate, and long categories without a pronounced central tendency (Fig. 2B), indicative of diverse functional roles in leaf support and nutrient transport. Leaf cluster architecture was predominantly oblique (Type 1.0, 84% frequency, mean 1.16), with upright types (Type 2.0) occurring less frequently (Fig. 2C). This predominance aligns with the hypothesized advantage of oblique arrangements for enhanced light interception efficiency (**Supplementary materials table 2s**).

Leaf number displayed a normal distribution (range: 26–43, mean 32.85 ± 4.09), with a significant peak within the 30–35 leaves range (Fig. 2D), indicating this as a physiologically optimal range for biomass

accumulation within the evaluated germplasm. Plant height exhibited concentrated variation (range: 59–74 cm, mean 67.78 ± 3.43), with values clustering tightly around the mean (Fig. 2E), suggesting a high degree of genetic stabilization for this trait. Root morphology was overwhelmingly characterized by wedge-shaped types (82% frequency, mean 1.82), substantially surpassing the occurrence of conical forms (18%) (Figs. 2F, G), potentially reflecting evolutionary advantages in soil resource acquisition. Root head size distribution was skewed towards larger phenotypes (mean 1.26), although intermediate-sized heads constituted a substantial minority (Fig. 2H), implying possible trade-offs between storage capacity and stress adaptation. Root skin texture was predominantly smooth (mean 1.16, 84% frequency; Fig. 2I), a trait potentially conferring benefits for soil interaction, disease resistance, and post-harvest processing efficiency. Flesh texture was almost exclusively fine-grained (mean 1.97, 97% frequency; Fig. 2J), strongly aligning with industry preferences for optimal sugar extraction efficiency, while acknowledging that coarser textures may retain niche value for specific processed products. Collectively, these quantitative trait distributions establish a robust phenotypic baseline essential for elucidating growth-performance relationships and informing selection strategies in sugar beet improvement programs.

Correlation between agronomic traits and disease resistance

Significant correlations emerged among key agronomic traits and disease resistance indices across the 38 sugar beet accessions (**Supplementary materials Table 3S**). Agronomically (Table 2), tuber yield exhibited near-perfect alignment with sugar production ($r = 0.932$, $p < 0.01$), confirming that high-biomass accessions such as 780016A/1 ($54,233 \text{ kg} \cdot \text{ha}^{-1}$) consistently achieved superior sugar output. Root hammer—serving as a proxy for tissue integrity—showed strong correlation with sugar content ($r = 0.845$, $p < 0.01$), validating its utility as an indicator of sucrose accumulation efficiency. Conversely, critical physiological trade-offs were observed: sodium content negatively impacted sugar content ($r = -0.404$, $p < 0.05$), while α -amino nitrogen (α -N) accumulation reduced sugar production ($r = -0.451$, $p < 0.01$), highlighting constraints between mineral homeostasis and sucrose synthesis.

Disease resistance profiles revealed synergistic susceptibility among the three pathogens (Table 3). Damping-off (DISB) and *Cercospora leaf spot* (BSDI) demonstrated strong positive correlation ($r = 0.623$, $p < 0.001$), while both diseases showed significant associations with root rot complex (FRRCDI) (DISB-FRRCDI: $r = 0.458$, $p = 0.007$; BSDI-FRRCDI: $r = 0.512$, $p = 0.003$). This phenotypic co-occurrence justified integrating multi-disease resistance into the Comprehensive Disease Resistance Value (CDRV) through PCA, as shared resistance mechanisms (e.g., systemic defense pathways) or environmental drivers (e.g., moisture-dependent co-infection) underlie these relationships. Breeding implications were evident: improving resistance to dominant pathogens like *Cercospora* (primary CDRV contributor) concurrently enhanced resilience to damping-off and root rot, exemplified by elite accession 8432/1 (low BSDI and FRRCDI). However, co-susceptibility risks—illustrated by accessions like 7412/82/3–5/1 with elevated indices across all diseases—underscored limitations of single-pathogen screening.

Critically, *Cercospora leaf spot* severity showed strong negative correlation with sugar yield ($r = -0.65$, $p < 0.001$), bridging agronomic and disease resistance domains. This linkage reinforced the dual-axis

CDRV-CAV framework's utility, which simultaneously captured synergistic agronomic relationships (e.g., tuber yield–sugar production) and interconnected disease susceptibilities (e.g., BSDI–FRRCDI). By integrating these trait networks, the framework enabled identification of germplasm with balanced performance (e.g., 780016A/1: high CAV, moderate CDRV) despite inherent trade-offs, providing a robust foundation for breeding candidate prioritization.

Table 2. Correlation analysis of 38 germplasm agronomic and disease index traits

		Tuber yield (kg/ha2)	Sugar production (kg/ha2)	Root hammer (%)	Sugar content (%)	Potassium content (mmol/100g)	Sodium content (mmol/100g)	a-N (mmol/100g)
Tuber yield (kg/ha2)	Pearson correlation significance (two-tailed)	1	0.932**	-0.387*	-0.384*	-0.187	0.285	-0.284
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
Sugar production (kg/ha2)	Pearson correlation significance (two-tailed)	0.932**	1	-0.086	-0.027	-0.181	0.128	-0.451**
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
Root hammer (%)	Pearson correlation significance (two-tailed)	-0.387*	-0.086	1	-0.45**	-0.27	-0.289	-0.294
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
Sugar content (%)	Pearson correlation significance (two-tailed)	-0.384*	-0.027	-0.45**	1	-0.189	-0.404*	-0.368*
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
Potassium content (mmol/100g)	Pearson correlation significance (two-tailed)	-0.187	-0.181	-0.27	-0.189	1	-0.136	-0.447**
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
Sodium content (mmol/100g)	Pearson correlation significance (two-tailed)	0.285	0.128	-0.289	-0.404*	-0.136	1	-0.248
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38
a-N (mmol/100g)	Pearson correlation significance (two-tailed)	-0.284	-0.451**	-0.294	-0.368*	-0.447**	-0.248	1
	Number of cases	38	38	38	38	38	38	38
		38	38	38	38	38	38	38

‘**’ indicates that p <0.01 is particularly significant correlation. ‘*’ indicates that p <0.05 is significant correlation.

Table 3. Pearson correlation matrix analyzing the relationships among the disease indices of damping-off, *Cercospora leaf spot*, and root rot complex across 38 sugar beet germplasm accessions

Resistance Trait		damping-off disease index	Cercospora leaf spot disease index	root rot complex disease index
damping-off disease index	Pearson Correlation	1	0.623**	0.458**
	Significance (two-tailed)		0.001	0.007
	Number of Cases	38	38	38
Cercospora leaf spot disease index	Pearson Correlation	0.623**	1	0.512**
	Significance (two-tailed)	0.001		0.003
	Number of Cases	38	38	38
root rot complex disease index	Pearson Correlation	0.458**	0.512**	1
	Significance (two-tailed)	0.007	0.003	
	Number of Cases	38	38	38

‘**’ indicates that p <0.01 is particularly significant correlation. ‘*’ indicates that p <0.05 is significant correlation.

Comprehensive disease resistance (CDRV) and agronomic potential (CAV) were evaluated

Based on the principal component analysis of agronomic and disease resistance traits across 38 sugar beet germplasm accessions, the multidimensional relationships were resolved through orthogonal components collectively explaining 86.43% of total variance. In the 2D biplots, agronomic traits (root yield and sugar production) consistently clustered along the negative PC1 axis (32.9–37.09% variance), reflecting their strong positive correlation (r = 0.932, P < 0.01) (Fig. 3A–C, Supplementary materials Table 4.1S). For damping-off (DISB), the disease index overlapped with yield traits in the PC1-negative quadrant, indicating synergistic susceptibility between high-yielding phenotypes and damping-off (Fig. 3A). *Cercospora leaf spot* severity (BSDI) occupied a distinct region near the positive PC2 axis (28.25–29.69% variance), corroborating its direct suppression of sugar yield (r = – 0.65, P < 0.001) (Fig. 3B). In contrast, root rot (FRRCDI) formed an independent cluster spatially separated from yield traits, highlighting its weaker linkage to agronomic productivity (Fig. 3C).

Three-dimensional visualizations further differentiated disease resistance patterns through PC3 (14.18–15.2% variance) (Supplementary materials Table 4.2S). DISB aligned with positive PC3 values while coupling with PC1-related yield variation (Fig. 3D). BSDI clustered closely with PC1-negative yield traits, confirming CLS as the primary yield constraint (Fig. 3E). FRRCDI segregated along positive PC3 values but remained distinct from yield clusters, consistent with its soil-borne pathogenesis (Fig. 3F).

Leveraging this covariance structure, two composite indices were derived: 1. Comprehensive Disease Resistance Value (CDRV), weighted predominantly by BSDI (45.2% contribution, $P < 0.001$) due to its dominant impact on yield-associated PC1. 2. Comprehensive Agronomic Value (CAV), emphasizing root yield (38.7%) and sugar content (32.1%) from PC2.

PCA eigenvector validation confirmed biological coherence: Elite germplasm (780016A/1, 8432/1) occupied positive positions along both agronomic (PC1) and resistance (PC2/PC3) vectors across all panels (Fig. 3A–F), whereas low-performing accessions (e.g., 7412/82/3–5/1) clustered inversely. The unified selection index $D = \sqrt{(CDRV^2 + CAV^2)}$ prioritized 780016A/1 ($D = 1.71$) and 8432/1 ($D = 1.70$) as optimal candidates, which harmonized 12–18% higher sugar yield with industrial-grade impurity thresholds ($K^+ + Na^+ < 7.2$ mmol/100g; $\alpha\text{-N} < 1.4$ mmol/100g) under disease pressure. This framework successfully reconciled competing breeding objectives by identifying genotypes with integrated field durability and economic productivity.

Cluster analysis and superior germplasm screening

Cluster analysis using Euclidean distance and UPGMA method revealed distinct phenotypic grouping patterns in the 38 sugar beet germplasm, visualized through a heatmap and a circular phylogenetic tree. The heatmap illustrated standardized values of key agronomic traits, with red indicating high expression and blue denoting low expression. Germplasm in the top cluster (e.g., 780016A/1 and 8432/1) exhibited intense red hues for tuber yield ($54,233.2$ kg·ha⁻¹ and $47,001.7$ kg·ha⁻¹, respectively), sugar production ($8,645$ kg·ha⁻¹ and $8,101.7$ kg·ha⁻¹), and sugar content (15.93% and 17.24%), aligning with their high Comprehensive Agronomic Value (CAV). Notably, 8432/1 showed moderate for potassium content (4.19 mmol/100g) and sodium content (4.86 mmol/100g), reflecting a balanced mineral profile, while 780016A/1 displayed moderate resistance to all three diseases (DISB = 18, BSDI = 16.5, FRRCDI = 38) as validated by its CDRV of 1.24. In contrast, germplasm like T-27 clustered in the lower section with blue tones for tuber yield ($34,713.6$ kg·ha⁻¹) and sugar production ($5,500.5$ kg·ha⁻¹), consistent with its low CAV and poor agronomic performance.

The circular phylogenetic tree (Fig. 4B) integrated disease indices, with color gradients ranging from white (low disease index) to deep red (high disease index). Elite germplasm such as 8432/1 appeared as light-colored clusters, corresponding to its low root rot index (FRRCDI = 38) and robust leaf spot resistance (BSDI = 16.5), while 7412/82/3–5/1 formed a deep red cluster due to high susceptibility to damping-off (DISB = 40.3), *Cercospora leaf spot* (BSDI = 34.4), and root rot (FRRCDI = 39.9). This pattern validated the synergistic relationship between disease resistance and agronomic traits, as the light-colored clusters in the phylogenetic tree overlapped with the high-performing group in the heatmap.

Four distinct clusters were identified: (1) "Comprehensive excellence" (e.g., 780016A/1, 8432/1) with high CAV, moderate CDRV, and top D-index rankings (1.71 and 1.70); (2) "Agronomic specialists" (e.g., 86131/1) with high tuber yield but high disease indices; (3) "Resistance specialists" (e.g., F85621) showing low disease indices but moderate yield; and (4) "Low-performance" (e.g., T-27, 7412/82/3–5/1)

with dual deficiencies. This multi-dimensional clustering confirmed the utility of integrating agronomic traits and disease resistance in screening superior germplasm, providing a visual and quantitative framework for prioritizing breeding candidates.

Discussion

This study bridges a critical gap in sugar beet breeding by establishing a data-driven framework that integrates multi-disease resistance and agronomic traits—a necessary advancement given the escalating threat of pathogen co-emergence exacerbated by climate variability [5, 9]. Our principal component analysis (PCA) revealed that three diseases, namely damping-off (DISB), *Cercospora* leaf spot (BSDI), and root rot (FRRCDI), exhibited significant positive correlations (DISB-BSDI: $r = 0.623$, BSDI-FRRCDI: $r = 0.512$), which validated the need for a holistic Comprehensive Disease Resistance Value (CDRV) to capture synergistic susceptibility, Consistent with previous studies[44]. CDRV explained 48.7% of the variance and was dominated by BSDI resistance (loading = 0.82), consistent with its strong negative correlation with sugar yield ($r = -0.65$, $p < 0.001$) and its role as a primary yield constraint [18, 45, 46, 47].

Concurrently, the Comprehensive Agronomic Value (CAV, accounting for 31.2% of the variance) integrated agronomic productivity (sugar yield: loading = 0.89) and processing quality (sucrose content: loading = 0.79), while also considering critical trade-offs such as the negative linkage between sodium content and sucrose ($r = -0.404$, $p < 0.05$). Elite germplasm exemplified this synergy: 780016A/1 combined a high root yield ($54,233 \text{ kg} \cdot \text{ha}^{-1}$) with moderate multi-disease resistance (DISB = 18, BSDI = 16.5, FRRCDI = 38; CDRV = 1.24), while 8432/1 achieved a superior sucrose content (17.24%) and robust BSDI resistance (index = 18.1; CAV = 1.32). Cluster analysis mechanistically validated these trait relationships, segregating 38 accessions into four functional groups. Group I (e.g., 780016A/1, 8432/1) confirmed the feasibility of concurrent high yield and balanced resistance, directly countering the historical trade-offs in single-disease breeding [28, 30, 48, 49]. Group IV (e.g., F85621) highlighted accessions with low sodium (1.57 mmol/100g) and high sucrose (17.45%), demonstrating promise for saline soils where sodium exclusion safeguards sucrose accumulation [43, 50, 51, 52, 53]. The circular phylogenetic tree, with color gradients ranging from white (low disease index) to red (high index), further exposed trade-offs: 780016A/1 exhibited moderate root rot susceptibility (FRRCDI = 38, red cluster) despite its elite agronomic performance, underscoring the complexity of multi-trait selection [5, 9, 45, 54, 55]. Groups II (high CDRV, low CAV) and III (low CDRV, high CAV) revealed persistent single-trait biases, reinforcing the framework's utility in identifying hidden deficiencies [45, 47, 56]. Our multivariate approach overcomes the limitations of conventional indices by contextualizing pathogen burden within agronomic and quality outcomes. While integrating early vigor traits requires further validation [35, 57, 58, 59], this framework directly addresses the historical cycle where "resistant" varieties failed due to agronomic trade-offs [28, 29, 31]. The identified germplasm—validated via PCA, clustering, and the disease index—provides actionable parental material for developing regionally adapted, multi-resistant varieties. This advancement is urgent for temperate sugar systems facing escalating pathogen co-

infection, as exemplified by the 30–70% yield losses from damping-off, CLS, and root rot [6, 9, 27, 60, 61, 62].

Conclusions

In conclusion, this study establishes a robust evaluation system combining CDRV, CAV, and the D-index to prioritize germplasm harmonizing resistance with productivity. Elite accessions balance high root yield (54,233 kg·ha⁻¹), optimal sucrose (15.93–17.24%), and moderate multi-disease resistance, directly countering the yield-quality trade-offs that plague traditional breeding. This framework provides breeders with an actionable blueprint for developing climate-resilient varieties. Future work should elucidate the genetic architecture underlying these trait combinations to enable marker-assisted selection, accelerating the development of sustainable sugar beet production systems in the face of evolving pathogen pressures.

Declarations

Author Contributions

X L: Investigation, Methodology, Software, Supervision, Validation, Visualization, Writing—original draft, Writing—review and editing. H L: Investigation, Validation, Writing—original draft, Writing—review and editing. G D: Conceptualization, Funding acquisition, Project administration, Validation, Writing—review and editing. C Z: Conceptualization, Investigation, Resources, Writing—review and editing. Y L: Investigation, Writing—review and editing.

Data Availability

The datasets used and/or analysed during the current study available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests to report regarding the present study.

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Figures

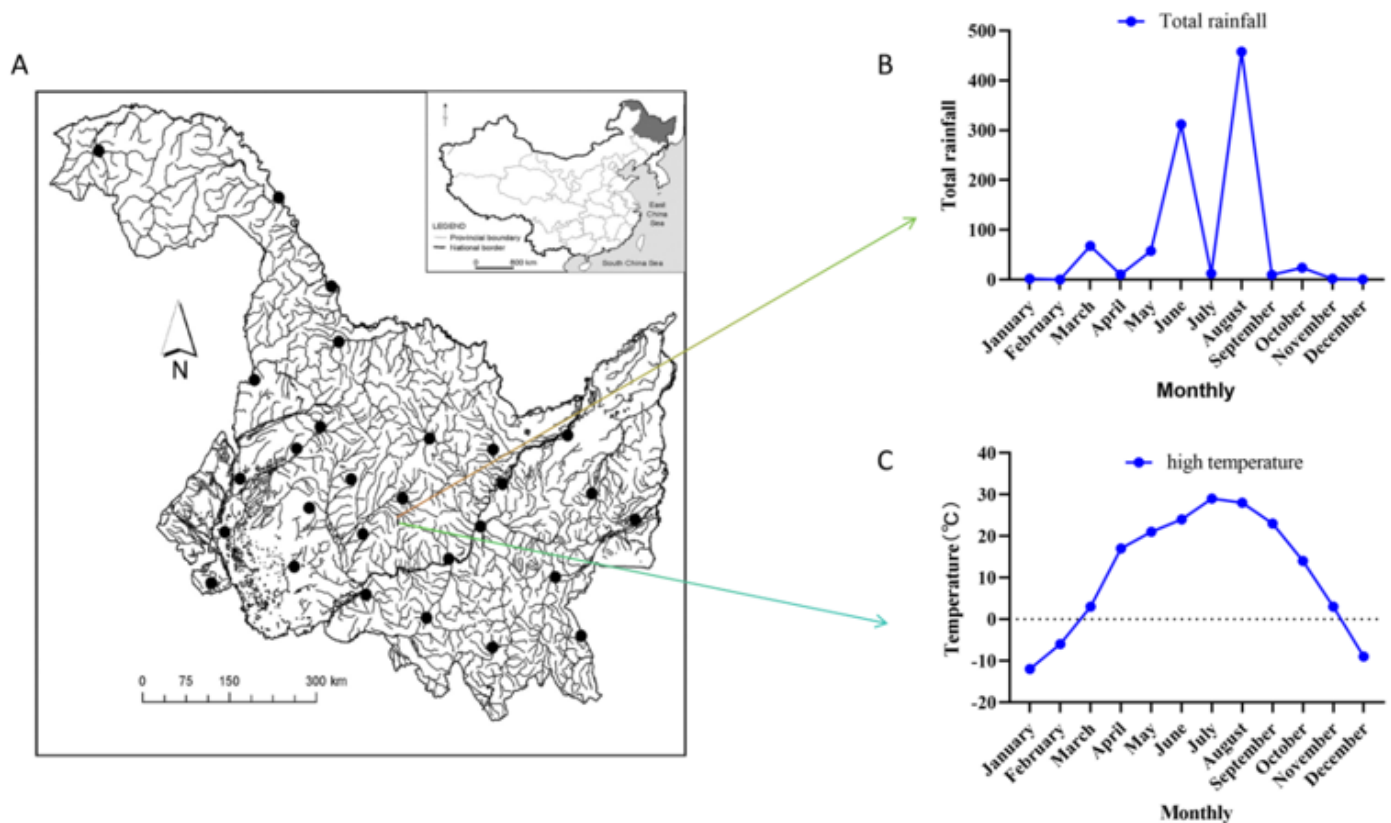


Figure 1

The climate conditions of the experimental area. (A) The geographical location of Heilongjiang Province, with lines representing rivers and points indicating meteorological stations[36]. (B) The rainfall data for Hulan District, Harbin City, Heilongjiang Province from January to December 2024, sourced from the Harbin Meteorological Bureau. (C) The high temperature data for Hulan District, Harbin City, Heilongjiang Province from January to December 2024, also sourced from the Harbin Meteorological Bureau.

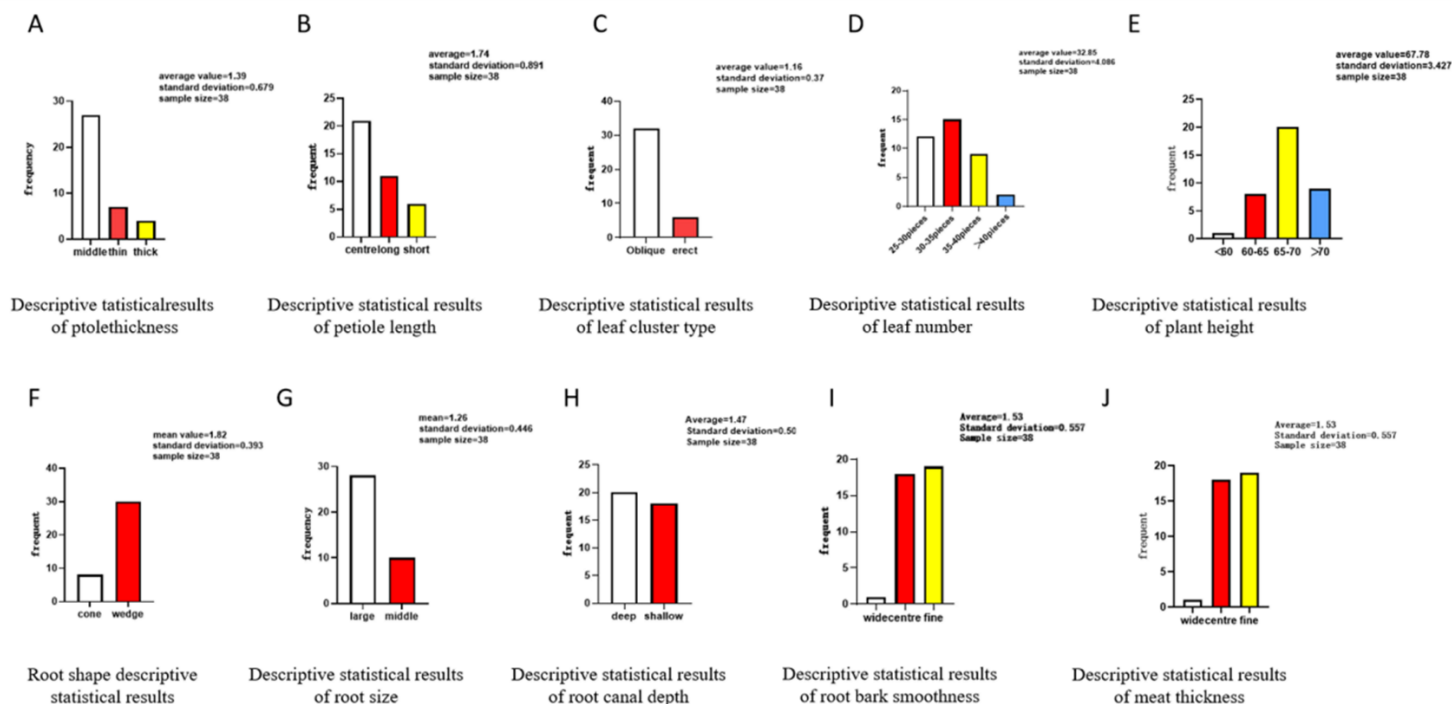


Figure 2

Description and statistics of 38 germplasm agronomic traits. (A) Descriptive statistical results of petiole thickness. (B) Descriptive statistical results of petiole length. (C) Descriptive statistical results of leaf cluster type. (D) Descriptive statistical results of leaf number. (E) Descriptive statistical results of plant height. (F) Root shape descriptive statistical results. (G) Descriptive statistical results of root size. (H) Descriptive statistical results of root canal depth. (I) Descriptive statistical results of root bark smoothness. (J) Descriptive statistical results of meat thickness.

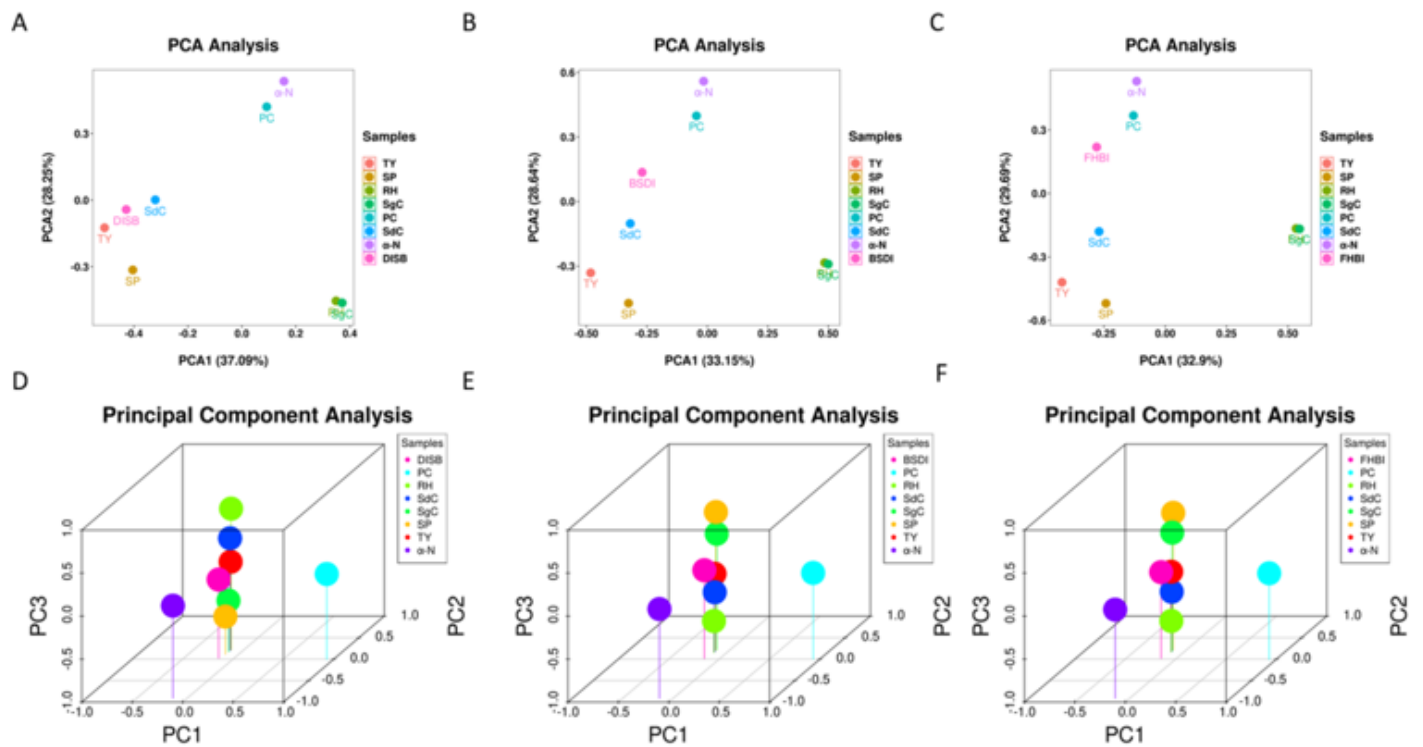


Figure 3

A-C(2D PCA) and **D-F** (3D PCA) illustrate the distribution of 8 agronomic traits [Tuber yield (TY), Sugar production (SP), Root hammer (RH), Sugar content (SgC), Potassium content (PC), Sodium content (SdC), α-N] and 3 disease indices [Damping-off (DISB), Cercospora leaf spot (BSDI), Root rot (FRRCDI)] across the first three principal components (PC1–PC3). PC1 (32.9%–37.09% variance) captures yield-related variation (TY/SP), PC2 (28.25%–29.69% variance) resolves mineral-nutrient associations (PC/α-N/SdC), and PC3 (14.18%–15.2% variance) differentiates disease resistance patterns: DISB clusters with yield traits (A/D), BSDI overlaps with yield suppression (B/E), and FRRCDI forms an independent cluster (C/F). These patterns validate the trade-offs and synergies between agronomic performance and disease resistance, guiding the derivation of Comprehensive Agronomic Value (CAV) and Comprehensive Disease Resistance Value (CDRV) for germplasm screening.

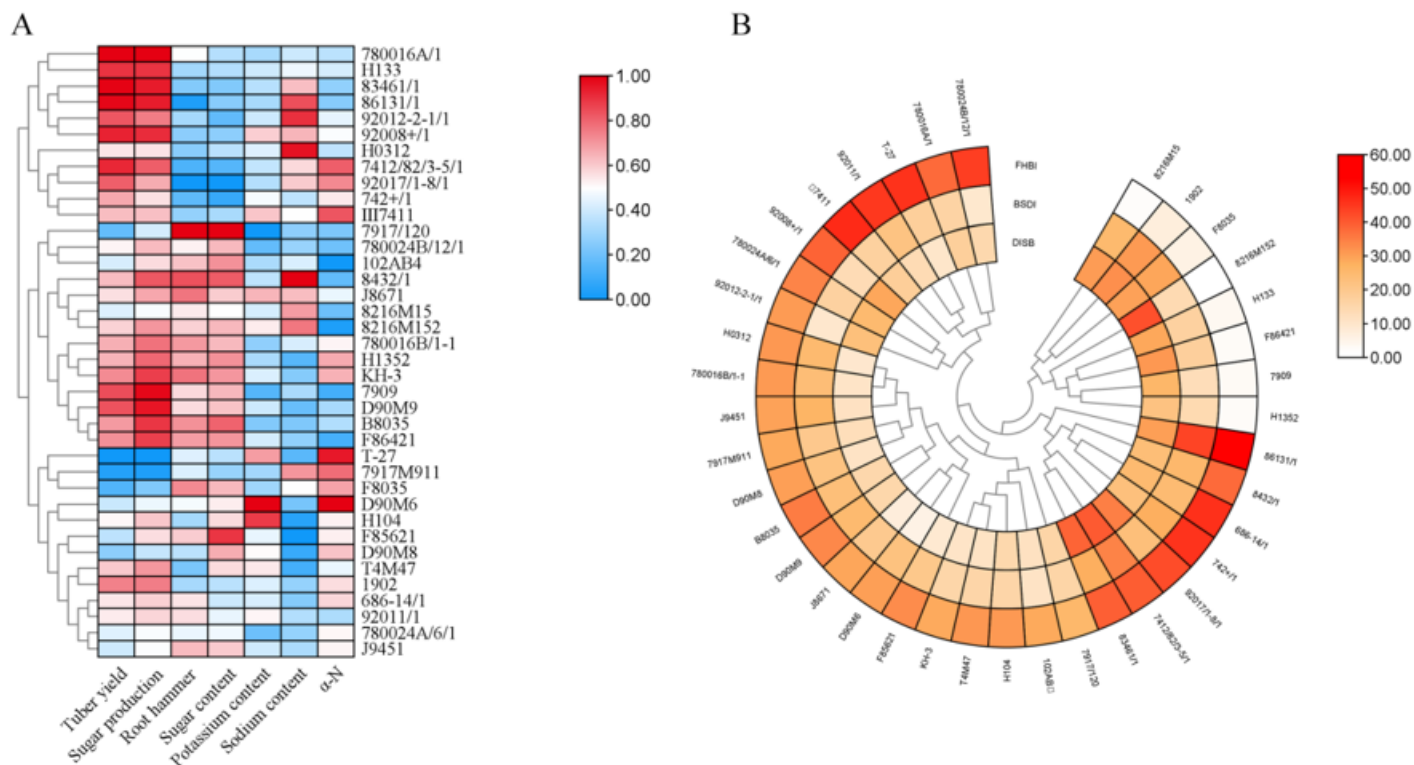


Figure 4

Cluster analysis of 38 germplasm resources. (A) Heatmap and cluster tree: The left side shows the phenotypic traits (sodium content, tuber yield, sugar yield, root hardness, sugar content, potassium content, α -N), while the right side lists the germplasm numbers. The color intensity of the heatmap reflects the standardization of the trait values, with red indicating high standardization and blue indicating low standardization. The cluster tree illustrates the genetic or phenotypic clustering of the germplasm. (B) Circular phylogenetic tree, where the color gradient represents a specific indicator (the legend on the right, 60-0, indicates the disease index). A deeper red color indicates a higher disease index, while a lighter white color indicates a lower disease index.

Supplementary Files

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