



Fenugreek Germplasm Trait Explorer: A digital platform for interactive trait visualization and core-set exploration of genetic resources

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Abstract

Phenotypic and genotypic information are fundamental to plant breeding, genetic improvement, and genomic research. Plant genetic resources conserved in gene banks provide an essential foundation for these activities by preserving genetic diversity and facilitating the identification and utilization of valuable traits. Digital information systems, databases, and repositories play an increasingly important role in the systematic management, accessibility, visualization, and exploration of germplasm information, thereby supporting data-driven breeding strategies. High Throughput Plant Phenotyping (HTPP) and genetic research. Considerable progress has been made globally in developing digital platforms for plant genetic resource management, crop-specific tools for interactive trait exploration remain essential for the effective characterization and utilization of germplasm collections across different crops. In this context, the present study introduces the Fenugreek Germplasm Trait Explorer, an interactive digital platform developed for the systematic organization, visualization, and trait-based exploration of fenugreek (*Trigonella foenum-graecum* L.) genetic resources. The platform incorporates phenotypic information on 712 fenugreek germplasm accessions, including a representative core collection of 71 accessions, characterized for 11 important phenotypic traits. These germplasm accessions are conserved at the ICAR–National Research Centre on Seed Spices (ICAR–NRCSS), Ajmer, India, which maintains a Medium-Term Storage (MTS) facility for the conservation of seed spice genetic resources. As India's dedicated national research centre for seed spices, ICAR–NRCSS plays an important role in the conservation, characterization, and utilization of these valuable genetic resources. The platform facilitates interactive trait visualization, comparative exploration of germplasm accessions, and identification of accessions belonging to the core collection. It provides a valuable digital resource for efficient germplasm characterization, trait-based selection, core collection exploration, and the identification of promising genetic resources for future fenugreek improvement programmes.

Keywords: Fenugreek (*Trigonella foenum-graecum* L.), digital platform, database, seed spices, core-set, Core-Hunter, germplasm, genetic resources

Introduction

Plant genetic resources and germplasm are foundation of crop improvement and breeding programmes, as they represent valuable reservoirs of genetic diversity and provide important insights into the biological,

morphological, agronomic, and genetic characteristics of crop species (Abhishek et al. 2024; Abiri et al. 2023; K. Singh et al. 2020). Worldwide, diverse germplasm collections are conserved in national and international gene banks to safeguard genetic diversity and ensure their

availability for research and crop improvement (Germeier and Unger 2019; Lee et al. 2005; Pathirana and Carimi 2022; K. Singh et al. 2020). These genetic resources are systematically collected, conserved, characterized, and evaluated for various traits to identify desirable accessions and potential sources of genes for use in breeding programmes. The effective conservation and utilization of plant genetic resources are also important prerequisites for sustainable agricultural and food production, which has become a critical global priority for meeting the growing food demands of an increasing population (Pathirana and Carimi 2022; K. Singh et al. 2020).

At another hand, Digital technologies play a vital role in enhancing agricultural productivity, resource-use efficiency, and sustainability (Ali and Zehra 2025). In this context, well-structured agricultural databases are essential for the systematic collection, storage, management, integration, and analysis of diverse datasets, irrespective of their size (Abbasi et al. 2022; Bolger et al. 2017). Such databases facilitate data-driven research, efficient utilization of genetic resources, informed decision-making, and the development of advanced artificial intelligence (AI) and machine learning (ML) based applications for sustainable agriculture.

Fenugreek (*Trigonella foenum-graecum* L.) is an important multipurpose seed spice crop valued for its medicinal, culinary, nutritional, and industrial applications (Zandi et al. 2015). It possesses considerable therapeutic and nutraceutical potential owing to its diverse bioactive compounds (Ahmad et al. 2016; Srinivasan 2006). India is one of the world's leading producers, consumers, and exporters of fenugreek. Consequently, the conservation, characterization, and systematic utilization of fenugreek genetic resources are essential for crop improvement and for advancing research in genomics, bioinformatics, metabolomics, and related disciplines. Given its medicinal significance, comprehensive germplasm characterization is particularly important for identifying promising accessions with desirable agronomic, nutritional, and therapeutic traits.

In this context, the ICAR–National Research Centre on Seed Spices (ICAR–NRCSS), Ajmer, conserves germplasm and serves as medium term storage centre and National Active Germplasm Site (NAGS) for germplasm. Therefore, the systematic phenotypic evaluation of fenugreek germplasm accessions work was started to assess their variability and potential for crop improvement. Subsequently, an interactive digital database, the Fenugreek Germplasm Trait Explorer, was

developed to facilitate the systematic organization, visualization, and exploration of phenotypic information. The platform enables plant breeders, geneticists, researchers, and other stakeholders to examine trait-wise variation, compare germplasm accessions, and gain a comprehensive understanding of the phenotypic diversity present within the collection. By providing rapid, user-friendly access to germplasm information, the platform supports the identification of promising genetic resources, informed selection of accessions, and the development of targeted breeding strategies. Furthermore, it establishes a valuable digital foundation for future integration of genomic, metabolomic, and bioinformatics data to support advanced fenugreek research and genetic improvement.

Material and Methods

Fenugreek Germplasm and Data Collection

The ICAR–NRCSS, Ajmer, is a national research institution dedicated to seed spice crops, including one of mandate crop i.e. fenugreek. The Centre maintains a Medium-Term Storage (MTS) facility for the conservation of seed spice genetic resources. Alongside research activities undertaken by State Agricultural Universities, their constituent colleges, and other research institutions, ICAR–NRCSS plays an important role in the collection, conservation, characterization, and utilization of fenugreek germplasm. These activities are essential for preserving genetic diversity, identifying desirable traits, and supporting crop improvement programmes, including conventional breeding, molecular characterization, and advanced genetic research. As part of its germplasm conservation efforts, the Centre maintains an extensive collection of fenugreek genetic resources, comprising both indigenous (Indian) and exotic germplasm accessions.

For the present study, 712 fenugreek germplasm accessions conserved at ICAR–NRCSS, Ajmer, were evaluated for their phenotypic characteristics. The experimental site is situated in Agro-climatic Zone IIIa (Semi-Arid Eastern Plain Zone) of Rajasthan, characterized by predominantly medium-textured sandy loam soil. The field experiments were conducted during two consecutive rabi seasons, 2022–23 and 2023–24, covering the crop-growing period from October to April. A total of 300 accessions were evaluated during 2022–23, followed by 412 accessions during 2023–24. The experiments were laid out in an Augmented Block Design (Federer and Raghavarao 1975).

Phenotypic observations were recorded for 11 important traits, comprising nine quantitative agronomic and yield-related traits and two disease-severity traits. The nine

quantitative traits included days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, test weight (1,000-seed weight, g), and seed yield per plant (g). Additionally, disease severity was assessed for two major fungal diseases of fenugreek, namely downy mildew and powdery mildew. The selected phenotypic traits are of considerable importance for germplasm characterization, genetic variability assessment, and crop improvement programmes, as they represent key agronomic, morphological, and yield-related characteristics (Abhishek et al. 2024; Zandi et al. 2015). These traits have been widely considered in previous fenugreek studies conducted across major fenugreek-growing regions of India and other countries, highlighting their relevance to breeding and germplasm evaluation (Choudhary et al. 2013; R. Singh et al. 2025; Srinivasan 2006; Zandi et al. 2015; V. S. Meena et al. 2025). In addition to these traits, disease severity associated with downy mildew and powdery mildew, two economically important diseases of fenugreek, was included in the present study (S. S. Meena 2026). The combined evaluation of these traits facilitates the identification of promising germplasm accessions with desirable agronomic characteristics, higher yield potential, and reduced disease susceptibility for future breeding programmes.

Development of a Phenotypic Database, Trait Explorer: Software & Technologies used

The software was developed using HTML5, CSS3, and JavaScript, following a client-side web application

architecture. HTML provides the structural framework, CSS supports responsive interface design, and JavaScript handles data processing, interactive filtering, sorting, visualization, and export operations. Phenotypic records are embedded in the application as structured JavaScript objects, allowing users to explore the dataset directly through a web browser without requiring a separate database server. Visualization using Dynamic HTML/CSS bar charts and summary statistics, Core-set identification using Accession matching using a JavaScript Set, Data export CSV generation using JavaScript Blob API and Multilingual support using Google Translate integration. The core-set developed borrows the principle of core hunter method (Beukelaer et al. 2012; De Beukelaer et al. 2018; Thachuk et al. 2009).

Results and Discussion

GUI Design and Interactive Features

The Fenugreek Germplasm Trait Explorer was developed as an interactive software application that can operate both through a web browser and in standalone mode. It facilitates the systematic organization, visualization, and exploration of phenotypic data from 712 fenugreek germplasm accessions, providing an accessible and user-friendly digital platform for researchers, academicians, and the broader scientific community. The platform integrates 11 phenotypic traits, comprising nine agromorphological and yield-related traits and two disease-severity parameters, along with the identification of accessions belonging to the representative core collection. The front end of the GUI is as shown in Fig.1.

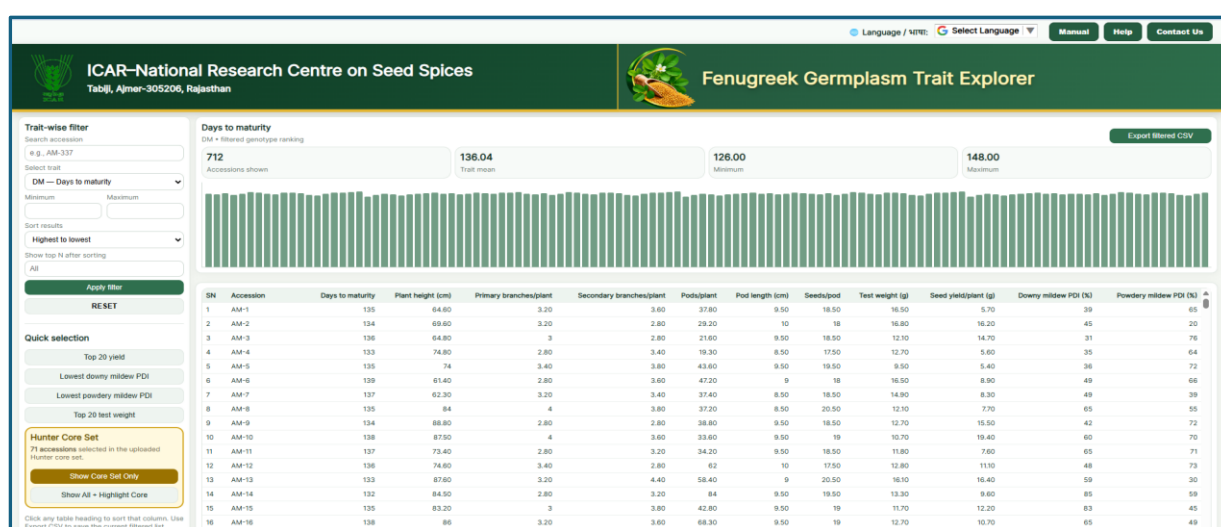


Fig.1: Main Page of the GUI Fenugreek Germplasm Trait Explorer. Graphical user interface of the Fenugreek Germplasm Trait Explorer showing the institutional header, trait-selection panel, accession-wise phenotypic database, summary statistics, and interactive visualization features.

The software provides trait-wise filtering and selection, allowing users to search germplasm accessions based on user-defined minimum and maximum trait values. It also offers sorting options and a Top-N selection feature, enabling users to specify the number of accessions to be displayed. The interactive visualization panel dynamically presents summary statistics, including the total number of accessions,

mean trait value, minimum and maximum values, and trait range. These statistics are automatically updated according to the selected filtering criteria, facilitating comparative assessment of either the entire germplasm collection or a user-defined subset of accessions. The interface has also multilingual support for users of different native Indian languages who grow fenugreek across India.

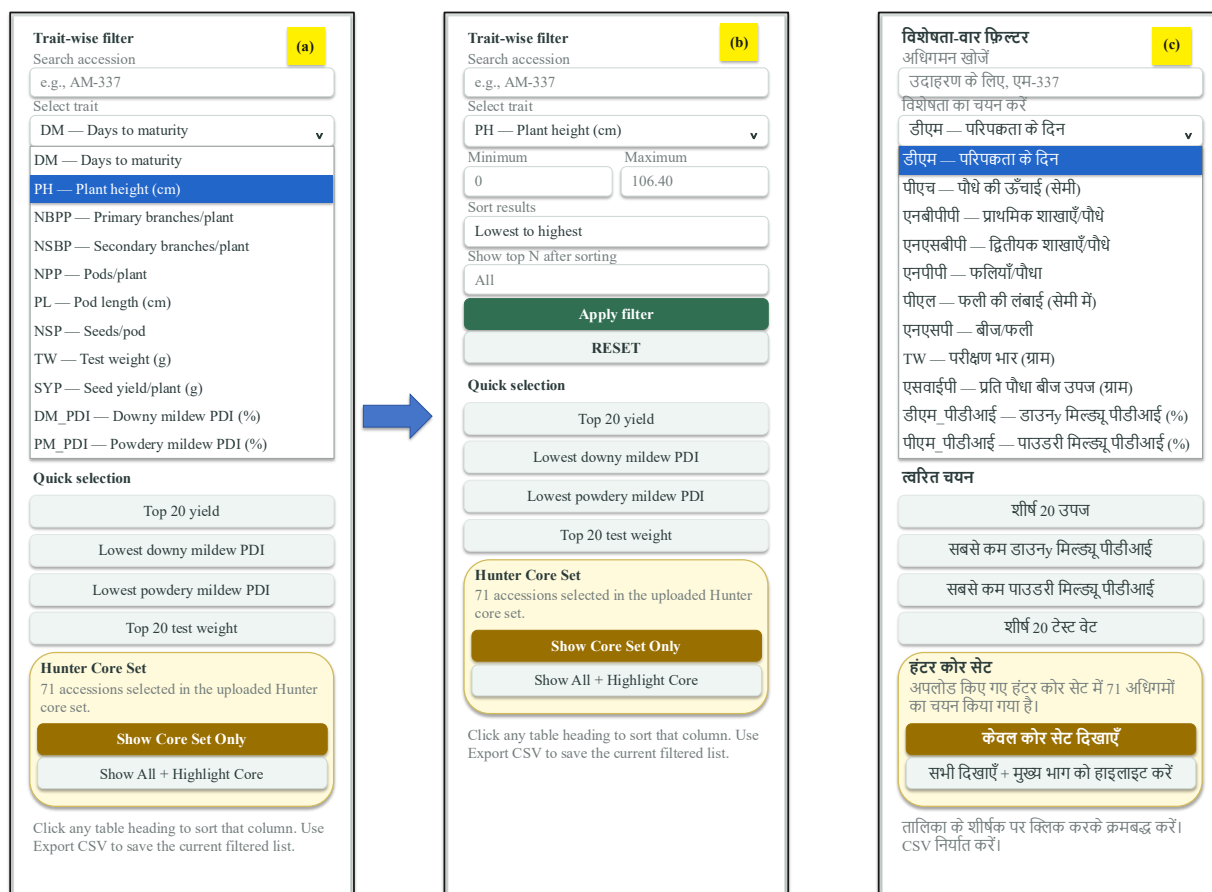


Fig.2: Interactive trait-wise selection and filtering interface of the Fenugreek Germplasm Trait Explorer: (a) selection of phenotypic traits (b) user-defined trait filtering based on minimum and maximum values, sorting order; and (c) Hindi-language interface demonstrating multilingual accessibility.

Dynamic trait exploration capability

One of the major functional outcomes of the developed platform is its dynamic trait exploration capability. Users can search individual accessions, select specific phenotypic traits, apply minimum and maximum thresholds, arrange accessions in ascending or descending order, and identify the top-performing entries. The filtering mechanism dynamically updates the displayed accession records and associated summary statistics, including the mean, minimum, and maximum values of the selected trait. This functionality facilitates rapid examination of phenotypic variability and the identification of accessions possessing

desirable characteristics. This operation is shown in Fig.2, Fig. 3 (a)-(b) and Fig.4.

Figure 2 illustrates the trait-wise selection and filtering interface of the Fenugreek Germplasm Trait Explorer, developed to facilitate interactive exploration and identification of desirable germplasm accessions based on specific phenotypic characteristics. Figure 2(a) presents the trait-selection panel, which allows users to search individual germplasm accessions by their unique accession numbers and select any of the 11 phenotypic traits, here in case like Plant Height. Figure 2(b) demonstrates the application of user-defined filtering criteria using plant height (cm) as an example. Users can specify minimum and maximum trait values,

arrange the results in ascending or descending order, and define the number of accessions (N) to be displayed. The *Apply Filter* option retrieves accessions satisfying the selected criteria, while the *Reset* function restores the default settings. This feature facilitates targeted screening and comparative assessment of germplasm accessions based on desirable trait values.

Figure 2(c) demonstrates the multilingual functionality of the software, with the trait-selection and filtering interface displayed in Hindi. The translated interface retains the principal search, filtering, quick-selection, and core-set exploration functionalities, thereby improving accessibility for Hindi-speaking researchers, breeders, and other stakeholders.

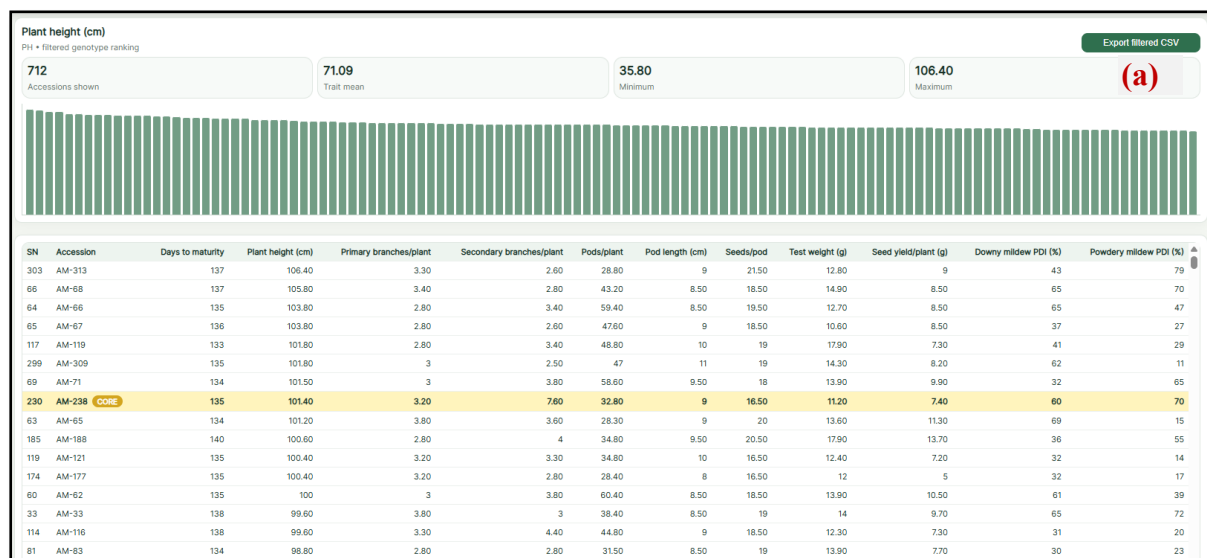


Fig.3:

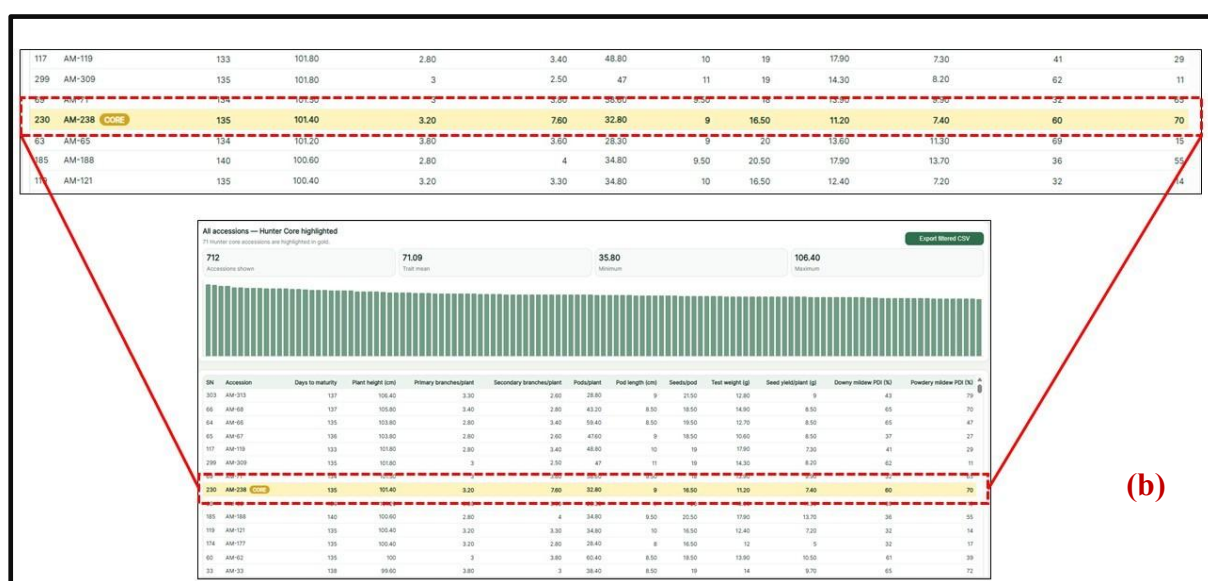


Fig.3: Core-collection exploration module of the Fenugreek Germplasm Trait Explorer: (a) identification and highlighting of 71 representative core accessions within the complete collection of 712 fenugreek germplasm accessions; and (b) enlarged inset showing a highlighted core accession.

The figure 3, illustrates the interactive visualization of 712 fenugreek germplasm accessions, displaying trait-wise summary statistics and accession-specific phenotypic data. The enlarged inset highlights accession AM-238, identified as a member of the 71-accession representative core collection and distinctly marked in gold for easy identification within the full

germplasm dataset. Similarly, Figure 4 illustrates the Hindi-language interface of the Fenugreek Germplasm Trait Explorer, displaying trait-wise summary statistics and accession-specific phenotypic data. The interface retains the core-set highlighting and interactive visualization features, enhancing accessibility for Hindi-speaking researchers and stakeholders.

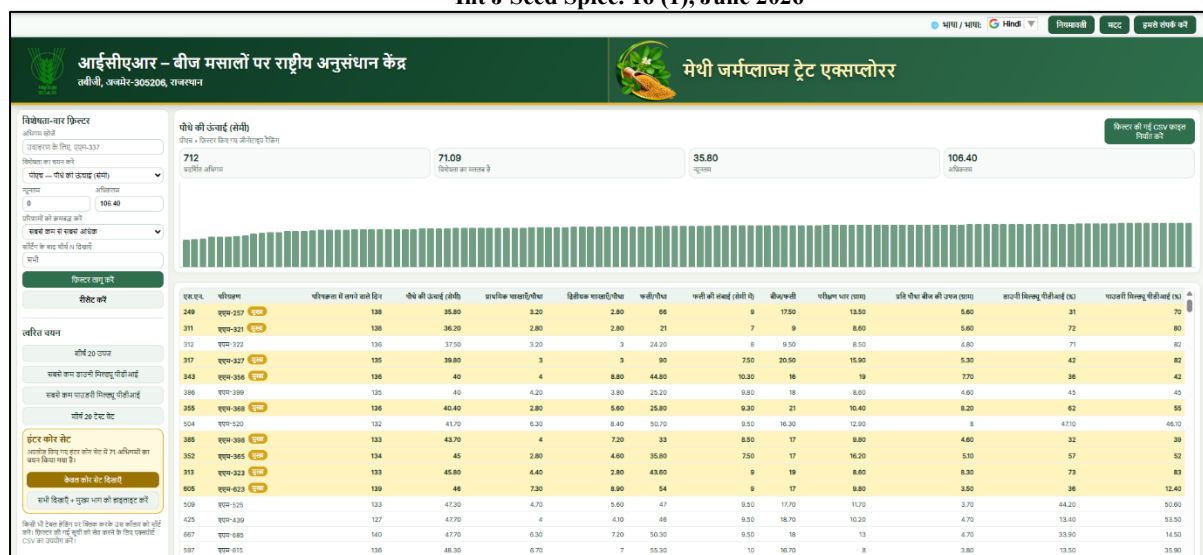


Fig.4: Identification of promising fenugreek germplasm accessions through predefined trait-based selection, sorting, and data-export functionalities.

Overall, the integrated trait-wise filtering, predefined selection criteria, core-set exploration, and multilingual interface provide a user-friendly approach to germplasm screening and phenotypic data exploration. These functionalities support the efficient identification and prioritization of promising fenugreek accessions for further evaluation and crop improvement programmes.

The interface also provides predefined quick-selection options for identifying the top 20 high-yielding accessions, accessions with the lowest downy mildew and powdery mildew percentage disease indices (PDI), and the top 20 accessions based on test weight. Additionally, the Hunter Core Set module enables users to explore 71 representative accessions separately or highlight them within the complete germplasm collection.

The software also incorporates trait-based graphical visualization, allowing users to compare accession-wise phenotypic values through dynamically generated bar charts. The graphical display changes automatically according to the selected trait and filtering criteria, thereby providing an intuitive representation of trait distribution among the displayed accessions. This feature is particularly useful for identifying accessions with relatively higher seed yield, greater test weight, or lower disease severity. The integration of tabular and graphical representations improves data interpretation and reduces the effort required for preliminary germplasm screening.

A distinctive feature of the developed application is the integration of the representative fenugreek core

collection comprising 71 accessions. A dedicated core-set exploration module allows users to display only core accessions or highlight them within the complete collection of 712 accessions. This functionality facilitates comparative assessment of representative germplasm against the entire collection and supports targeted identification of potentially useful genetic resources. The integration of core-set information within the phenotypic database provides a practical interface for prioritizing accessions for further characterization and breeding-related investigations.

Additionally, the application provides predefined selection options for identifying accessions with high seed yield, higher test weight, and relatively low downy mildew or powdery mildew severity. The CSV export facility enables users to download filtered phenotypic records for subsequent statistical analysis and documentation. The inclusion of multilingual translation support, a user manual, and an integrated help section further improve the accessibility and usability of the software for researchers, plant breeders, and other stakeholders.

Overall, the developed Fenugreek Germplasm Trait Explorer demonstrates the feasibility of integrating phenotypic datasets, interactive visualization, and core-collection information into a unified digital platform. The software offers a practical approach to converting conventional germplasm characterization records into an accessible and searchable digital resource. Although the present version primarily supports descriptive analysis and interactive exploration, its modular web-based structure provides a foundation for future integration of advanced statistical methods, relational

database management, and predictive analytical tools. Thus, the platform has potential to strengthen digital germplasm documentation, preliminary trait-based selection, and data-driven decision-making in fenugreek improvement programmes.

Conclusion

The Fenugreek Germplasm Trait Explorer was developed as an interactive, web-based platform for the digital documentation, visualization, and exploration of phenotypic data from 712 fenugreek germplasm accessions conserved at ICAR–NRCSS, Ajmer. The software integrates 11 agro-morphological, yield-related, and disease-severity traits, enabling accession-wise searching, trait-based filtering, comparative visualization, and identification of promising germplasm. The integration of the 71-accession representative core collection further facilitates targeted exploration of genetic resources based on their phenotypic characteristics. The platform provides a user-friendly digital resource for germplasm management, trait assessment, and informed selection of accessions for future breeding programmes. Future development will focus on transforming the existing standalone application into a more comprehensive, scalable, and dynamically managed germplasm information system. The Jupyter Notebook environment, supported by Python-based analytical tools, will be utilized for further data processing, statistical analysis, advanced visualization, and prototyping of additional analytical features. The front-end interface will be further enhanced using modern web-development technologies to improve interactivity, accessibility, and user experience. These developments are expected to establish the Fenugreek Germplasm Trait Explorer as a comprehensive digital platform for germplasm characterization, conservation, and seed spices crop improvement research.

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Conflict of Interest

Authors declare no conflict of interest

Authors Contributions

MKV: Conceptualization of the study- database preparation, software development, and manuscript drafting; SSM: Experimental design and execution, germplasm evaluation, and manuscript review; RSM, SS, YK, and RDM: Assistance in conducting field

experiments and germplasm evaluation; VB: Administrative support and manuscript review; all approved the manuscript.

References

- Abbasi, R., Martinez, P., & Ahmad, R., (2022). The Digitization of Agricultural Industry – a systematic literature review on agriculture 4.0. *Smart Agric. Technol.* 2 (December): 100042. <https://doi.org/10.1016/j.atech.2022.100042>.
- Abhishek, G.J., Deepika D.D., Jagdeesh M, S., Ragi, S., Bhatt, K.C., & K.R., (2024). Comprehensive overview of plant germplasm augmentation: strategies, techniques and applications. *J. Adv. Biol. Biotechnol.* 27 (9): 1009–18. <https://doi.org/10.9734/jabb/2024/v27i91371>.
- Abiri, R., Rizan, N., Balasundram, S.K., Shahbazi, A, B., & Hamid, A, H., (2023). Application of digital technologies for ensuring agricultural productivity. *heliyon* 9 (12): e22601. <https://doi.org/10.1016/j.heliyon.2023.e22601>.
- Ahmad, A., Alghamdi, S.S., Mahmood, K., & Afzal, M., (2016). Fenugreek a multipurpose crop: potentialities and improvements. *Saudi J. Biol. Sci.* 23 (2):300–310. <https://doi.org/10.1016/j.sjbs.2015.09.015>.
- Ali, S., and Zehra, O., (2025). Digital technologies for precision agriculture: current approaches, advances and future perspectives. *Plant Sci. Today*, ahead of print, October 30. <https://doi.org/10.14719/pst.8318>.
- Beukelaer, De, H., Smýkal, P., Davenport, G. F., & Fack, V., (2012). Core hunter II: fast core subset selection based on multiple genetic diversity measures using mixed replica search. *BMC bioinformatics* 13(1):312. <https://doi.org/10.1186/1471-2105-13-312>.
- Bolger, M., Schwacke, R., Gundlach, H., Schmutzer, T., Chen, J., Arend, D., Oppermann M., Weise, S., Lange, M., Fiorani, F., Spannagl, M., Scholz, U., Mayer, K., & Usadel, B., (2017). From plant genomes to phenotypes. *J. Biotechnol.* 261 (November): 46–52. <https://doi.org/10.1016/j.jbiotec.2017.06.003>.
- Choudhary, S., Meena, R.S., Singh, R., Vishal, M.K., Choudhary, V., & Panwar, A., (2013). Assessment of genetic diversity among Indian fenugreek (*Trigonella Foenum-Graecum* L.) varieties using morphological and RAPD markers. *Legume Res.* 36 ((4)): 289–298.
- Beukelaer, De, H., Davenport, Guy, F., & Fack, V., (2018). core hunter 3: flexible core subset selection. *BMC bioinformatics* 19 (1):203. <https://doi.org/10.1186/s12859-018-2209-z>.

- Federer, W.T., & Raghavarao. D., (1975). On augmented designs. *biometrics* 31 (1): 29. <https://doi.org/10.2307/2529707>.
- Germeier, C, U., & Unger, S., (2019). Modelling crop genetic resources phenotyping information systems. *Front. Plant Sci.* 10 (June): 728. <https://doi.org/10.3389/fpls.2019.00728>.
- Lee, J, M., Davenport, Guy, F., Marshall, D., et al. (2005). GERMINATE. A generic database for integrating genotypic and phenotypic information for plant genetic resource collections. *Plant Physiol.* 139 (2): 619–31. <https://doi.org/10.1104/pp.105.065201>.
- Meena, S.S., Meena, R.D., Meena, R.S., Sharma, Y.K., Kumar, S., Meena, N.K., Meena, S.S., & Ravi Y., (2025). Gamma irradiation induced powdery mildew disease resistance in fenugreek (*Trigonella Foenum-Graecum* L.). *Int. J. Seed Spices* 15 (1): 74–81. <https://doi.org/10.56093/IJSS.v15i1.6>.
- Meena, V, S., Meena, V, K., Bhardwaj, R., Singh, K., Shekhawat, N., & Shukla, A. K., (2025). Genetic diversity and agromorphological characterization of fenugreek (*Trigonella Foenum-Graecum* L.) germplasm provides insight for breeding and crop improvement. *Scientific Reports* 16 (1): 2324. <https://doi.org/10.1038/s41598-025-32066-y>.
- Pathirana, R., & Carimi, F., (2022). Management and utilization of plant genetic resources for a sustainable agriculture. *Plants* 11 (15): 2038. <https://doi.org/10.3390/plants11152038>.
- Singh, K., Gupta, K., Tyagi, V., & Rajkumar, S., (2020). Plant genetic resources in India: management and utilization. *Vavilov J. Genet. Breed.* 24 (3): 306–14. <https://doi.org/10.18699/VJ20.622>.
- Singh, R., Meena, R, S., Choudhary, S., Meena, N.K., Meena, R.D., Verma, A.K., Mahatma, M.K., Yathendranaik, R., Lal, S., Shekhawat, P.K., & Bhardwaj, V., (2025). Deciphering agronomic traits, biochemical components, and color in unique green-seeded fenugreek (*Trigonella Foenum-Graecum* L.) genotypes. *Front. Nutr.* 12 (February): 1542211. <https://doi.org/10.3389/fnut.2025.1542211>.
- Srinivasan, K., (2006). Fenugreek (*Trigonella Foenum-Graecum*): A review of health beneficial physiological effects. *Food Rev. Int.* 22 (2): 203–24. <https://doi.org/10.1080/87559120600586315>.
- Thachuk, C., Crossa, J., Franco, J., Dreisigacker, S., Warburton, M., & Davenport, Guy, F., (2009). Core hunter: An algorithm for sampling genetic resources based on multiple genetic measures. *BMC bioinformatics* 10 (1):243. <https://doi.org/10.1186/1471-2105-10-243>.
- Zandi, P., Basu, S, K., Khatibani, L, B., Balogun, M, O., Aremu, M, O, Sharma, M., Kumar, A., Sengupta, R., Li, X., Li, Y., Tashi, S., Hedi, A., & Cetzal-Ix. W., (2015). Fenugreek (*Trigonella Foenum-Graecum* L.) seed: A review of physiological and biochemical properties and their genetic improvement. *Acta Physiol. Plant.* 37 (1): 1714. <https://doi.org/10.1007/s11738-014-1714-6>.