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GISP: online data management system for pigeonpea germplasm

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ABSTRACT

Germplasm Information System for Pigeonpea (GISP) addresses the data management need by producing a online user-friendly menu driven system that allows users to store, modify and update germplasm information. System has two basic functional modules *viz.*, Germplasm Data Management Module, Germplasm Reports Module. Presently, the database contains information on 1058 accessions (221 early and 837 late maturing lines) evaluated for 22 important descriptors (11 qualitative traits and 11 quantitative traits) for each accession. Statistical analysis of the data was done on the variable with continuous variation to determine the mean, range, variance standard deviation, skewness and kurtosis. Total 4 main reports have been designed to enable quick and accurate retrieval of data *viz.*, Qualitative Report, Quantitative Report, Query-based Report, and Details report. Passport, characteristic, and evaluation data on available germplasm can be reviewed and retrieved through the use of a menu-driven system. Crop breeders can use these data to determine the existence of germplasm that could be useful in their research programs. Requests for germplasm then can be created and forwarded to the appropriate germplasm maintenance site.

Keywords: GISP, ASP.NET, SQL Server 2008, Data Management, Database, DUS, Descriptors

Pigeonpea is one of the most important protein rich perennial pulse crops and is globally cultivated on 7.03 m ha land and 4.89 m tones production in about 50 countries. India has the distinction of being top producer of pigeonpea and alone accounts for 80% of the world acreage and 67% of the world producer(Anonymous 2015). The major pigeonpea producing states in the country are Maharashtra, Karnataka, Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, Gujarat, Jharkhand, Odisha and Tamilnadu. It is crop of resource poor farmers that provides them not only quality food and fodder but also fuel wood (Singh *et al*., 2008). Pigeonpea is well-suited to a large number of cropping systems and constitutes an important place in vegetarian diets.

Indexing the genetic variability is a huge task for plant breeders to provide the end users with easily accessible as well as assessable information on materials they are working with (Miliar *et al.* 1982; Mundankar *et al.* 2008). Ambiguous germplasm identification, difficulty in tracing different characteristics of germplasm data and lack of integration between genetic resources, characterization, evaluation and utilization data have been recognized as one of the major constraints to break the yield plateau (Chen *et al.* 2007; Kumar *et al.* 2013). An extensive utilization of the existing variability already available in the country may play a key role in genetic enhancement of pigeonpea. The number of pigeonpea germplasm collected and evaluated is being maintained without proper electronic data management system. Hence, there is a need to develop online data management system for pigeonpea plant genetic resource data by crop breeders and information technicians to allow users to interact search and locate information of required traits of the germplasm (Ravisankar *et al.* 2009). Presently, the database contains information on 1058 accessions (221 early and 837 late maturing lines) evaluated for 22 important descriptors (11 qualitative traits and 11 quantitative traits) for each accession.

MATERIALS AND METHODS

The database of pigeonpea germplasm has been designed on the basis of information collected during the exploration, evaluation, conservation and distribution levels at Indian Institute of Pulses Research (IIPR), Kanpur. The database facilitates to store germplasm data on agro-morphological traits characterized and evaluated as per DUS (Distinctiveness, Uniformity and Stability) descriptor. A total of 11 important morphological (qualitative traits) evaluation data were included in the database. The details of descriptors and distinguishing states are shown in Table 1. In addition to this, the database also contains agronomical evaluation data. In DUS descriptors for pigeonpea, some of the characters *viz.*, days to flower initiation, days to 50% flowering; days to 75% flowering, plant height at maturity, number of primary branches, number of secondary branches, number of racemes, pod length, numer of seeds per pod, 100-seed mass and yield per plant have been included. Details of these agronomical evaluation data (11 quantitative traits) for pigeonpea germplasm are presented in Table 2. Statistical analysis of the data was done on continuous variation to determine the frequency distribution and summary of statistics (mean, range, variance, standard deviation, skewness and kurtosis).

Proposed system has been developed as online application having client-server three tier architecture comprising Client side interface layer, Server side application layer and Database layer (Dahiya *et al.* 2008; Kumar *et al.* 2006) shown in Fig. 1. The system operates on Windows

2008 Server using SQL Server 2008 and IIS 7.0 for database management server and web server, respectively. Server side application layer is being implemented using ASP.NET with C#.

Table 1. Descriptors (Morphological Evaluation Data) and descriptor states selected for pigeonpea accessions

Descriptor	Descriptor States
Base flower colour(BFC)	Ivory
	Light yellow
	Orange yellow
	Yellow
Growth Habit (GH)	Compact
	Spreading
	Semi-spreading
Vigour at 50% flowering(VF)	Good
	Medium
	Poor
Stem Colour (SC)	Sun red
	Green
	Purple
Plant stand(PS)	Good
	Medium
	Poor
Pattern of streaks(POS)	Dense streaks
	Few streaks
	Medium streaks
	None
Flowering pattern(FP)	Determinate
	Non-determinate
	Semi-determinate
Pod Colour (PC)	Dark purple
	Green
	Mixed, green and purple
	Purple
Seed colour pattern (SCP)	Mottled
	Mottled & speckled
	Plain
	Ringed
	Speckled
Base seed colour(BSC)	Brown
	Black
	Cream
	Dark brown
	Dark grey
	Dark purple
	Grey
	Light brown
	Light cream
	Light grey
	Orange
	Purple
	Reddish brown
	White
Seed shape(SS)	Elongate
	Oval
	Pea
	Square

RESULTS AND DISCUSSION

The proposed system is online, user-friendly, menu driven and allows users to store, modify and update germplasm information as and when required and perform search and retrieve operations efficiently (Pratheepa *et al.* 2014). System has two basic functional modules *viz.*, Germplasm Data Management Module, Germplasm Reports Module. Germplasm Data Management Module of the system has been designed for data entry, updation and submission. Under this module, a data entry form has been designed and developed for entering the basic information related to each accession of pigeonpea germplasm. A sample screen-shot provides the interface to add records of new germplasm into the database (Fig. 2). System has the facility of drop down menu options for selecting the appropriate descriptor state for a particular descriptor (Devraj *et al.* 2016).

Table 2. Agronomical evaluation data selected for pigeonpea accessions

Descriptor	Description
Days to flower initiation (DFI)	Number of days when plants had initiate flowers
Days to 50% flowering (DF)	Number of days when 50% plants had flowers
Days to 75% maturity (DM)	Number of days when 75% pods matured
Plant Height at maturity (PH)	Plant height measured in centimeter
Number of primary branches (NPB)	Branches arising from main shoot were counted
Number of secondary branches (NSB)	Branches arising from secondary shoot were counted
Number of racemes (NR)	Counted in numbers
Pod length (PL)	Length of premature pod measured in centimeter
Number of seeds per pod (NSP)	Number of seeds per pod were counted
100-Seed mass (SM)	After harvest, 100 seeds were counted and weighted in gram
Yield per plant (YP)	Grain yield per plant was recorded in gram

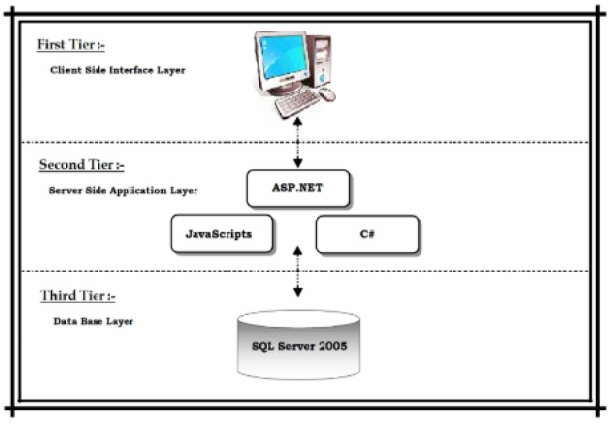

Fig. 1. Proposed system architecture.

The germplasm reports module has been developed to retrieve/search germplasm information based on single character or combination of more than one characters. User customized reports have been designed in PDF format to generate the information on various parameters of pigeonpea accessions. Under this module, total four main reports have been designed *viz.*, Qualitative report, Quantitative report, Query-based report and Detail report. Reports on qualitative characters (morphological evaluation data), generate information about summary of statistics in tabular form and frequency distribution for a particular

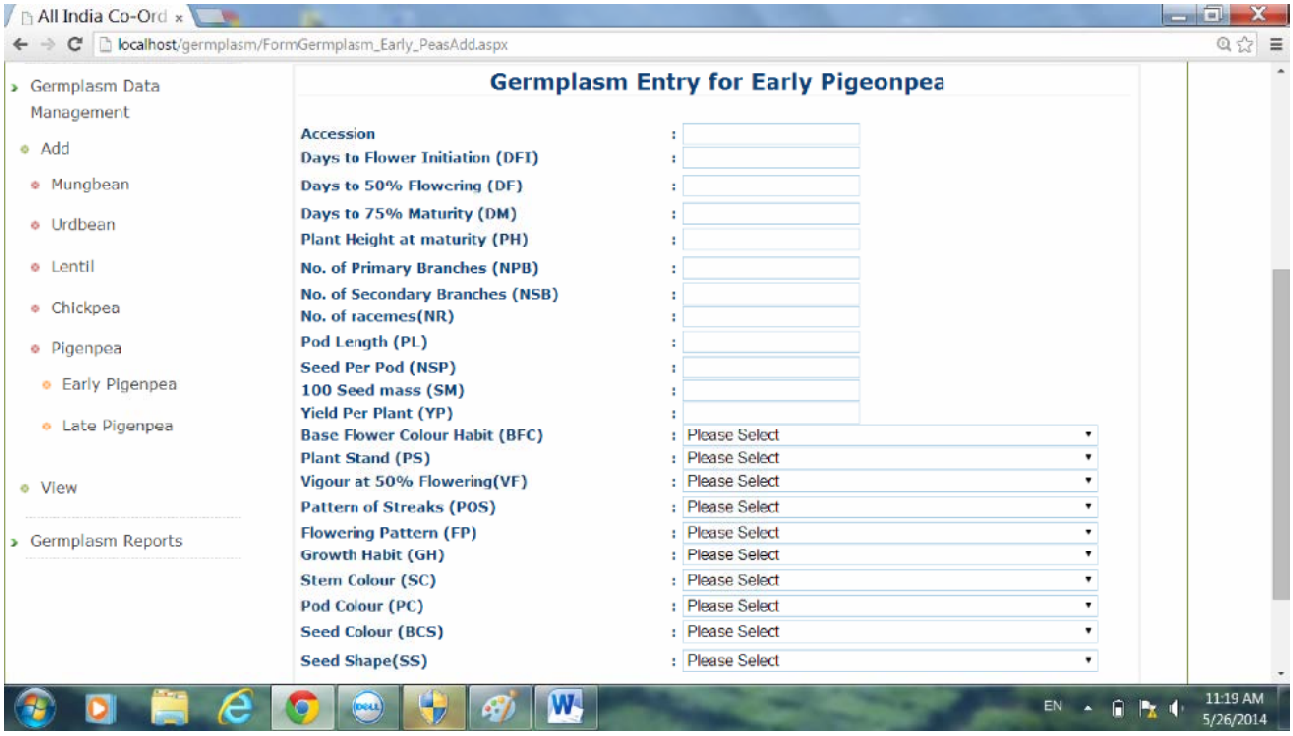

Fig. 2. Screen showing Data Entry for Pigeonpea Gerplasm

character in graphical form(Pie-Chart) (Fig. 3). Similarly, system also generates report on all qualitative characters. Reports on quantitative characters (agronomical evaluation data) show the summary of statistics and frequency distribution for a selected character and/or all characters. Summary of statistics for selected character contains: Number of accessions, Minimum value, Maximum value, Mean, Variance, SD (Standard Deviation), Skewness and Kurtosis and frequency distribution comprising graphical representation (Bar-Chart) of all accessions in a given range (Fig. 4).

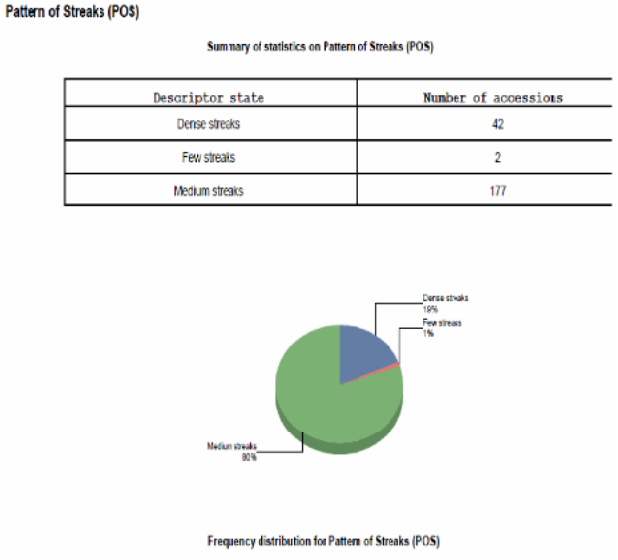

Fig. 3. Screen showing Report on Qualitative Characters.

A query-based report generates report on single character and report on more characters. After selecting the required parameters (Descriptor Name, Descriptor State and Value) and selection based on more than one characters (combination of both morphological as well as agronomical characters), the output screen (Fig. 5) is generated. Detailed report (Fig. 6) displays all the information for each and every accession. After generating this report, it can be saved as PDF format in tabular form.

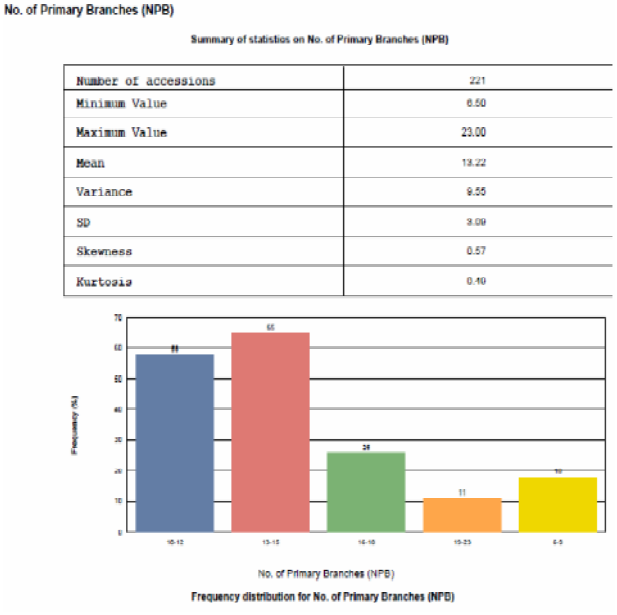

Fig. 4. Screen showing Report on Quantitative Characters.

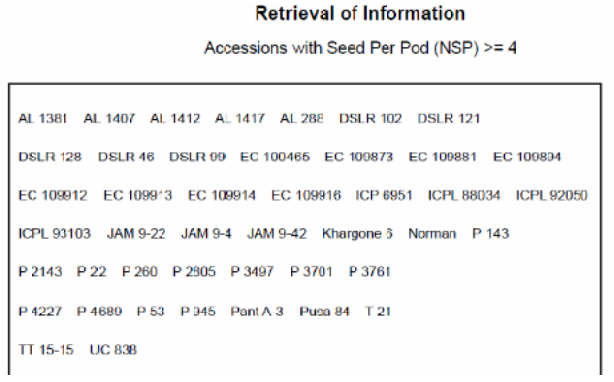

Fig. 5 Screen showing retrieval of information.

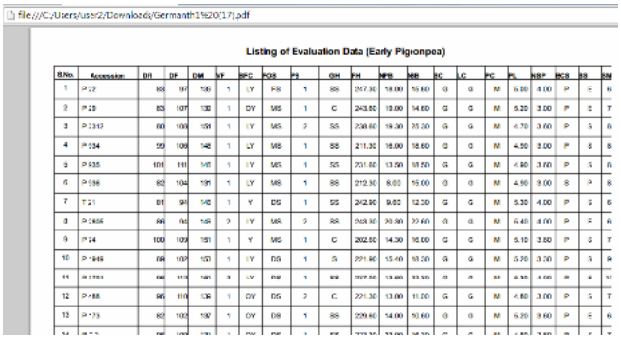

Fig. 6. Screen showing detailed report of early pigeonpea germplasm.

CONCLUSION

Data management system for pigeonpea germplasm is online, user-friendly and menu driven system that can be used by various users *viz*., genetic resource specialists, crop breeders, researchers, planners, extension specialists and farmers. For accessing the system, user needs web browser and internet connectivity. The database of the system can also be updated by the valid users who are authorized and having rights for updation. The system contains information on 1058 pigeonpea accessions (221 early and 837 late maturing lines), including 11 morphological and 11 agronomical descriptors. It will help in retrieving the information for a single attribute or any combination of attributes by identifying the most appropriate accessions with particular traits of interest. The system also provides statistical summary for each evaluation descriptor and its various descriptor states. The system is expected to be of great significance to the end users and will help them in identification and selection of desired genotype. Nevertheless a continuous updation of the system is required to have most recent information on pigeonpea germplasm accessions to make it more useful.

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