

TNAU PDB - Tamil Nadu Agricultural University Proteome DataBase

- Black Gram Proteome

S. Swathi¹, N. Senthil^{1*}, V. Vinod Kumar¹, S. Sathish², N. Jagadeesh
Selvam¹ and M. Raveendran¹

¹Department of Plant Molecular Biology & Bioinformatics, Tamil Nadu
Agricultural University, Coimbatore, Tamil Nadu, India.

²Department of Seed Science and Technology, Seed Centre, Tamil Nadu
Agricultural University, Coimbatore, Tamil Nadu, India.

ABSTRACT

Tamil Nadu Agricultural University Proteome DataBase (TNAU PDB) – Black gram proteome is an open accessible database that focuses on proteome of Black gram (*Vigna mungo* L.). Currently, the database contains reference maps of Two-Dimensional Polyacrylamide Gel Electrophoresis (2D-PAGE) of proteins obtained from artificially aged black gram seeds of variety TNAU blackgram CO 6, which is compared to that of fresh seeds. The database provides information about experimentally identified properties, such as molecular weight, pI value, of the differentially expressed protein due to accelerated ageing and protein sequences obtained using MALDI-TOF mass spectrometry. This database runs on WAMP server with HTML as the front end and MySQL as the backend using PHP as interface and it is hosted in TNAU genomics domain. The basic intention of this database is to provide the detailed information about proteome of black gram. This will help us to understand adaptive and general protective mechanism related to seed aging and effect of ageing on germination.

Web page link: <http://www.tnaugenomics.com/proteome/blackgram.php>

Keywords: Accelerated ageing, Black gram, Database, Proteomics, Proteome database, TNAU PDB.

1. INTRODUCTION

Black gram (*Vigna mungo* L) is a protein rich food, containing about 26 per cent protein, which is almost three times that of cereals. It ranks fourth among the major pulses cultivated in India. Black gram supplies a major share of protein requirement of vegetarian population of the country. It is consumed in the form of split pulse as well as whole pulse, which is an essential supplement of cereal based diet. In India, black gram

*Corresponding author: Email: senthil_natesan@tnau.ac.in

occupies 12.7 per cent of total area under pulses and contribute 8.4 per cent of total pulses production. However, area and production of black gram has declined from 3.01 million ha and 1.30 million tonnes in 2000-01 to 2.97 million ha and 1.23 million tonnes, respectively in 2009-10 [1]. In the current scenario of flourishing “omics” segment that provides deep insight into the mechanism of crop physiology and assist in further crop improvement, proteomics of blackgram is not yet completely exploited as that of cereals like paddy [2]. Since analysis of the proteome provides a direct link of genome sequence with biological activity, data on proteomes are slowly mounting [3]. Currently, in our lab, proteome study on blackgram crop were set in motion. Since seed is the prime source of crop production [4] and storage is inevitable for carryover seeds [5], knowledge on molecular basis of seed ageing is warranted for effective maintenance of seed quality during storage. Accelerated ageing has been widely used to study the pattern of seed deterioration in various crops [6-9]. As a initial phase of proteome study in blackgram, proteome of seed ageing was analysed through comparative study of accelerated aged and fresh seeds and differentially expressed proteins due to ageing were identified. This growing data on proteome of blackgram and unavailability of no separate database concentrating on proteomes of black gram had encouraged us to develop a database to integrate the essential data derived in our lab which would help the researchers to understand the biological process and thereby assists in further research. The main objective of this database is to promote quantitative and qualitative proteome research in black gram that helps in understanding the mechanism of various biotic and abiotic stress related proteins which in turn helps in annotating their function. Currently detailed proteome information about the blackgram variety TNAU blackgram CO 6 seeds are made available in the database.

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61 2. METHODOLOGY

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63 2.1. Database content and source

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The black gram proteome database consists of proteome information about pods, leaves, stem and root. Currently, only proteome data of pods alone is made available. Possible changes in proteins due to artificial ageing on dry seeds of blackgram variety TNAU blackgram CO 6 were analyzed and the quantitative and qualitative proteome changes were recorded. Artificial ageing was done for 6 days by packing seeds in perforated butter paper bags and placed in an ageing jar containing 100 ml of distilled water to maintain $98 \pm 2\%$ relative humidity and incubated at a temperature of $40 \pm 1^\circ \text{C}$ [10]. In the first dimension, 150 μg of protein was loaded on a 17 cm IPG strip with a linear gradient of pH 4-7. In the second dimension, 12% SDS-PAGE gels were used with

74 molecular weight standards. Proteins were visualized by silver staining as suggested by
75 Blum *et al* [11]. Their properties such as molecular weight, pI values and their expression
76 were calculated using image analyzer software. Significant spots were cut, digested in
77 trypsin and analysed in MALDI-TOF for sequencing [12]. The generated data were
78 uploaded in the database.

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80 **2.2. Languages and Software's Used**

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82 The front end of the web application is developed on HTML 5.0 (Hyper Text Markup
83 Language) and the validations are done using javascript. The server side scripting was
84 done on PHP 5.3.0 (Hypertext Pre Processor) and the application was connected to the
85 database using MySQL 5.0.8. Web application was created by using wamp server 2.2
86 and each spot in the gel image was linked to the corresponding protein information with
87 the help of Macromedia dreamweaver.

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89 **2.3. Database Architecture**

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91 The application is built on a three tier architecture model consisting of presentation layer,
92 logic layer and the database layer. The presentation layer is the front end of the
93 application created using HTML with which the user interacts. The middle layer is the
94 application server or logical layer created using PHP, which serves the application with
95 data and accepts the requests from the user. The data layer contains the relational
96 database which contains the data to be fetched by the application.

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98 **3. RESULT AND DISCUSSION**

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100 **3.1. Flow of Data**

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102 Proteome database of blackgram has been added as a sub link under TNAU genomics
103 web page which has home page under the link <http://www.tnaugenomics.com>. From the
104 home page the blackgram database can be reached through the drop down link named
105 TNAU PDB under the tab databases. The flow of data and the procedure to access the
106 database were meticulously depicted in Fig (1). Similar flow of data can also be seen in
107 a database developed for maize [13].

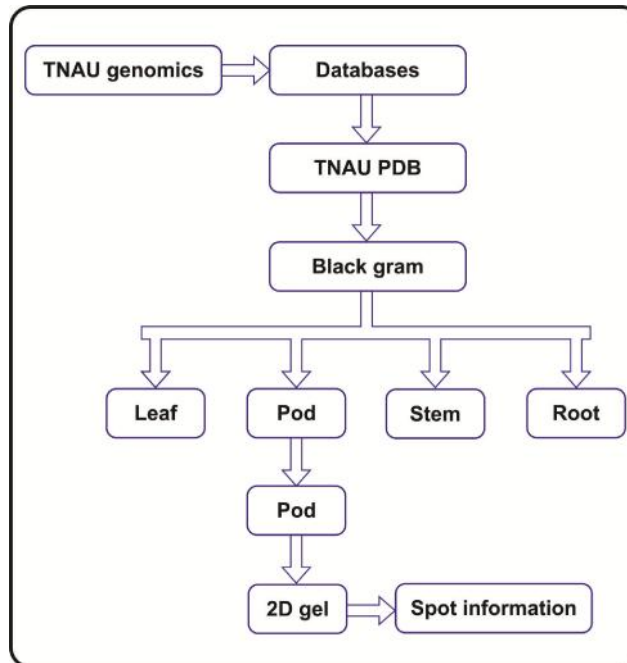


Fig. 1. Flow of data

3.2. Database schema and its features

The data is classified based on the tissue such as pods, leaf, stem, root, etc. from which it is identified. Proteomes obtained using the 2D PAGE and MALDI-TOF methods are displayed using image analyzer software. The description of each spot is stored in the database and they are mapped to the corresponding spots. Based upon the request from the user, the application queries the database and fetches the spot information.

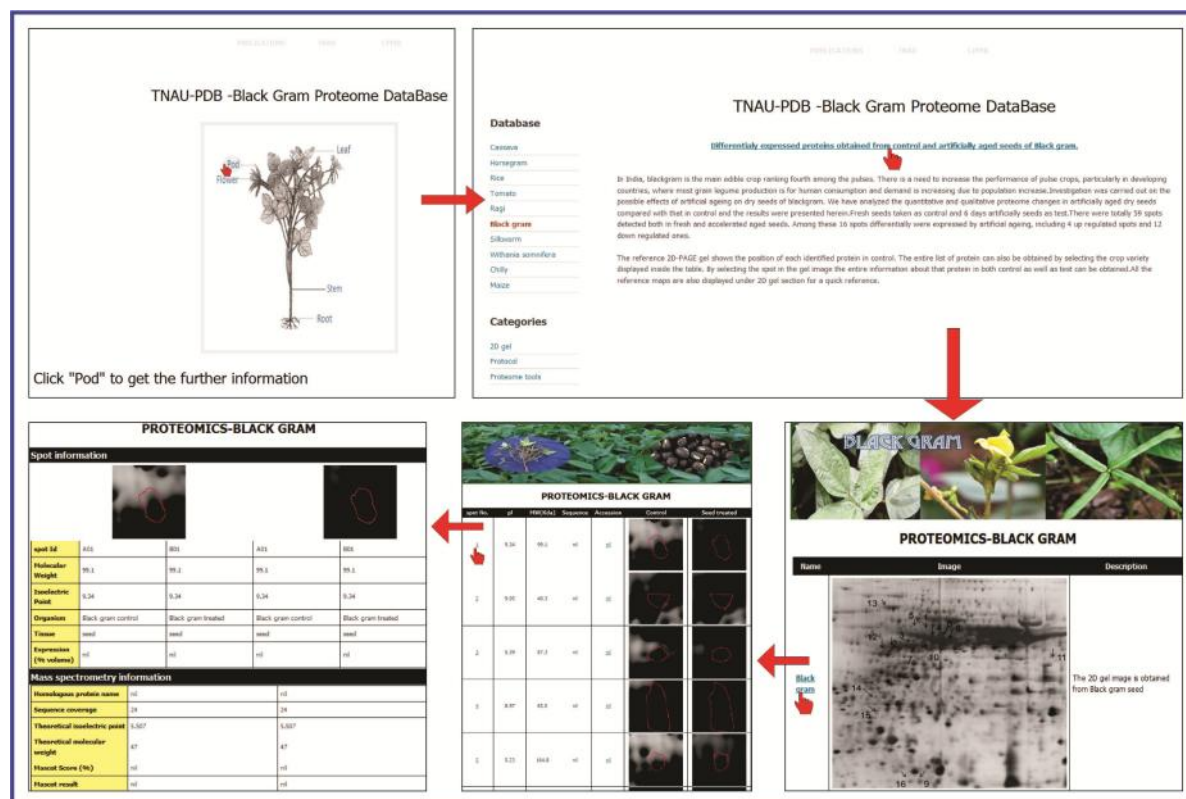


Fig. 2. Procedure to access differentially expressed proteins due to artificial ageing in blackgram seeds

Currently, database contains the proteome information obtained from pods of black gram. The reference 2D-PAGE gel shows the position of each identified protein in that crop. The entire list of protein can also be obtained by selecting the crop name displayed inside the table. By selecting the spot in the gel image the entire information about that protein can be obtained. The results are displayed in such a manner that they are also compared with their control (Fig. 2). All the reference maps are also displayed under 2D gel section for a quick reference. The experiment protocols are listed under the protocol section. Some of the major proteomics tools like includes Mascot, Compute pI/Mw tool in ExPASy and ExPASy Proteomics tools are displayed under proteome tools section. Similar advanced proteome databases were developed for Arabidopsis and maize by Cornell university [14] and DynaProt 2D for dynamic online access to proteomes and two-dimensional electrophoresis gels [15].

3.3. Utility

137 The primary users of this database will be plant breeders, seed technologist, students
138 and other researchers concentrating on blackgram improvement. It shows the proteome
139 changes that could take place at the dry state of aged seeds. Determination of the
140 expression patterns in response to stress, and an understanding of their functions in
141 stress adaptation will provide the researchers with the basis for effective genetic
142 engineering strategies for improving the tolerance of crops to various stresses.

143 **3.4. Future Developments**

144 The database content will be updated routinely. In the near future proteome data for
145 whole plant parts such as root nodules, stem, leaves and expression of protein under
146 different environmental stress conditions will be made available. With the availability of
147 ample proteome data, architecture of the web page might be modified to suit to the
148 excess flow of information.

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150 **AUTHORS' CONTRIBUTIONS**

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152 This work was carried out by the first author SS in collaboration between all authors.
153 Guided by the expertise advice of the second author NS and last author MR, the
154 corresponding author NS designed the study, first author SS and third author VVK
155 designed the web page and wrote the first draft of the manuscript. Fourth author SS and
156 fifth author NJS did the proteomic analysis. All the authors managed the analyses of the
157 study. However, all authors read and approved the final manuscript.

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