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Leveraging web-based tool for phenological data management in climate-sensitive fruit crops like mango

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Abstract

Phenological studies play a crucial role in understanding mango flowering dynamics across diverse climates. However, managing the extensive data generated from observations using the modified BBCH scale poses significant challenges. To address this, we developed a web-based tool in PHP to efficiently manage mango phenology data. This tool aids researchers in organizing phenological data on a timescale by decoding phenophases and presenting them as images, facilitating data summarization through frequency tables of different phenophases. Additionally, the tool incorporates a module that simultaneously depicts phenophases according to the BBCH scale and as a line graph, providing a clear representation of flowering phenology dynamics. The primary objective of this tool is to provide computational assistance to researchers working on mango phenology, accessible worldwide through the link (https://hortportal.org/mangifera_res/site/phenology/). It enables data collected in an Excel sheet in a standard format to be depicted as a series of small images, facilitating the correction or cleaning of raw data. The corrected data file can then be utilized to calculate frequencies and generate an Excel sheet for developing graphs using graphical software. Furthermore, the tool features a built-in module for creating graphs with selective phenophases, allowing simultaneous selection of different phenophases for a line graph depiction, indicating their duration and time of peak occurrence.

Key words: Mango phenology, web-based tool, BBCH scale, PHP platform, data management, frequency tables, line graph visualization

Introduction

Phenological research has gained paramount importance in recent years, especially in the context of climate change and its impact on fruit crop production (Menzel *et al.*, 2020). Understanding the timing and duration of phenological events such as bud burst, flowering, and fruit ripening is critical for assessing the effects of shifting environmental conditions on plant growth and development (Rajan, 2012; Rajan *et al.*, 2013; Ramírez Kumar *et al.*, 2014; Kisvarga, 2023). In this regard, mango (*Mangifera indica* L.), a climate-sensitive fruit crop, stands as a notable example wherein phenological stages are highly susceptible to fluctuations in temperature, rainfall, and humidity (Rajan, 2012). Consequently, the management and analysis of phenological data have become indispensable for predicting crop yields and implementing adaptive agricultural practices (Rajan *et al.*, 2013).

The sheer volume and complexity of phenological data necessitate sophisticated tools for efficient management and analysis. Traditionally, such data were managed manually, posing significant challenges in terms of accessibility, integration, and scalability (McKellip *et al.*, 2010). However, the emergence of web-based tools has transformed the landscape of phenological research by providing scalable, accessible, and user-friendly platforms for data management and analysis (Cope *et al.*, 2017). These tools leverage advancements in cloud computing, data analytics, and collaborative technologies to streamline data collection, storage, visualization, and sharing processes. Additionally, the integration of disparate datasets facilitated by web-based tools enables researchers to derive meaningful insights and foster interdisciplinary collaborations in phenological research (Rosemartin *et al.*, 2018).

Despite these advancements, there remains a need for software solutions capable of facilitating access, integration, and analysis of cross-scale, multi-platform phenological data (Morisette *et al.*, 2021; Pearson *et al.*, 2020). To address this gap, the “Pheno-Synthesis Software Suite” (PS3) was developed, offering a comprehensive set of tools for integrating and analyzing phenological and ancillary data across various scales and platforms. By leveraging PS3, researchers can investigate and interpret phenological processes ranging from individual organisms to landscapes, and from short-term observations to long-term trends (Morisette *et al.*, 2021). Moreover, PS3 holds promise in enhancing phenological modeling, forecasting, and supporting agricultural and natural resource management decisions.

The aim of this study was to develop and evaluate a web-based tool for managing phenological data in climate-sensitive fruit crops, with a specific focus on mango. This tool aims to streamline the organization, interpretation, and visualization of mango phenology data collected using a modified BBCH scale (Rajan *et al.*, 2013). By leveraging PHP and associated technologies, we seek to provide researchers with a user-friendly platform for efficiently managing and analyzing large datasets of mango phenological observations. Through a comprehensive evaluation and validation process, we aim to demonstrate the effectiveness and reliability of our web-based tool in supporting phenological research and promoting sustainable fruit crop management practices in the face of climate change.

Materials and methods

Development of the web-based Tool: For observing phenophases in mango, a modified BBCH scale was generated (Rajan *et al.*, 2011) to facilitate phenological studies. To handle the voluminous dataset generated from these observations, a software tool was developed at the Central Institute for Subtropical Horticulture, Rehmankhera, Lucknow, using the PHP platform. This tool arranges phenological data on a time scale by decoding phenophases and presenting them as images, facilitating easy interpretation of data generated by frequency tables. The dynamics of phenophases, as per the BBCH scale, were depicted through line graphs to provide a clear understanding of various aspects of flowering phenology. The data collected in Excel sheets were formatted into a standard format and represented as a series of small images, aiding researchers in correcting or cleaning raw data. Additionally, a phenophases frequency sheet was generated on a time scale, which could be directly utilized for developing graphs using graphical software.

Resources used: The web tool was developed using XAMPP (Cross Platform + Apache + MYSQL + PHP + PERL), a free open-source web server and PHP development environment. Alternatively, the tool was built on the Apache HTTP Server utilizing PHP server-side scripting language. To read Excel files with extensions (.xls) and (.xlsx), the package "Spreadsheet_Excel_Reader" and class "SimpleXLSX" were employed, respectively. The frequency ratio of specific phenological stages was visualized using the "SVG Graph Library" and "JP Graph Library" for multi-line graph representation.

Methodology: Initially, the tool was designed for users possessing both types of Excel files with extensions (.xls) and (.xlsx). Upon browsing the Excel file, the classes "SimpleXLSX" and "Spreadsheet_Excel_Reader" computed the sheets within the file and fetched the data row-wise. Predefined images corresponding to phenophases were displayed based on the total number of shoots in a tree and the number of weeks. Subsequently, the total number of particular BBCH codes in a week was computed, and the frequency ratio of each phenophase per week was calculated. This allowed for the determination of shoot growth percentage and the identification of phenophases with the highest shoot growth each week. The tool also facilitated the visualization of graphs for at least six phenocodes simultaneously, employing the "JP Graph Library" for displaying shoot development over time.

Results and discussion

In this study, we developed a novel web-based tool to observe dyanamics of phenophases in mango trees, utilizing a modified BBCH scale adapted for phenological studies (Rajan *et al.*, 2011). This tool, created at the Central Institute for Subtropical Horticulture, Rehmankhera, Lucknow, offers a comprehensive platform for organizing and interpreting voluminous phenological data. Leveraging the PHP platform, the tool arranges phenological observations on a temporal scale, decoding phenophases and presenting them as images for intuitive interpretation. Through dynamic line graphs, the tool provides a clear depiction of mango flowering phenology based on the BBCH scale, facilitating deeper insights into various aspects of the growth cycle. Additionally, the tool streamlines data formatting and cleaning processes, enabling researchers to efficiently correct raw data and generate phenophase frequency sheets for graphical representations. By harnessing open-source technologies such as XAMPP and Apache HTTP Server, coupled with libraries for Excel file parsing and graph visualization, this tool offers a user-friendly interface for researchers to analyze and comprehend mango phenological data effectively.

The tool was designed to accommodate users with both types of Excel files, denoted by the extensions ".xls" and ".xlsx", representing Microsoft Office Excel versions 97-2003 and 2007 and above, respectively.

Upon selecting an Excel file from the system by clicking the browse button, the tool utilizes the classes "SimpleXLSX" and "Spreadsheet_Excel_Reader" to parse the file. Subsequently, it systematically retrieves data row by row, moving through each cell. The tool generates predefined images corresponding to the phenophases based on the total number of shoots in a tree and the number of weeks. After displaying the data on the screen, the next step involves calculating the total number of particular BBCH codes occurring in a given week, derived from the total number of shoots in a tree. This computation is denoted by the equation fij = fij + 1, where 'fij' represents the cumulative count of a specific BBCH code occurring in week 'j'.

Fig. 1. The initial screen of the Mango Phenology Monitoring System (MPMS) introduces its outputs and provides options for the type of Excel data sheet to be used.

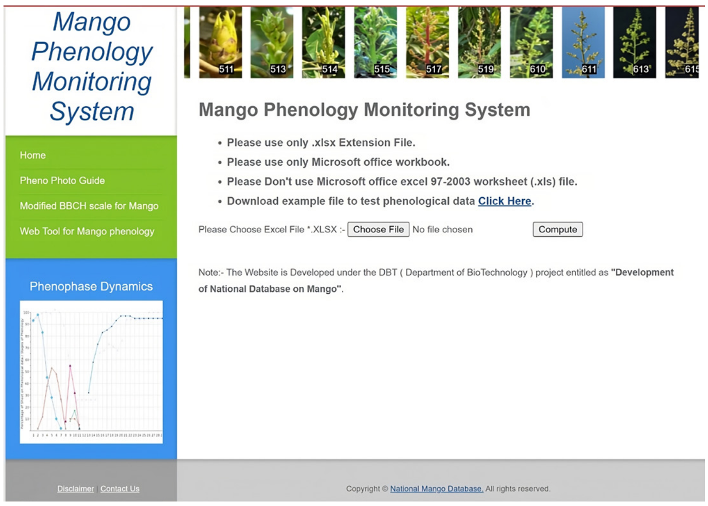

Fig. 2. Use of Microsoft Office workbooks from various versions of Excel, accompanied by an example file for demonstration.

Subsequently, the tool computes the frequency ratio of each phenophase per week, denoted by ‘fij’, where ‘i’ represents the BBCH code and ‘j’ represents the week number. The percentage of shoot growth (PSij) for a particular BBCH code under a specific week is then calculated using the formula PSij = (fij * 100) / s, where ‘s’ represents the total number of shoots (Fig. 3). The tool also separately displays the phenocode with the maximum occurrence in a particular week.

Furthermore, the tool generates a graph based on the frequency ratio, depicting upto six phenocodes simultaneously. To achieve this, a multi-line graph was employed, leveraging the capabilities of the “JP Graph Library”. This graph visually represents the development of shoots over time, offering insights into phenological dynamics (Fig. 4).

The development of the web-based tool for managing phenological data in climate-sensitive fruit crops like mango marks a significant advancement in agricultural research. Leveraging a modified BBCH scale for observing phenophases in mango (Rajan *et al.*, 2011), the tool allows for efficient organization and interpretation of phenological data. By decoding phenophases and presenting them visually through line graphs, researchers can gain valuable insights into mango flowering dynamics across different climates.

The utilization of the PHP platform in developing the tool offers several advantages. It facilitates the arrangement of phenological data on a time scale, enabling researchers to track the progression of phenophases over time. Additionally, the tool’s ability to generate frequency tables of different phenophases aids in identifying patterns and trends in mango flowering behavior. The graphical representation of phenophase dynamics enhances the clarity and interpretability of the data, thereby supporting informed decision-making in agricultural management practices.

The incorporation of features such as importing data from Excel sheets and representing it as a series of small images streamlines the data management process. Researchers can easily correct or clean raw data, ensuring the accuracy and reliability of the analysis. Moreover, the tool’s compatibility with both (.xls) and (.xlsx) file formats enhances its versatility and usability for researchers with varying data preferences.

The future scope of the tool includes providing online correction in phenological data, expanding its functionality to study vegetative growth in mango, and enabling the download of improved/corrected data in Excel sheets. These enhancements aim to further enhance the utility and accessibility of the tool, facilitating collaborative research efforts and promoting sustainable fruit crop management practices.

Week No.			10	11	13	17	19	110	111	115	119	311	312	315	317	319	510	511	513	514	515	517	519	610	611	613	615	617	619	710	711	713	715	719	810	811	819	911	916	Max Number
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	510
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	510
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	511
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30	40	22	5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	511
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25	15	50	7	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	513
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	23	33	15	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	513
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	28	18	35	12	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	514
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	17	13	27	22	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	515
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	2	50	15	12	3	2	2	0	0	0	0	0	0	0	0	0	0	0	519
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	3	7	23	52	0	0	0	0	0	0	0	0	0	0	0	0	615
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	18	57	22	2	0	0	0	0	0	0	0	0	0	0	615
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	65	13	0	0	0	0	0	0	0	0	2	0	617
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53	0	0	0	0	0	0	0	0	22	25	619
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0	28	53	916
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	83	916

Fig. 3. Computing Phenophase Frequency Ratios and the phenocode with the maximum occurrence in a particular week.

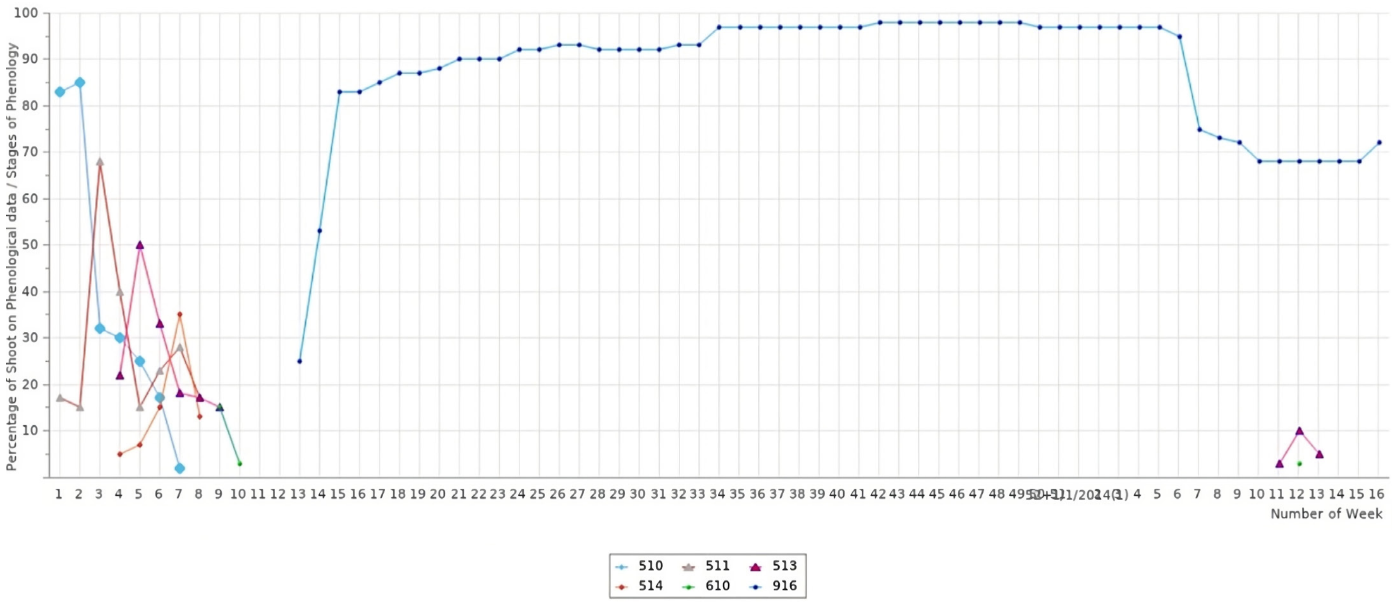

Fig. 4. Visualization of phenocode frequency ratios with multi-line graph

Utilizing BBCH scale-based data, a line graphs were also generated to highlight phenological stages with the highest occurrence rates across various standard weeks and months (see Fig. 4). This graph illustrates fluctuations in different phenophases for identified shoots over time, facilitating the identification of predominant stages. Interpretation of phenophase occurrences was linked to prevailing temperature and rainfall conditions. Analysis of the dataset revealed notable transition patterns in mango phenophases. The data covered observations from the first week of August 2015 (week 33) to the last week of June 2016 (week 24) in Lucknow. Notably, during August (weeks 33-36), stage 010 exhibited the highest percentage of shoots, remaining static from weeks 46 to 51 (November to December), indicating a growth cessation period. However, from week 4 (last week of January), the frequency of stage 010 declined before increasing from week 13, reaching a prominent peak in May, highlighting the cyclic nature of mango growth. The decline in the percentage of shoots at stage 010 suggested a transition to other phenophases. Variations in the duration between stages 010 and 319 throughout the year indicated periods of both slow and rapid growth, as discerned through the scale. Additionally, an alternate flushing pattern was observed in the vegetative growth of mango cv. Langra, with a gradual decrease in the re-flushing frequency of primary and subsequent flushes within the same year.

The tool's future enhancements include providing online correction in phenological data, expanding its functionality for studying vegetative growth in mango, enabling the download of improved/corrected data in Excel sheets, allowing the selection of any number of phenocodes for graph display, and incorporating features to visualize graphs with changes in climatic conditions. These developments aim to further improve the utility and versatility of the web-based tool for managing phenological data in climate-sensitive fruit crops like mango.

Web-based tools like the USA National Phenology Network (USA-NPN) facilitate citizen science data collection on plant and animal life cycle events, aiding in understanding climate impacts. However, accessibility challenges prompted the development of features like climate data overlay, interactive maps, and customizable graphs, improving data exploration and sharing (Auer *et al.*, 2011). The recent advancements in high-resolution remote sensing technology, coupled with sophisticated software pipelines and machine learning algorithms, have enabled the collation, analysis, and application of big data systems in agriculture, particularly in addressing the complex interactions within ecophysiological systems previously considered too challenging to resolve (Potgieter *et al.*, 2021).

Extensive research has delved into the distinct impacts of various global change drivers, particularly climate warming, on plant phenology. While it is widely acknowledged that climate warming typically accelerates the flowering phenology, leading to earlier leaf out and flowering in plants (Liu *et al.*, 2016; Menzel *et al.*, 2006; Sparks & Menzel, 2002; Stuble *et al.*, 2021), other factors such as precipitation can also induce a spectrum of phenological shifts. These shifts exhibit diverse directions and magnitudes across different ecosystems (Liu *et al.*, 2016; Peñuelas *et al.*, 2004; Reyes-Fox *et al.*, 2014; Wang & Tang, 2019). Furthermore, the interactions among these drivers can further complexify phenological responses, posing challenges in accurately predicting future plant phenology amidst global change scenarios (Rice *et al.*, 2021; Ganjurjav *et al.*, 2021; Reyes-Fox *et al.*, 2014). Hence, unraveling these intricate interactions and their repercussions on mango phenology stands as a pivotal endeavor, crucial for enriching our comprehension of ecosystem reactions to ongoing global transformations.

Strengthening the mango phenological network with large-scale phenological data managed and analyzed by this web-based tool will be instrumental in comprehending the impact of climate change. By leveraging such a tool, researchers can systematically gather and analyze vast amounts of phenological data from diverse geographic regions. This holistic approach facilitates a comprehensive understanding of how climate change drivers influence mango phenology across different landscapes. By elucidating the intricate interplay between climate variables and mango phenological responses, this enhanced network can provide invaluable insights into the dynamics of mango ecosystems under changing environmental conditions. Ultimately, the strengthened mango net phenological network will serve as a robust foundation for informed decision-making and proactive management strategies aimed at mitigating the adverse effects of climate change on mango cultivation.

In conclusion, the web-based tool represents a valuable resource for researchers working on mango phenology, offering computational assistance in managing and analyzing large datasets. Its user-friendly interface and robust features make it a valuable asset in advancing our understanding of phenological dynamics in climate-sensitive fruit crops, ultimately contributing to improved agricultural resilience and sustainability in the face of climate change.

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