The operation instructions of BreedingEIS

We established a breeding evaluation information system (BreedingEIS) for improving breeding efficiency. The full system is composed of a web client and a mobile client. The system has two core functions: breeding evaluation and germplasm resource evaluation, meeting the needs of various species and different personnel. We are in the process of establishing the germplasm resource information system. The following focuses on the detailed functions of the breeding evaluation information system.

1. Selection of available systems

The user can select the deployed system. The system's accounts are currently provided offline. Users can apply to us via email for organization accounts to directly use this system. At the same time, the system also supports full deployment to its own server to ensure data privacy.

The system supports two deployment methods: 1) a method that utilizes a Docker container, which does not require secondary development and code adjustment but only needs to deploy an available environment; 2) a method that installs components step-by-step and start services. This method is applicable to computer staff with a certain development foundation, which needs to conduct secondary development through the code and install, deploy and test the modified program. For the detailed installation and deployment process, please refer to the pdf file, "The installation manual of BreedingEIS". The deployment file can be downloaded from our homepage (www.nnyshj. com) or from GitHub (https://github.com/qikaijie/BreedingEIS-M).

2. Access rights of the account

The system's account has three levels of management mechanisms (super administrator account, administrator account and data record user account) with different permissions and functions (Table 1). The system sets up a super administrator account with the highest authority, which is mainly used to establish/delete accounts at all levels and carry out system maintenance. One administrator account was set up for each user unit/organization/individual, with the authority to establish/delete the user account of the data record under this account, fill in basic data, generate the barcode, review and

count the germplasm resources and hybrid evaluation data of this account. The data record user account is only used to distinguish different filling users, and the authority is mainly to fill in new data and use statistical functions.

Table 1. Authority of each account

Account type	Establish/delete administrator account	Establish/delete data record user account	Data statistics	Data filling
Super administrator	Yes	Yes	No	No
Administrator	No	Only this account	Only this account	Yes
Data record user	No	No	Only this account	Yes

3. Presetting a web client

3.1 System login

Through the BreedingEIS website (www.nnyshj.com), the user can access the system login page and can click the box on the top right to switch the language from English Chinese to Chinese (Figure 1). The user enters the username, password, and verification, code and then clicks the sign-in button to enter the system homepage (Figures 1, 2). The test account username is test1, and the password is test1234.
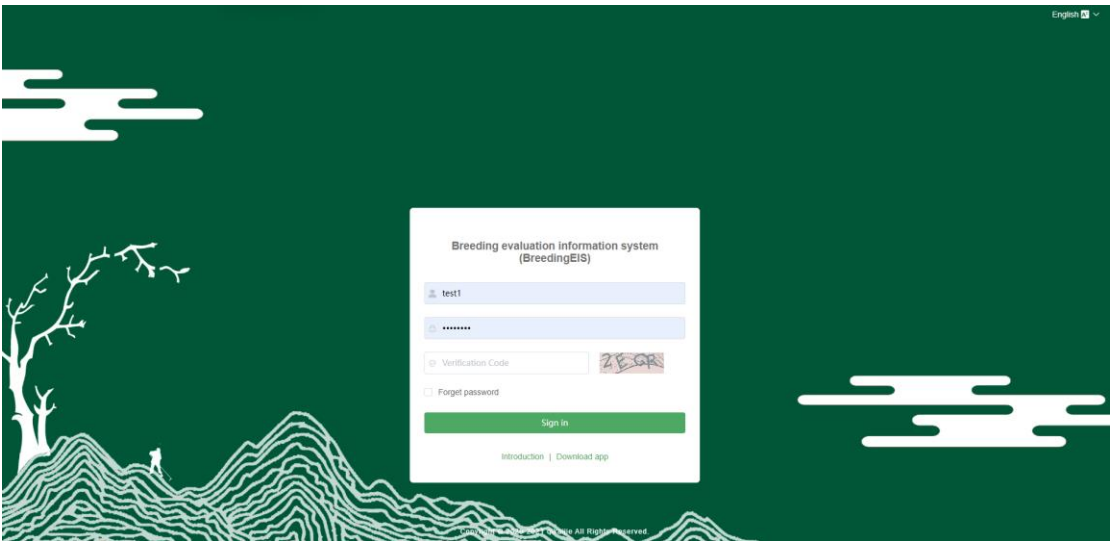
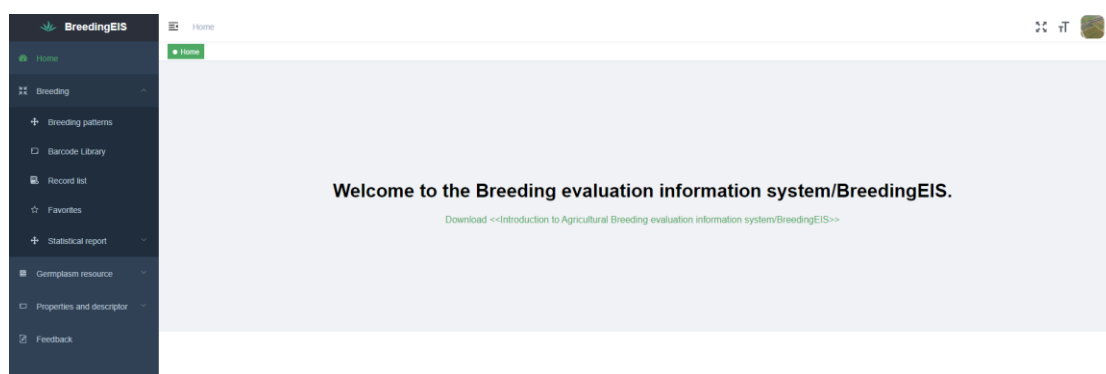Figure 1. Interface of the system login

Figure 2. Home interface of the system

3.2 Personal center

After logging into the system, click the drop-down arrow next to the upper right image. The personal center module is used to enter the basic information of the account manager and to change the account password (Figure 3).
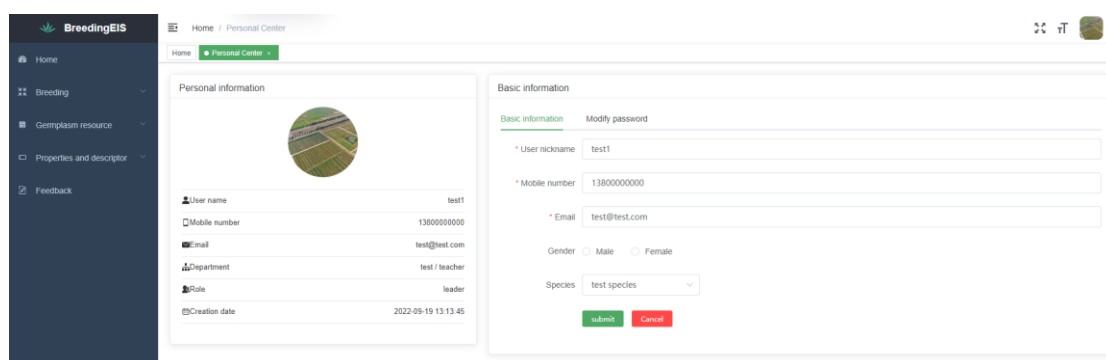

Figure 3. Account information modification interface

3.3 Breeding patterns in the breeding module

The breeding module includes five subfunctions: breeding patterns, barcode library, record list, collection information and statistical reports, which are mainly used to comprehensively interpret and apply the information from the breeding patterns, as well as to establish a barcode library and to view the details of existing records (Figures 4-6).

The breeding patterns are used to manage the existing breeding method and focus on the unique numbering for each new group (Figures 4, 5). The user first adds breeding combinations by clicking the new breeding population button. Users can also add

parental information, breeding date, breeding code, and quantity of the breeding materials on this page. After registering this information, it is displayed in the middle of the page. When the number of combinations is large, the page search function can be enabled by using parent and breeding year information.

Taking cross breeding as an example, this function can record the details of pollination, seed collection, sowing, planting and other information relevant to the hybrid combinations (Figure 5). This content is the basic information of breeding and the main raw data of the system. For the users' convenience, we also added an import function. After downloading the fixed format template, the relevant data are copied to the template according to the template format, which enables the uniform addition of information after uploading (Figure 6). Later, the data for the current year can be filled in according to the phenological periods within a year.
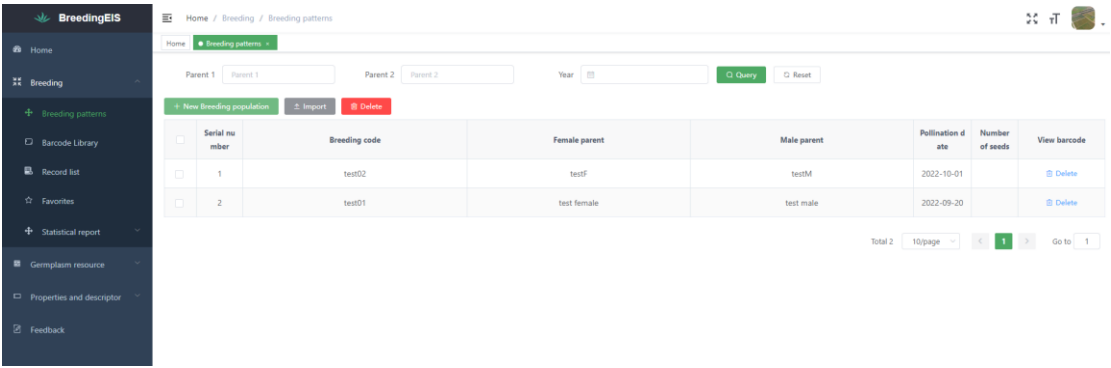
Figure 4. Main interface of breeding management
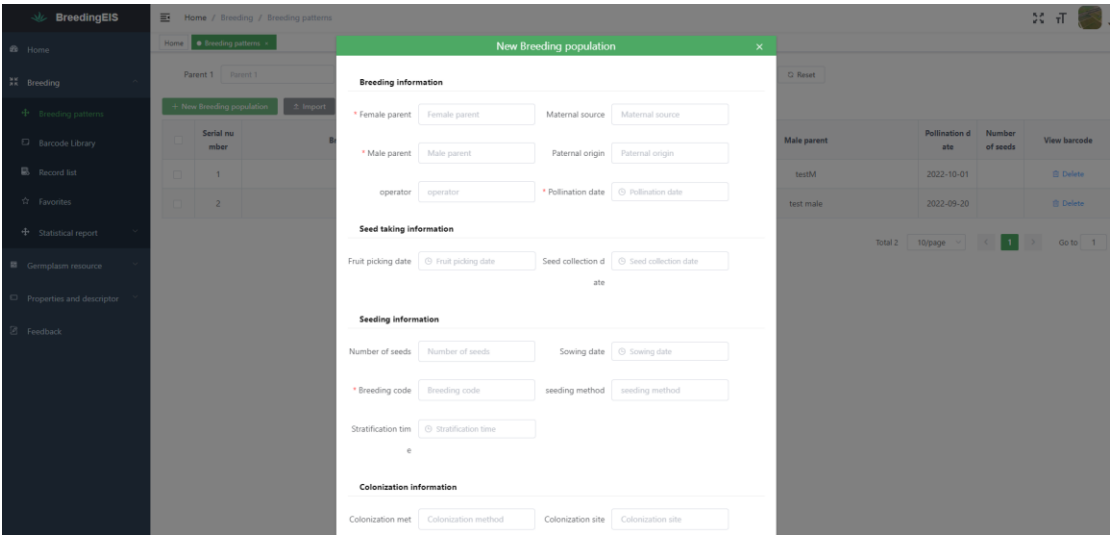
Figure 5. Interface of a new breeding population
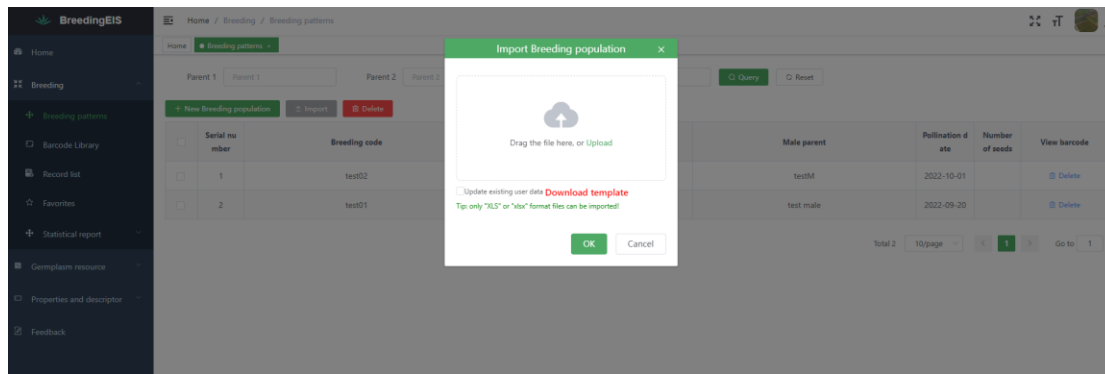
Figure 6. Import interface of breeding information

3.4 Barcode library in the breeding module

The barcode library was used to generate identity codes for individual plants of every population (Figure 7). Users enter this page and first use the breeding year, parent name or breeding code information registered by breeding patterns to quickly locate the target population. Then, users click the generate barcode button to register the information of Base code+Nursery code+ridge number+row number (the number of rows per ridge) +max number (the maximum number of individual plants per row) (Figure 8A). Considering the complexity of land resources and the diversity of utilization in agricultural production, the system is set to draw a planting map according to the maximum number of individual plants in the whole row of this nursery (Figure 8B). Users can use the operation mode of left-clicking to select and right-clicking to delete to number the individual plants of the population in the corresponding area of the planting map according to the actual situation. Finally, users can click submit, and a prompt box of successful generation pops up (Figure 9). Through this function, each individual plant has its own identity code or QR code. The identity code consists of the long code (base code + region code + ridge number + line number + serial number) and short code (breeding code + an individual plant tracking number). At this time, the barcode and creation date information of each single plant of the combination have been displayed in the main interface of this function. Users can click the export QR code or export barcode to batch output the identity code or the QR code of this population (Figure 7). In addition, users can click the red Delete button to delete the barcode information of all the individual plants in this population. Users click the Generate QR code and Delete options under the individual plant's operation information column to view the QR code information of the individual plant and delete all the information of the individual plant (Figure 7).

Figure 7. Interface of the barcode library

Figure 8. Interface of a newly generated barcode

A. Interface for setting the coding rules for the current breeding pattern; B. Interface for setting the coding for individual plants by clicking the selection method.
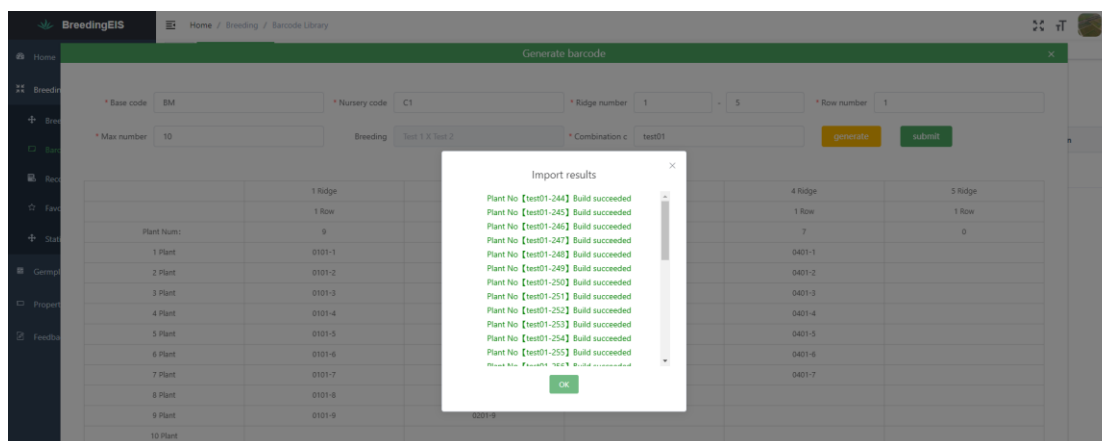
Figure 9. Prompt box of successfully generating individual plant numbers

3.5 Properties and descriptor module

The properties and descriptor module includes three subfunctions: species management, additive properties, and properties classification (Figures 14-18).

The species management subfunction mainly involves system compatibility and embeds information about various crop species (Figure 14). Users can select the desired species types and add user-defined groups according to the evaluation schedule at different stages. Users can click the "Add category" button to group the properties and descriptor generated by the "Properties and descriptor" function (Figure 15). Users can group according to the evaluation period and evaluation type, such as phenology and fruit development period, or customize the grouping. The set grouping information will be displayed synchronously on this function interface and mobile app. Users can sort, modify, hide and delete groups on the web page for easy statistics.
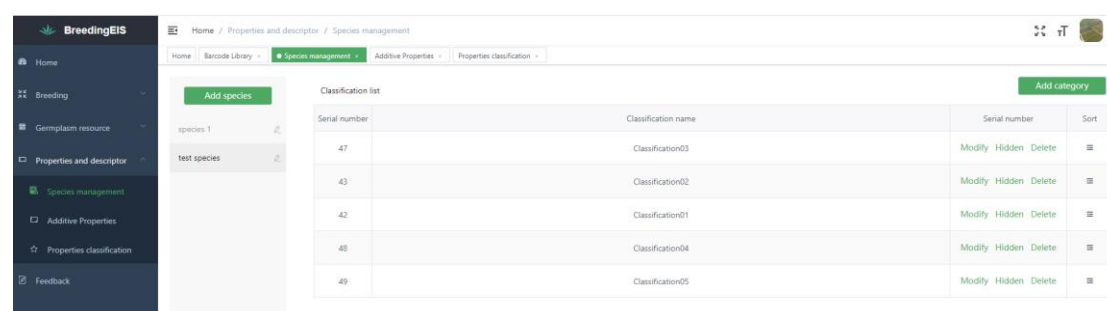

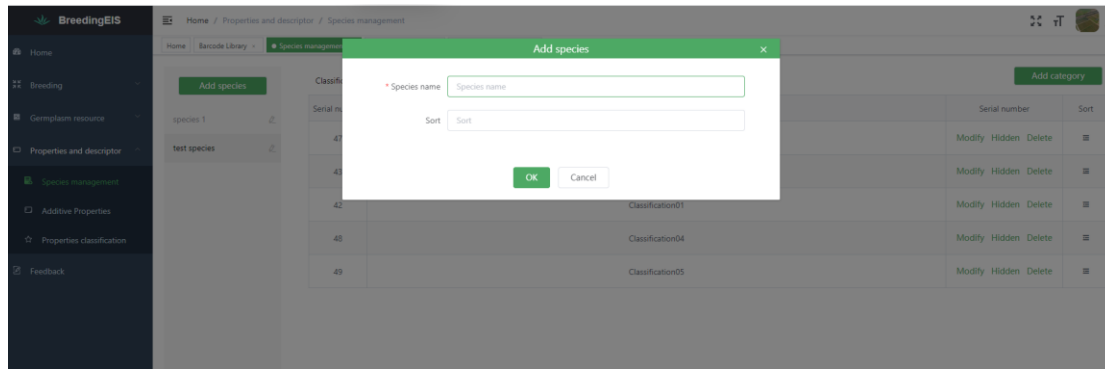Figure 14. Classification interface of species and traits

Figure 15. Interface of the add category

The subfunction of additive properties is mainly to add and import the characteristics and descriptors required for breeding evaluation of the corresponding crop species (Figure 16). This content expands the user's authority and can be customized according to actual needs to facilitate the personalized content evaluation. At present, we added the main characteristics and corresponding descriptors of 17 common fruit trees (strawberry, pear, citrus, prunus mume, plum, kiwifruit, loquat, apple, peach, grape, persimmon, melon, watermelon, apricot, red bayberry, cherry, jujube), including fruit color, single fruit weight, soluble solids content, stone cells, etc. Users can directly search and use the descriptor library of the fruit tree. In addition, users can click the "Additive properties" button, enter the character name, and select species and type to customize and add properties (Figure 17). The type includes five patterns: single choice, multiple choice, date, number box, and text box. Single choice, multiple choice and date are all developed based on the click selection mode. For example, the fruit color can be set to red, slightly red, green and other different colors for single choice, while the fruit shape can be set to long, round, oblate and other different types for multiple choice. Additionally, the phenological period can be set to date selection mode. The number box and text box are used to enter corresponding information. The number box defines the number type, and the text box can enter any content. For example, single fruit weight and plant height can be set as the number type; maturity prejudgment and memo can be set as the text box. The set properties and descriptor will be displayed on the main interface of this function. Many descriptors used in the initial stage can be uploaded through templates (Figure 16).

Figure 16. Interface of the distribution statistics in the statistical report subfunction
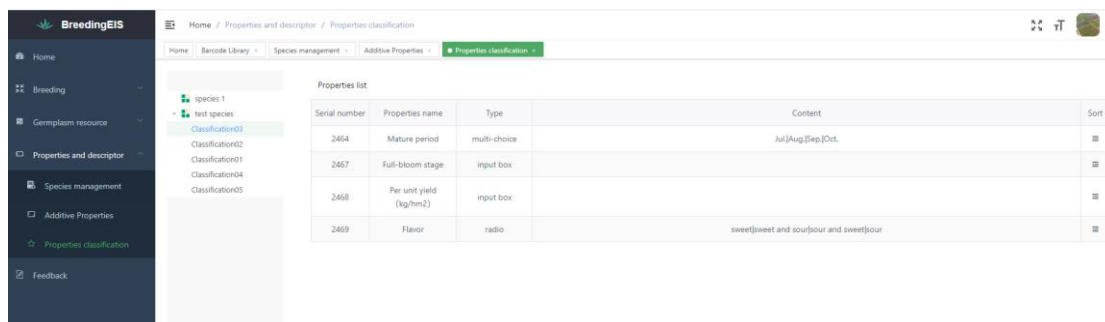
Figure 17. Interface of the additive properties function

The property classification subfunction classifies and sorts the characteristics in the above evaluation group to facilitate the rapid screening of the required characteristics during field evaluation with the mobile client and to improve the system's efficiency (Figure 18). Users can sort the characteristics by dragging the icon under the sort column (Figure 18). This sort is also displayed synchronously with the mobile app.

Figure 18. Interface of property ranking

4. Collection of mobile client data

The main functions of the mobile client are focused on field evaluation work, including barcode recognition, evaluation data input, image and video file collection, real-time viewing and comparison of early evaluation data, and real-time upload and download of all relevant data. The user downloads and installs the app package (BreedingEIS-M) from the web client (http://www.nnyshj.com/#/download) or mobile app store (Figure 19).
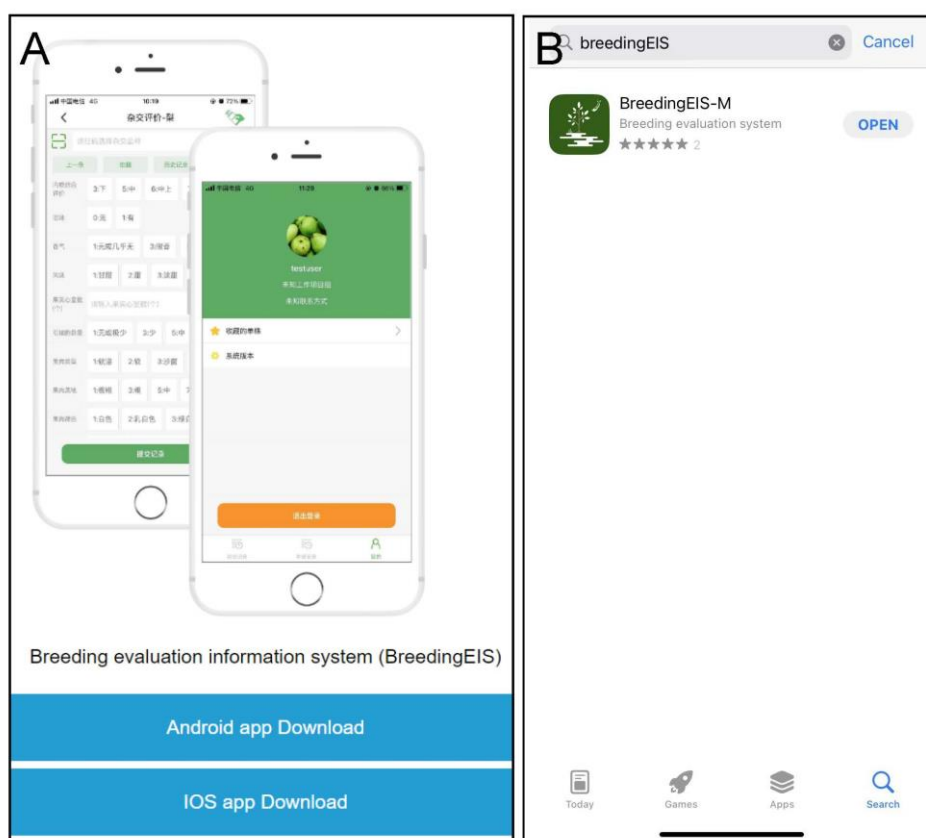

Figure 19. Download of the mobile software BreedingEIS-M in web client interface (A) and IOS appstore (B).

4.1 System login

After the software is installed, it opens the app, enters the username and password (the account and password are the same as those on the web page), and clicks Login to enter the main interface (Figure 20).
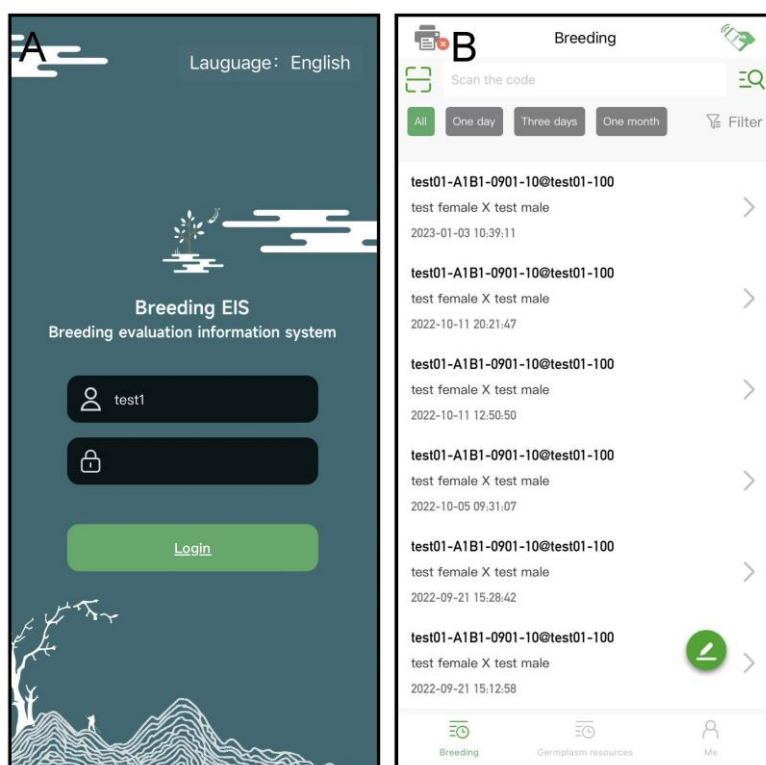

Figure 20. Homepage of mobile software

A. App login interface; B. Homepage of software after login

4.2 Introduction to operation interface

The homepage of the software is divided into three main parts: identity code selection area, screening function area and record list area (Figure 20B).

In the identity code selection area, the user clicks the scanning function button to scan the QR code label and can quickly locate all the investigation and evaluation records of the corresponding individual plant for the label (Figure 21A, B). The user can also enter the short code to search by pressing the search function button (Figure 21C). In addition, the mobile client device can make direct contact, termed 'snuggling,' with the NFC tag on this interface to search and locate the evaluation data. Note that the snuggle function is only applicable on the Android system. The iOS system requires the user to click the

"Code scanner" icon on the upper right to call the NFC function (Figure 21B). Moreover, when clicking the printer icon on the top left, the system can connect to the portable label machine through Bluetooth for printing QR codes, which can be attached to the sample to be evaluated to facilitate the detection of relevant indicators in the laboratory later (Figure 20B).

In the screening function area, the corresponding investigation and evaluation records can be quickly filtered by one specific day, a period of three days and a period of one month by clicking the corresponding time button (Figure 22). The user can click the filter button to quickly screen the corresponding investigation and evaluation records according to the breeding year, breeding parents and other information.
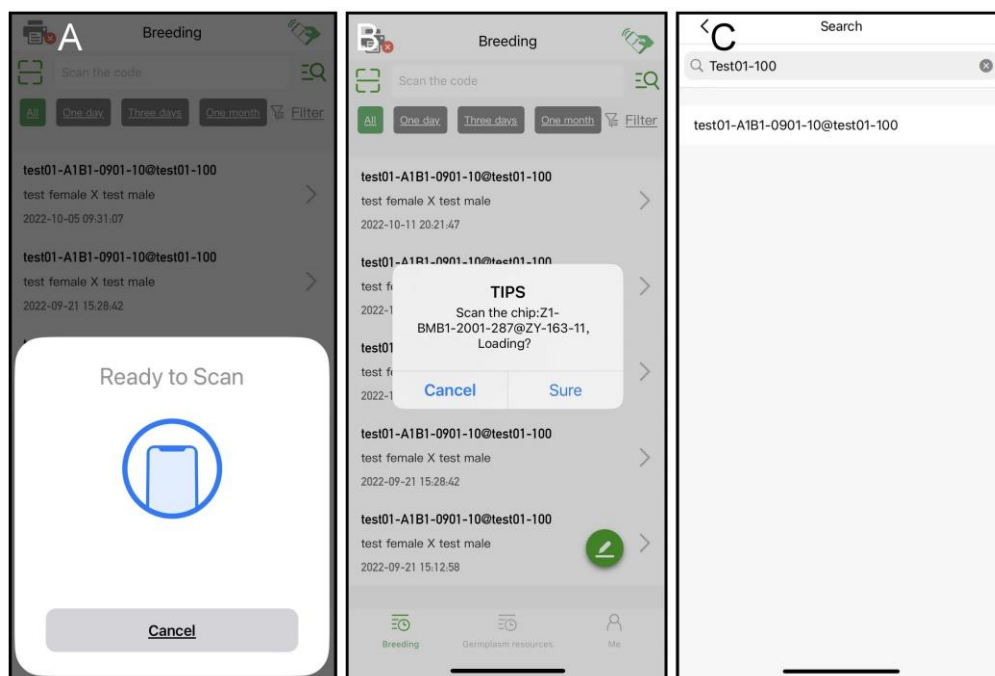

Figure 21. The interface of three query methods for the entry code in the home page.

A. Start NFC function interface on the iOS system; B. Reading interface of NFC; C. Users can enter the short code search interface.
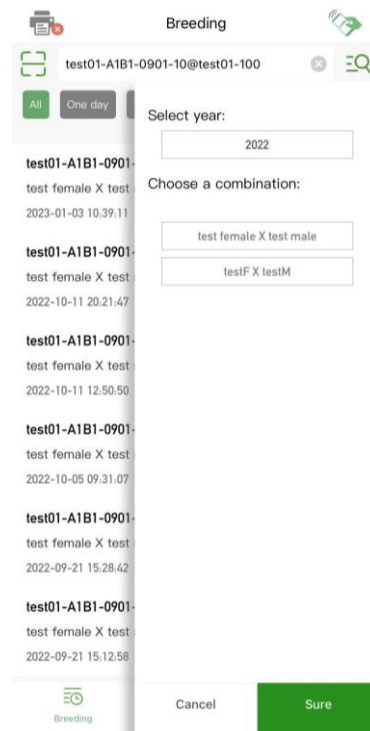
Figure 22. The interface of the screening function on the home page

The user can click the evaluation function button of the pen icon to enter the breeding evaluation system (Figure 20B). First, the user selects the characteristic classification for evaluation (Figure 23A). Here, the evaluation classification and the characteristics included in each classification are preset and sequenced through the web. The user clicks the upper category button to quickly locate the required category (Figure 23A). The characteristics under each classification can be selected as a group or individually. After grouping and characteristic selection, users click "Next" to enter the main page of evaluation (Figure 23B). The main evaluation page is divided into three main functional areas for display: 1) The area marked with a red box is the identity code identification function area (Figure 23B). The upper end is marked with the corresponding species type, such as 'apple'. The lower end is marked with the code scanning function button on the left, the middle part is the identity code display area of the identified individual plant, and the Favorites function button is on the right side. 2) The area marked with a blue box is the evaluation function area (Figure 23B). 'Previous' and 'Next' correspond to the previous or next identity code in relation to the current identity code. The identity code can be switched directly to simplify the scanning operation process. 'Capture' means calling the camera to capture images or record videos (Figure 24). Users can click 'Capture' to add multiple images and video and

click "submit" to upload them to the server in real-time (Figure 24). After confirmation, users can also enter the interface again to add or delete uploaded images or videos. The 'History' function can provide a real-time and convenient view of the historical evaluation data and provide a reference for the current evaluation (Figure 25). At the same time, users can copy the previous evaluation content by clicking the Clone button, and the current evaluation can be modified based on this information to reduce the workload (Figure 25). In this system, an individual line and its expanded progeny are given the same identity code, which is distinguished only by additional characters and recorded as primary selection, multiple selection and final selection records, and all evaluation data of the individual plant, such as maturity, appearance characteristics, internal quality, etc., can be displayed in real-time and conveniently in the historical record to facilitate comparative evaluation and improve the accuracy and stability of evaluation data. 3) The area marked with a yellow box is a quick evaluation area for characteristics and their descriptors (Figure 23B). Different classifications, characteristics and preset descriptors for this item are displayed in large font. The user directly clicks to complete the record of evaluation content and to support characteristics entered as text. After clicking or filling, the user then clicks 'Submit Record' at the bottom to upload relevant data, images, and video to the server in real-time and to save them in the database in order (Figure 26). At this time, the button color changes from green to gray (Figure 26B), indicating that the user has uploaded successfully but can still continue to make changes and resubmit.
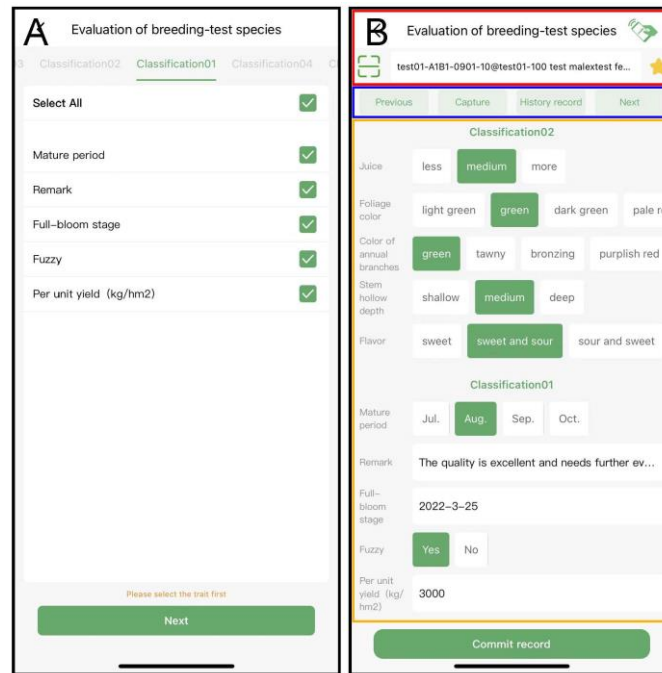
Figure 23. Main interface of characteristic classification (A) and evaluation (B).

A. Interface for characteristic classification selection; B. Main page of evaluation. The area marked with a red box is the identity code identification function area, the area marked with a blue box is the evaluation function area, and the area marked with a yellow box is a quick evaluation area for characteristics and their descriptors.
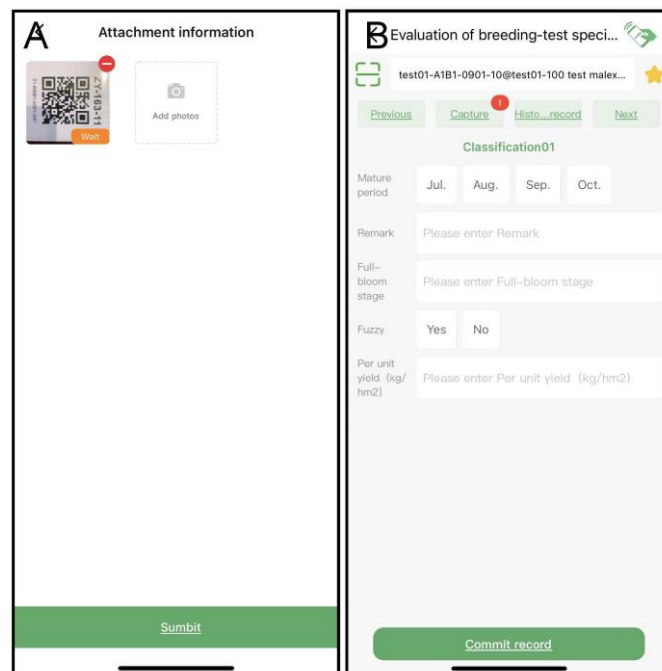

Figure 24. Image and video capture interface

A. Upload image or video interface; B. Interface after uploading image or video.
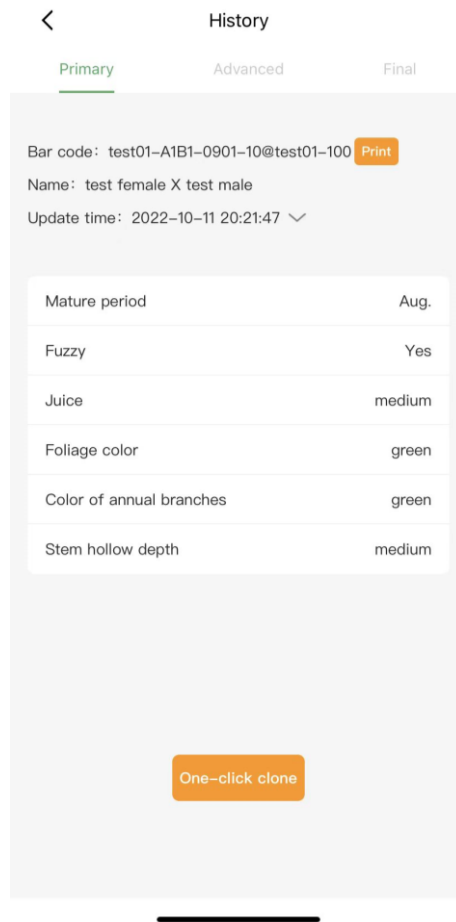
Figure 25. Interface of History function
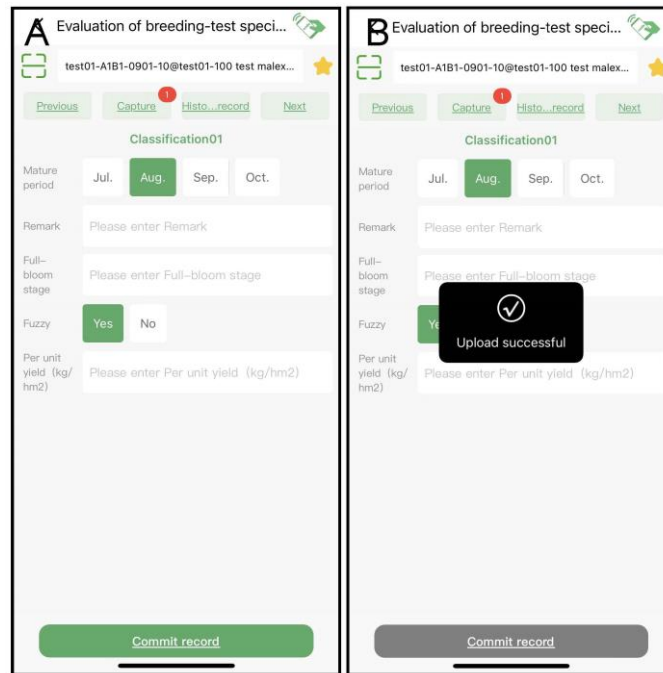
Figure 26. Display interface after evaluation

A. Fill in the page; B. Submit page

In addition, by clicking the 'Me' button at the bottom of the homepage, the user can enter the Personal Center (Figure 27). Similar to what is seen in the web client, this area provides a feedback function (Figure 27). Moreover, it also provides access to collection information and software version number information (Figure 27). The Favorites function is mainly used to mark superior plants (Figure 28). Click this function button to view all the individual plant directories in the Favorites (Figure 28C). Click the identity code to view the detailed information of each evaluation record of the individual plant. The first Favorites is marked in yellow, and the second collection is marked in red. We can change the Favorites level and delete the record (Figure 28D). All records are uploaded to the server in real-time and synchronized with the web client.
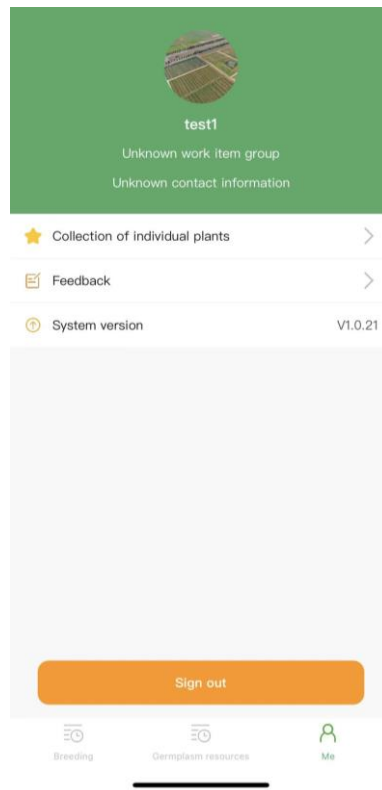
Figure 27. Main interface of the "Me" function
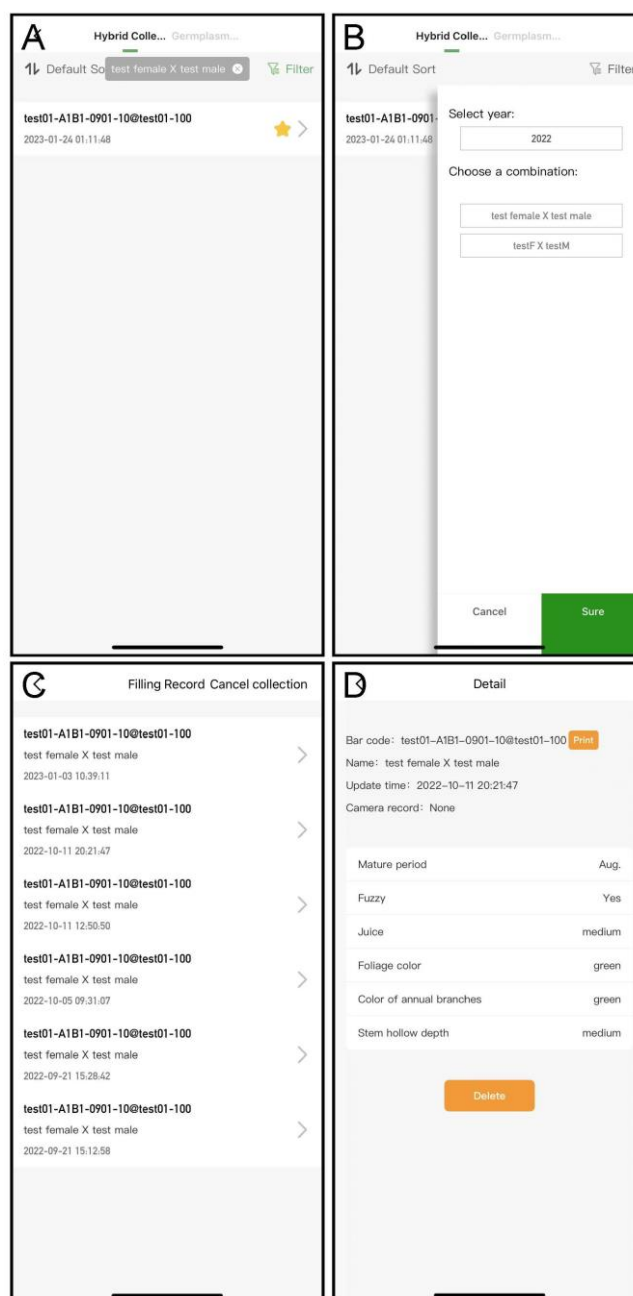
Figure 28. Interface related to the Favorites function

A. Main interface of the Favorites function; B. The interface of the screening function in the Favorites; Specific evaluation directories (C) and detailed information of each record (D) of individual plants marked with the Favorites function

5. Data analysis of the web client

5.1 Record list

A record list is used to record all breeding data from a detailed analysis of the data in the current user account (Figure 29). Enter this page, first use the breeding year, parent name or breeding code information registered by breeding patterns to quickly locate the

target population. Users can also add an evaluation date range for filtering. The first page of this function displays the evaluation records of all individual plants of this population. At the same time, users can upload laboratory-measured experimental data according to the corresponding template through the Import function on this page. Users can also download all the evaluation record data of the population through the Export function.

Figure 29. Interface of the record list

5.2 Favorites

The Favorites subfunction information is used to mark excellent germplasm resources to facilitate later searches and comparisons and to enable further evaluation screening (Figure 30). Individual plants in the favorites are displayed on the main page of this function. Users can view all the evaluation records of the individual plant by clicking barcodes. According to the breeding specifications of new crop varieties, the selected individual plants should generally meet the stable expression of excellent target traits for more than two years and retain relevant evaluation data for new variety approval/identification. Therefore, this subfunction also enables secondary collection. When the user clicks on the Favorites button for the first time in the first year/stage, the color changes from white to yellow, and when the user clicks again in the next year/stage, the color changes to red. At the same time, we can change the Favorites level by clicking the text under the Operation column. For potential new cultivars to meet the requirement of stable expression of excellent target traits over the course of two years, the next step can be arranged according to the details of the actual situation.

This can enable users to track whether an individual plant meets the requirement of stable expression of excellent target traits over the course of two years and can be used as an important tool for targeting an individual plant.
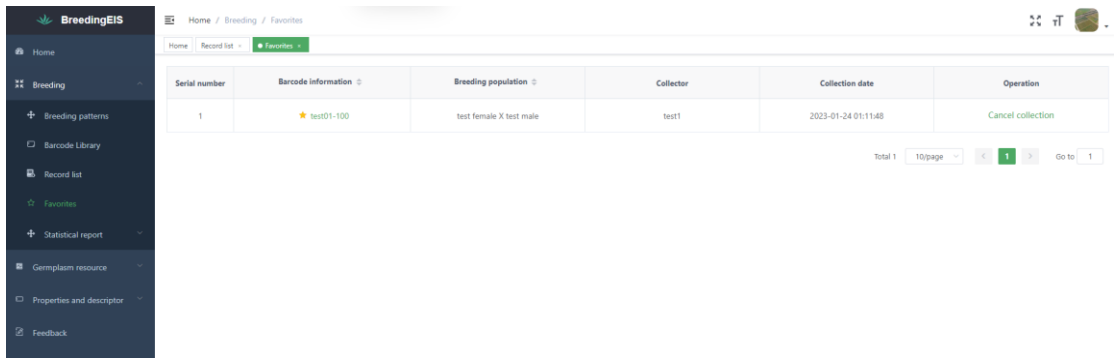

Figure 30. The Favorites interface

5.3 Statistical report

The statistical report subfunction is itself divided into three subfunctions: the entire population (Figure 31), individual plant evaluation (Figure 32), and distribution statistics (Figure 33). The entire population is used to count all the traits of an individual plant from a single population in a year, that is, to list the detailed evaluation data of all individual plants of the population in a certain year in the form of a table (Figure 31). Enter this page; first, use the breeding year and parent name information registered by breeding patterns to quickly locate the target population. In this function interface, all the individual plant information of the population is displayed according to the properties. Users can sort breeding target traits by clicking the arrow at the bottom right of the trait to facilitate rapid selection of superior plants.

Individual plant evaluation is used to analyze and compare the evaluation data of individual plants for many years and is often used for in-depth analysis and screening of target traits in population evaluation (Figure 32). Enter this function page, quickly locate the information of the individual plant using the individual plant code, and display all the annual information of the individual plant according to the properties on this interface. Through this function, users can check whether the traits of the individual plant are stable in different years.

Distribution statistics are used to intuitively understand the survey times of an individual plant of a certain population in different years, and they are mainly used to count the fruiting or flowering time and the number of fruits or flowers (Figure 33). Once enter this page, users can use the breeding year and parent name information

registered by breeding patterns to quickly locate the target population. In this function interface, the evaluation times of the individual plant are displayed according to different years.

Figure 31. Interface of the entire population in the statistical report subfunction

Figure 32. Interface of individual plant evaluation in the statistical report subfunction

5.4 Feedback

The Feedback subfunction is used to collect users' suggestions on our system and to answer users' questions during the use process (Figure 34).
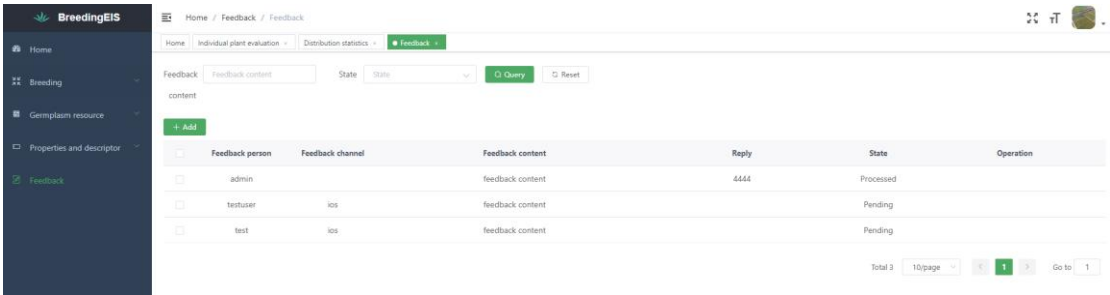
Figure 34. Interface of the feedback function

6. Application instance

We take pear cross breeding as an example.

In 2013, we gave the pollen of 'Zaoguan' to the stigma of 'Yuluxiang' pear and collected the seeds of the offspring of the hybrid combination. In 2014, we obtained the hybrid combination ('Zaoguan' × 'Yuluxiang') of seedlings of the offspring, and then we generated a barcode through the web client, BreedingEIS (Figures 35, 36), and hung it on the corresponding individual plant in 2019 (Figure 37).
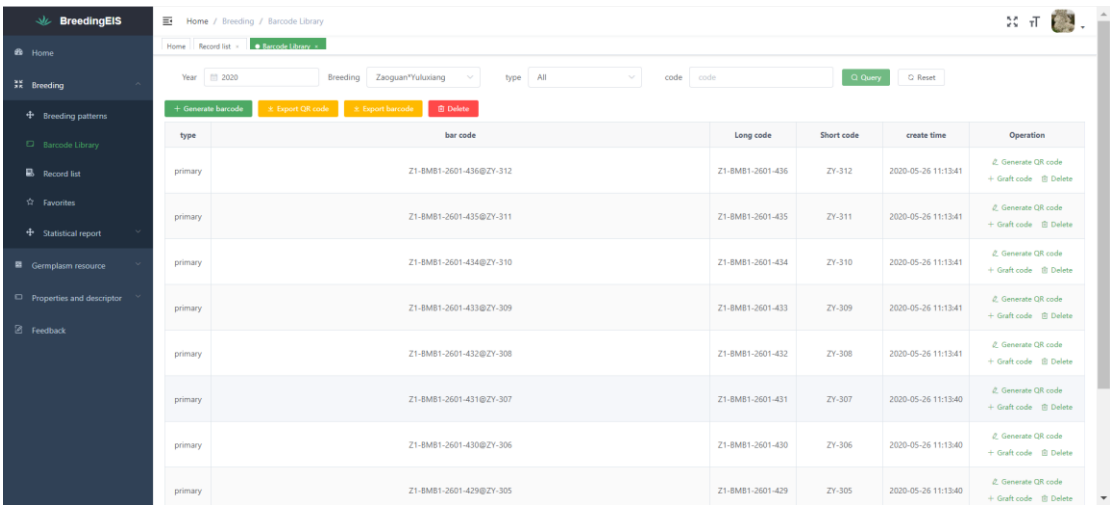
Figure 35. Generate barcode for hybrid combination ('Zaoguan' × 'Yuluxiang')
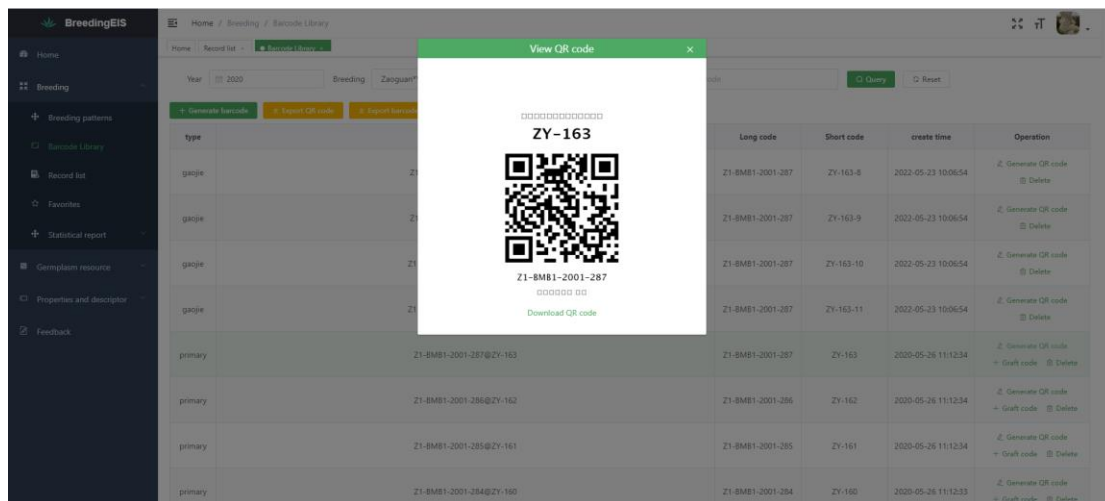
Figure 36. Example of specific QR code information for individual plants

Figure 37. Each individual plant with an identity code
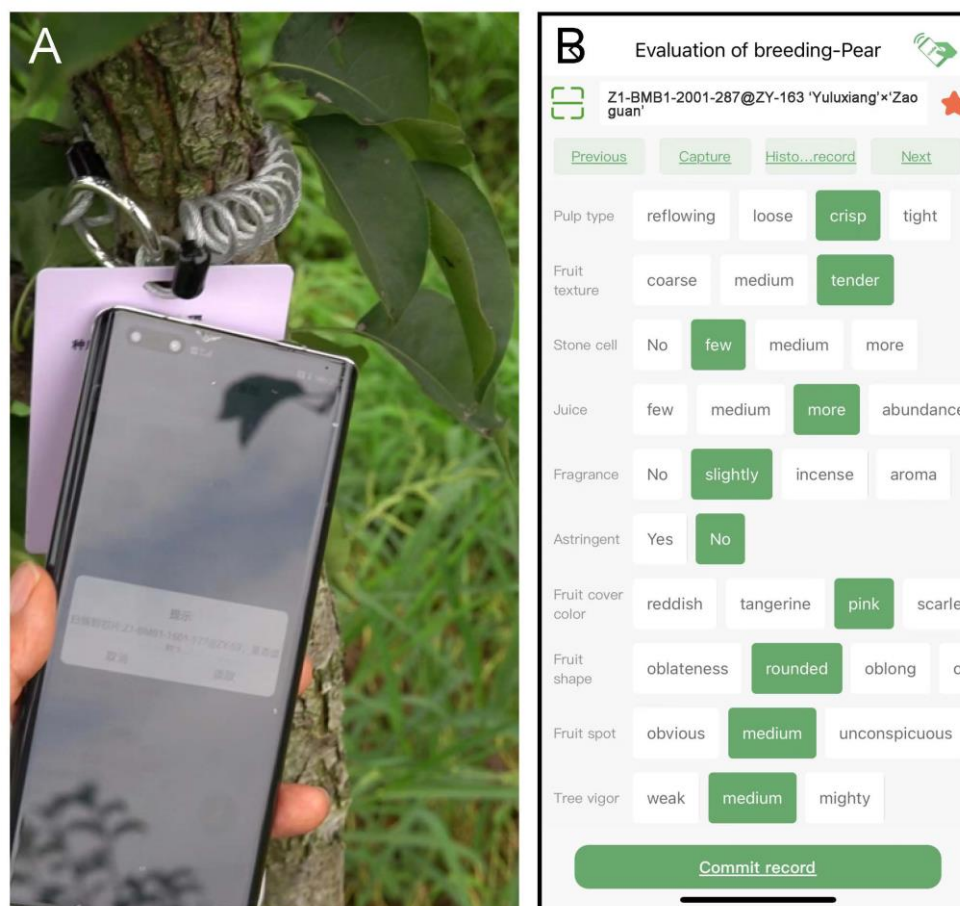
Figure 38. Mobile scans of the identity code of the individual plant (A) and the software evaluation interface (B).

Afterward, we scanned the code using a mobile phone to make field records (Figure 38A, B). Then, we analyzed the evaluation data on the web client. As there are few red peel pear resources in Asia and most Asian pears fruits grow for more than 160 days with a mature later, we focused on fruit development period, appearance traits, internal quality and hoped to obtain new varieties of a high-quality early-maturing red peel pear. In the entire population, according to the ranking of comprehensive evaluation indicators of appearance and fruit maturity, we found the top individual plant, Z1-BMB1-2001-287@ZY-163 (Figure 39). In 2020, we evaluated this individual plant as a superior line. Therefore, in the same year, we grafted its branches onto a 6-year-old tree for further evaluation (Figure 40A). In 2021, we re-evaluated the individual plant and found that its quality was excellent and its character was stable (Figure 40B). In

2022, we evaluated the grafted pear tree of this individual branch and found that its comprehensive performance was similar to that of the seedling tree and its character was still stable (Figure 40C).

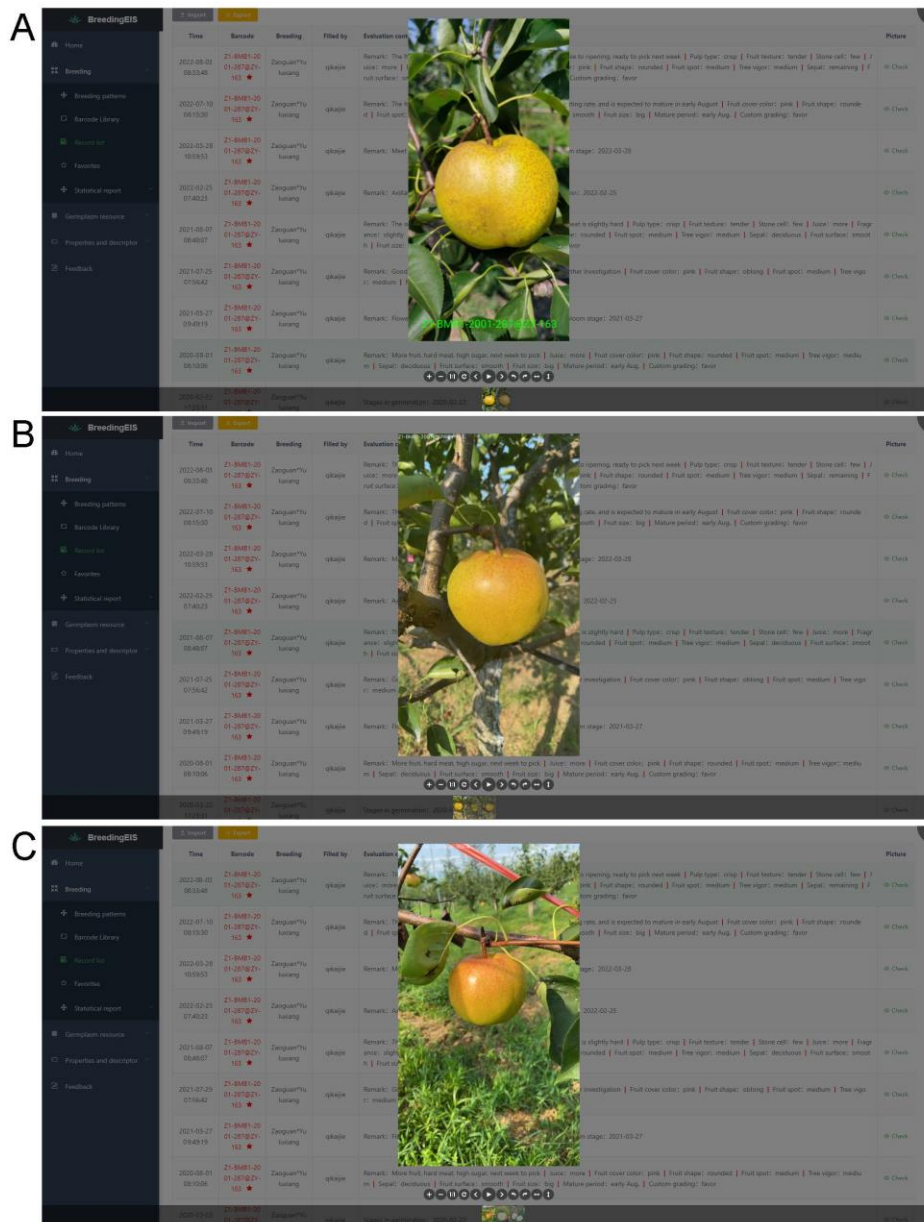Figure 39. Entire population analysis of individual plant evaluation results in hybrid combination ('Zaoguan' × 'Yuluxiang')

Figure 40. Evaluation record of individual plant Z1-BMB1-2001-287@ZY-163 in different years in 2020 (A), 2021 (B), and 2022 (C).

Using the Individual plant evaluation and Favorites function, we checked the detailed evaluation data of the individual plant again and found that the individual plant showed excellent traits in the evaluation for three consecutive years (2020-2023), meeting the standards of the Distinctness, Uniformity and Stability (DUS) test (Figures 41, 42).

Figure 41. Character stability analysis of individual plant, Z1-BMB1-2001-287@ZY-163 by Individual plant evaluation function.

Figure 42. Favorite records of individual plant, Z1-BMB1-2001-287@ZY-163.

Finally, we screened the superior strain, Z1-BMB1-2001-287@ZY-163 (Figure 43), and prepared it to apply for plant variety rights.

Figure 43. Fruiting state of individual plant, Z1-BMB1-2001-287@ZY-163.

Note: If you have any questions, please feel free to contact us via email (Shutian Tao: taost@njau.edu.cn or Shaoling Zhang: slzhang@njau.edu.cn).