



# User Perspectives SPBase NaCRRI

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# Outline

- Why sweetpotatobase?
- Routine plant breeders task
- Progress in the use of sweetpotatobase
- Way forward
- Conclusion
- Acknowledgement



# Why sweetpotatobase

- Archive and retrieval of all information associated to trials
- Trial management
- Electronic data capture
- Plot / plant tracking made easy
- Continuous update of features on the base

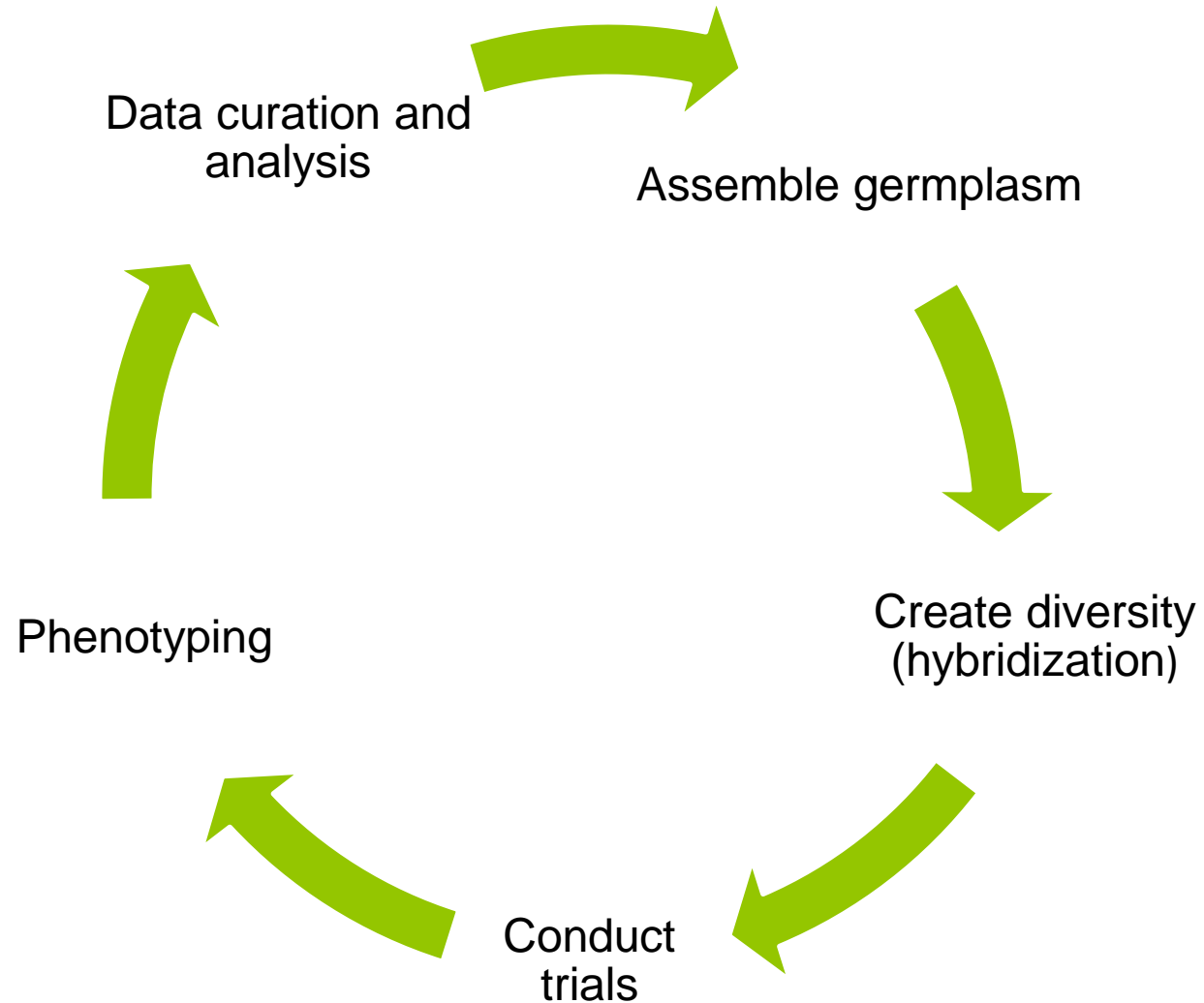


# Why sweetpotatobase

- Data sharing
- Data manipulation
- Simple statistics
- Open source <https://sweetpotatobase.org/>
- Data integrity and security
- Documentation and support



# Routine plant breeders task



# Progress on the use of sweetpotatobase

- 3475 accessions
- 5 cross trials designed
- 38 trials

The screenshot shows the SweetPotatoBase Search Wizard interface. At the top, there is a navigation bar with the SweetPotatoBase logo and links for Search, Manage, Analyze, Genomes, and About. The main heading is "Search Wizard" and the sub-heading is "Explore the database using metadata".

The interface includes a "Login to start from a list" button with a refresh icon. Below this, there are four dropdown menus for selecting search criteria:

- breeding\_programs**: A list of countries including Ghana, GT4SP-CIP, Lima, Mozambique, NCSU, and **Uganda** (selected).
- trials**: A list of trial names including "NKB\_IntermediateYieldTrial\_BUZARDI2011", "NKB\_IntermediateYieldTrial\_NaCRRRI", "NKB\_IntermediateYieldTrial\_NaCRRRI2015", "NKB\_IntermediateYieldTrial\_NaSARRI", "NKB\_IntermediateYieldTrial\_NaSARRI2011", "NKB\_IntermediateYieldTrial\_RwebitabaZambia", "NKB\_IntermediateYieldTrial\_RwebitabaZambia", "Phenotyping 8 x 8 Mwanga diversity panel", "Phenotyping 8 x 8 Mwanga diversity panel", "SPYLOT2011\_UG-NaSARRI", and "SPYLOT2012\_UG-NaCRRRI".
- accessions**: A list of accession numbers including "2017/APA 356/OP/1" through "2017/APA 356/OP/18".
- please select**: An empty dropdown menu.

Below the dropdown menus, there are "Select All" buttons and "OR (v)" operators. At the bottom, there are four boxes showing the number of items and selected items for each dropdown:

- breeding\_programs: Items: 6, Selected: 1
- trials: Items: 68, Selected: 38
- accessions: Items: 3475
- please select: No Selection

# Manage accessions

- Accession lists

Show  entries Search:

| List Name  | Count | Type       | Validate | View | Delete | Download | Share | Group                    |
|--|-------|------------|----------|------|--------|----------|-------|--------------------------|
| 2016 OP seedlings                                | 451   | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| 2017 check list for Weevil resistant OP seedling | 4     | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| 2017 Weevil resistant OP seedling                | 730   | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| 2017On Farm genotypes                            | 12    | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| 8 x 8 checks                                     | 2     | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| AYT locations                                    | 35    | locations  | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| Checks for NKB flowering trial                   | 2     | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| IYT check  | 1     | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| NC-07-847 accession list                         | 189   | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |
| NC-08-427genotypes                               | 30    | accessions | ✓        | ☰    | ✗      | ↓        | ➔     | <input type="checkbox"/> |

[View Public Lists](#)



# Manage trials

- Designing multilocation trials
- All 2017 experiments, 2018
- 5 Locations added
- Type of designs: CRBD
  - Alpha lattice
  - Augmented

The screenshot displays a web interface for managing trials. On the left, there is a search bar and a section titled "Download Trial Phenotypes" with a blue button labeled "Download Phenotypes". Below this, instructions state: "Double click trial (🌿) or folder (📁) to view detail page." and "Breeding programs (🏠)". A "Folders" section contains three buttons: "Create new folder", "Move trial(s) to folder", and "Move folder". On the right, a tree view shows a folder named "Uganda" containing several trials and sub-folders. The trials listed are: 16BBTKaZARDI, 16BBTNaCRRRI, 16BBTNaSARRI, 18AAYTUganda, 18ACRFBCIP, 18ACRFBtrial, 18ASPVDLima, 2015Ug, 2016Ug, 2017Ug, 2017A, and 2017B. The 2017B folder is expanded to show sub-trials: 20017B\_OBS5734NaSARRI, 2017BNC427-30BUZ, 2017BNC435-30BUZ, 2017BOnFarm12ABI, 2017BPYT2013E-30ABI, and 2017B\_Observation210ABI.



# Manage crosses

## 2018 Cross trials

- Yield
- SPVD
- Alternaria blight
- Weevil resistance
- Dry matter content

The screenshot shows the SweetPotatoBase web application interface. At the top, there is a navigation bar with the SweetPotatoBase logo and menu items: Search, Manage, Analyze, Genomes, and About. A search bar contains the text "chelangat". Below the navigation bar, the page title is "Manage Crosses".

The main content area is divided into two panels. The left panel, titled "Information", contains a search box, a "Double click crossing trial (🌿) or folder (📁) to view detail page." instruction, and a "Breeding programs (📁)" section. The right panel, titled "Breeding Programs -- Folders -- Crossing Trials", contains a "Refresh" button and a tree view of the data structure.

The tree view shows the following structure:

- Mozambique
- Uganda
  - 2016ASPGH\_FUMESUA\_CROSSES
  - 2017B80A50NaCRRRI
  - 2018 Crossing Trials
    - Alternaria\_CT
    - Drymatter\_CT
    - Processing\_CT
    - SPVD\_CT
    - SPW resistance hybridization
    - Yield\_CT
- Ghana
- NCSU
- Lima
- GT4SP-CIP

# Phenotyping

- Historic trial curation and upload
- Simplified with fieldbook app

**Folders**

Create new folder

Move trial(s) to folder

Move folder

2015A\_MAPPON\_NKB287AbiZARDI

2015A\_MAPPON\_NKB287RwebitabaZARDI

BUZARDI NKBM Mapping population phenotyping

NKB\_IntermediateYieldTrial\_ABIZARDI

NKB\_IntermediateYieldTrial\_BUZARDI

NKB\_IntermediateYieldTrial\_NaCRRRI

NKB\_IntermediateYieldTrial\_NaSARRI

NKB\_IntermediateYieldTrial\_RwebitabaZARDI

2015B

NKB\_IntermediateYieldTrial\_ABIZARDI2015B

NKB\_IntermediateYieldTrial\_BUZARDI2015B

Manage Analyze Genomes About

chelangat

NKB\_IntermediateYieldTrial\_RwebitabaZARDI2015B

2016Ug

2017Ug

2017A

2017B

20017B\_OBS5734NaSARRI

2017BNC427-30BUZ

2017BNC435-30BUZ

2017BOnFarm12ABI

2017BPYT2013E-30ABI

2017B\_Observation210ABI

2018Ug

2018A

Phenotyping 8 x 8 Mwanga diversity panel for sweetpotato weevil resistance

Phenotyping 8 x 8 Mwanga diversity panel for sweetpotato weevil resistance\_AbiZARDI

Phenotyping 8 x 8 Mwanga diversity panel for sweetpotato weevil resistance\_NaCRRRI, Uganda

Phenotyping 8 x 8 Mwanga diversity panel for sweetpotato weevil resistance\_NaSARRI, Uganda

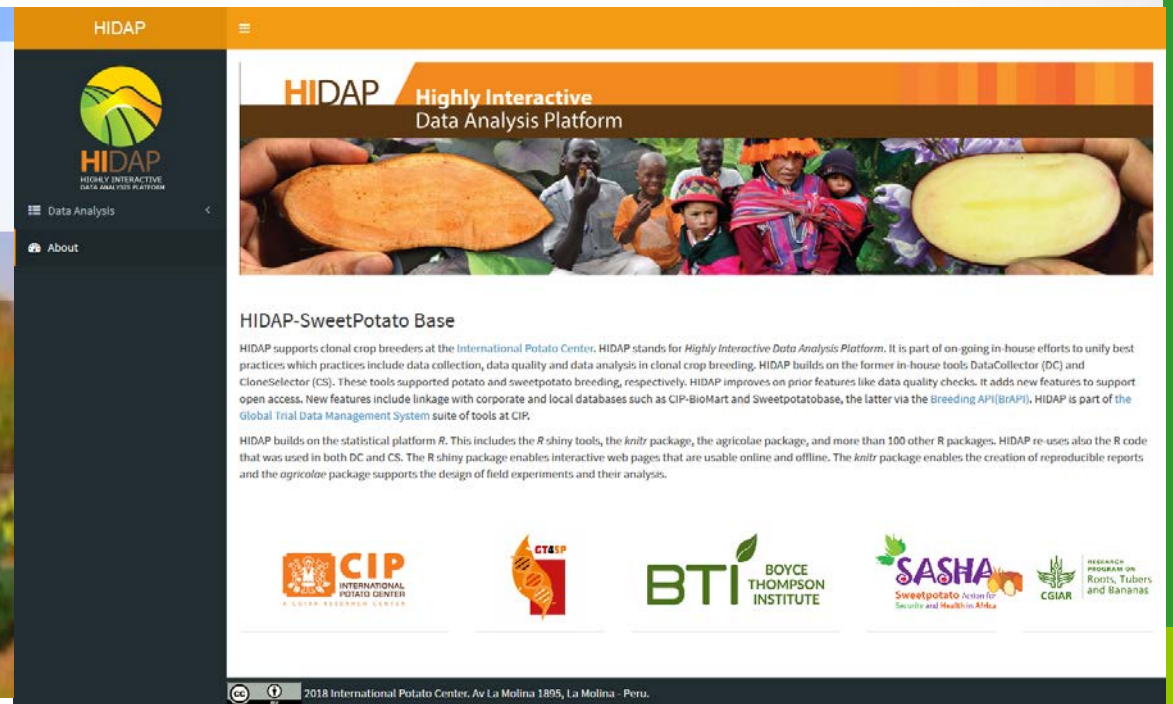
# Curation and data analysis

- Simple statistics  Sweetpotatobase
- Quality check, complex analysis and report  HIDAP



Phenotypic Analysis  
Upload and access sweetpotato breeding data

Upload Phenotypes  
Upload FieldBook file  
Summary Statistics  
Download data with Lists  
Download data with Wizard



HIDAP

**HIDAP** Highly Interactive Data Analysis Platform

HIDAP-SweetPotato Base

HIDAP supports clonal crop breeders at the International Potato Center. HIDAP stands for *Highly Interactive Data Analysis Platform*. It is part of an on-going in-house efforts to unify best practices which practices include data collection, data quality and data analysis in clonal crop breeding. HIDAP builds on the former in-house tools DataCollector (DC) and CloneSelector (CS). These tools supported potato and sweetpotato breeding, respectively. HIDAP improves on prior features like data quality checks. It adds new features to support open access. New features include linkage with corporate and local databases such as CIP-BioMart and Sweetpotatobase, the latter via the *Breeding API (BrAPI)*. HIDAP is part of the *Global Trial Data Management System* suite of tools at CIP.

HIDAP builds on the statistical platform *R*. This includes the *R* shiny tools, the *knitr* package, the *agricolae* package, and more than 100 other *R* packages. HIDAP re-uses also the *R* code that was used in both DC and CS. The *R* shiny package enables interactive web pages that are usable online and offline. The *knitr* package enables the creation of reproducible reports and the *agricolae* package supports the design of field experiments and their analysis.

CIP INTERNATIONAL POTATO CENTER  
GT4SP  
BTI BOYCE THOMPSON INSTITUTE  
SASHA Sweetpotato Sensor for Security and Health in Africa  
CGIAR RESEARCH PROGRAM ON ROOTS, TUBERS and BANANAS

2018 International Potato Center, Av La Molina 1895, La Molina - Peru.

# Way forward

- Continue uploading existing phenotype data
- Bar coding all plots in field trials while maintaining identity
- Obtain all necessary bar code material
- Fully incorporate HIDAP use



# Conclusion

- NaCRRI has fully adopted Spbase
- Label using label designer tool
- Electronic data capture
- Adoption attributed to readily available support and documentation



# Acknowledgement

## Sweetpotatobase support team

- Alex Ogonna
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**BMGF**

