

Highly Interactive Data Analysis Platform (HIDAP): Advances in Collecting & Analyzing Breeding Data

Standardized information on the performance of progenies and selected clones across environments is necessary to assist breeders to efficiently make decisions about selection and variety release. For clonal crop breeders, the new HIDAP tools facilitates collecting and analysing breeding data on a platform that can work on-line or off-line.

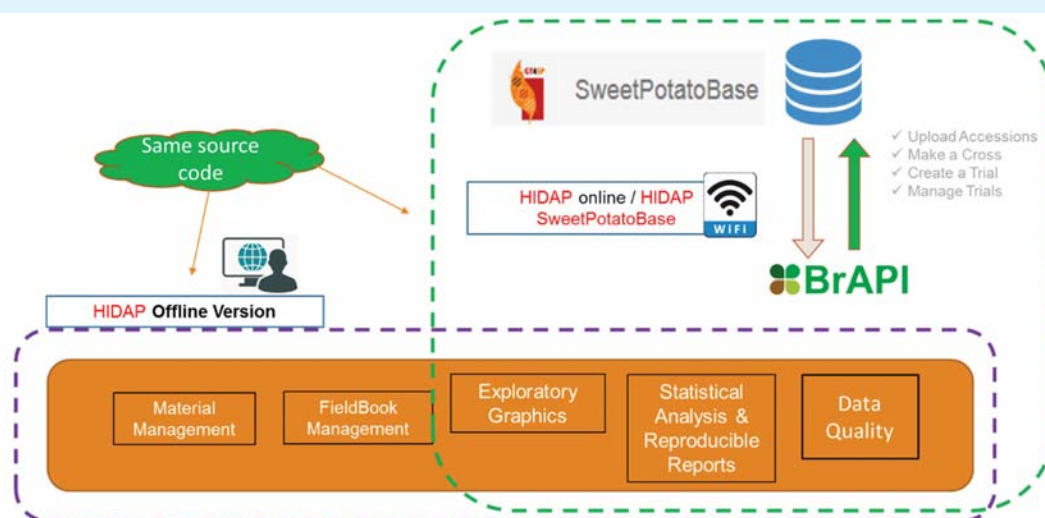


Fig. 1 HIDAP and SweetPotatoBase interaction to enable breeders to collect and analyze data either on-line or off-line

► What is the problem?

Breeding programs involve large investments of time and money but have the potential to pay very large returns on investment in the form of improved varieties which benefit farmers, societies and the environment. For the right decisions to be made, well-structure protocols need to be in place for data collection, and tools that can address the needs of vegetatively propagated crops.

► What do we want to achieve?

HIDAP stands for Highly Interactive Data Analysis Platform and has been developed by CIP. The platform supports clonal crop breeders with data collection and design of experiments, data quality checks and processing by use of statistical methods, statistical analysis and reproducible reports for breeding data. HIDAP has been built to support compliance with Open Access, open standards such as the potato and sweetpotato crop ontologies and linkages with relevant corporate and community databases, for example CIP's Corporate Database (<https://research.cip.cgiar.org/gtdms/biomart>) and the SweetPotatoBase (www.sweetpotatobase.org) (Fig. 1). The latter has been implemented via the Breeding API (BrAPI). BrAPI specifies a standard interface for

plant phenotype/genotype databases to link their data to crop breeding applications like HIDAP.

The SweetPotatoBase is a web-based global database for SweetPotatoBase breeding data developed by the Boyce Thomson Institute (BTI). It is part of a family of roots, tuber and banana databases: CassavaBase, MusaBase, and YamBase. Development of SweetPotatoBase and HIDAP are part of on-going efforts to unify best practices for breeding data management. SweetPotatoBase offers web-based trial management features. Statistical analyses of these trials is by HIDAP via BrAPI. Both SweetPotatoBase and HIDAP are compatible with the Open Source Android based phenotyping app, Field Book, by Kansas State University. Figure 1 provides of the interaction between SweetPotatoBase and HIDAP:

► Where and with whom are we working?

HIDAP is a software tool developed in by the International Potato Center (CIP) in Lima, Peru, and the SweetPotatoBase by the Boyce Thomson Institute (BTI) in New York, USA. Both tools are being used by clonal crop breeders within CIP and its partners around the world. Two national breeding programs, Uganda and Ghana, have also received advanced training on the use of these advanced tools and are active users.



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GENOMIC TOOLS
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RESEARCH
PROGRAM ON
Roots, Tubers
and Bananas

Partners:

- International Potato Center (CIP)
- North Carolina State University
- Boyce Thompson Institute, Cornell University
- CGIAR Research Program on Roots, Tubers & Bananas (RTB)

► How are we going to make it happen?

SweetPotatoBase is available online at www.sweetpotatobase.org. Users are required to create an account before they can manage their trials on this database. SweetPotatoBase offers a lot of advanced trial management functionalities to breeders including:

1. Management of breeding programs.
2. Management of accessions.
3. Field Trials: Add new trials and create field layouts.
4. Genotyping Trials: Upload and manage Institute for Genomic Diversity genotyping trials.
5. Locations: Manage locations. Add/remove locations.
6. Crosses: Create new crosses.
7. Phenotyping: Upload phenotype information for accessions in the database.
8. Creation of files for the Android based Field Book application, upload files from Field Book to the database.
9. Barcodes: Download barcodes for accessions and plots.
10. Download Data: Download phenotypic and genotypic data by trial, trait and location.
11. Advanced search function for accessions and plots, field trials, genotyping trials, traits, markers, images and people.
12. Analysis: Inbuilt Selection Index, Genomic Selection, Accession Usage, Trial Comparison and Graphical Filtering. Advanced statistical analysis for breeding trials implemented by HIDAP via BrAPI.

► Who are we working with?

In Africa, CIP breeders at the three Sweetpotato Support Platforms (SSPs) in Uganda, Mozambique and Ghana have received training and are using the software. CIP is also providing technical backstopping on how to use the program to national breeding programs in at least 14 target countries for the Sweetpotato for Health Initiative (SPHI). HIDAP has been developed with the support of Genomic Tools 4 Sweetpotato Improvement project (GT4SP), The United States Agency for International Development (USAID), the CGIAR Research Program on Roots, Tubers & Bananas (RTB) and the Sweetpotato Action for Security and Health in Africa (SASHA) project.

HIDAP builds on the statistical platform R. This includes the Shiny R package (<https://shiny.rstudio.com/>), the knitr package (<https://yihui.name/knitr/>), and a collection of in-house developed R packages. Both versions of the software are available at <https://research.cip.cgiar.org/gtdms/hidap/>. A link to the online HIDAP is also available on Sweetpotatobase. Key features of HIDAP include:

1. Available both as an online platform and as an offline software package.
2. Easy to install. End users can download the latest version of the offline version from <https://research.cip.cgiar.org/gtdms/hidap/> and follow a friendly graphical interface to complete the set up.
3. Ability to read information (pedigree and passport) from CIP's Corporate Database

(<https://research.cip.cgiar.org/gtdms/biomart/>). Experimental data can also be uploaded to the corporate database via the Field Book Registry Tool (Fig. 2).

(<https://research.cip.cgiar.org/gtdms/fieldbook>) and published on CIP's Open Data repository (<https://data.cipotato.org>).

4. The offline version supports creation of Field books, which can be manipulated using Excel.
5. Analysis for various statistical designs, including multi-environment analyses.
6. Reproducible reports, available in both MS Word and HTML formats.

► What have we achieved so far?

In May 2018, two webinars were offered to sweetpotato breeders on the use of SweetPotatoBase and HIDAP. In 2017 and 2018, participants at the annual sweetpotato breeders' meeting spent one-and-a-half-days in each meeting training on the use of SweetPotatoBase and HIDAP. Follow up in-country trainings were held in July and August 2017 for Sweetpotato breeders based at Ethiopia's Southern Agricultural Research Institute (SARI) and Tigray Agricultural Research Institute (TARI) and Tanzania's Ukiriguru Agriculture Research Institute (LZARDI). In July 2018, one in-country training was delivered to breeders in Burkina Faso. In-country trainings allow for more in-depth discussions than is possible at the annual breeders meeting.

The use of the Field Book app for phenotyping was demonstrated during the 2018 breeders meeting. An experimental version of the Field Book app with integrated mobile printing capabilities was also demonstrated.

The latest version of HIDAP is 1.0.3, and the offline version has been downloaded over 300 times. The SweetPotatoBase is hosting over 300 trials, 33,237 accessions and 648,833 phenotypic observations. Over 100 different traits have also been measured on SweetPotatoBase.

► What's next?

Sweetpotatobase and HIDAP now have stable public releases, but significant development is still on-going based on user feedback. A key focus area is on refining the SweetPotatoBase-HIDAP integration. Four in-country trainings have been scheduled to take place by the end of 2018 targeting breeding programs in Mozambique, Malawi, Zambia, Burundi, Rwanda and Kenya. In early 2019, the technical teams behind the development of these tools will get together to review progress and discuss the next steps. Finally, improvements on the Field Book app itself, an open source phenotyping software, are at an advanced stage to incorporate the ability to print barcode labels using Zebra mobile printers.



Fig. 2 Field Book app in action (Credit A. Kamweru)

CONTACTS

Luka Wanjohi (CIP, SSA)
L.Wanjohi@cgiar.org

Raul Eyzaguirre (CIP, Lima)
R.Eyzaguirre@cgiar.org

Henry Juarez (CIP, Lima)
H.Juarez@cgiar.org

Bryan Ellerbrock (BTI, Ithaca, New York)
bje24@cornell.edu