

HIDAP: A unified platform for clonal crops breeders

Background

Breeding programs involve large investments of time and money, but can pay very large returns on investment in the form of improved varieties which benefit farmers, societies and the environment. International breeding efforts involving multiple partners and targeting regionally important constraints have great potential for efficiently and rapidly achieving impact. Standardized information on the performance of progenies and selected clones across environments is necessary in order to assist breeders to efficiently make decisions about selection and variety release. Standardized methods also facilitate sharing and reporting of breeding program results with colleagues and the agencies that support us. A number of tools already exist to help with standardised breeding information management. For clonal crop breeders, the challenge has been how to improve the usability and power of existing tools, leveraging on advancements in various open source software technologies in the breeding space. The Highly Interactive Data Analysis Platform (HIDAP) has been developed to address the above challenge

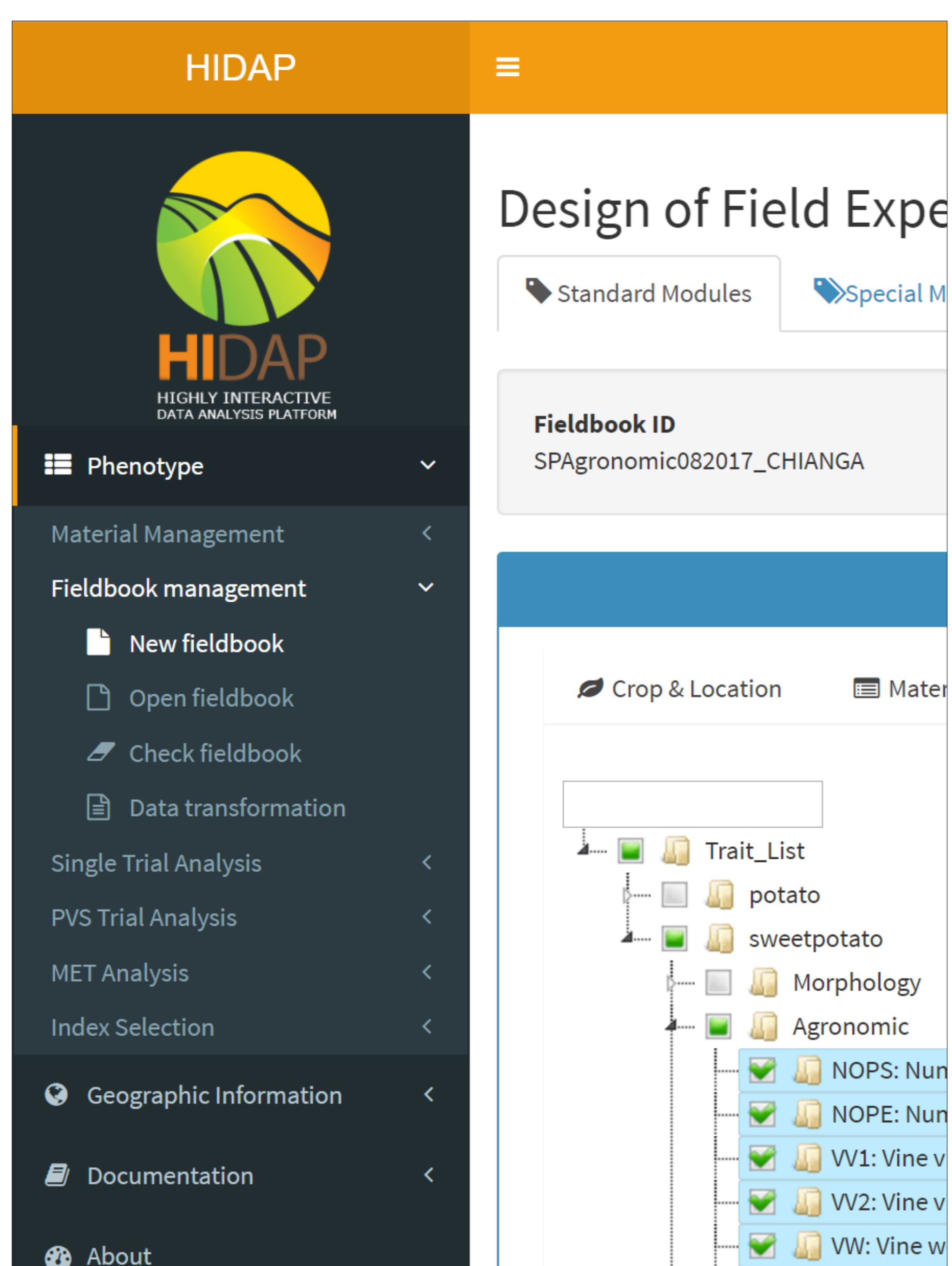


Figure 1. HIDAP software screenshot.

HIDAP has been developed by the International Potato Center (CIP). It is part of on-going in-house efforts to unify best practices. These 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 now provides a single platform for use by potato and sweetpotato breeders, as well as improved usability and data quality checks. It also has new features built to support compliance with Open Access, open standards such as the potato and sweetpotato crop ontologies.

HIDAP is also linked 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). The latter will be implemented via the Breeding API (BrAPI). BrAPI specifies a standard interface for plant phenotype/genotype databases to serve their data to crop breeding applications like HIDAP.

Key features

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 the R code that we used in both DC and CS. The R shiny package enables implementation of interactive web pages that are usable online and offline. The knitr package enables the creation of reproducible reports. The statistical analysis is performed using R and R functions developed at CIP. The software is available for download at

<https://research.cip.cgiar.org/gtdms/hidap/>.

Key features of HIDAP include:

1. Easy to install. End users can download a stable release of the software from <https://research.cip.cgiar.org/gtdms/hidap/> and follow a friendly graphical interface to complete the set up. CloneSelector in particular had an ineluctably complex installation process.
2. Provides a unified platform for clonal crops breeders.
3. Supports offline usage. Online usage has been successfully tested and will be ready in 2018.
4. Can read information (pedigree and passport genotypes) from CIP's Corporate Database (<https://research.cip.cgiar.org/gtdms/biomart/>). The experimental data can also be uploaded to the database via the Field Book Registry Tool (<https://research.cip.cgiar.org/gtdms/fieldbook/>) and can be published in Open Access through CIP's Dataverse (<https://data.cipotato.org/>).
5. Entirely Open Source.
6. Has an improved web based user interface, making it easy to present users with a more refined look and feel compared to the Excel based interfaces from both CS and DC.
7. Has improved usability and data quality checks.
8. Supports design of field experiments under several different experimental designs.
9. Supports creation of FieldBooks, which can be manipulated using Excel.
10. Supports analysis of single and multi-environment experiments.
11. Custom analysis with results output in the form of reproducible reports, available in both MS Word and HTML formats.

Key achievements so far

1. First major stable release done early 2017, with two major updates mid 2017.
2. A series of webinars accompanied release first release.
3. Reference manuals and training materials from the introductory webinars available for download to the public on the HIDAP website.
4. HIDAP introduced to several sweetpotato breeders from across SSA during the 2017 annual sweetpotato breeders meeting in Kigali, Rwanda.
5. Two follow up in-country trainings 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).

2.3.3. Plot of means

It is always good to have some visualization of the data. Because the number of genotypes in your experiment is not so big, we can plot the data for each genotype:

Dotplot with means \pm 1 standard deviations

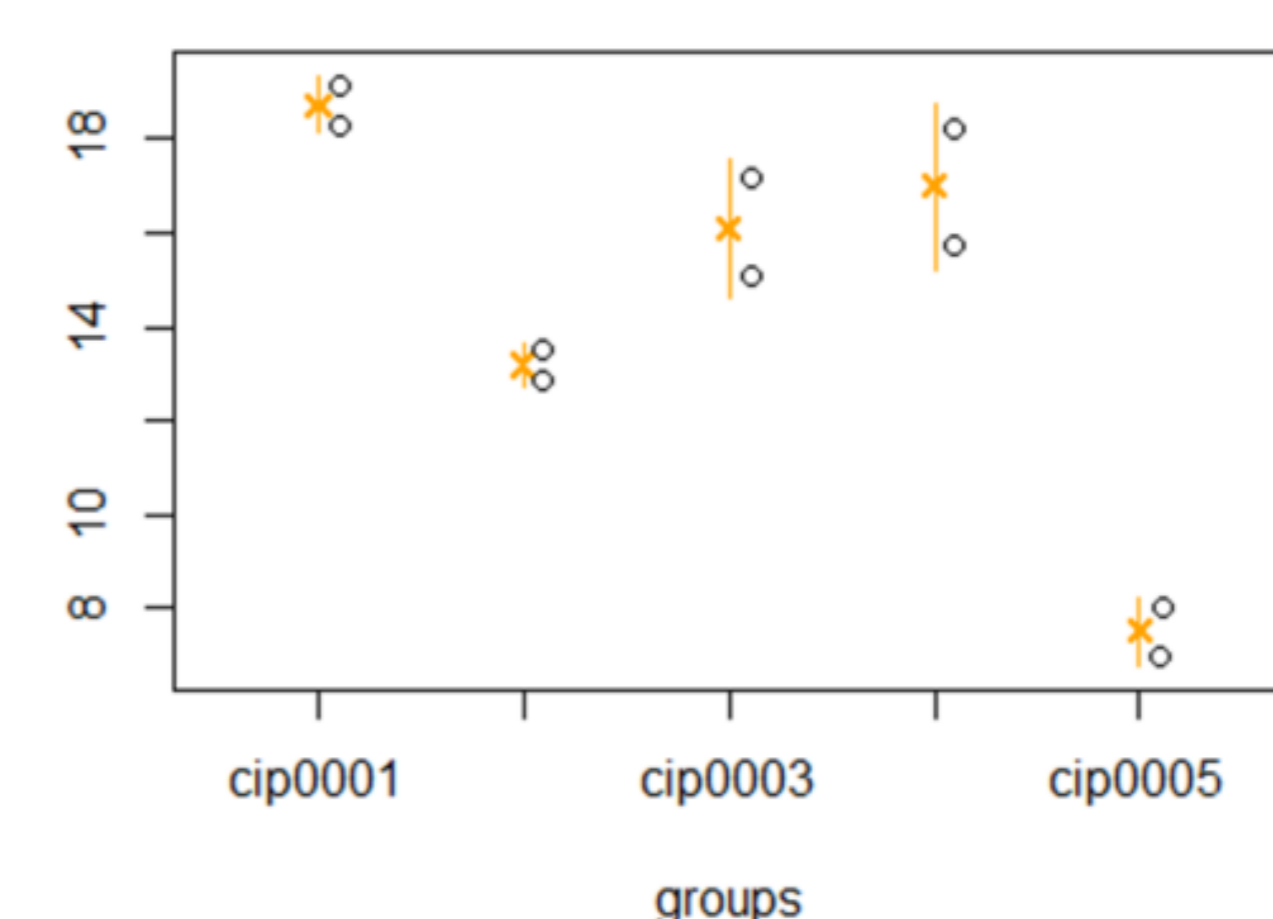


Figure 2. Sample dot plot from HIDAP.

Future plans

The development of HIDAP is led by the Research Informatics Unit (RIU), based at CIP headquarters in Lima, Peru. End user feedback from both within CIP and external partners informs a lot of the development work. Some of the major focus areas will include the integration of mobile data collection and management of data exchange with external databases.

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.