



KDMManage
Data Management

KDMManage Documentation

Release 1.9.19

DArT Team

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Welcome to the KDManage application user guides. Navigate this help using the left-hand menu. This help is also available within KDManage.

For a quick start with KDManage it is suggested you follow the order of the help index however before you do please see the following for a:

- [Brief Overview of KDManage Application](#)
- Overview of the KDDart environment see: [Introduction to the KDDart Environment](#) .

For more information please explore the following websites:

- www.diversityarrays.com
- www.kddart.org

This documentation is a growing resource which will change shape as improvements are made and more content is added and extended.

INTRODUCTION TO KDMANAGE

This help provides an introduction to the KManage application. Beforehand it is beneficial to briefly look at the following *KDDart Environment Overview* as this will assist with understanding the role this application performs and how it may overlap, intentionally, in functionality with other KDDart applications. This will place you in a better position to choose the most appropriate tool for a specific time consuming or possibly repetitive task.

To quickly gain success with KManage it is suggested you initially follow the order of the help index.

Please Note: As part of DArT's continuous improvement all KDDart application help resources are 'works in progress', hence we would be most grateful for any *feedback* regarding errors, omissions or suggestions. You may even have some valuable tips and experiences to share with others to better leverage these tools.

1.1 Audience

This document is intended for the following audience although it is not strictly confined to the roles listed:

Table 1: Roles and Responsibilities

Role	Responsibility
Technical User	An administrator of the KDDart database implementation who is familiar with how various activities of breeding trials and data needs to be organised for your organisation. This role does not require you to be an IT programmer.
Data Analyst	Analytical tools may use data retrieved from KDDart for analysis by using DAL. The results from analysis tools along with insertions (updates) may also be stored in the database using DAL.
Trial Manager	The manager of a trial/experiment.

1.2 KDDart Environment Overview

The KDDart environment consists of a three layered architecture consisting of:

- The Applications Layer, containing KManage and other applications;
- A Data Access Layer which is an API we refer to as 'the DAL' that connects the applications with your data; and
- A Database Layer containing the underlying databases.

Benefits of this well established architecture include much greater long term stability and efficiency for both users and developers of the platform.

Note: As depicted in the following KDDart System Architecture diagram, KManage has an important role within the Applications Layer

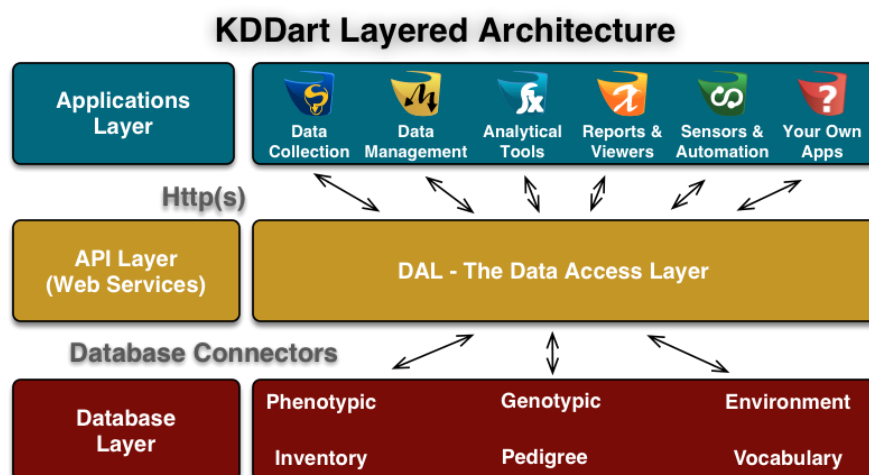


Fig. 1: The KDDart System Architecture

The application layer provides an opportunity for applications to be built or modified to suit end user requirements and provide specific functionality to best suit their tasks. Applications designed in this manner, to specialise in a specific role, may have overlapping functionality provided for convenience. Therefore it is recommended that the correct ‘tool’ is chosen for the job at hand.

The following table lists current the KDDart environment application software suite and describes the roles they perform. This should assist in choosing the most appropriate application for a task.

Table 2: KDDart Applications

Application	Description
KDManage	The KDManage application provides a web interface to KDDart allowing users to update and maintain their data using a web browser on their workstations. The application provides an authenticated user the means to add and amend database records, upload and export data.
KDXplore	KDXplore is a versatile modular application for online/offline Trial management, Curation, Seed Preparation and Harvest, Genexplore, Inventory and Trial/Nursery design. It is a useful tool for breeders, researchers, technicians, curators and developers.
KDSmart	KDSmart is designed to operate on a variety of Android handheld devices to collect data in the field. Containing data selectively exported from your KDDart database, KDSmart allows you to capture and store your phenotypic Trial data in the field for subsequent uploading to KDXplore then KDDart.
KDCompute	KDCompute is an application that provides capabilities for extensible data analysis in an efficient and customisable framework. As a tool it allows the technical detail of preparation and configuration of algorithms to be performed by a ‘technical user’ and an interface for ‘analyst users’ to easily employ those algorithms to undertake their research. Using a cooperative plugin framework for processing algorithms KDCompute is designed for multiple, longer running tasks. Using a queuing server, workstations are free to perform other tasks and demand for KDDart resources is effectively managed.
KDSens	The KDSens application provides an interface between the KDDart database and various generic environmental sensors, such as weather stations, soil probes, etc. Sensor definitions are maintained within KDDart.
DAL	Not an application, but an Application Programming Interface (API). The Data Access Layer, we refer to as ‘the DAL’, connects the applications with databases containing your Trial data. The KDDart DAL API simplifies application development so organisations can develop their own applications, or plugins and algorithms for existing applications.

These applications provide functionality to leverage your trial and nursery data when it is stored in the KDDart environment. They employ some of the diverse capabilities of the KDDart environment and demonstrate opportunities for others to build upon and extend the application layer.

Whether you choose to further enhance an application or develop new ones, the data storage capabilities of KDDart and the DAL API layer are extensible enough to meet current and long term needs.

1.3 When to use KDManage?

KDManage allows users to manage their Trial and Nursery data that is stored in a KDDart database using a web browser on their workstation.

During KDDart database setup, KDManage enables administrative tasks to be performed to create entity dependencies. Relationships are not always hierarchical such as this simple example: before adding a Trial, the Site for the trial must be defined which in turn requires the Organisation to be defined for site ownership.

Beyond initial KDDart setup many other functions can be performed, grouped under the menus for Germplasm and Experiment. Within Germplasm, KDManage manages Genus, Genotype, Specimen, Trait and Treatment, whilst Experiment contains Site, Trial, Design Type, Unit Position and Breeding Method. In KDDart the Specimen represents the unit upon which Trials are performed and trait measurements are taken.

As Trials are defined in KDDart and are in progress, other activities within KDManage become more frequent. These include activities such as importing Trial results, data extraction/exporting to perform analysis, etc.

Direct access to data stored within KDDart is possible using other applications such as KDCompute, without first needing to extract data, as it is 'already there'. This is a big difference to user activity such as moving and manipulating data stored in individual files and spreadsheets. Once data is in place in KDDart, it can be called upon time and again for review and analysis tasks.

1.4 Data Dependencies

Before adding Genotypic data to KDDart for your Trial or Nursery, any data dependencies must first be added to the database, many of which appear in selection lists (i.e. drop downs). As KDDart becomes more populated, various dependences will be already been met making further data addition easier. The order of the following list briefly illustrates dependencies that must be met, however the following diagram provides more complete detail:

1. Organisation(s)
2. Contact(s) - belonging to Organisations
3. Sites
4. Genotypes and Specimens
5. Trials.

Note: Without delving into data analysis explanations, Trials and Nurseries are well understood and KDDart design has them resolved to a common data model as *Trials*.

The following diagram provides a simplified illustration of KDDart data dependencies to assist understand the structure.

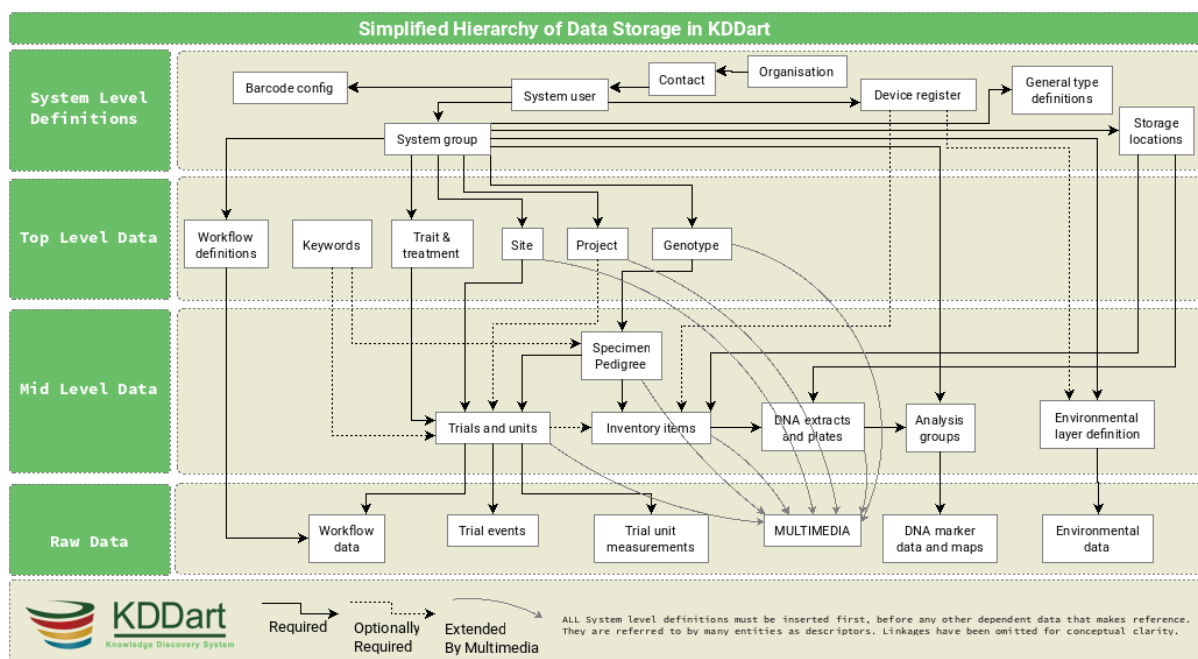


Fig. 2: Simplified hierarchical view of KDDart data dependencies

1.5 Importing

Frequently pre-existing data will exist that needs ‘importing’ into KDDart such as Genotypes and Specimens.

Tip: Until you are familiar with the import functionality or have large files to import it is recommended that you:

1. Backup the KDDart database prior to performing large imports
2. Ensure all data *Data Dependencies* have been addressed beforehand
3. Import a small selection of data before embarking on a large import.

Performing **item 3** above is important to establish that the:

- Input file has the correct format; and
- Imported data has correctly populated the desired KDDart fields.

Note: KDManage is not the only tool capable of importing data. KDXplore or KDCompute may be better suited to the task, especially if a very large time consuming import is to be performed.

1.6 Deleting

As of KDManage Version 1.9.12, delete function has been added for some KDDArT entities. They are:

- Trials
- Genotypes
- Specimens
- Items

Since individual KDDArT entities are a part of a network of dependencies, deleting entities may not always be possible. The following restrictions are in place

- Trials cannot be deleted if there is trial data uploaded to trial.
- Genotypes can not be deleted if there are Genotype Pedigree entries, Specimen entries or Extract entries that are associated with Genotype.
- Specimens can not be deleted if there are Specimen Pedigree entries, Specimen keywords, Item entries that are associated with Specimen. Specimens also can not be deleted if Specimen is used in a Trial.
- Items can not be deleted if it is attached to a Specimen in a Trial Unit. Items also can not be deleted if Item is part of an Item Group or has Item Logs recorded on it.

As such, delete should only be used to reverse accidentally additions or removing test/practice data. To remove data, please contact your Administrator for options. Alternatively, contact the KDDArT team for further options.

1.7 Login and Switch Group

KDDart is designed to accomodate many users of the system and Groups enable user access to the data stored within (see the following section *Access Settings and Permissions*).

To commence using KDManage you need a valid userid and password to login/authenticate to the KDDart database.

Once logged into KDManage the user must choose the Group to use for the session if they belong to multiple Groups, much like having multiple roles.

Note: Group selection is automatic if the user is attached to a single Group.

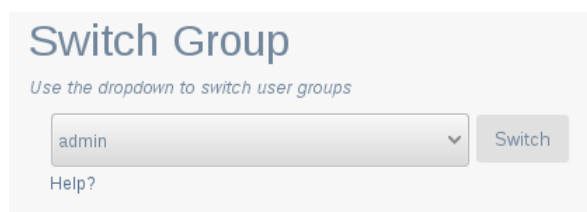


Fig. 3: KDManage switch Group selection after login

1.8 Access Settings and Permissions

A brief introduction to how KDDart manages access and security is described in this section to assist you entering and managing your data.

The following Permission Matrix table outlines what a user can perform with a selected permission setting when creating or updating the user.

Table 3: Permission Matrix

Task	Admin and Manager	Admin and NOT a Manager	Manager	User	Guest
See all records regardless of the record permission	Yes	Yes	No	No	No
Change record permission regardless of the permission	Yes	No	No	No	No
Add and remove users, add and remove groups, add and remove users from a group and reset user password	Yes	No	No	No	No
See their own records	Yes	Yes	Yes	Yes	No
Update their own records	Yes	Yes	Yes	Yes	No
Change permission of their own records	Yes	No	Yes	No	No
Add and update types, design, breeding method etc. (vocabulary entities)	Yes	No	Yes	No	No
See public records	Yes	Yes	Yes	Yes	Yes

Firstly a look at Groups, then the permissions settings that feature on some KDManage screens.

1.9 Groups

The security model used by KDDart is a common construct based upon *record level permissions* of which ownership of a record is assigned to a 'Group'. Simply put, 'Groups' own records, not users. Users, however are assigned to Groups.

Groups are managed by 'Group Administrator(s)' who are users with the ability to:

- Assign or add users to the Group
- Assign other users of the Group as a Group Administrator
- Delete records (when available) owned by the Group (except where data dependencies restrict deletion).

Note:

- Group Administrators can only conduct administration activities for a Group they are assigned to as Group Administrator.
 - The creator of a Group automatically has Group Administrator capability for that Group.
-

Tip: Whilst creating and arranging your Groups and users, those users requiring an administrative capacity should be assigned to the new Group as a 'Group Administrator'.

1.10 Permissions

First, some understanding of record access permissions is required, to ensure you and the necessary colleagues have the correct access to perform their tasks within KDDart.

Permission setting is mandatory in the following KDManage screens, so this topic has been singled out to avoid repetition:

All the following Add screens have the same requirements for permission settings:

- Genotype
- Trait
- Trial
- Specimen List (also referred to as ‘Specimen Group’)
- Marker Data Management.

The screenshot shows a form with four dropdown menus and one button. The labels and their selected values are:

- Owner Permission*:** Read/Write/Link
- Access Group*:** admin
- Access Permission*:** Read/Write/Link
- Public Permission*:** Read/Link

An **Add** button is located at the bottom right of the form.

Fig. 4: Permission settings common to the KDManage screens listed above

Note: Permission fields, as above, do not appear on many KDManage screens, however permissions are inherited and full data integrity is maintained internally by the system.

1.10.1 What Permissions Can You Set?

The following table describes the permission settings for the record. These values are available for selection from the three permission field drop downs.

Table 4: Permission Settings

Permission	Permission Description
None	No access to the record.
Read	The record may only be read.
Read & Link	The record may be read or linked to, which refers to the ability to create an association, or link, with the record.
Read & Write	The details of the record may be read or written/updated.
Read & Write & Link	The details of the record may be read or written/updated or linked to.

Note: Record deletion does not appear as this capability is not selectable (not available in KDManage) and is limited to users assigned as Group Administrator.



1.10.2 Who is it Set For?

Permission settings must be set for the three Groups shown in the following table:

Table 5: Group Permissions

#	Group	Group Description
1.	Owner	The 'Owner Group' is the Group inherited from the user at the time the record was being created. E.g. if the user's Group is set to 'A' the record created will have an 'Owner Group' = 'A'.
2.	Access	The 'Access Group' is for the primary users of the record(s), who are <i>not</i> the 'administrator of the record'.
3.	Public	The 'Public Group', is 'the remainder' of KDDart users who are neither within the Owner or Access Groups. Note: They are still authenticated users within this installation of KDDart.

1.11 Logout

The Logout button  appears in the Admin Bar  at the top right of the KDManage screen.

Automatic logoff from KDDart may occur following a period of inactivity if the timeout has not been programmatically overridden by the application at logon.

The inactive time period setting and automatic logoff option can vary depending upon the configuration chosen for each installation of KDDart.

1.12 Map Selections

Maps are used in several locations to define areas such as Sites and Trials.

To commence selecting an area on the map:

1. Scroll to the location required and double click on the map to zoom to that location. Keep zooming until you have the required level of detail.
2. Select the 'Draw a new object' button which will result in a blue circle and central dot appearing.

For moving the selected area or altering its shape select the middle button and the drawn area will highlight in another colour. The connection corners will show circular handles.

- To move the shape select the middle handle and move to the desired location.
- To alter the shape select the desired corner hand and stretch the boundary. Where the centre of a line has been moved new midway handles will appear allowing further fine adjustment of the area.
- Select the middle button to exit from this map edit mode.

1.13 More Information

For more information on KDDart and Diversity Arrays Technology see the following websites:

- www.kddart.org
- www.diversityarrays.com

NEW FEATURES IN 1.9.19

KDManage v1.9.19 includes the following bug fixes.

- Fixed issue where Genotype Factors weren't being included in *Import Genotype*
- *Trial Super Import* Trial Import error handling related to dates improved
- Issues related to *Trial Design* fixed.

KDManage v1.9.19 has included functionality to allow users to reset their password. See *User Passwords*.

ADMINISTRATIVE SETTINGS

The administrative settings for KDMange are can be found in the **Admin Bar** which appears at the top right of any KDMange screen. This page introduces the various administrative settings available to KDMange users. See the table and image below for more information on the **Admin Bar**.

The screenshot displays the KDMange interface. At the top right, the **Admin Bar** is highlighted with a red box, showing the user's identity: 'Username: admin | Group: admin' and a set of utility icons. The main dashboard area features a 'Welcome' message and four summary cards for 'Total Projects' (1), 'Total Trials' (22), 'Total Nurseries' (7), and 'Total Analysis Groups' (6). Below these are two data tables: 'Trials' and 'Nurseries'. Both tables show a list of entries with columns for Id, Trial Name, Trial Type, Site, Start Date, End Date, and Action. The 'Trials' table lists 5 entries (IDs 25-29) and the 'Nurseries' table lists 5 entries (IDs 25-29).

Id	Trial Name	Trial Type	Site	Start Date	End Date	Action
29	FB04	Yield trial	Narrabri	2017-09-19 00:00:00		👤
28	YieldHeightCross	NURSERY2	Narrabri	2017-09-19 00:00:00		👤
27	FB03	Yield trial	Narrabri	2017-09-19 00:00:00		👤
26	FBNurserySelection	NURSERY2	Narrabri	2017-09-19 00:00:00		👤
25	FB02	Yield trial	Narrabri	2017-09-19 00:00:00		👤

Fig. 1: Admin Bar

Table 1: UI Elements of the Admin Bar

UI Element	Description
Username	Displays the username of the logged in user.
Group	Displays the group that user has logged in as.
Home Button	Navigates the user to the KDManage Main Screen
Help Button	Navigates the user to the KDManage User Guide (this document).
Administrative Settings Button	Displays the Administrative Settings Menu .
KDCompute Button	Navigates the user to KDCompute.
Logout Button	Logs the user out of the current session.

Note: The **Username** and **Group** elements are one combined button that will navigate the user to the **Switch Group Page**.

3.1 Satisfying Dependencies

Data relationships within KDDart are hierarchical, hence data needs to be populated in a specific order to ensure it is available when needed to create other, 'related' elements.

The following list shows items of the **Administrative Settings Menu** to illustrate the order of dependency, and the diagram below provides a visual representation of data dependency:

1. *Organisations*
2. *Contacts*
3. *Types*
4. *Device Registrations*
5. *Barcode Configurations*

- 6. *Projects*
- 7. *Units*
- 8. *Users*
- 9. *Groups*
- 10. *Factors*
- 11. *Keywords*
- 12. *Keyword Groups*
- 13. *Workflows*

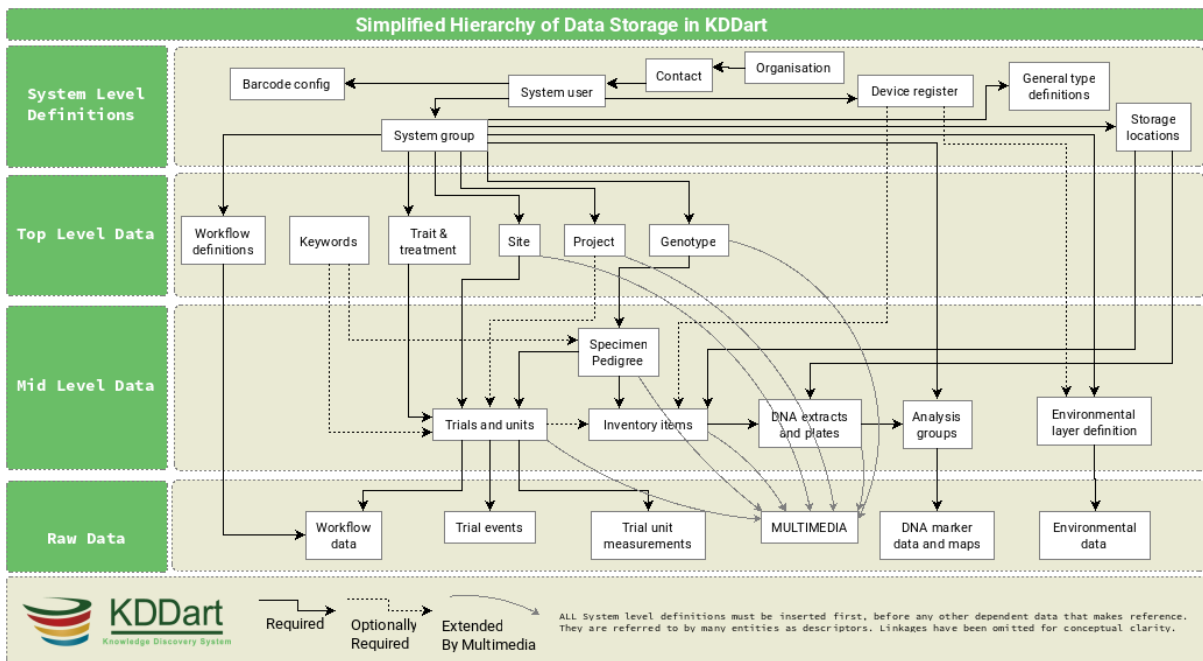


Fig. 2: Simplified Hierarchical View of KDDart Data Dependencies

Note: A user must have *Group Administrator* privileges to perform these administrative actions, otherwise actions will fail with the following error message:

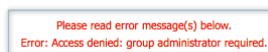
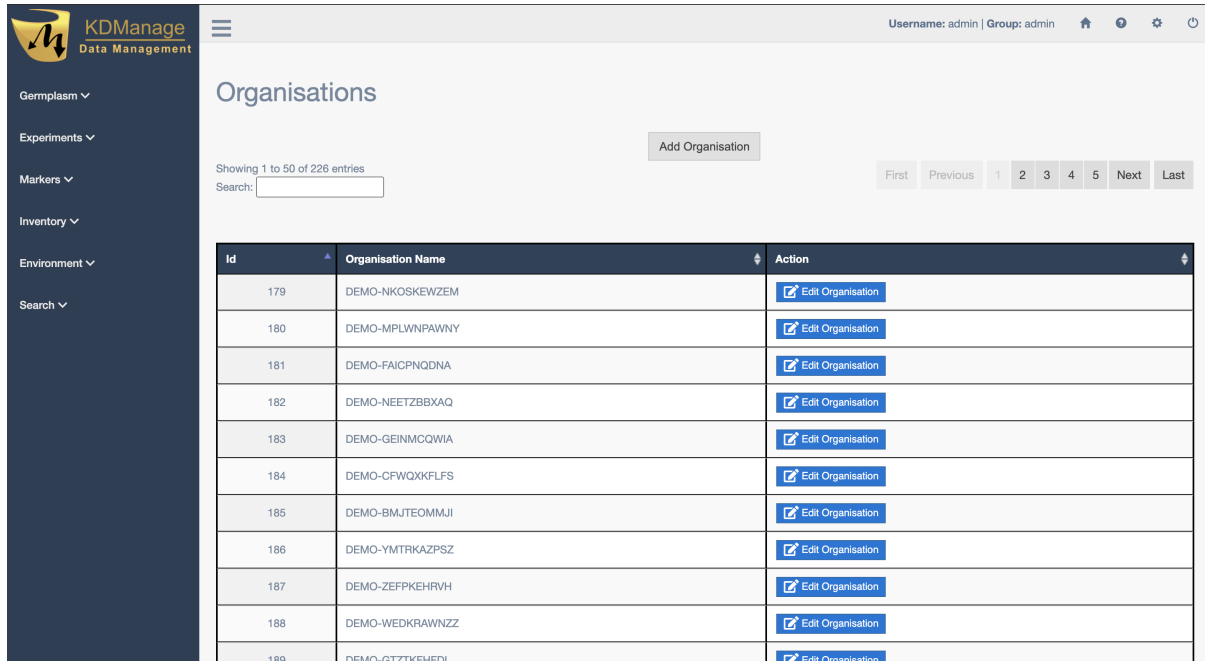


Fig. 3: Access Denied Error Message

3.2 Organisations

The organisation name defines an entity which may be an external or internal collaborating organisation.



The screenshot shows the 'Organisations' page in the KDManage application. The page header includes the KDManage logo and 'Data Management' text. The user is logged in as 'admin' with the group 'admin'. The page title is 'Organisations'. Below the title, there is a search bar and an 'Add Organisation' button. The table below shows 10 organisations, each with an 'Id', 'Organisation Name', and an 'Action' button labeled 'Edit Organisation'.

Id	Organisation Name	Action
179	DEMO-NKOSKEWZEM	Edit Organisation
180	DEMO-MPLWNPAPWNY	Edit Organisation
181	DEMO-FAICPNQDNA	Edit Organisation
182	DEMO-NEETZBBXAQ	Edit Organisation
183	DEMO-GEINMCQWIA	Edit Organisation
184	DEMO-CFWQXKFLFS	Edit Organisation
185	DEMO-BMJTEOMMI	Edit Organisation
186	DEMO-YMTRKAZPSZ	Edit Organisation
187	DEMO-ZEFPKEHRVH	Edit Organisation
188	DEMO-WEDKRAWNZZ	Edit Organisation
189	DEMO-GTZTKHFIDL	Edit Organisation


Fig. 4: Organisation Page

To add a new organisation, select the **Add Organisation Button** which will open the **Add Organisation Window** as seen in the image below:



The screenshot shows the 'Add Organisation' window. The window has a title bar with the text 'Add Organisation' and a close button. Below the title bar, there is a text input field for 'Name of Organisation*' and an 'Add' button.

Fig. 5: Adding a New Organisation

The organisation name can be updated by selecting the  **Edit Button** and then entering a new name.

3.3 Contacts

The **Contacts Page** defines contacts for an organisation which may include KDDart system users, collaborators, material providers, etc.

Contacts within KDDart refer to those people who have a relevant role or responsibility in relationship to the data. For example, a *site manager* needs to be entered as a *contact* as they are required to be referenced when defining a *site*. However, they may not necessarily be a *user* who logs into the KDDart system.

Select the **Add Contact Button** to add a new contact. See the image and table below for more information:

The following image illustrates the fields for Contacts. All fields except ‘Contact Location’ are mandatory. The map view, not illustrated, appears below the form and enables the selection of the contact’s geographic location.

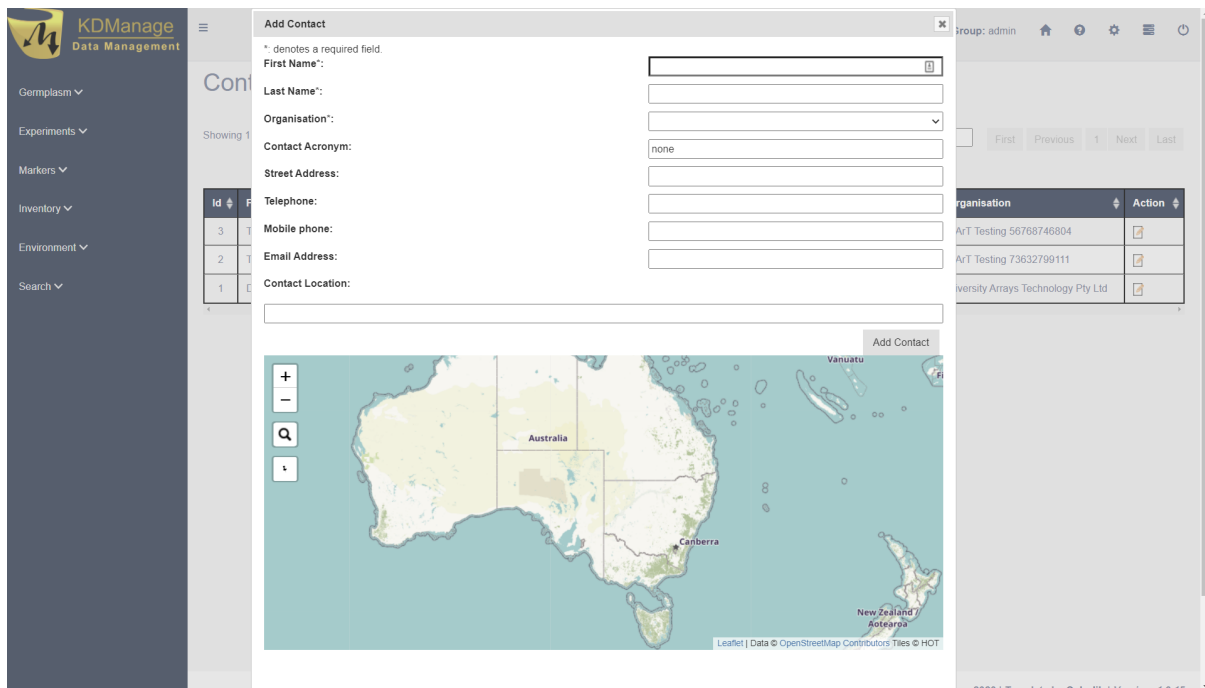


Fig. 6: Adding a New Contact

Table 2: Adding a New Item

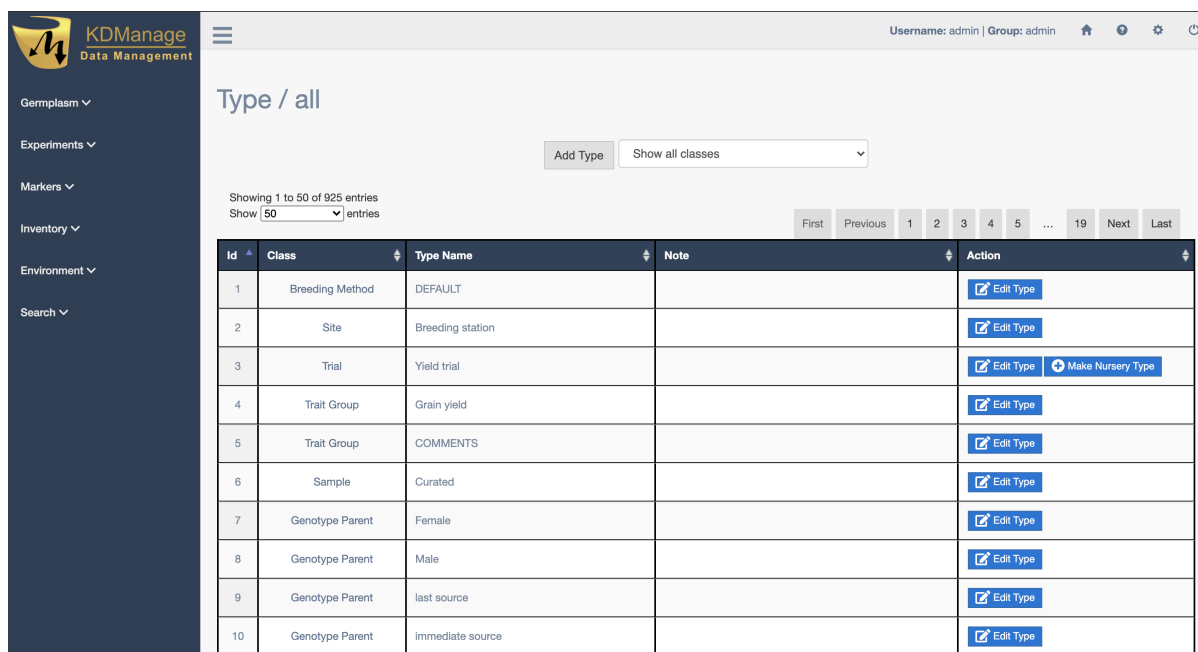
Step
1. Select the Add Contact Button to display the Add Contact Window .
2. Enter all known details about the contact. The <i>first name</i> , <i>last name</i> , and <i>organisation</i> fields are all mandatory.
3. Select the Marker Button from the map and place it on the place that the contact is located.

The contact can also be updated after it has been created by selecting the **Edit Button** and then editing the details.

Note: Please note that the *organisation name* must already exist before contacts can be added.

3.4 Types

Types are used as part of KDDart's global vocabulary to support classification. Each *Type* that is created must be assigned to a *Class*. An example of a type is a *seed bag* which belongs to the *item* class. The image below shows the **Type Page**



The screenshot shows the 'Type / all' page in the KDManage application. The page includes a sidebar with navigation options like Gemplasm, Experiments, Markers, Inventory, Environment, and Search. The main content area displays a table of types. Above the table, there are controls for 'Add Type' and 'Show all classes'. The table has columns for Id, Class, Type Name, Note, and Action. The Action column contains 'Edit Type' buttons for each row. The table lists 10 types, including Breeding Method, Site, Trial, Trait Group, Sample, and Genotype Parent.

Id	Class	Type Name	Note	Action
1	Breeding Method	DEFAULT		Edit Type
2	Site	Breeding station		Edit Type
3	Trial	Yield trial		Edit Type Make Nursery Type
4	Trait Group	Grain yield		Edit Type
5	Trait Group	COMMENTS		Edit Type
6	Sample	Curated		Edit Type
7	Genotype Parent	Female		Edit Type
8	Genotype Parent	Male		Edit Type
9	Genotype Parent	last source		Edit Type
10	Genotype Parent	immediate source		Edit Type

Fig. 7: Type Page

New types may be created within the **Type Page**. The following image of the **Add Type Window** shows the fields required for adding a new type. The *Is Active* field allows a type to be enabled or disabled as required.

Setting a type to *Inactive* removes the item from future selection lists, however, the classification remains historically present for those records still referencing it.

The screenshot shows the 'Type / all' page in the KDManage application. The page header includes the KDManage logo and 'Data Management' text. The user is logged in as 'admin' with the group 'admin'. The page title is 'Type / all'. There is a search bar with 'Add Type' and a dropdown menu set to 'Show all classes'. Below the search bar, it indicates 'Showing 1 to 50 of 925 entries' and a 'Show 50 entries' dropdown. A pagination control shows 'First', 'Previous', '1', '2', '3', '4', '5', '...', '19', 'Next', and 'Last'. The main content is a table with the following data:

Id	Class	Type Name	Note	Action
1	Breeding Method	DEFAULT		Edit Type
2	Site	Breeding station		Edit Type
3	Trial	Yield trial		Edit Type Make Nursery Type
4	Trait Group	Grain yield		Edit Type
5	Trait Group	COMMENTS		Edit Type
6	Sample	Curated		Edit Type
7	Genotype Parent	Female		Edit Type
8	Genotype Parent	Male		Edit Type
9	Genotype Parent	last source		Edit Type
10	Genotype Parent	immediate source		Edit Type

Fig. 8: Adding a New Type

Types can also be updated after they have been created by selecting the **Edit Button** and then editing the details.

3.5 Device Registrations

Any device that is used in conjunction with KDDart must be registered within the **Device Registrations Page**. This could include any device which is used for measuring or capturing information such as weather instruments, scales, soil monitors, etc.

Device registration can assist with record keeping and accountability. This can later assist in identifying and if necessary, isolating the information or data that a specific instrument produced or assisted in producing.

For example, if a device was discovered to be needing recalibration, or providing questionable results it's data can be isolated, either to ignore during analysis or to apply specific adjustments.

Devices belong to the *Device Register* class. They are classified with a *Device Type* of *Device Register Class* and optionally may have a specific geographic location recorded. The image below shows the **Device Registration Page** with the **Register Device Window** open:

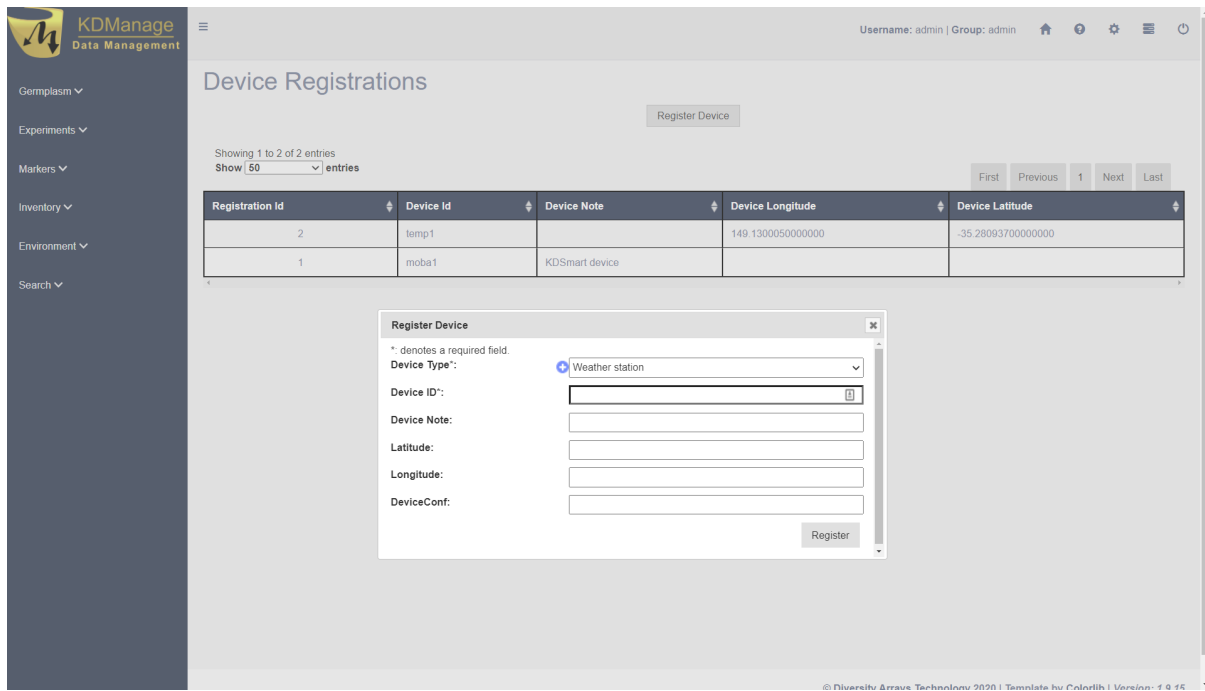


Fig. 9: Registering a Device

Note: Registered devices cannot be edited after they are registered.

3.6 Barcode Configurations

The **Barcode Configuration Page** lists all barcode configurations available to the user and provides the ability to create new barcode configurations. Barcode configuration defines how barcodes are created for various applications.

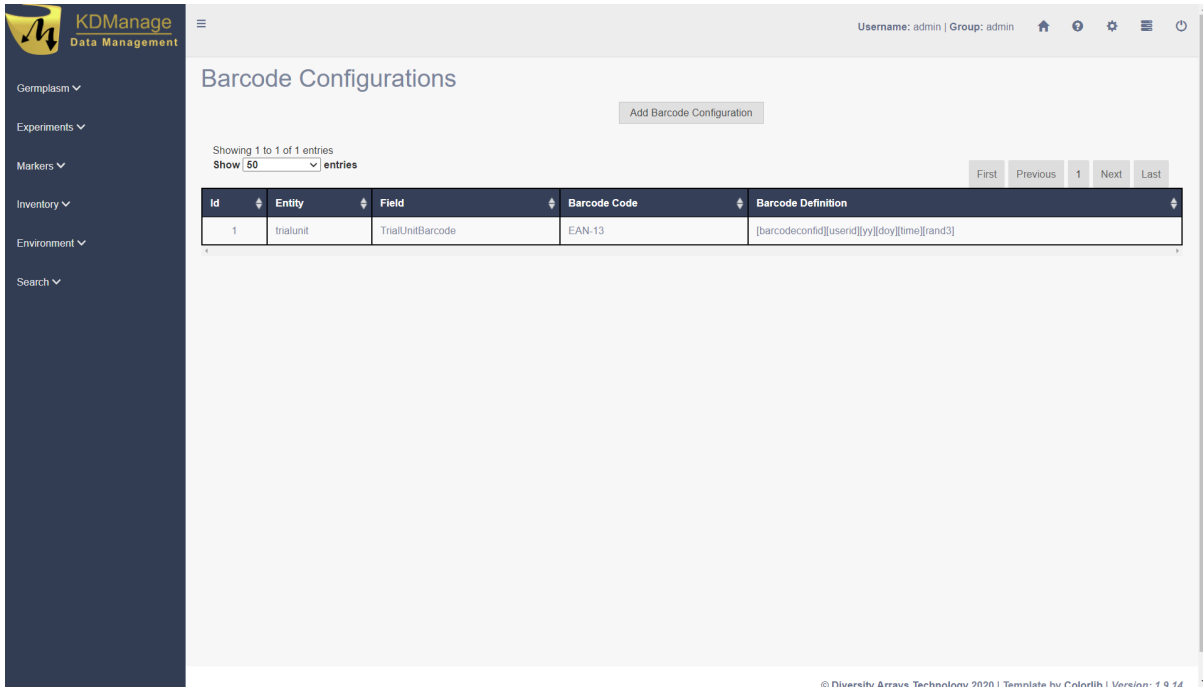


Fig. 10: Barcode Configuration Page

New barcode configurations can be created by selecting the **Add Barcode Configuration Button** which displays the **Add Barcode Configuration Window**. The image below shows the window with an example of the creation of a barcode configuration used for specimens:

The 'Register Device' window is a modal form with the following fields and controls:

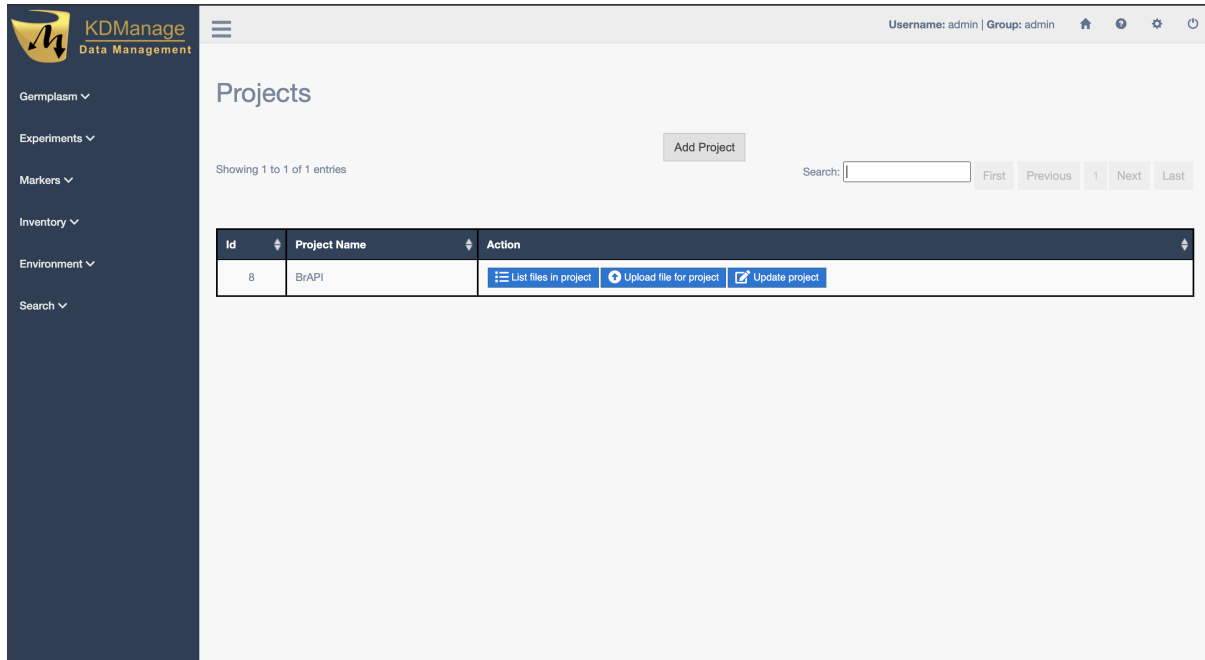
- Device Type*:** A dropdown menu with a blue plus icon on the left and a dropdown arrow on the right.
- Device ID*:** A text input field with a lock icon on the right.
- Device Note:** A text input field.
- Latitude:** A text input field.
- Longitude:** A text input field.
- DeviceConf:** A text input field.
- Register:** A button at the bottom right.

A note at the top left of the form states: '*: denotes a required field.'

Fig. 11: Adding a Barcode Configuration

3.7 Projects

Project entities can be created and are designed to help with progress and file tracking for various projects your organisation may be undertaking. Project types are created via the **Type Page**.



The screenshot displays the 'Projects' page in the KDManage application. The top navigation bar shows the user is logged in as 'admin' with the group 'admin'. The left sidebar contains a menu with categories: Gemplasm, Experiments, Markers, Inventory, Environment, and Search. The main content area is titled 'Projects' and features an 'Add Project' button. Below the button, it indicates 'Showing 1 to 1 of 1 entries' and includes a search bar and pagination controls (First, Previous, 1, Next, Last). A table lists the project details:

id	Project Name	Action
8	BrAPI	List files in project Upload file for project Update project

Fig. 12: Project Page

New projects can be added in the **Add Project Window** (pictured below) which can be found by selecting the **Add Project Button**:

✕
Add Project

*: denotes a required field.

Project Name*:

Project Type*: +

Manager Name*:

Project Status:

Start Date:

End Date:

Note:

Fig. 13: Adding a New Project

3.8 Units

Units enable the custom definition of the units of measurement for items, traits and trial events. The image below shows the **Units Page**:

- Gemplasm ▾
- Experiments ▾
- Markers ▾
- Inventory ▾
- Environment ▾
- Search ▾

Units


Username: admin | Group: admin
🏠 ⚙️ 🔌

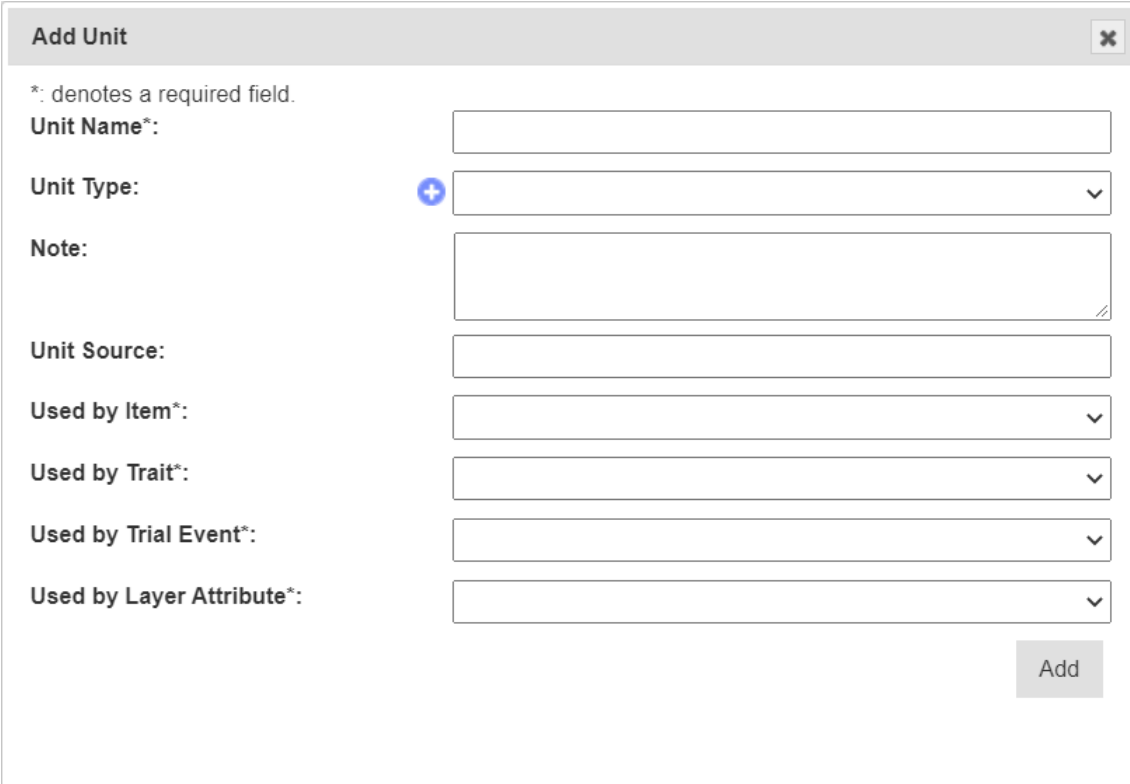
Showing 1 to 8 of 8 entries

Search:
First Previous 1 Next Last

id	Unit Name	Unit Type Name	Unit Note	Action
8	Gram (g)	Weight	Gram unit for seed weight	🔗 Update Item Unit
7	degCx		Note degCx	🔗 Update Item Unit
6	Kg/ha		Kilogram per hectare	🔗 Update Item Unit
5	Gram per 7.6			🔗 Update Item Unit
4	NO UNIT			🔗 Update Item Unit
3	Percentage			🔗 Update Item Unit
2	cm		centimetre	🔗 Update Item Unit
1	Date Unit			🔗 Update Item Unit

Fig. 14: Units Page


New units can be created in the **Add Unit Window** which is accessed by selecting the **Add Unit Button**. Unit types are created via the **Type Page** or can also be accessed via the quick link button  without leaving the **Add Unit Window** (pictured below).



Add Unit

*: denotes a required field.

Unit Name*:

Unit Type: 

Note:

Unit Source:

Used by Item*:

Used by Trait*:

Used by Trial Event*:

Used by Layer Attribute*:

Add

Fig. 15: Adding a Unit

3.9 Groups

Users need to be assigned to appropriate groups to provide them with their required level of access.

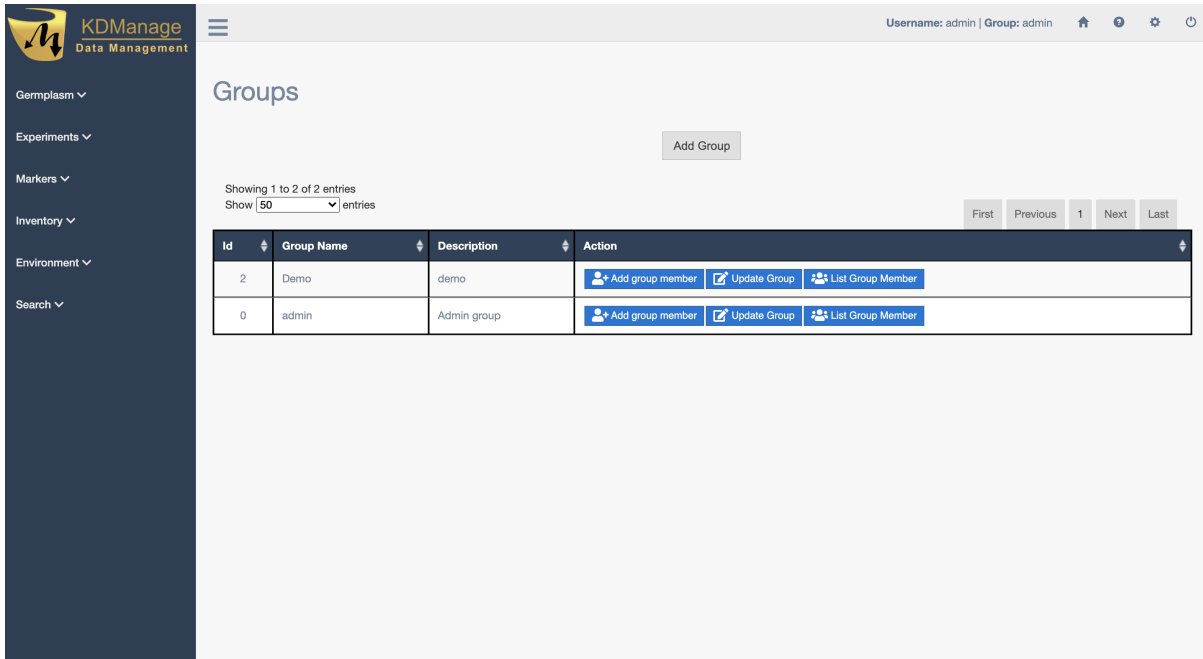


Fig. 16: The Groups Page

Add Group ✕

*: denotes a required field.

Group Name*:

Group Description*:

Fig. 17: Adding a New Group

Once a group is created, existing users can be added to the group and if needed, made an Administrator of that group. See the image and instructions below for more details:


Table 3: Adding a New Group

Step
1. On the Groups Page , select the Add Group Button . This will display the Add Group Window as seen in the above image.
2. Enter a group name and a group description.
3. Select the Add Button to complete the

Groups need to have users assigned to them. See the information below on how to assign a user to a group:

Fig. 18: Assigning a User to a Group

Table 4: Assigning a User to a Group

Step	Action
1.	On the Groups Page , find the required group in the list.
2.	Select the  Add group member (Add group member) from the Action Column of the required group. This will display the Add User to Group Window .
3.	Select the username from the dropdown menu and then from the second dropdown menu, choose whether the user will be a group administrator or not.
4.	Select the Add Button to complete the addition of the user to the group. Repeat with more users if necessary.

3.10 Users

An administrator of a group can create new users and assign them to the appropriate groups for their required access.

New users can be added by selecting the **Add User Button** on the **Users Page**. This will open the **Add User Window** as seen in the image below:

The screenshot shows a window titled "Add User" with a close button in the top right corner. The window contains several input fields:

- User Name*:** A text box containing "tester" and a help icon.
- Password*:** A password field with masked characters and a help icon.
- Re-type Password*:** Another password field with masked characters and a help icon.
- Contact*:** A dropdown menu showing "Diversity Arrays".
- User Type*:** A dropdown menu showing "PEOPLE".
- Group Membership*:** A list box containing "admin", "Demo", and "Train".

 An "Add User" button is located at the bottom right of the window.

Fig. 19: Adding a New User

The following permission matrix table outlines what a user can perform with a selected permission setting when creating or updating the user:

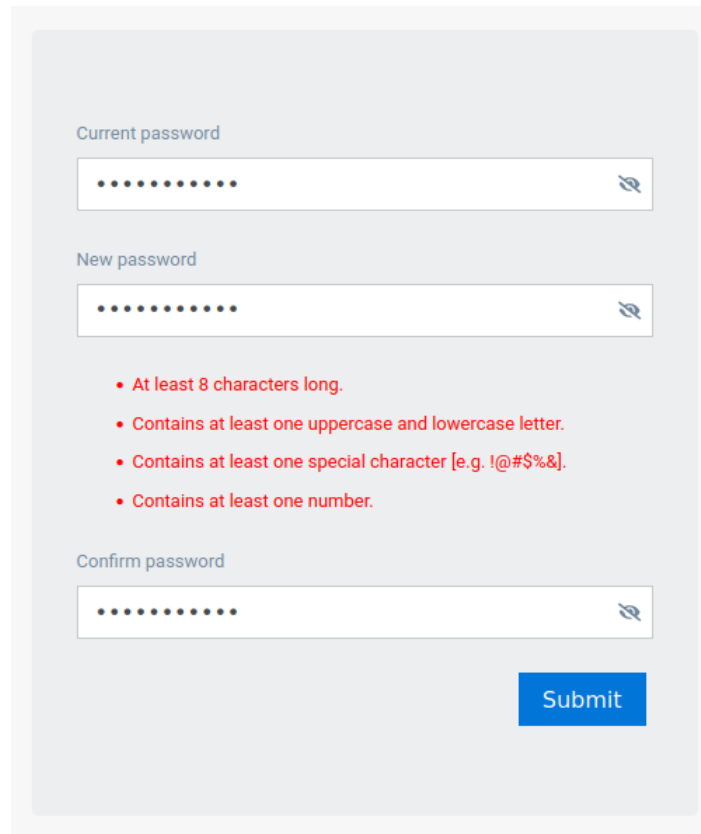
Table 5: Assigning a User to a Group

Task	Admin	Admin and a Manager	Admin and a NOT Manager	Admin and a Guest	Admin and a User
See all records regardless of the record permission	Yes	Yes	No	No	No
Change record permission regardless of the permission	Yes	No	No	No	No
Add and remove users, add and remove groups, add and remove users from a group and reset user password	Yes	No	No	No	No
See their own records	Yes	Yes	Yes	Yes	No
Update their own records	Yes	Yes	Yes	Yes	No
Change permission of their own records	Yes	No	Yes	No	No
Add and update types, design, breeding method etc. (vocabulary entities)	Yes	No	Yes	No	No
See public records	Yes	Yes	Yes	Yes	Yes

3.11 User Passwords

Users can reset their own passwords using the Password Reset Page.

Users must use their current password and fulfil the requirements listed on the page.



The screenshot shows a password reset form with the following elements:

- Current password:** A text input field with a masked password (10 dots) and a toggle icon.
- New password:** A text input field with a masked password (10 dots) and a toggle icon.
- Requirements:** A list of four red bullet points:
 - At least 8 characters long.
 - Contains at least one uppercase and lowercase letter.
 - Contains at least one special character [e.g. !@\$%&].
 - Contains at least one number.
- Confirm password:** A text input field with a masked password (10 dots) and a toggle icon.
- Submit:** A blue button labeled "Submit".

Fig. 20: Password reset page

3.12 Factors

Factors are custom fields that administrators can add to different entities.

For example, an extra field for *Trials* can be added for organisation specific information requirements.

Warning: Whilst an administrator can create new factors, it is recommended that factors are used sparingly with careful consideration of the KDDart schema.

To add a new factor follow these instructions:

Fig. 21: Adding a New Factor

Table 6: Adding a New Factor

Step
1. Go to the Factors Page and select the Add Factor Button . This will display the Add Factor Window .
2. Select the Add Factor button
3. Fill in the mandatory fields. The factor name must not have any spaces and the factor validation rule must be a valid Boolean expression and regular expression.
4. Select the Add Button to finalise the creation of the factor.

Once a factor is successfully created, a new field will appear in the appropriate entity Add/Update windows.

3.13 Keywords

Keywords can be attached to trial units and specimens to assist grouping related entities together.

After a keyword is created, it can be attached to Trial Units (see *Adding a Keyword to a Trial Unit*).

A new keyword can be added by selecting the **Add Keyword Button** which will open the **Add Keyword Window** as seen in in the image below:

Fig. 22: Adding a New Keyword

3.14 Keyword Groups

When keywords exist in KDDart they can be organised into *keyword groups*. A keyword can exist in multiple keyword groups if required.

The following example shows the **Add Keyword Group Window** and instructions on how to make a new keyword group:

Keyword Id	Keyword name	Keyword note
3	keyword3	An example of a keyword.
2	keyword2	An example of a keyword.
1	keyword1	An example of a keyword.

Keyword Id	Keyword Name	Keyword Note
3	keyword3	An example of a keyword.
2	keyword2	An example of a keyword.
1	keyword1	An example of a keyword.

Keyword group name*: Keyword Group Example 1

Fig. 23: Adding a New Keyword Group

Table 7: Adding a New Keyword Group

Step	Action
1.	From the Keyword Groups Page , select the Add Keyword Group Button . This will display the Add Keyword Group Window as seen in the image above.
2.	Enter a name for the keyword group ('Keyword Group Example 1' in the example above).
3.	Select the keywords to be included or added to the group.
4.	Drag the selected keywords to add to the keyword group into the New Keyword Group Panel (the lower panel).
5.	Select the Add Button to finalise the creation of the new keyword group.

3.15 Workflows

KDDart provides a workflow structure which:

- Enables documenting process steps or events that occur throughout parts of the trial/nursery lifecycle;
- Are sharable across multiple trials/nurseries;
- Cater for important activities e.g. soil preparation and conditioning before planting;
- At the conclusion of a trial or nursery a historical reference of activities undertaken is maintained; and
- Facilitates organisations developing their own applications, using the DAL API, to meet specific business requirements e.g. to move towards more automation or email warnings and alerts of upcoming or overdue tasks.

The order of the following sections show the dependency order for using workflows:


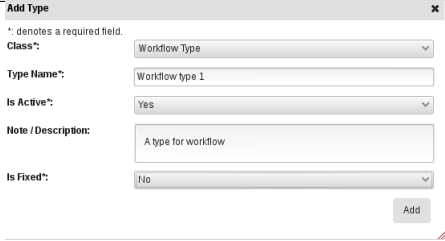
1. Create a workflow type
2. Create a workflow
3. Create the workflow definition
4. Assign a workflow to a trial/nursery

3.15.1 1. Creating a Workflow Type

A *workflow type* provides a means to group workflows for different purposes. These may be to associate workflows for trials vs nurseries, different crops, etc.

To add a new workflow type, follow these instructions:

Table 8: Creating a Workflow Type

Step	Action
1.	Select the  Administrative Settings Button at top right of any KDManage page, then select the <i>Types</i> option from the list.
2.	Select the Add Type Button . This will display the Add Type Window .
3.	At <i>Class</i> , select <i>Workflow Type</i> .
	
	<p>Fig. 24: Add a New Class: Workflow Type</p>
4.	Complete the mandatory fields.
5.	Select the Add Button to create the new Workflow type.

3.15.2 2. Creating a Workflow

Once the required workflow type exists, the next step is to create the workflow entity. To create the workflow:

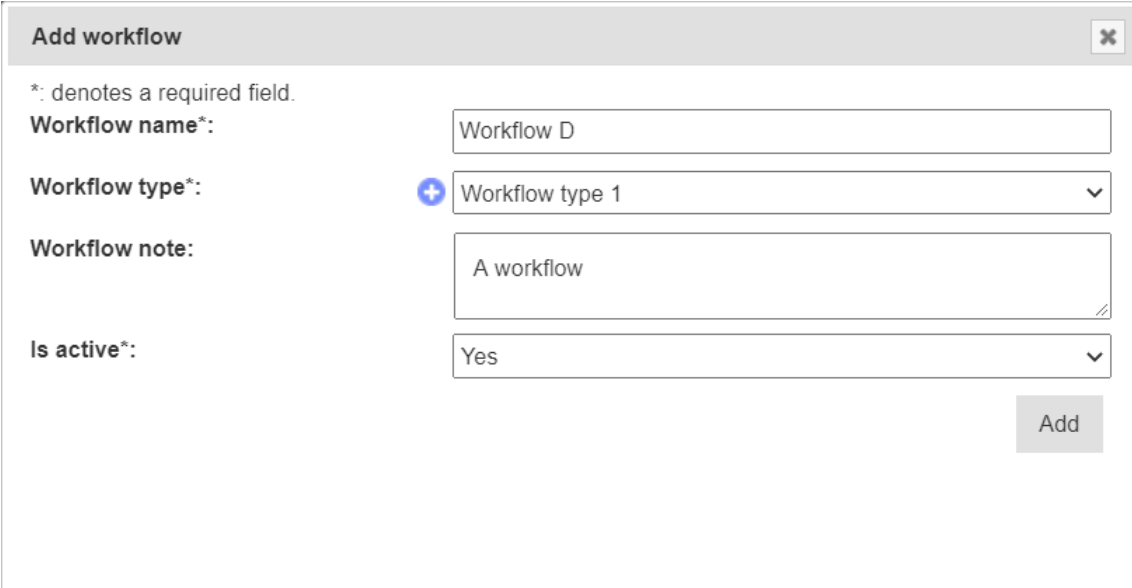


Fig. 25: Creating a Workflow

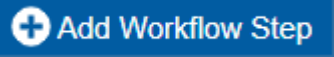
Table 9: Creating a Workflow

Step	Action
1.	From the Workflow Page , select the Add Workflow Button . This will display the Add Workflow Window .
2.	Complete the required details and selecting a workflow type.
3.	Select the Add Button to create the workflow entity. The new Workflow entity will now appear in the list of Workflows.


3.15.3 3. Creating, Updating, and Listing Workflow Definitions

Workflow definitions (which are the workflow steps) can now be created. This helps define what steps are needed in a specific workflow. To add definitions to the workflow:

Table 10: Creating a Workflow Definition

Step	Action
1.	From the Workflows Page , select the  (add workflow) for the workflow that you want to add a definition to. This will display the Add Step to Workflow Window .
2.	Enter the <i>step name</i> , <i>step order</i> and optional <i>step note</i> .
3.	Select the Add Button to finalise the creation of the definition.
4.	Repeat steps 2-3 as required.

Note: Step order must be numerical. This defines what order this definition is in the workflow (i.e. users must do step 1 before step 2).

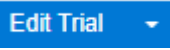



Workflow definitions can be listed for a specific workflow by selecting the  (List workflow steps).

3.15.4 4. Assign a Workflow to a Trial

At the **Trial Page**, a workflow can be added to an existing trial or a new trial created with a workflow (if the workflow is already defined).

To add a workflow to a trial:

Table 11: Adding a Workflow to an Existing Trial

Step	Action
1.	From the Main Menu , select <i>Experiments</i> , then <i>Trials</i> to navigate to the Trials Page .
2.	At the required trial, select the  (edit trial) in the Action Column to display the Update Trial Window
3.	At the <i>Current Workflow</i> field select a workflow from the dropdown list. The workflow choices that are available will depend on the workflows that have already been created.
4.	Select the Update Button to finalise the workflow assignment.
5.	After the workflow has been assigned to the trial, choose “Assign a workflow to Trial” (under  dropdown) and choose the relevant step.
5.	After a workflow step has been added to a trial, users may select the  Tick Button to mark the step as completed or the  Cross Button to mark the step as incomplete.

Note: The *step ID* is the ID shown in the **Workflow Definition Table**, not the *step number* of the Workflow Definition*.

A workflow may also be added to a new trial as it is being created. When the user is entering the trial details, there will be a dropdown option for the workflow.

GERMPLASM MENU

The **Germplasm Menu** contains various pages with tools that can be used to manage germplasm data and related data.

The following pages of the **Germplasm Menu** illustrate the *order of dependency*:

1. *Genus*
2. *Genotype*
3. *Specimen*
4. *Specimen Lists*
5. *Traits*
6. *Trait Groups*
7. *Treatment*.

This order of dependency means that a *genus* must first be created for a *genotype* to be added to it, and a genotype must exist for a specimen to be added to it as well.

4.1 Genus

The **Genus Page** contains a list of all genus that are contained in KDDart. *Genus* refers to a logical grouping of genotypes which may optionally be botanically related.

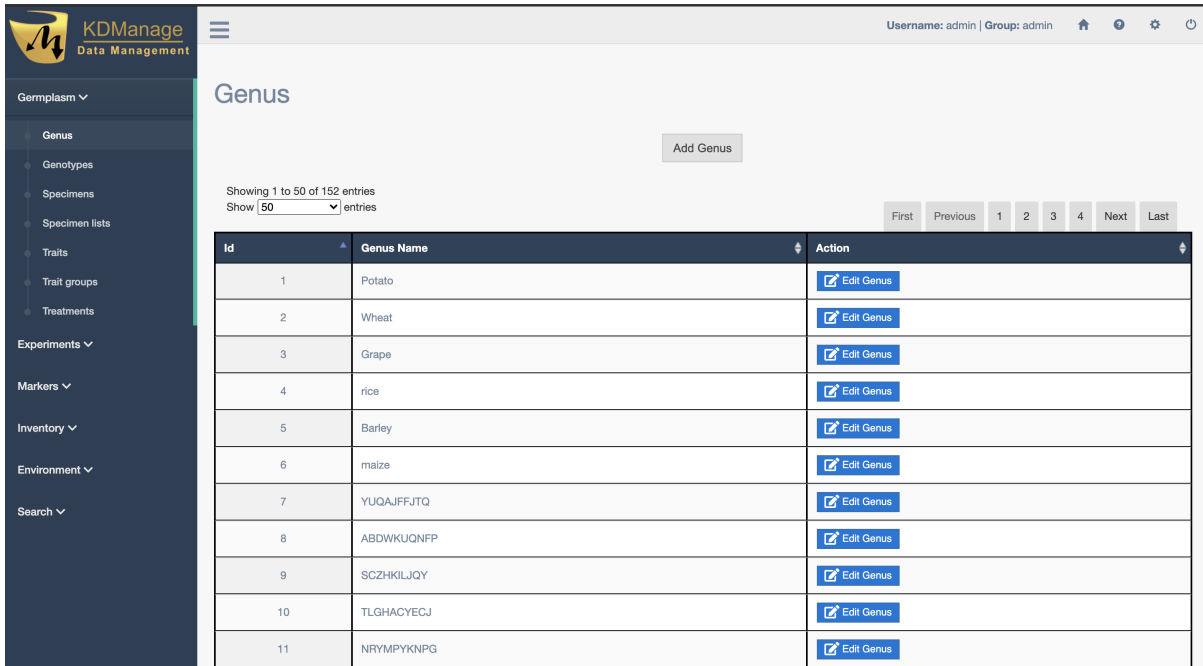



Fig. 1: Genus Page

A new genus can be added to KDDart by selecting the **Add Genus Button** which displays the **Add Genus Window** as seen in the image below:



Fig. 2: Add Genus Window

Once created in KDDart, the name of a genus may be edited by selecting the  **Edit Button** of the required genus.

4.2 Genotype

Genotype refers to the set of an individual's genes. Each genotype in KDManage is listed in the **Genotypes Page**. A synonym for genotype can be *variety* and should be used as a generic category. As stated in the *order of dependency*, each genotype must be associated with a genus.

The screenshot displays the 'Genotypes' page in the KDManage application. The page header shows the user is 'admin' with the group 'admin'. The main content area features a table with 11 entries, each representing a genotype. The table columns are: Id, Genotype Name, Genus Name, Species Name, Acronym, and Action. The Action column contains three buttons: 'View Genotype', 'Update Genotype', and 'Delete Genotype'. The page also includes a sidebar with navigation options and a top navigation bar with utility icons.

Id	Genotype Name	Genus Name	Species Name	Acronym	Action
1	1:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
2	2:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
3	3:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
4	4:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
5	5:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
6	6:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
7	7:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
8	8:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
9	9:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
10	10:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype
11	11:ZWB14	Wheat	Triticum		View Genotype - Update Genotype - Delete Genotype

Fig. 3: Genotypes Page

Genotype records may either be entered manually or imported from a file (see the *Import Genotype* section).

To add a genotype manually, select the **Add Genotype Button** on the **Genotypes Page** which will open the **Add Genotype Window**. The window and a table describing the fields for manual genotype addition can be seen below:

Add Genotype ✕

*: denotes a required field.

Genotype Name*:

Genus*: +

Genotype Colour:

Species Name:

Genotype Acronym:

OriginId*:

Can Published?*

Note:

Owner Permission*:

Access Group*:

Access Permission*:

Other Permission*:

Fig. 4: Add Genotype Window

Table 1: Add Genotype Window Fields

Field	Mandatory?	Description
Genotype Name	Mandatory	The name of the genotype.
Genus	Mandatory	The name of the genus that the genotype belongs to. Select the + or go to the Genus Page to create a new genus.
Genotype Colour		Can be used for plant variety rights information.
Species Name		Latin name - common naming conventions should be established.
Genotype Acronym		Abbreviated name of genotype.
OriginId	Mandatory	Source Identifier - possible part of plant variety rights information - could refer to organisation or contact.
Can be Published	Mandatory	Indicate if genotype is publicly available.
Note		Any notes regarding the genotype.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

4.2.1 Genotype Actions

For the management of Genotypes, there are various actions to help manage Genotypes. The following table explains what they do and use cases:

Table 2: Genotype Actions

Action	Description	Parent Button
View Genotype	Link to Genotype page	
List Genotype Alias	List all alias for genotype	View Genotype
List Genotype Trait	List all assigned traits for genotype	View Genotype
Show Pedigree of Genotype	Show Pedigree chart of Genotype	View Genotype
Update Genotype	Update Genotype Information	
Add Genotype Alias	Add an alias to a Genotype	Update Genotype
Add Genotype Trait	Add an assigned trait to a Genotype	Update Genotype
Merge Genotype	Reassign another Specimens of another Genotype and attach them to current Genotype.	Update Genotype
Clone Genotype	Create another Genotype with fields of current Genotype copied over to new Genotype and allow an explicit pedigree link to the two Genotypes	
Create Specimen	Create a new Specimen and link it to current Genotype	

4.2.2 Import Genotype

New genotype records may be imported into KDDart and if required, specimens for the genotype records can be automatically created within the process.

Select the **Import Genotype Button** to display the **Import Genotype Window** (pictured below). The following image and table show the fields required in an input file to import genotypes and create specimens if required.

Import Genotype [Close]

*: denotes a required field.

Genus*: [+] [v]

Number of Specimens: [1] [v]

Breeding Method: [+] [v]

Genotype File*: [Choose File] No file chosen

Genotype Name Column*: [v]

Species Name Column*: [v]

Genotype Acronym Column: [v]

Genotype Note Column*: [v]

Number of Specimen Column: [v]

Genpedigree start column: [v]

[Import]

Fig. 5: Import Genotypes Window

Table 3: Import Genotype Fields

Field	Mandatory?	Description
Genus	Mandatory	The genus name for the genotypes.
Breeding Method		Select from the list of breeding methods (Use Default if not required/important)
Number of Specimens		A value must be selected from 0-9. The value specified here applies to all genotype records being imported unless overridden by the Number of Specimen Column (see the example below).
Genotype File	Mandatory	Select the input file for the import.
Genotype Name Column	Mandatory	Column number for genotype name.
Species Name Column	Mandatory	Column number for the species name.
Genotype Acronym Column		The acronym column is optional.
Genotype Note Column	Mandatory	Column number for notes regarding the genotype.
Number of Specimen Column		The number of specimens to be created for a, individual record (see example below).
Genpedigree Start Column		Begins a genotype name and genotype pedigree type pairings. Use genotype names and type names.

Access Fields (see the [Access Settings and Permissions](#) topic) do not appear in the **Import Genotype Window**. These fields are automatically set with the owning group set to the group used to perform the import as follows:

Table 4: Group Privileges

Group	Privilege
Owner (Group used for import)	Read & Write
Access	Read & Link
Public	Read & Link

When importing genotypes from a file, KDManage can optionally create specimens for each or selected genotypes if required. The following applies to the import window:

- **Number of ‘Specimens greater than zero’** - The specified number of specimen records will be created for each genotype record imported unless overridden by the individual record.
- **Numeric value in the ‘Number of Specimen Column’** - Directs the import to check that column in the file for each record and create the specified number of specimens for the genotype. Within the file where a:
 - **Value for a record = blank** - The *Number of Specimens* value entered will apply for the genotype.
 - **Value for a record = zero** - No specimen will be created for the genotype.
 - **Zero < Value < 10** - This number (value) of specimens will be created for the genotype.

Import Genotype Example

The following example shows a small genotype input CSV file:

```
GenotypeName,SpeciesName,GenotypeNote,Specimen Number
G1,Triticum aestivum,None,1
G2,Triticum aestivum,None,0
G3,Triticum aestivum,None,2
G4,Triticum aestivum,None,0
G5,Triticum aestivum,None,1
```

Fig. 6: Example Genotype CSV Import File

The following image shows the completed import fields for this file.

The import file shown above will create five genotype records and four specimen records when imported using the following KDManage form settings.

Note: The records in the file with a zero in the specimen number column will *not* have a specimen record created.

Import Genotype
✕

*: denotes a required field.

Genus*: + VKTMUSVZZP

Number of Specimens: 0

Breeding Method: + DEFAULT

Genotype File*: Choose File testgenotype.csv

Genotype Name Column*: GenotypeName

Species Name Column*: SpeciesName

Genotype Acronym Column:

Genotype Note Column*: GenotypeNote

Number of Specimen Column: Specimen Number

Genpedigree start column:

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
GenotypeName	G1	-
SpeciesName	Triticum aestivum	Species Name Column
GenotypeNote	None	Genotype Note Column
Specimen Number	1	Number of Specimen Column

Import

Fig. 7: Example Genotype CSV Import

After a successful import, all genotypes will be available in the list of the **Genotypes Page** as seen below:

Id	Genotype Name	Genus Name	Acronym	Species Name	Action
7249518	G5	VKTMUSVZP		Triticum aestivum	
7249517	G4	VKTMUSVZP		Triticum aestivum	
7249516	G3	VKTMUSVZP		Triticum aestivum	
7249515	G2	VKTMUSVZP		Triticum aestivum	
7249514	G1	VKTMUSVZP		Triticum aestivum	

Fig. 8: Imported Genotypes

Another example below shows how specimens that were automatically created based when genotypes were imported. Note how the specimen name was treated when:

- A single specimen is created the specimen name matches the genotype name
- Multiple specimens are created for a genotype, the specimen name is given the genotype name with a numeric suffix (e.g. for a genus called ‘GenoA’, specimen names would be GenoA__1, GenoA__2, etc).

Id	Specimen Name
7247811	Geno_833
7247810	Geno_103_1
7247809	Geno_103_2
7247808	geno_123

Fig. 9: Automatically Generated Specimens

Import Genotype with Genpedigree Example

Genpedigree entries can also be included in the CSV by including each Genpedigree pair following the column specified in the window. See the example below:

```
GenotypeName,SpeciesName,GenotypeNote,GenotypeParent1,GenotypeParentType1,GenotypeParent2,GenotypeParentType2
Ge1,Triticum aestivum,None,,
Ge2,Triticum aestivum,None,,
Ge3,Triticum aestivum,None,Ge1,Male,Ge2,Female
Ge4,Triticum aestivum,None,Ge3,Male,G1,Female
Ge5,Triticum aestivum,None,G1,Female,G2,Male
```

Fig. 10: Genotype CSV with Genpedigree Example

Tip: Parents listed in CSV can either be genotypes that are in the CSV or existing genotypes that have already been added or imported.

This will result in the following genpedigree being created for genotype *Ge3*:

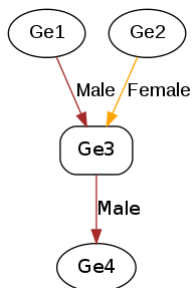


Fig. 11: Imported Genpedigree Example

4.2.3 Import Genpedigree

New Genpedigree entries for existing genotypes can also be imported. Select the **Import Genotype Pedigree Button** to display the **Import Genotype Pedigree Window** as seen in the image below (along with a table to outline the fields):

Note: The **Import Genotype Pedigree Window** will match column names once users select a file for import.

Import genotype pedigree ✕

*: denotes a required field.

Genotype Pedigree File*: Choose File No file chosen

Genotype ID Column*:

Parent Genotype ID Column*:

Genotype Parent Type Id Column*: +

Use Name*:

Fig. 12: Import Genotype Pedigree Window

Table 5: Import Genpedigree Fields

Field	Mandatory?	Description
Genpedigree File	Mandatory	Select the input file for the import.
Genotype ID Column	Mandatory	Column number for genotype ID. These are the <i>children</i> genotypes.
Parent Genotype ID Column	Mandatory	Column number for parent genotype ID. These are the <i>parent</i> genotypes.
Genotype Parent Type ID Column	Mandatory	Column number for genotype parent type ID.
Use Name	Mandatory	Flags whether to use genotype ID or genotype name.

4.2.4 Genotype Alias

Genotypes may also have a *genotype alias* added to help with identifying. To add an alias to a genotype, find the required genotype in the list on the **Genotypes Pages** then select “Add Genotype Alias” (under **Update Genotype** dropdown) to display the **Add Genotype Alias Window**. The window and a table that explain the related fields can be found below:

Fig. 13: Add Genotype Alias Window

Table 6: Add Genotype Alias Fields

Field	Mandatory?	Description
Alias Name	Mandatory	Alias name for genotype.
Type Name		Alias type.
Status		Status of alias.
Language		Language of alias.
Genotype Name?		Flag that alias is genotype name or not.

4.2.5 Genotype Super Import

The **Genotype Super Import** provides a single function whereby multiple genotypes can be created, updated or replaced in a single csv. The aliases, genpedigrees and traits of these genotypes can also be included in the import. This function enables bulk uploads/updates of genotypes into the system.

Prerequisite: Before the Genotype Super Import can be used, a .csv file containing the relevant data must be prepared. This .csv file should contain the columns listed within the Genotype Super Import Form.

Where a genotype already exists, the row will be **ignored** unless a flag from below is set to allow for updates:

- **Update Existing Genotype** - determines whether existing genotypes should be updated with given information.
- **Replace Existing Pedigree** - determines whether existing genotype pedigree for an existing genotype should be replaced with given information.
- **Create Specimens** - determines whether a corresponding set of specimens should be created with the genotypes. **NOTE:** this will only work when creating new genotypes.

To use the Genotype Super Import, select the **Super Import Genotype** button to display the Super Import Genotype window.

The following illustration shows the Super Import Genotype window, it displays the fields which represent the columns required for the super import to run.

Genotype File*: No file chosen

Genus*:

Genotype Name Column*:

Species Name:

Genotype Acronym Column:

Genotype Note Column:

Genotype Colour Column:

Aliases Start Column:

Aliases End Column:

Trait Start Column:

Trait End Column:

Factor Start Column:

Factor End Column:

Female Parent Column:

Male Parent Column:

New Name Column:

Owner Group*:

Access Group Permission*:

Access Group*:

Other Group Permission*:

Update Existing Genotype:

Replace Existing Pedigree:

Create Specimens:

These fields are only for new Specimens

Specimen Name:

Breeding Method:

Selection History Column:

Pedigree Column:

These fields are only for new Specimens

Breeding Method:

Selection History Column:

Pedigree Column:

Owner Group*:

Access Group Permission*:

Access Group*:

Other Group Permission*:

Import CSV

Field	Mandatory?	Description
Genotype File	Mandatory	The prepared .csv file containing the columns below.
Genus	Mandatory	Dropdown to select the Genus of given genotypes.
Genotype Name Column	Mandatory	The column that contains the names of the given genotypes.
Species Name		Textfield to select the species of given genotypes.
Genotype Acronym Column		The column that contains the acronym for given genotypes.
Genotype Note Column		The column that contains the note for given genotypes.
Aliases Start Column		The starting column that contains the aliases for given genotypes.
Aliases End Column		The ending column that contains the aliases for given genotypes.
Trait Start Column		The starting column that contains the traits for given genotypes.
Trait End Column		The ending column that contains the traits for given genotypes.
Factor Start Column		The starting column that contains the factors for given genotypes.
Factor End Column		The ending column that contains the factors for given genotypes.
Female Parent Column		The column that contains the female parent for given genotypes.
Male Parent Column		The column that contains the male parent for given genotypes.
New Name Column		The column that contains the new name for given genotypes.

continues on next page

Table 7 – continued from previous page

Field	Mandatory?	Description
Update Existing Genotype		Flag to determine whether existing genotypes should be updated with given information.
Replace Existing Pedigree		Flag to determine whether existing genotype pedigree for an existing genotype should be replaced with given information.
Create Specimens		Flag to determine whether a corresponding set of specimens should be created with the genotypes. NOTE: this will only work when creating new genotypes.
Breeding Method		(Only required if creating specimens) Dropdown to select the breeding method of the specimens to be created.
Selection History Column		(Only required if creating specimens) The column that contains the selection history for the specimens to be created.
Pedigree Column		(Only required if creating specimens) The column that contains the pedigree for the specimens to be created.
Owner Group	M	Dropdown to select the owner's access permissions to given genotypes.
Access Group Permission	M	Dropdown to select the access group's access permissions to given genotypes.
Access Group	M	Dropdown to select the access group to given genotypes.
Other Group Permission	M	Dropdown to select the other groups' permissions to given genotypes.

Note: Since genotypes can have an arbitrary number of aliases, traits, and factors, this import function requires that the start and end columns for them. This means:

1. The columns for aliases, traits and factors must be next to each other.
2. If there is only a single column, the start and end columns will be the same.

Once the .csv file has been uploaded under **Genotype File**, an additional view will be generated in the window that contains all the columns of the .csv file.

Super Import Genotype

Genotype File*: Choose File genotype_super.csv

Genus*: + ▼

Genotype Name Column*: ▼

Species Name: sativa

Genotype Acronym Column: ▼

Genotype Note Column: ▼

Aliases Start Column: ▼

Aliases End Column: ▼

Trait Start Column: ▼

Trait End Column: ▼

Factor Start Column: ▼

Factor End Column: ▼

Female Parent Column: ▼

Male Parent Column: ▼

New Name Column: ▼

Update Existing Genotype:

Replace Existing Pedigree:

Create Specimens:

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
Genotype	RAOm1123	-
CLJBDMABZA	Alias123random1	-
variety	varietone1123	-
Cross	32	-
Pedigree	123	-
Male	Its a Winner_93444	-
Female	Hot Cocoa_93444	-
what1	1	-
what2	11	-

Now, the remaining fields can be selected using the dropdowns to match the requisite columns to the columns that exist within the uploaded file.

The existing columns on the right will turn green when they have been selected once, and turn red if they have been selected more than once. In the case where the starting and ending columns are the same, the super import function will still complete despite the column highlighting as red.

Super Import Genotype
✕

Genotype File*: genotype_super.csv

Genus*: + Wheat

Genotype Name Column*: Genotype

Species Name:

Genotype Acronym Column:

Genotype Note Column:

Aliases Start Column: CLJBDMABZA

Aliases End Column: CLJBDMABZA

Trait Start Column: what1

Trait End Column: what2

Factor Start Column:

Factor End Column:

Female Parent Column:

Male Parent Column:

New Name Column:

Update Existing Genotype:

Replace Existing Pedigree:

Create Specimens:

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
Genotype	RAOm1123	Genotype Name Column
CLJBDMABZA	Alias123random1	Aliases Start Column, Aliases End Column
variety	varietone1123	-
Cross	32	-
Pedigree	123	-
Male	Its a Winner_93444	-
Female	Hot Cocoa_93444	-
what1	1	Trait Start Column
what2	11	Trait End Column

Once all the needed columns have been selected, click the **Import CSV** button to run the super import. When the super import completes, a prompt should be shown with a report on the super import.

Import Results
✕

Completed Import. Individual results displayed below.

```

=====
RAOm1123: Successfully updated (Genotype Id: 10957) Unable to add its a winner_93444 to RAOm1123 as male parent
Unable to add hot cocoa_93444 to RAOm1123 as female parent GenotypeAliasName (Alias123random1): already exists.
RAOm1124: Successfully updated (Genotype Id: 10958) Unable to add its a winner_93444 to RAOm1124 as male parent
Unable to add hot cocoa_93444 to RAOm1124 as female parent GenotypeAliasName (Alias123random2): already exists.
RAOm1125: Successfully updated (Genotype Id: 10959) Unable to add its a winner_93444 to RAOm1125 as male parent
Unable to add hot cocoa_93444 to RAOm1125 as female parent GenotypeAliasName (Alias123random3): already exists.
RAOm1126: Successfully updated (Genotype Id: 10960) Unable to add its a winner_93444 to RAOm1126 as male parent
Unable to add hot cocoa_93444 to RAOm1126 as female parent GenotypeAliasName (Alias123random4): already exists.
RAOm1127: Successfully updated (Genotype Id: 10961) Unable to add its a winner_93444 to RAOm1127 as male parent
Unable to add hot cocoa_93444 to RAOm1127 as female parent GenotypeAliasName (Alias123random5): already exists.
RAOm1128: Successfully updated (Genotype Id: 10962) Unable to add its a winner_93444 to RAOm1128 as male parent
                    
```

The report will include the status of each row. Green denotes a success while yellow denotes a warning.

4.2.6 Genotype Data Page

The **Genotype Data Page** provides the data/details about each genotype that is contained in your KDDart instance. This can display the following entities related to the genotype being viewed:

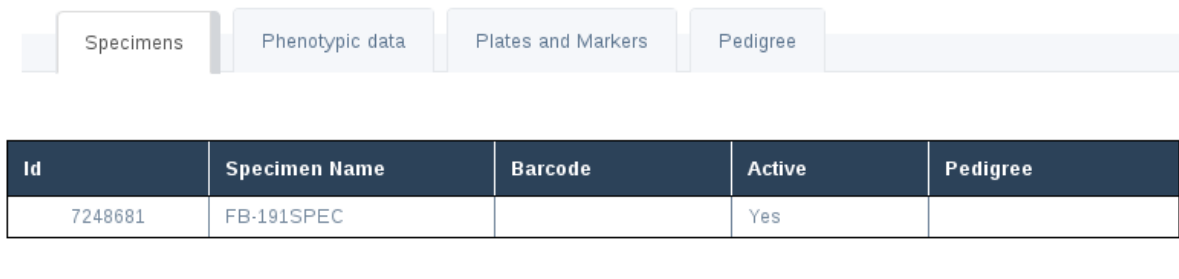


Fig. 14: Specimens Associated with the Genotype

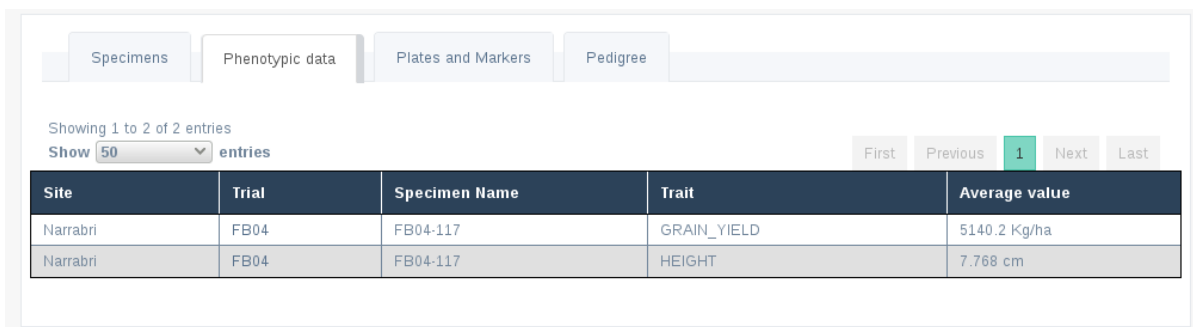


Fig. 15: Phenotypic Data Associated with a Genotype

Genus name: **Wheat** Species name: **none** Acronym:

Genotype details: **Genotype color:**

Genotype alias: **Note:** CROSSING

Factors: *There are no factors for Genotypes*

Id	Specimen Name	Barcode	Active	Pedigree
7248896	FB04-116		Yes	

Fig. 16: DNA and Marker Data Associated with Genotype

Genus name: **Wheat** Species name: **none** Acronym:

Genotype details: **Genotype color:**

Genotype alias: **Note:** CROSSING

Factors: *There are no factors for Genotypes*

Id	Specimen Name	Barcode	Active	Pedigree
7248896	FB04-116		Yes	

Fig. 17: Genpedigree Data of Genotype

4.3 Specimen

A *specimen* is the physical representation of a genotype and this facilitates the recording of vital characteristics such as where and when it was grown.

For example, in horticulture one specimen may be composed of two genotypes (rootstock and scion). The KDDart environment anticipates these scenarios and caters for this requirement.

Id	Specimen Name	Barcode	Breeding Method	Active	Pedigree	Selection History	Filial Generation	BreedingMethodName	Item Count	Action
1	1:2WB14		DEFAULT	Yes	BECARD/CHYAK	CMSS07B00236S-099M-099Y-099M-24WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
2	2:2WB14		DEFAULT	Yes	KACHU/BECARD/WBLL1*0BRAMBLING	CMSS07B00580T-099T0PY-099M-099NJ-099MJ-10WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
3	3:2WB14		DEFAULT	Yes	ROLF07/PAURAOUE #1	CMSS08Y00016S-099Y-099M-099Y-08WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
4	4:2WB14		DEFAULT	Yes	QUAJU #1/SUP152	CMSS08Y00075S-099Y-099M-099MJ-13WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
5	5:2WB14		DEFAULT	Yes	FRET2/FUKURUJ/FRET2/3PRL	CMSS08Y00125S-099Y-099M-099Y-2M-0WGY	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
6	6:2WB14		DEFAULT	Yes	HELO/MILAN/MUNA/3/KRITATI2*TRCH	CMSS08Y00127S-099Y-099M-099MJ-30WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
7	7:2WB14		DEFAULT	Yes	KACHU/KRITATI2*TRCH	CMSS08Y00152S-099Y-099M-099Y-2M-0WGY	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
8	8:2WB14		DEFAULT	Yes	KACHU/KRITATI2*TRCH	CMSS08Y00152S-099Y-099M-099MJ-19WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen
9	9:2WB14		DEFAULT	Yes	KACHU/KRITATI2*TRCH	CMSS08Y00152S-099Y-099M-099MJ-40WGY-0B	0	DEFAULT	0	Update Specimen Show Name Delete Specimen

Fig. 18: Specimens Page

Specimens can also be imported by selecting the **Import Specimen Button** which will display the **Import Specimen Window**. An example of the window and a table which explains the relevant fields can be found below:

Import Specimen ✕

*: denotes a required field.

Genus*: +

Breeding Method*: +

Specimen File*: No file chosen

Specimen Name Column*:

Is Active Column:

Pedigree Column:

Selection History Column:

Filial Generation Column:

Genotype Start Column*:

Genotype End Column:

Fig. 19: Import Specimen Window

Table 8: Import Specimen Fields

Field	Mandatory?	Description
Genus	Mandatory	Select an existing genus for all the specimens in the input file.
Breeding Method	Mandatory	Select an existing breeding method for all the specimens in the input file.
Specimen File	Mandatory	Browse to locate the input specimen CSV file.
Specimen Name Column	Mandatory	The specimen name column in the input file, numbered from zero.
Is Active Column		An indicator to show if the specimen is still active (i.e. in production).
Pedigree Column		Could be a generated Purdy string from male and female parent ID (or some other than Purdy standard).
Selection History Column		Optionally siblings clones etc, where genotype name is the same.
Filial Generation Column		Level of specimens being <i>selfed</i> , required when full selection history is unavailable.
Genotype Start Column	Mandatory	The genotype name column in the input file, numbered from zero.
Genotype End Column		The second genotype name column in the input file, numbered from zero.

4.3.1 Import Pedigree

New pedigree entries for existing specimens can be imported by selecting the **Import Pedigree Button** which will display the **Import Pedigree Window**. The window is displayed below with a table that details the relevant fields:

Fig. 20: Import Pedigree Window

Table 9: Import Pedigree

Field	Mandatory?	Description
Pedigree File	Mandatory	Select the input file for the import.
Specimen ID Column	Mandatory	Column number for specimen ID. These are the <i>children</i> genotypes.
Parent Specimen ID Column	Mandatory	Column number for parent specimen ID. These are the <i>parent</i> genotypes.
Specimen Parent Type ID Column	Mandatory	Column number for specimen parent type ID.
Use Name	Mandatory	Flags whether to use specimen ID or specimen name.

4.4 Specimen Lists

Specimens can be added to *specimens lists* for an organisation. The **Specimen Lists Page** can be seen in the image below:

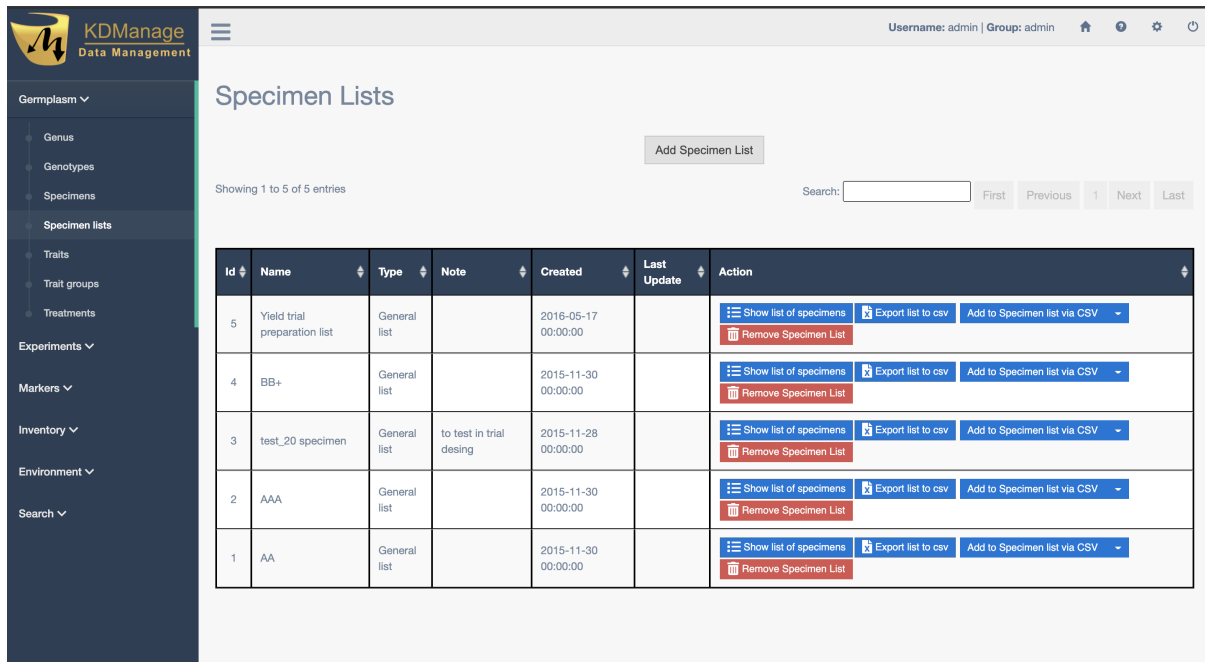


Fig. 21: Specimen Lists Page

A new specimen list can be added by selecting the **Add Specimen List Button** which will display the **Add Specimen List Window**. The window and a table with the relevant fields can be found below:

Add Specimen List
✕

*: denotes a required field.

Name*:

Type*: +

Status*: +

Date Created*:

Note / Description:

Owner Permission:

Access Group:

Access Permission:

Other Permission:

Specimen

	<input checked="" type="checkbox"/>	Specime Id	Specimen Name	Pedigree
+	<input type="checkbox"/>	7248897	FB04-117	
+	<input type="checkbox"/>	7248896	FB04-116	
+	<input type="checkbox"/>	7248895	FB04-115	
+	<input type="checkbox"/>	7248894	FB04-114	
+	<input type="checkbox"/>	7248893	FB04-113	
+	<input type="checkbox"/>	7248892	FB04-112	
+	<input type="checkbox"/>	7248891	FB04-111	
+	<input type="checkbox"/>	7248890	FB04-110	
+	<input type="checkbox"/>	7248889	FB04-109	
+	<input type="checkbox"/>	7248888	FB04-108	

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Selected Specimen for new List: please drag a single or multiple specimens from list above.

<input checked="" type="checkbox"/>	Specimen Id	Specimen Name

Page 1 of 0 | 10 | No records to view

Fig. 22: Add Specimen List Window

Table 10: Add Specimen List Fields

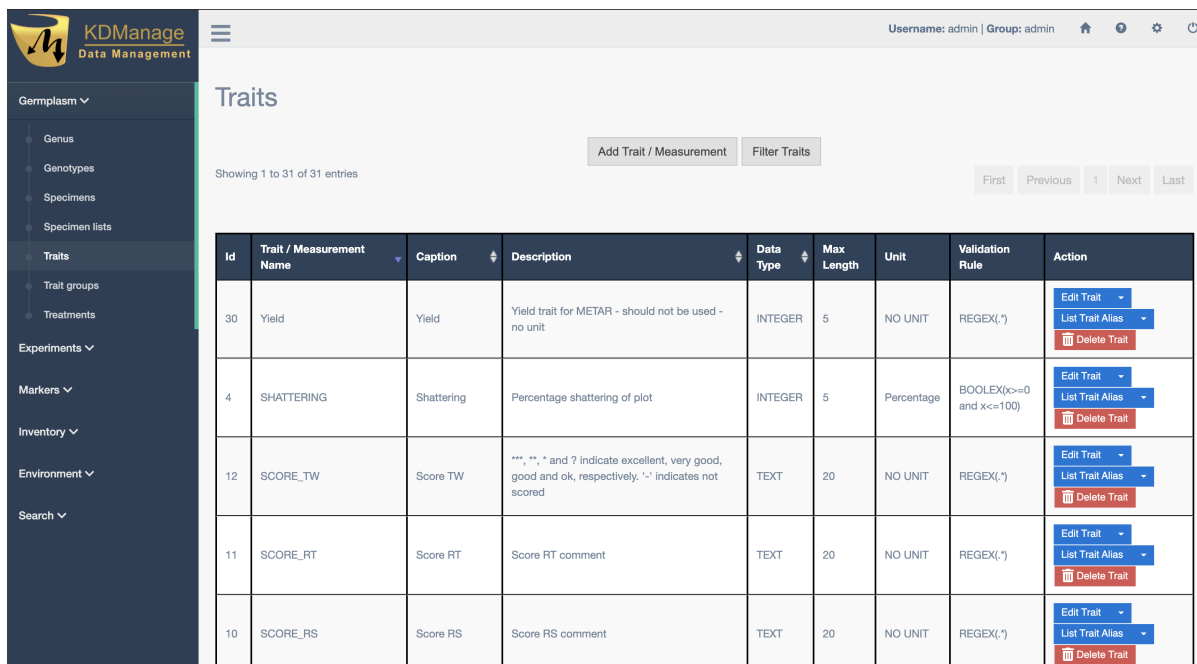
Field	Mandatory?	Description
Name	Mandatory	Name of specimen list.
Type	Mandatory	Type of specimen list see the <i>Administrative Settings</i> topic.
Status	Mandatory	Status of specimen list see the <i>Administrative Settings</i> topic.
Date Created	Mandatory	Date that specimen list is created.
Note/Description		Notes of specimen list.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

4.4. Specimen Lists

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4.5 Traits

Traits are important descriptors of what is to be measured and what the permissible values are in those measurements. The **Trait/Measurement Page** enables the definition and quantification of a trait or characteristic of the trial/experiment. This includes a description and notes, the data type, units of measurement, maximum value and validation rule.



The screenshot shows the KDManage interface for the Traits page. The page title is "Traits" and it shows "Showing 1 to 31 of 31 entries". There are buttons for "Add Trait / Measurement" and "Filter Traits". A table lists the following traits:

Id	Trait / Measurement Name	Caption	Description	Data Type	Max Length	Unit	Validation Rule	Action
30	Yield	Yield	Yield trait for METAR - should not be used - no unit	INTEGER	5	NO UNIT	REGEX(,)	Edit Trait List Trait Alias Delete Trait
4	SHATTERING	Shattering	Percentage shattering of plot	INTEGER	5	Percentage	BOOLEX(x>=0 and x<=100)	Edit Trait List Trait Alias Delete Trait
12	SCORE_TW	Score TW	***, **, * and ? indicates excellent, very good, good and ok, respectively. '-' indicates not scored	TEXT	20	NO UNIT	REGEX(,)	Edit Trait List Trait Alias Delete Trait
11	SCORE_RT	Score RT	Score RT comment	TEXT	20	NO UNIT	REGEX(,)	Edit Trait List Trait Alias Delete Trait
10	SCORE_RS	Score RS	Score RS comment	TEXT	20	NO UNIT	REGEX(,)	Edit Trait List Trait Alias Delete Trait

Fig. 23: Traits Page

Traits need to be defined before they can be assigned to a trial. Once traits are added here they will appear in the selection list for *Add Traits to a Trial*.

New traits can be added by selecting the **Add Trait Button** which displays the **Add Trait Window**. The window and all fields available in it are demonstrated in the image and table below:

Add Trait ✕

*: denotes a required field.

Trait / Measurement Name*:	<input style="width: 95%;" type="text" value="plant_height"/>
Trait level*:	<input style="width: 95%;" type="text" value="Trial Unit"/>
Caption*:	<input style="width: 95%;" type="text" value="height"/>
Description / Note*:	<input style="width: 95%;" type="text" value="The height of the plant."/>
Group Type:	<input style="width: 95%;" type="text" value=""/>
Data Type*:	<input style="width: 95%;" type="text" value="DECIMAL"/>
Max Length*:	<input style="width: 95%;" type="text" value="8"/>
Unit*:	<input style="width: 95%;" type="text" value="cm"/>
Used for Analysis*:	<input style="width: 95%;" type="text" value="Yes"/>
Type of Validation Rule:	<input style="width: 95%;" type="text" value="Boolean expression"/>
Validation Rule*:	<input style="width: 95%;" type="text" value=""/>
Validation Error Message*:	<input style="width: 95%;" type="text" value="The plant height must be between 0cm and 200cm."/>
Owner Permission*:	<input style="width: 95%;" type="text" value="Read/Write/Link"/>
Access Group*:	<input style="width: 95%;" type="text" value="admin"/>
Access Permission*:	<input style="width: 95%;" type="text" value="Read/Write/Link"/>
Other Permission*:	<input style="width: 95%;" type="text" value="Read/Link"/>
AltIdentifier:	<input style="width: 95%;" type="text" value=""/>

Fig. 24: Add Traits Window

Field	Mandatory?	Description
Trait/Measurement Name	Mandatory	The name to identify the trait or measurement.
Caption	Mandatory	An abbreviated or shortened trait name (e.g. name without spaces). Could be used for display.
Description/Note	Mandatory	A description or note about the trait.
Data Type	Mandatory	The trait's data type. Selection from class <i>Trait Data Type</i> in Types (see Types section in <i>Administrative Settings</i>)
Max Length	Mandatory	The maximum length of the value (e.g. 12).
Unit	Mandatory	Unit of measurement for the trait (e.g. kg/h, colour, etc).
Used for Analysis	Mandatory	May be used as an indicator (e.g export all traits need analysis).
Type of Validation Rule	–	Indicator for the type of validation rule (either a Boolean, Regular, Range or a Choice expression). Upon selecting a rule, a helper will appear that you can use to make sure you use the correct format.
Validation Rule	Mandatory	A validation rule for the value of the trait.
Validation Error Message	Mandatory	An error message to display when the validation rule criteria is not met.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

4.6 Trait Groups

Traits can be added to *trait groups* which allows for traits to be added in groups for convenience. Trait groups are listed in the **Trait Groups Page** as seen in the image below:

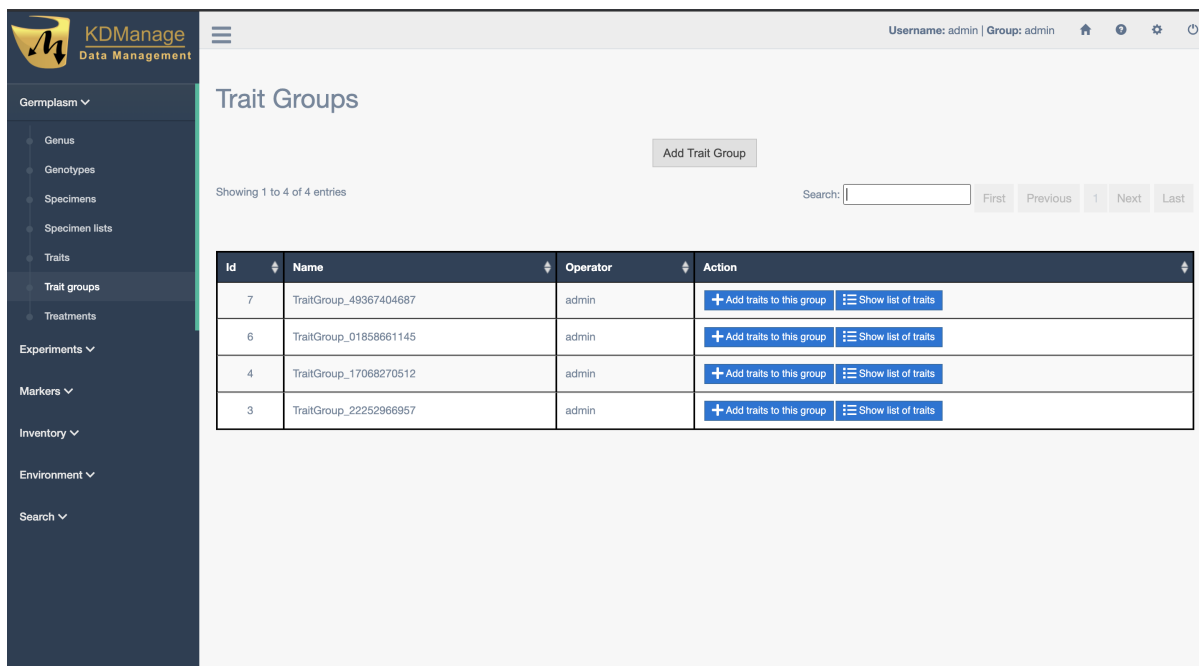


Fig. 25: Trait Groups Page

The image below demonstrates a trait group for a wheat trial:

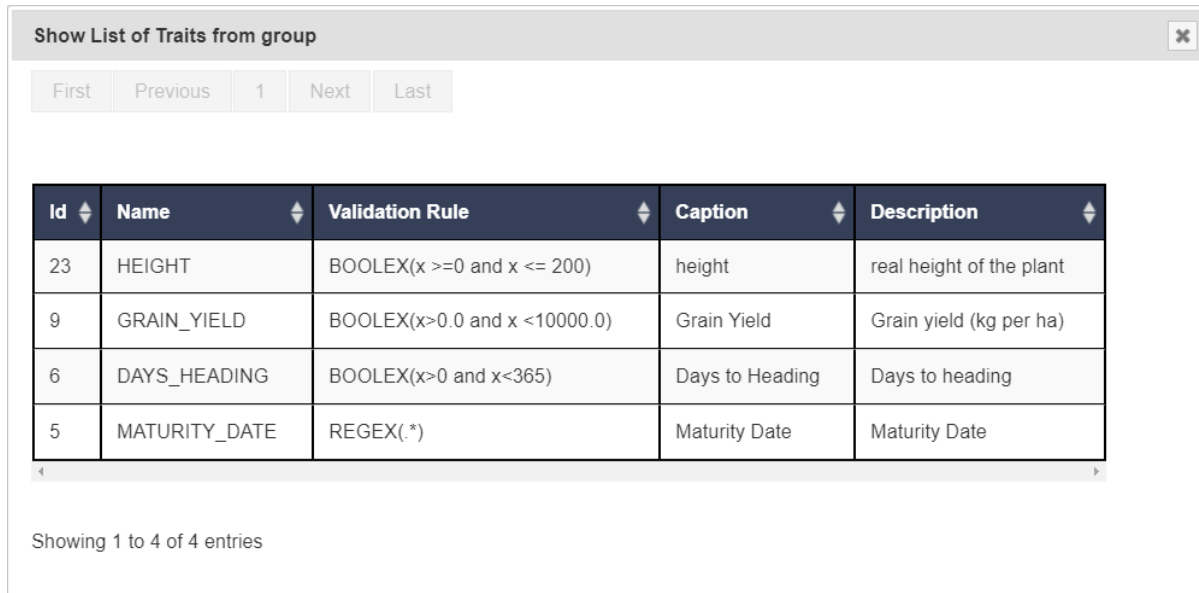


Fig. 26: Trait Group

New trait groups can be created by selecting the **Add Trait Group Button** which will display the **Add Trait Group Window** (see below) where a name for the new group and traits can be selected.

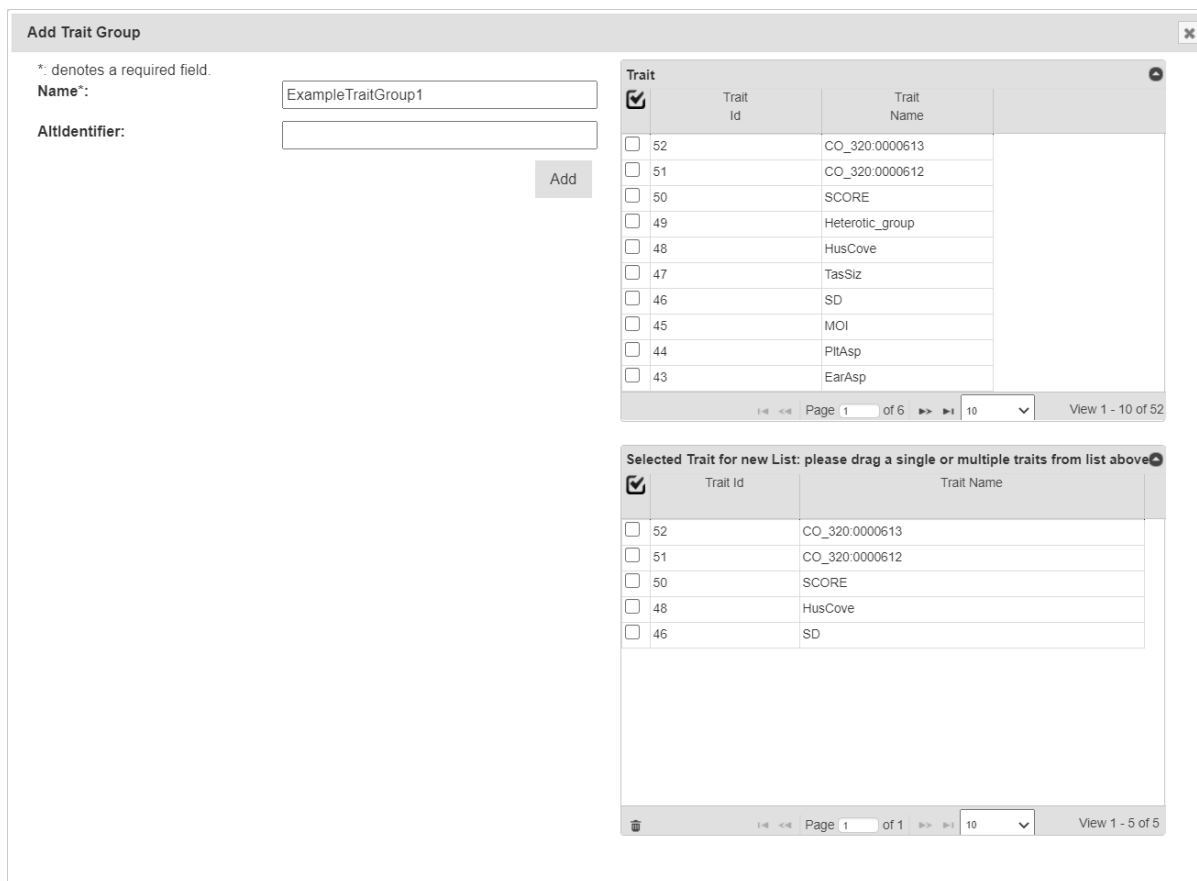


Fig. 27: Add Trait Group Window

Note: Traits must already exist in KDDart before they are added to trait groups.

4.7 Treatment

Treatment describes or quantifies an action performed on a trial unit to induce a measurable response, such as to a certain level of fertilisation (e.g. adding nitrogen) quantity of irrigation, etc. The **Treatment Page** lists all treatments that are available in your KDDart instance.

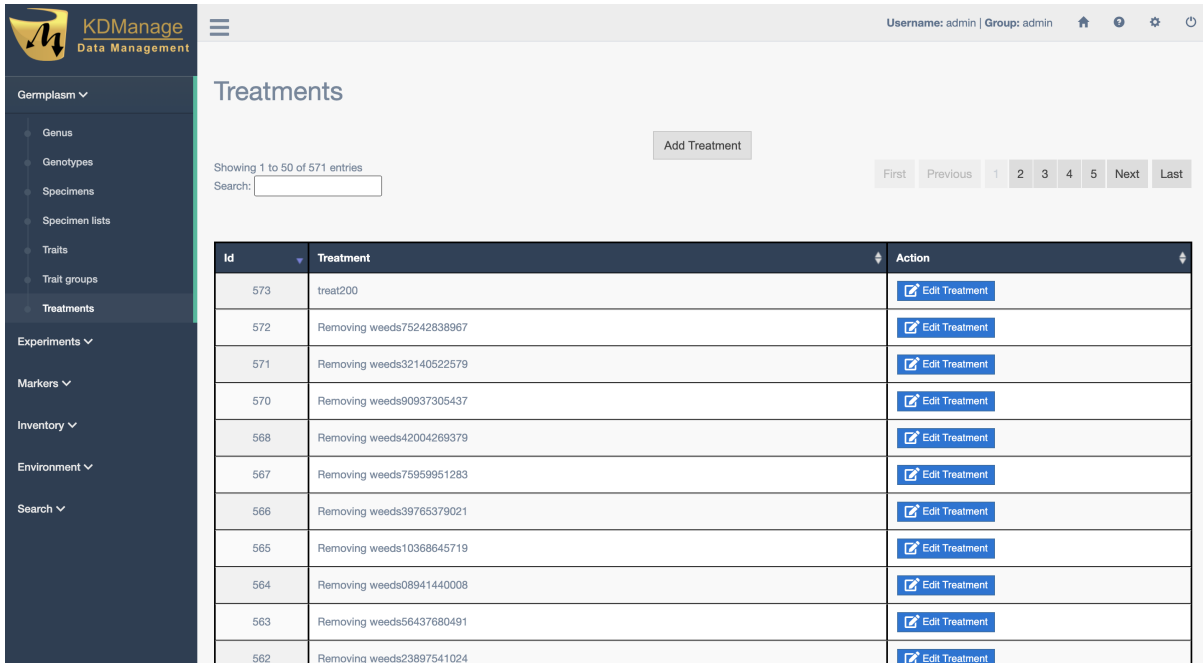


Fig. 28: Treatments Page

New treatments can be added by selecting the **Add Treatment Button** which displays the **Add Treatment Window** as seen in the image below:

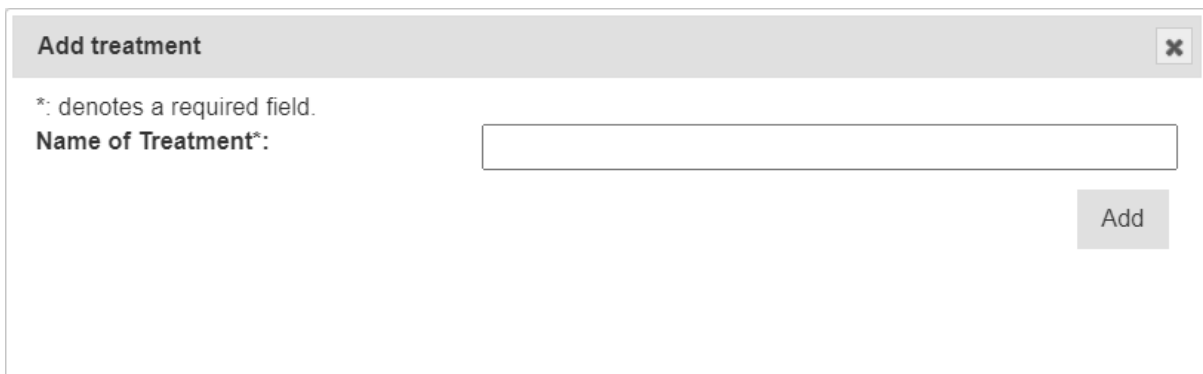


Fig. 29: Add Treatments Window

EXPERIMENT MENU

The **Experiment Menu** contains various pages with tools that can be used to create and manage the entities in KDDart that represent experiments and methods.

The following items of the **Experiment Menu** illustrate the *order of dependency*:

1. *Site*
2. *Design Type*
3. *Breeding Method*
4. *Trials*
5. *Nurseries*

This order of dependency means that a *site* must first be created before a *design type* can be added to it.

5.1 Site

Sites are high-level groupings of *trials* which may equate to places where breeding/variety evaluation occurs such as a *breeding station*. Geographic coordinates can be assigned to enable illustration on a map. A *site* may consist of a whole farm, breeding station or any other general environmentally homogeneous area, where planting occurs.

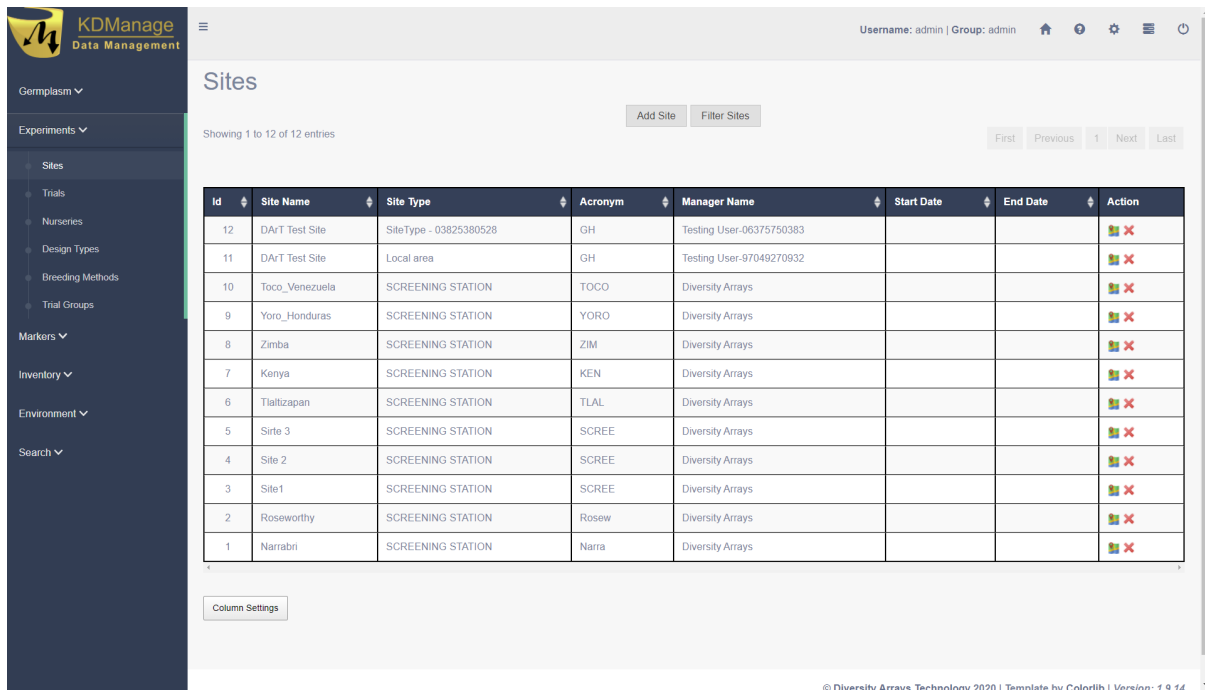


Fig. 1: Sites Page

Sites can be added by selecting the **Add Site Button** which will display the **Add Site Window** which provides options for creating a new site. An image of the **Add Site Window** and a table describing its fields can be found below:

Add site
✕

*: denotes a required field.

Site Name*:

Site Type*: + Local area ▼

Site Acronym*:

Site Manager*: ▼

Start Date:

End Date:

Site Geometry*:

Manual Site Longitude:

Manual Site Latitude:

Add site

Search values: OpenStreetMap Data offer by nominatim.osm.org

Fig. 2: Add Sites Window

Table 1: Add Site Fields

Field	Mandatory?	Description
Site Name	Mandatory	A name to identify the site.
Site Type	Mandatory	Selection from defined or classified site types. Site types must have already been created.
Site Acronym	Mandatory	Abbreviated site name (e.g. may conform to the trial naming convention).
Site Manager	Mandatory	An existing contact - a person currently managing the site (not necessarily a user of this system).
Start Date	Mandatory	Date the site commenced operation (format YYYY-MM-DD).
End Date	Mandatory	Date the site stopped operation (format YYYY-MM-DD).
Site Geometry	Mandatory	This field contains the geographic coordinates of the site. It is populated by the selection of the site on the displayed map.

5.2 Design Type

A *design type* defines how a trial or experiment is to be conducted.

The fields capture the layout/method that will be used to plant the genotypes, the number of replicates, etc. The data entered here is used as input for external software, such as DiGger, which may be used to create the design.

Id	Name of Design	Name of Software	Template File	Genotype Format	Factor Alias Prefix	Action
13	XITEHSFVRG					Edit Design Type
12	XFRXUWEDRC					Edit Design Type
3	Other					Edit Design Type
2	CIMMYT					Edit Design Type
1	Digger					Edit Design Type

Fig. 3: Design Types Page

KDCompute can generate a trial layout using DiGger which will consume the data entered here.

Note: Whilst an external application can be used to construct the trial design it is not mandatory.

New design types can be added by selecting the **Add Design Type Button** which will open the **Add Design Type Window**. The window and a table which explains the relevant fields can be found below:

Add Design Type ✕

*: denotes a required field.

Name of Design*:

Name of Software:

Template File:

Genotype Format:

Factor Alias Prefix:

Fig. 4: Add Design Type Window

Field	Mandatory?	Description
Name of Design	Mandatory	A name to identify the design type.
Name of Software	Mandatory	The software used for preparing the design. For example, DiGger could be used to create a randomised block design.
Template File	Mandatory	Defines how the parameters need to be inserted in the input file for the design software.
Genotype Format	Mandatory	Format in which the genotype name and genotype ID will be exported into the trial design input file. The DesignGenotypeFormat must be GenotypeName GenotypeId (eg VENTURA 41) to satisfy DiGger requirements.
Factor Alias Prefix	Mandatory	Prefix used to find the factor for the trial design parameter while importing trial design from the output file generated by the trial design software.

5.3 Breeding Method

A *breeding method* is an additional descriptor of a specimen which complements pedigree information and caters for a controlled vocabulary.

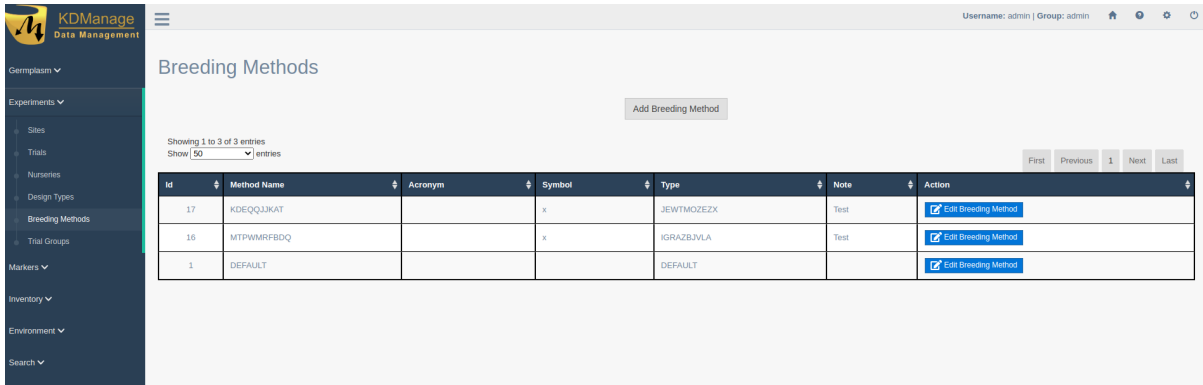


Fig. 5: Breeding Methods Page

A new breeding method can be added by selecting the **Add Breeding Method Button** which will display the **Add Breeding Method Window**. The window, along with a table explaining its fields can be found below:

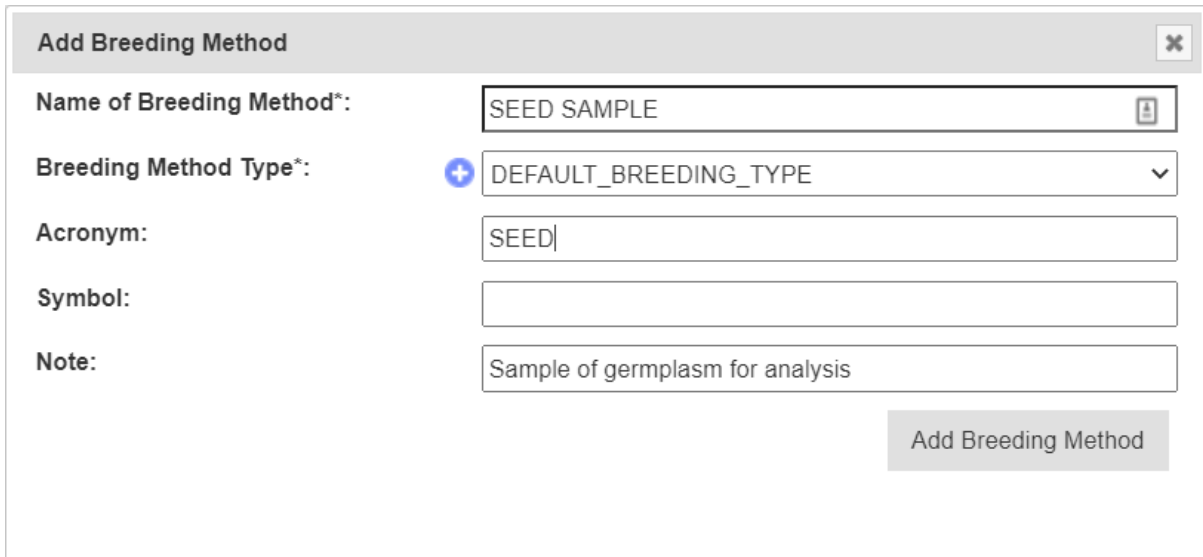



Fig. 6: Add Breeding Method Window

Field	Mandatory?	Description
Name of Breeding Method	Mandatory	Name of the breeding methodology.
Breeding Method Type	Mandatory	Type of breeding method. A new breeding method type can be created by selecting the  Add Button .
Acronym		Acronym for the name of the breeding method.
Symbol		Symbol to represent the breeding method.
Note		A short description of the breeding methodology.

Note: Where it is not important to specify a Breeding Method use the 'Default' Breeding Method.

5.4 Trials

Trials are the equivalent to field or nursery experiments that are performed within a *Site*.

The **Trials Page** displays the list of defined trials which the user/group has permission to view as shown in the following image:

The screenshot shows the 'Trials' page in the KDManage application. The page header includes the KDManage logo, a navigation menu, and user information (Username: admin | Group: admin). Below the header, there are buttons for 'Add Trial', 'Filter Trials', and 'Trial Super Import'. A pagination bar indicates 'Showing 1 to 17 of 17 entries' with 'First', 'Previous', 'Next', and 'Last' buttons. The main content is a table with the following data:

ID	Trial Name	Trial Type	Site	Manager	Start Date	End Date	Trial Status	Action
18	MLGAZGFVKA	BRWBCHLZYP	ZDYDDIQXAJ	CJUECHCFQM Tester	2021-01-27 00:00:00		Layout Added	View trial - Edit Trial - Delete trial
17	SWBLOEVHTU	IAPKIFQNSW	PODBJLOKC	HONYJHMKEN Tester	2021-01-27 00:00:00		Layout Added	View trial - Edit Trial - Delete trial
16	Test Maca	Yield trial	Test Maca	Diversity Arrays	2016-05-17 00:00:00		Data Uploaded	View trial - Edit Trial - Download CSV Template - Delete trial
15	Test22	Yield trial	Narrabri	Diversity Arrays	2015-11-23 00:00:00		Layout Added	View trial - Edit Trial - Delete trial
14	Test20	Yield trial	Narrabri	Diversity Arrays	2015-11-23 00:00:00		Ready for Upload	View trial - Edit Trial - Download CSV Template - Delete trial
13	Tlaltl Optim - outlier - not for METAR	Optim	Tlaltzapan	Diversity Arrays	2013-07-03 00:00:00		Ready for Upload	View trial - Edit Trial - Download CSV Template - Delete trial
12	Zimba_Stress	Stress	Zimba	Diversity Arrays	2014-07-03 00:00:00		Data Uploaded	View trial - Edit Trial - Download CSV Template - Delete trial

Fig. 7: Trials Page

In the image above, the **Trials Page** shows several trial records. Each record contains a trial’s ID in KDDart as well as its name and available actions.

5.4.1 Trial Actions

The following table lists all the actions that can be performed for the selected Trial in KDManage.

Note: The presence of action types is dependent upon the trial state - not all action types will be available for all trials.

Action	Description	Parent Button
Add Trait to Trial	Add a trait to the trial.	Edit Trial
Download	Download trial data.	Download CSV Template
Edit Trial	Edit the trial.	
Download CSV Template	Down the CSV template for the trial.	
List Trait for Trial	List the traits for the selected trial.	View Trial
Import CSV Scoring Data	Import a data file for trial	Download CSV Template
Display Trial Unit for Trial	Display the trial units/layout for the selected trial.	View Trial
Upload File	Uploads files to this trial.	View Trial
List files for Trial	List all files that have been uploaded to this trial	View Trial
Delete Trial	Delete this trial. This can only be done if there is no trial data uploaded to this group and this trial is not part of an existing trial group. Users can also choose to clear the trial of trial units and trial traits if they wish.	

Three of the actions are relevant to KDSmart. These are:

- **Download Trial Data** - produces a CSV file for importing into KDSmart which contains a trial's trait results.
- **Download CSV Template** - produces a CSV file for importing into KDSmart without any of a trial trait's results.
- **Import CSV Scoring Data** - loads data back into KDDart from scoring in KDSmart.

5.4.2 Adding Trials

New trials can also be created in KDManage. To add a new trial, select the **Add Trial Button** which will display the **Add Trial Window**. The window, along with a table that explains the relevant fields can be found below:

✕
Add Trial

*: denotes a required field.

Trial Name* :	<input style="width: 90%;" type="text" value="FB04"/>
Trial Number* :	<input style="width: 90%;" type="text" value="4"/>
Trial Type* :	+ <input style="width: 90%;" type="text" value="Yield trial"/>
Season* :	+ <input style="width: 90%;" type="text" value="UnknownSeasonFromMigration"/>
Site* :	<input style="width: 90%;" type="text" value="Narrabri"/>
Project ID:	<input style="width: 90%;" type="text" value="BrAPI"/>
Current Workflow:	<input style="width: 90%;" type="text"/>
Trial Acronym* :	<input style="width: 90%;" type="text" value="FB"/>
Design Type* :	+ <input style="width: 90%;" type="text" value="CIMMYT"/>
Trial Manager* :	<input style="width: 90%;" type="text" value="Diversity Arrays"/>
Start Date* :	<input style="width: 90%;" type="text" value="2020-09-01"/>
End Date:	<input style="width: 90%;" type="text" value="2021-09-01"/>
Note:	<div style="border: 1px solid #ccc; height: 30px; width: 100%;"></div>
Owner Permission* :	<input style="width: 90%;" type="text"/>
Access Group* :	<input style="width: 90%;" type="text"/>
Access Permission* :	<input style="width: 90%;" type="text"/>
Other Permission* :	<input style="width: 90%;" type="text"/>

Add this trial to the following trial groups: Stress Grouping Multilocation Yield Testing

Add trial

Fig. 8: Add Trial Window

Table 2: Add Trial Fields

Field	Mandatory?	Description
Trial Name	Mandatory	The name of the trial. A naming convention is suggested (e.g. a concatenation of site, type, date, number).
Trial Number	Mandatory	The Number of the trial, which could be sequentially assigned.
Trial Type	Mandatory	Select from the list of trial types (A general type as opposed to design type which is a trial specific definition).
Season	Mandatory	Season that the trial is taking place.
Site	Mandatory	Select from the list of sites to specify where the trial is to occur.
Project ID		Select from a list of projects.
Current Workflow		Select a related workflow from the list.
Trial Acronym	Mandatory	An alternative abbreviated name for the trial.
Design Type	Mandatory	Select a design type that identifies the trial design.
Trial Manager	Mandatory	Someone currently managing the trial and defined in contacts although they are not necessarily a system user.
Start Date	Mandatory	The date the trial commenced (Format YYYY-MM-DD).
End Date	Mandatory	The date the trial has/will end (Format YYYY-MM-DD).
Note	Mandatory	Descriptive notes for the trial.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

Note: Before a trial can be added, the site to be used must exist. When defining the trial Location, the trial must be contained within the boundaries defined for the Site.

5.5 Trial Design

The trial design page allows data visualisation (e.g specimens) with XYZ dimensions.

To add the data to map, select from the search results and click on the button **Add Specimens to Design**. Data added will show in the Layout List and can be removed by clicking **Remove Specimen**.

Search Resultss

>>
Use all

Showing 51 to 75 of 24588 entries

First Previous 1 2 3 4 5 Next Last

#	Barcode	Note	Action
men	MegaTestttt37_specimen_barcode	MegaTest1 timing	Add Specimens to Design
men	MegaTestttt19_specimen_barcode	MegaTest1 timing	Add Specimens to Design
men	MegaTestttt30_specimen_barcode	MegaTest1 timing	Add Specimens to Design
men	MegaTestttt34_specimen_barcode	MegaTest1 timing	Add Specimens to Design
men	MegaTestttt31_specimen_barcode	MegaTest1 timing	Add Specimens to Design
men	MegaTestttt29_specimen_barcode	MegaTest1 timing	Add Specimens to Design

Layout List

S
Save Trial

R
Reset Trial

R
Randomise

Max X

Max Y

Max Z

Showing 1 to 6 of 6 entries
Show entries

First Previous 1 Next Last

Specimen	X	Y	Z	Repeat	Action
MegaTest33_specimen	1	1	1	1	Remove Specimen
MegaTest19_specimen	2	1	1	1	Remove Specimen
MegaTest30_specimen	3	1	1	1	Remove Specimen
MegaTest33_specimen	4	1	1	2	Remove Specimen
MegaTest31_specimen	5	1	1	1	Remove Specimen
MegaTest29_specimen	6	1	1	1	Remove Specimen

Fig. 9: Search Results and Layout List

The map will be displayed in the New Layout Visualised section using XYZ dimensions. Each unit comes with the drag and drop function and can be adjusted with the following settings:

New Layout Visualised

S
Save Trial

R
Reset Trial

R
Randomise

C
Recolour

R
Rotate

Select Orientation:
Map Size:

MegaTest33_...	MegaTest19_...	MegaTest30_...	MegaTest33_...	MegaTest31_...	MegaTest29_...	MegaTest32_...	MegaTest27_...	MegaTest23_...	MegaTest22_...
MegaTest8_s...	MegaTest7_s...	MegaTest1_s...	MegaTest31_...	MegaTest12_...	MegaTest16_...	MegaTest9_s...	MegaTest23_...	MegaTest20_...	MegaTest33_...
MegaTest21_...	MegaTest33_...	MegaTest32_...	MegaTest22_...	MegaTest33_...	MegaTest30_...	MegaTest33_...	MegaTest24_...	MegaTest25_...	MegaTest28_...
MegaTest2_s...	Empty	Empty	Empty	Empty	Empty	Empty	Empty	Empty	Empty

Fig. 10: Trial Design Map

Table 3: Trial Design Map Settings

Field	Description
Max X	Maximum units show in a row.
Max Y	Maximum rows show in a block.
Max Z	Maximum blocks show in the map.
Map Size	Size of the map (e.g. 10x10, 20x20, 50x50, 100x100).
Orien-tation	View Direction either from top left, top right, bottom right and bottom left.
Zoom In	Enlarge the size of the map/ specific zone of the map.
Zoom Out	Reduce the size of the map.

There are also list of actions that can be performed to the map including:

- **Save Trial** - Save the current arrangement of the map for future use.
- **Reset Trial** - Start over again from initial stage of trial design page.
- **Randomise** - Shuffle the arrangement of layout.
- **Recolour** - Colour the units based on the frequency of a specimen has been used.
- **Rotate** - Change the view direction of the map.

5.5.1 Trial Super Import

Prerequisite: Before the Trial Super Import can be used, a .csv file containing the relevant data must be prepared. This .csv should contain the columns listed within the Trial Super Import form.

This function allows the user to upload trial units for multiple trials with a single .csv file.

Where a trial already exists, it will update the existing trial. Otherwise, a new trial will be created with the given information within the csv. Similarly, existing trial units will be updated or created as necessary.

There are also flags that can be set in this super import function that will prevent certain actions:

- **Allow creation of Specimens/Genotypes** - determines whether specimens and genotypes that don't exist should be created.
- **Update existing Trial Information** - determines whether an existing trial should be updated with given information.
- **Update existing Trial Units/Plots** - determines whether existing trial units/plots should be updated with given information.

Generally, it is useful to prevent these actions where it is certain that the data is uploaded exclusively for updating existing trials/ trial units. This way, spelling and other administrative errors will be caught instead of automatically added as a new trial/trial unit/ specimen/ genotype.

To use the Trial Super Import, select the **Trial Super Import** button to display the Trial Super Import window.

The following illustration shows the Trial Super Import window, displaying the fields which represent the columns required for the super import to run. There are in total 4 steps:

Step 1: Trial Information

Super Import Trial Data

*: denotes a required field.

Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Trial Data File*: No file chosen

Trial Name Column*:

Site Column*:

Trial Start Date Column*:

Trial Manager Name Column*:

Trial Type*:

Update existing Trial Information*:

Next

Field	Mandatory	Description
Trial Data File	M	The prepared .csv file containing the columns below.
Trial Name Column	M	The column that contains the trial names.
Site Column	M	The column that contains the sites for each trial.
Trial Start Date Column	M	The column that contains the Trial Start Date for each trial.
Trial Manager Name Column	M	The column that contains the manager for each trial.
Trial Type	M	The column that contains the Trial Type for each trial.
Update existing Trial Information	M	Flag to determine whether the super import should update existing trial information with given data.

Step 2: Trial Unit Dimensions

Super Import Trial Data

*: denotes a required field.

Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

X Column:

Y Column:

Z Column:

EntryId Column:

Position Column:

Replicate Number Column:

Barcode Column:

Use Barcode for Update*:

Automatically generate empty barcodes*:

[Previous](#) [Next](#)

Field	Mandatory	Description
X Column	(!)	One of the trial dimension columns as part of XYZ which will be added to new trials, to create new trial units and to identify existing trial units.
Y Column	(!)	One of the trial dimension columns as part of XYZ which will be added to new trials, to create new trial units and to identify existing trial units.
Z Column	(!)	One of the trial dimension columns as part of XYZ which will be added to new trials, to create new trial units and to identify existing trial units.
EntryId Column	(!)	One of the trial dimension columns which will be added to new trials, to create new trial units and to identify existing trial units.
Position Column	(!)	(NOT CURRENTLY IN USE) One of the trial dimension columns which will be added to new trials, to create new trial units and to identify existing trial units.
Replicate Number Column		The column where the replicate number is listed for the Trial Unit.
Barcode Column	(!)	One of the trial dimension columns which will be added to new trials, to create new trial units and to identify existing trial units.
Use Barcode for Update	M	Flag to determine whether the super import should update existing trial units barcode with given data.
Automatically generate empty barcodes	M	Flag to determine whether the super import should generate random barcodes for trial units.

Step 3: Specimen & Genotype & Trial Unit

Super Import Trial Data

*: denotes a required field.

Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Specimen Name Column*:

Genotype Name Column:

Specimen Number Column:

TUS Label Column:

Plant Date Column:

Treatment Column:

Notes Column:

Source Trial Unit Barcode:

Allow creation of Specimens/Genotypes*:

Update existing Trial Units/Plots*:

[Previous](#) [Next](#)

Field	Mandatory	Description
Specimen Name Column	M	The column where the specimen names within each trial unit are listed. For existing trial units, these will just be used to validate the correctness of the .csv file. The specimen number column is the primary identification of specimens within trial units.
Genotype Name Column		The column where the specimen's genotype is defined and will be added to the specimen. For new genotypes, they will be created automatically.
Specimen Number Column		The column where a specimen's number within a trial unit is defined. For existing trial units, these values will be used as the primary identification of specimens within trial units.
TUS Label Column		The column where label for the Trial Unit Specimen are given.
Plant Date Column		The column where the plant dates are given.
Treatment Column		The column where an existing treatment name is listed for the Trial Unit.
Notes Column		The column where descriptive notes for the Trial Unit are given.
Source Trial Unit Barcode		The column where the source trial unit's barcode is listed for the Trial Unit.
Allow creation of Specimens and Genotypes	M	Flag to determine whether the super import should automatically create new specimens and genotypes.

continues on next page

Table 6 – continued from previous page

Field	Mandatory	Description
Update existing Trial Units/Plots	M	Flag to determine whether the super import should update existing trial units with given data.

Step 4: Item Information

Super Import Trial Data

*: denotes a required field.

Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Item Type:

Item Unit:

Amount Column:

Storage Barcode:

Item Barcode:

[Previous](#) [Import](#)

Field	Mandatory	Description
Item Type		The column that contains the Item Type for each item. Also, a flag to determine whether this super import should create new items and add to specimen.
Item Unit		The column that contains the Item Unit for each item.
Amount Column		The column that contains the Item Amount for each item.
Storage Barcode		The column that contains the Storage Barcode for each item.
Item Barcode		The column that contains the Item Barcode for each item.

Note: (!) in the mandatory column denotes that at least one of these fields must be given.

Once the .csv file has been uploaded under **Trial Data File**, an additional view will be generated in the window that contains all the columns of the .csv file.

Super Import Trial Data
✕

*: denotes a required field.
 Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Trial Data File*: genotype-trial-inventory-demo (2).csv

Trial Name Column*:

Site Column:

Trial Start Date Column:

Trial Manager Name Column:

Trial Type*:

Update existing Trial Information*:

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
TrialName	Megatest-Trial13	-
TrialManager	Diversity Arrays	-
TrialStartDate	27/7/2021	-
Site	Sydney	-
GenotypeName	MegaTest1	-
Specimen	LKFVJTMLE	-
SelectionHistory	DD1	-
Note	MegaTest1 timing	-
ColourDay1	Red	-
ColourDay2	Black	-
CommonName	MegaTest1_regular	-
CommercialName	MegaTest1_commercial	-
Pedigree		-
GF1	34.64	-
GF2	97.01	-
LODGING	75	-
Height	56	-
Male		-
Female		-
NewName	YY1	-

Now, the remaining fields can be selected using the dropdowns to match the requisite columns to the columns that exist within the uploaded file.

The existing columns on the right will turn green when they have been selected once, and turn red if they have been incorrectly selected more than once.

Super Import Trial Data
✕

*: denotes a required field.
 Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Trial Data File*: genotype-trial-inventory-demo (2).csv

Trial Name Column*:

Site Column:

Trial Start Date Column:

Trial Manager Name Column:

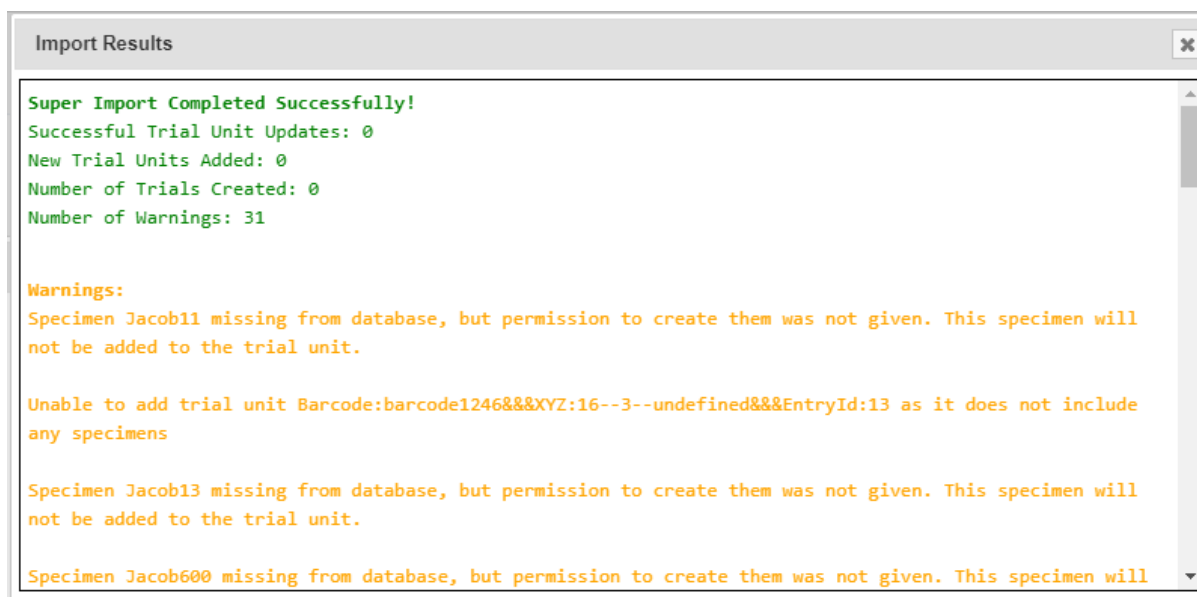
Trial Type*:

Update existing Trial Information*:

This is a preview of your CSV file

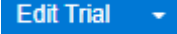
CSV headers	First row	Column will be mapped as:
TrialName	Megatest-Trial13	Trial Name Column
TrialManager	Diversity Arrays	Trial Manager Name Column
TrialStartDate	27/7/2021	Trial Start Date Column
Site	Sydney	Site Column
GenotypeName	MegaTest1	-
Specimen	LKFVJTMLE	Specimen Name Column
SelectionHistory	DD1	-
Note	MegaTest1 timing	-
ColourDay1	Red	-
ColourDay2	Black	-
CommonName	MegaTest1_regular	-
CommercialName	MegaTest1_commercial	-
Pedigree		-
GF1	34.64	-
GF2	97.01	-
LODGING	75	-
Height	56	-
Male		-
Female		-
NewName	YY1	-

Once all the needed columns have been selected, select the **Import** button to run the super import. When the super import completes, a prompt should be shown with some statistics on the super import.




The general statistics are displayed at the top, while all the warnings will are printed in yellow below.

5.5.2 Add Traits to a Trial

Selecting **Add a Trait to Trial** (under  dropdown) adjacent to the selected Trial will display the following Add Trial Trait window. The Trait is selected from a list of predefined Traits (refer to the *Traits* topic).

When the Compulsory field is set to 'yes' the capturing of the trait will become mandatory when recording Trial data.

Trials need *traits* added to them before they can be measured in the field. To add traits to a trial, select the  **Add Button** (adjacent to the relevant trial) which will display the **Add Trial Trait Window** which can be seen in the image below:

*: denotes a required field.
Please use plus or cross action icon to add a new row or delete an unwanted one!

Trait*:	Compulsory*:	Action
<div style="border: 1px solid gray; padding: 5px;"> pER PH PLANT_HEIGHT PLANT_MATURITY_ZAVOK PltAsp pRL pSL rEPH rEPP SCORE SCORE_EA SCORE_HUERTA SCORE_RS SCORE_RT SCORE_TW SD SHATTERING TasSiz Yield </div>	<input checked="" type="checkbox"/>	+ -

Fig. 11: Add Trial Trait Window

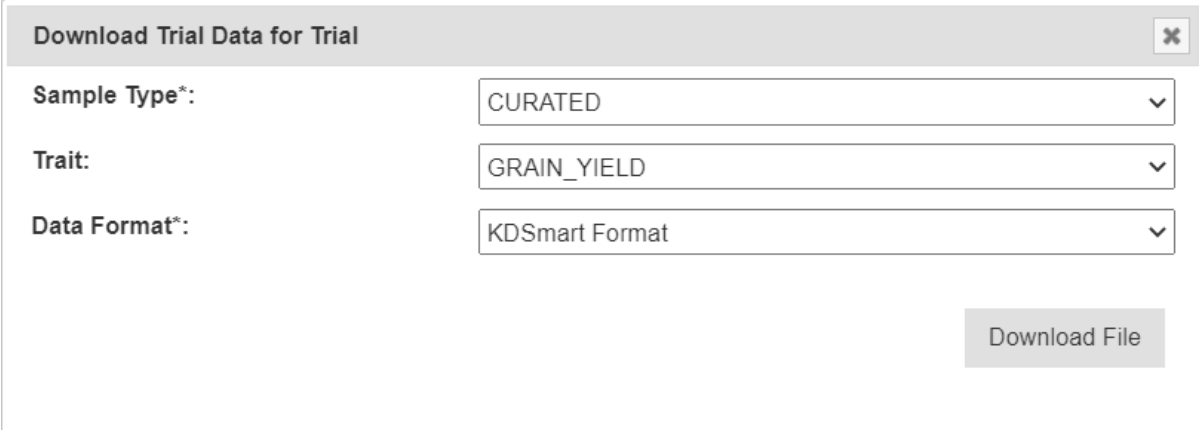
The trait is selected from a list of predefined traits (refer to the [Traits](#) topic).

When the **Compulsory Checkbox** is set to *yes*, the capturing of the trait will become mandatory when recording trial data.

More traits can be added by selecting “Add Trait to trial” (under **Edit Trial** dropdown) from the **Action Column**.

5.5.3 Downloading Trial Data

To download trial data in CSV format, select “Download Trial Data” (under **Download CSV Template** dropdown) for the required trial. This will display the **Download Trial Data Window** (seen below) which provides some options for data to download. The file can be downloaded in one of three formats: KDManage format, KDSmart format or Direct DAL format.



Download Trial Data for Trial

Sample Type*: CURATED

Trait: GRAIN_YIELD

Data Format*: KDSmart Format

Download File

Fig. 12: Download Trial Data Window

5.5.4 Editing Trials

To edit an existing trial select the  **Edit Button** to display the **Update Trial Window** as seen in the image below:

Update Trial 29
✕

*: denotes a required field.

Trial Name* :	<input style="width: 90%;" type="text" value="FB04"/>
Trial Number* :	<input style="width: 90%;" type="text" value="4"/>
Trial Type* :	+ <input style="width: 90%;" type="text" value="Yield trial"/>
Season* :	+ <input style="width: 90%;" type="text" value="UnknownSeasonFromMigration"/>
Site* :	<input style="width: 90%;" type="text" value="Narrabri"/>
Project ID:	<input style="width: 90%;" type="text" value="BrAPI"/>
Current Workflow:	<input style="width: 90%;" type="text"/>
Trial Acronym* :	<input style="width: 90%;" type="text" value="FB"/>
Design Type* :	+ <input style="width: 90%;" type="text" value="CIMMYT"/>
Trial Manager* :	<input style="width: 90%;" type="text" value="Diversity Arrays"/>
Start Date* :	<input style="width: 90%;" type="text" value="2017-09-19 00:00:00"/>
End Date:	<input style="width: 90%;" type="text"/>
Note:	<div style="border: 1px solid #ccc; height: 30px; width: 100%;"></div>
Owner Permission* :	<input style="width: 90%;" type="text" value="Read/Write/Link"/>
Access Group* :	<input style="width: 90%;" type="text" value="admin"/>
Access Permission* :	<input style="width: 90%;" type="text" value="Read/Write/Link"/>
Other Permission* :	<input style="width: 90%;" type="text" value="Read/Link"/>

Fig. 13: Update Trial Window

Note: This window is the same as the **Add Trial Window** so the fields are described in the *Adding Trials* section.

5.5.5 Deleting Trials

KDManage can be used to delete trials from a KDDart database by selecting the `[[kdmanage-button-deletetrial]]` **Delete Button** for the relevant trial.

Trials will not be able to be deleted if any of the conditions apply: - Trials that contain trial data/sample measurements; - Trials that are part of a trial group.

Trials may be deleted if they contain trial units, traits, and uploaded multimedia. However, these will be removed and will not be retrievable.

Users may also wish to delete trial units and trial traits from a trial. This effectively resets the trial for use. This is only possible if there is no trial data in the trial.

If any of the above criteria is not met, the selection of the **Delete Button** will display a warning message such as the one pictured below:

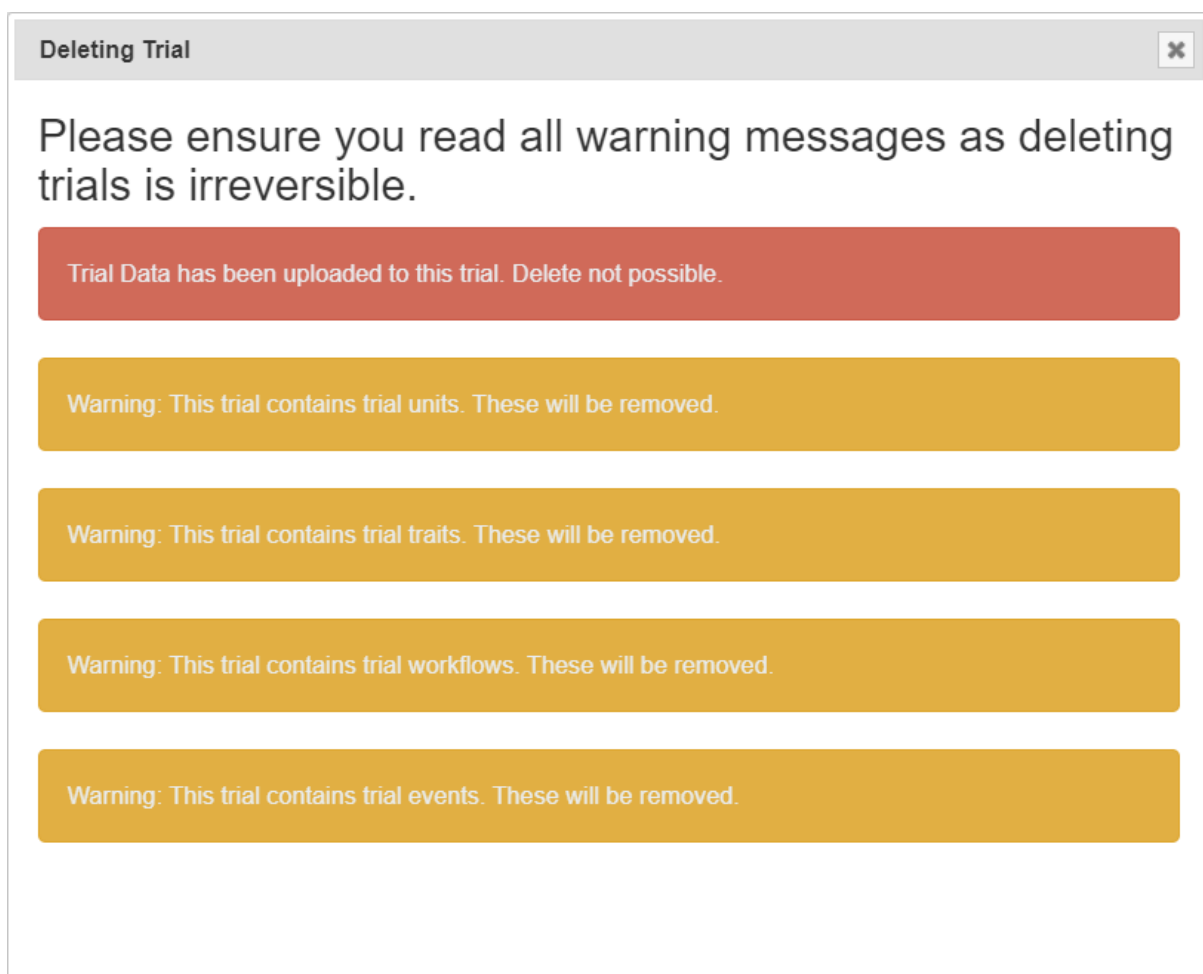


Fig. 14: Update Trial Window

5.5.6 List Traits

To display the traits for a trial, select the “List Trait in Trial” (under **View trial** dropdown). This will display the following list of traits in the **Trait List Window**:

Id	Trait Name	Unit	Max Length	Validation Rule	Compulsory
23	HEIGHT	cm	8	BOOLEX(x >=0 and x <= 200)	No
5	MATURITY_DATE	Date Unit	10	REGEX(.*)	No
6	DAYS_HEADING	NO UNIT	3	BOOLEX(x>0 and x<365)	No
9	GRAIN_YIELD	Kg/ha	8	BOOLEX(x>0.0 and x <10000.0)	No

Fig. 15: Trait List Window

5.5.7 Trial Data CSV Format

KDManage can accept trial data (sample measurements) in the following three formats:

KDManage CSV Format

This is the standard format where each row points to either trial data for the plot or specific specimens in the plot (i.e. sub-plot data). Multiple instances of traits are separated in different columns and can be paired with the preceding column for the date.

For trait column headers, different instances are identified by a ‘:’(colon). For example, *YIELD:3* indicates the third instance point of the trait *YIELD* of the line. If date columns are used, the date columns match to the trait columns before it (i.e. if *YIELD:1* is column 3, column 4 will be used as *DATE-YIELD__1*).

KDSmart CSV Format

This is the standard format for the KDSmart Android application. Each row corresponds to a single plot with each instance of each specific specimen or subplot data is identified by separate columns. Dates can be paired with the preceding column.

Each trait column header name must be in the following formats:

Plot data: [TRAITNAME]:[INSTANCENUMBER] Sub-plot data: [TRAIT-NAME]:[INSTANCENUMBER]#[SPECIMENNUMBER]

Dates are formatted by :

Plot data: Date-[TRAITNAME]:[INSTANCENUMBER] Sub-plot data: Date-[TRAITNAME]:[INSTANCENUMBER]#[SPECIMENNUMBER]

For example, *PLANT_HEIGHT:3#4* will correspond to the third instance of *PLANT_YIELD* of Specimen 4 (which is stored as 0 in DAL). *YIELD:3* will correspond to the third instance of *YIELD* of the plot.


Note: The instance divider can also be set to “__” (double underscore) in import.

Direct DAL CSV Format

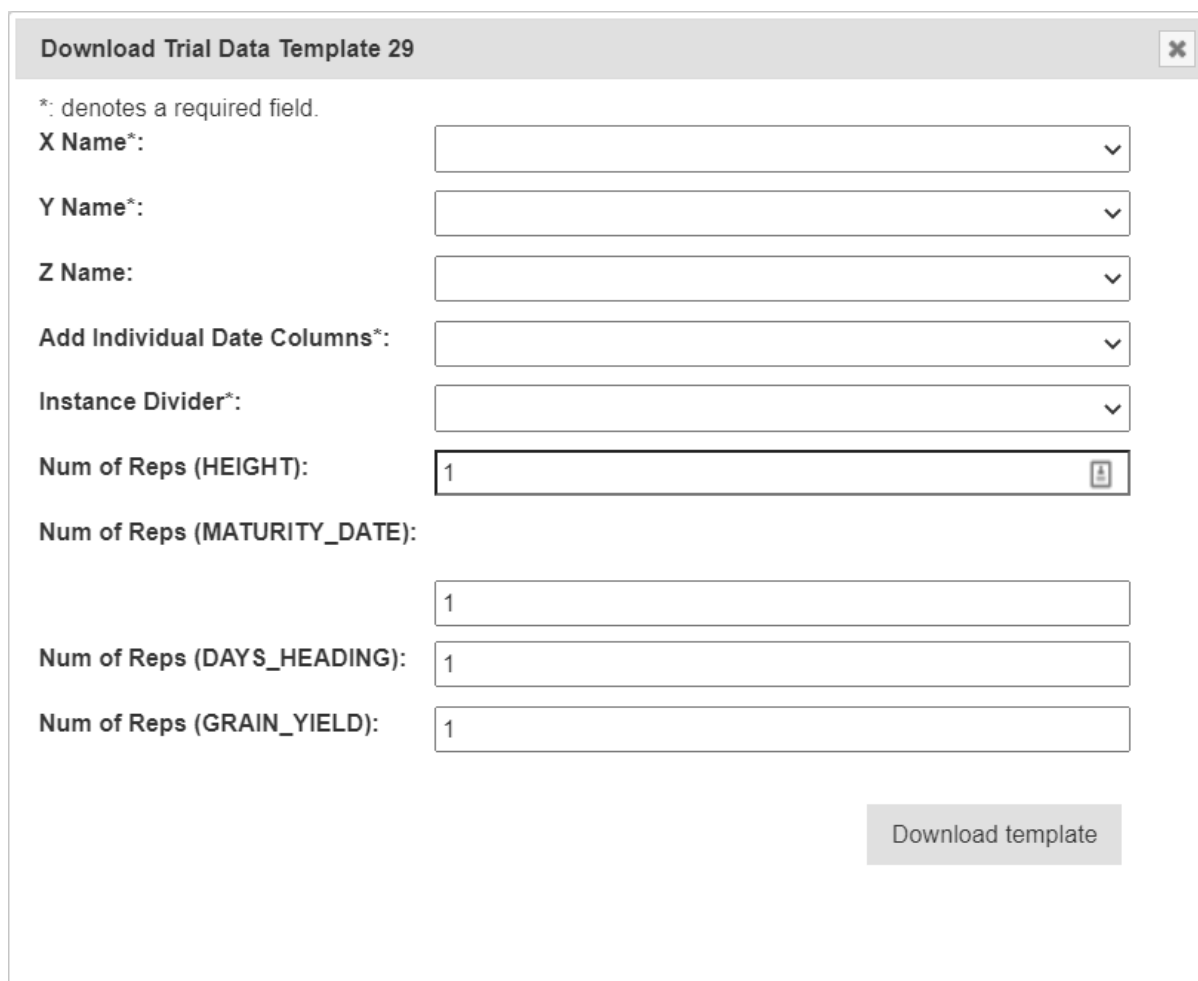
This is also called the *sample measurement format* and is the format that uses the Database ID identities (including TrialUnitId, TrialUnitSpecimenId and TraitId) to directly upload data to the database. This is only recommended for advanced users as it requires a good understanding of the KDDArT database schema.

For best examples, use the following feature to download a scoring template for a correctly formatted CSV.

5.5.8 Exporting a CSV Template

A CSV template can be used to enter data into so that it can be imported into KDSmart and KDManage. The  **Export Template Button** will open a window that provides options for exporting either a KDManage CSV template or a KDSmart CSV template (both options seen in the images below). The KDSmart format can be loaded into the KDSmart application for scoring trials in the field.

The download requires entry of the unit position for the row and column, and for each trait, the number of repetitions to be entered (default is one). When a trait is not required, zero should be entered to suppress the trait from the download file.



Download Trial Data Template 29

*: denotes a required field.

X Name*:

Y Name*:

Z Name:

Add Individual Date Columns*:

Instance Divider*:

Num of Reps (HEIGHT):

Num of Reps (MATURITY_DATE):

Num of Reps (DAYS_HEADING):

Num of Reps (GRAIN_YIELD):

Download template

Fig. 16: Exporting a KDManage CSV Format Template

Download KDSmart Template 29
✕

*: denotes a required field.

X Name:

Y Name:

Z Name:

Position Name:

Entry Id Name:

Instance Divider*:

Use Same Date per Plot:

Specimen Number Start Offset :

Num of Reps (HEIGHT):

Num of Reps (MATURITY_DATE):

Num of Reps (DAYS_HEADING):

Num of Reps (GRAIN_YIELD):

Fig. 17: Exporting a KDSmart CSV Format Template

For the KDManage format, users will be given the choice to add date/time columns per trait instance per plot/sub-plot row.

For KDSmart format, users will be given the option to offset the specimen number. This should normally set to 0 unless legacy trials have specimen number 0.

Once the export has completed the number of trial units and trait columns in the file are displayed as (shown in the following image). Select one of the links to download the template.



Fig. 18: CSV Template Download Window

Note: The trial template file contains empty trait columns, without results.

5.5.9 Importing CSV Data

To import trial data from a CSV file, select “Import CSV Scoring Data” (under **Download CSV Template** dropdown) in the **Action Column** for required trial (or select the **Import Trial Data Button** in the **Trial Map Tab** in the *Trial View Page*) and then choose the format of the CSV file that you want to import. See the section below for more information on each format.

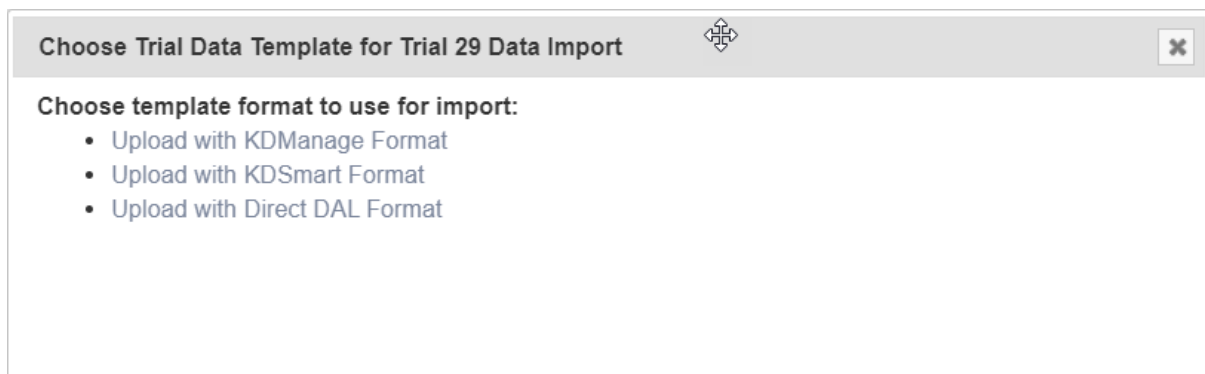


Fig. 19: Choose Trial Data Format Window

Importing CSV Data - KDManage Format

When selecting the *Upload with KDManage Format* option from the **Choose Trial Data Format Window**, the **Import Trial Data Window** will look like the image below.

The screenshot shows a window titled "Import Trial Data 29" with a close button in the top right corner. Below the title bar, there is a note: "*: denotes a required field." The main area contains several input fields, each with a dropdown arrow on the right:

- Data File*:** Includes a "Choose File" button and the text "No file chosen".
- Data Start Column*:** A dropdown menu.
- Data End Column*:** A dropdown menu.
- X Column:** A dropdown menu.
- Y Column:** A dropdown menu.
- Z Column:** A dropdown menu.
- Barcode:** A dropdown menu.
- Specimen Number*:** A dropdown menu.
- Sample Type*:** A dropdown menu.
- Individual Date per Data Point?***: A dropdown menu.
- Instance Divider*:** A dropdown menu.

At the bottom right of the window, there are two buttons: "Curate" and "Import".

Fig. 20: Import Trial Data Window - KDManage Format

The table below outlines the fields that are present in this version of the **Import Trial Data Window**:

Table 8: Import KDManage Trial Data Format Fields

Field	Description
Data File	Browse to locate and select the appropriate CSV file for import.
Data Start Column	The first column in the CSV file containing data for import.
Data End Column	The last column in the CSV file containing data for import.
X Column	The column that contains the X position of the plot.
Y Column	The column that contains the Y position of the plot.
Z Column	The column that contains the Z/block position of the plot.
Barcode Column	The column that contains the barcode of the plot.
Specimen Number Column	The column that contains the specimen number of the plot. For rows that correspond to plot data, the number can be empty or 'PLOT'.
Sample Type	The type of sample, as defined in type definitions.
Individual Date per Data Point?	Whether if the trial data has individual columns for dates per trait instance. If trial data does not contain individual date columns, the uploaded sample measurements will use the current date/time as measured date/time.
Instance Divider	Choose the character set that identifies the instance number of scored data

Note: For referencing the CSV file contents, column numbering commences with zero.

Importing CSV Data - KDSmart Format

When selecting the *Upload with KDSmart Format* option from the **Choose Trial Data Format Window**, the **Import Trial Data Window** will look like the image below.

Import Trial Data 29
✕

*: denotes a required field.

Data File*: Choose File No file chosen

Data Start Column*:

Data End Column*:

X Column*:

Y Column*:

Z Column:

Plot Measure Date :

Sample Type*:

Instance Divider*:

Remove Outliers:

Specimen Number Offset:

If you are not using a single date column, each date for each plot/instance/subplot must come after the matching trait value column. If you are using a Plot date, the Plot Date column must be outside the range of Data columns.

Fig. 21: Import Trial Data Window - KDSmart Format

The table below outlines the fields that are present in this version of the **Import Trial Data Window**:

Table 9: Import KDSmart Trial Data Format Fields

Field	Description
Data File	Browse to locate and select the appropriate CSV file for import.
Data Start Column	The first column in the CSV file containing data for import.
Data End Column	The last column in the CSV file containing data for import.
X Column	The column that contains the X position of the plot.
Y Column	The column that contains the Y position of the plot.
Z Column	The column that contains the Z/block position of the plot.
Plot Measure Date	If used, all measurements will use a single date defined in the Plot Measure Date Column .
Sample Type	The type of sample, as defined in type definitions.
Instance Divider	The character on how different instances are marked out in the trait columns
Remove Outliers	Option to remove outliers with given method.
Specimen Number Offset	Use if KDSmart and KDDart specimen numbers are misaligned. This will add the offset from KDSmart CSV to match KDDart specimen number.

Note: For referencing the CSV file contents, column numbering commences with zero.

5.5.10 Importing Sample Measurements

To import sample measurements from a CSV file, select the **Import Sample Measurements Button** in the **Trial Data Tab** in the **Trial View Page**. This will display the **Import Sample Measurements Window** which can be seen in the image below along with a table that describes the related fields:

Sample CSV*: dal_import_sampl...374565574207.csv

Trial Unit Id Column*:

Sample Type Id Column*:

Trait Id Column*:

Operator Id Column*:

Measure date/time Column*:

Instance number Column*:

Trait Value*:

Trial unit specimen Column*:

Note: manual sample measurements must be uploaded as a group.

Sample Measurement Group Name*:

Sample Measurement Group Status*:

Sample Measurement Group Note*:

CSV headers	First row	Column will be mapped as:
OperatorId	0	Operator Id Column
TraitValue	727.893926247167	Trait Value
InstanceNumber	1	Instance number Column
TrialUnitId	6298	Trial Unit Id Column
MeasureDateTime	"2018-01-01 13:00:05"	Measure date/time Column
TrialUnitSpecimenId		Trial unit specimen Column
SampleTypeId	6	Sample Type Id Column
TraitId	57	Trait Id Column

Fig. 22: Import Trial Sample Measurements Window

Note: For referencing the CSV file contents, column numbering commences with zero.

Table 10: Import Trial Sample Measurement Fields

Field	Mandatory	Description
Data File	Mandatory	Browse to locate and select the appropriate CSV file for import.
Trial Unit ID Column	Mandatory	The column in the CSV that contains trial unit IDs of each sample measurement.
Sample Type ID	Mandatory	The column in the CSV that contains sample type IDs of each sample measurement.
Trait ID	Mandatory	The column in the CSV that contains trait IDs. These traits must be included in the trial as trial traits (see <i>List Traits</i>)
Operator ID	Mandatory	The column in the CSV that contains the user IDs of each sample measurement.
Measure Date/Time Column	Mandatory	The column in the CSV that contains date/time of each sample measurement.
Instance Number	Mandatory	The column in the CSV that contains an instance of each sample measurement.
Trait Value	Mandatory	The column in the CSV that contains a trait value (or measured value of trait) of each sample measurements
Trial Unit Specimen		The column in the CSV that contains the trial unit specimen ID of each sample measurement, if applicable.

If required, sample measurements can also be uploaded and added to a new sample measurement group.

Table 11: Sample Measurement Group Fields

Field	Mandatory	Description
Sample Measurement Group Name	Mandatory	Name for new sample group measurement. New sample measurements cannot be added to existing groups so these names must be unique.
Sample Measurement Group Status		Status for sample measurement group
Sample Measurement Group Note		Note for sample measurement mroup

5.5.11 Listing Sample Measurements Groups

To list all sample measurement groups in a trial, select the **List Sample Measurement Groups Button** in the **Trial Data Tab** of the **Trial View Page**. This will display the **Sample Measurement Groups List Window** which can be seen in the image below:

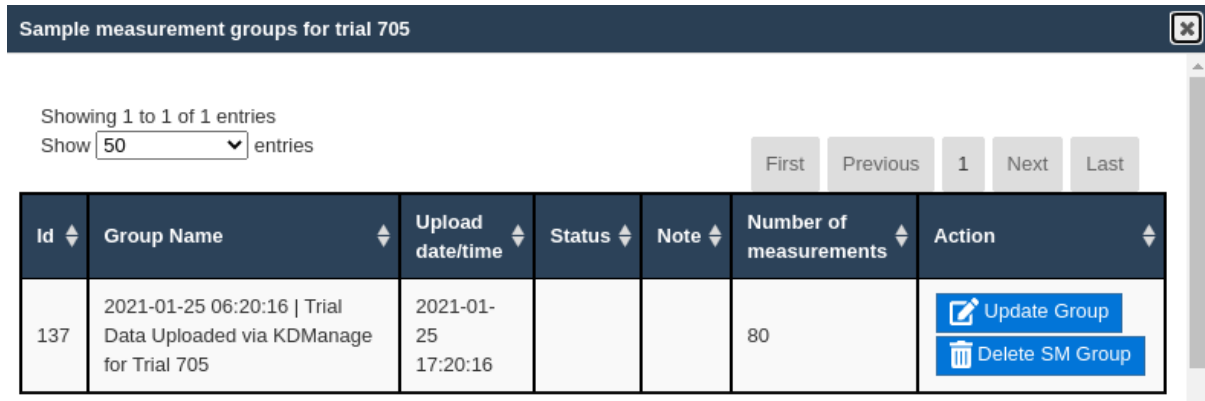


Fig. 23: Sample Measurement Groups List

The following table lists all the actions that can be performed for the selected sample measurement groups in KDManage.

Table 12: Sample Measurement Group Actions

Action	Description	Parent Button
Update SM Group	Edit name, note and/or status of the sample measurement group.	
Delete SM Group	Delete sample measurement group and all sample measurements in the group.	

Note: Deleting sample measurement groups is irreversible.

5.5.12 Displaying Trial Unit Layouts

To view the trial units of a trial, select “Display Trial Layout for Trial” (under **View trial** dropdown) in the **Action Column** to display the **List of Trial Units Window**:

List of Trial Unit(s) in Trial 18									
Showing 1 to 10 of 80 entries									
Show 10 entries									
First Previous 1 2 3 4 5 ... 8 Next Last									
Barcode	Note	Specimen[0]	Pedigree[0]	TUS Label[0]	Replicate	X (Row)	Y (Column)	Z (Block)	Action
10021026041017ED3		Jocelyn_22033	EMPTY/TESTING		1	1	1	1	Add Keyword Show Items Show Specimens
10021026041017EL8		Fruitee_22033	EMPTY/TESTING		1	1	2	1	Add Keyword Show Items Show Specimens
10021026041017CQ3		Full Sail_22033	EMPTY/TESTING		1	1	3	1	Add Keyword Show Items Show Specimens
10021026041017L0		Gemini_22033	EMPTY/TESTING		1	1	4	1	Add Keyword Show Items Show Specimens
10021026041017SA2		Geraldine_22033	EMPTY/TESTING		1	1	5	1	Add Keyword Show Items Show Specimens

Fig. 24: List of Trial Units Window

5.5.13 Uploading a File to a Trial

To add a file to a trial, select “Upload file” (under [View trial](#) dropdown) in the **Action Column** to display the **Upload File Window** (below image). File types are defined in the *Types* page.

Upload File for Trial 29 ✕

*: denotes a required field.

File*: Choose File No file chosen

File Type*: [Dropdown]

Upload

Fig. 25: Upload File Window

To view all files that have been uploaded, select “List files for Trial” (under [View trial](#) dropdown) which will display the **List of Files Window** as seen in the image below:



Fig. 26: List of Files Window

5.5.14 Adding a Trial Event

To add a trial event to a trial, select the **+ Button** and then **Add Trial Event** in the **Trial Data Tab** of the **Trial View Page**.

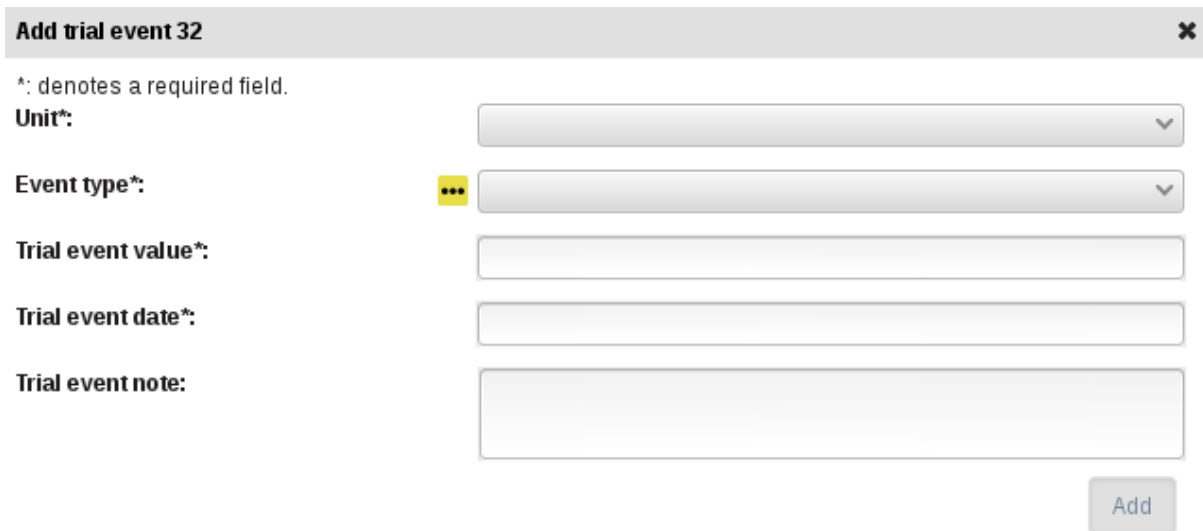


Fig. 27: Add Trial Event Window

Table 13: Add Trial Event Fields

Field	Mandatory	Description
Unit	Mandatory	Unit of trial event.
Event Type	Mandatory	The type of event, as defined in type definitions.
Trial Event Value	Mandatory	Value of trial event.
Trial Event Date	Mandatory	Date of trial event.
Trial Event Note		Note of trial event.

5.5.15 Adding a Trial Location

Once a trial has been added within a site, a geographic location can be added to the trial. A Google map will be displayed in the **Trial Location Tab** of the **Trial View Page**. Drag the map to the appropriate location then *double click* repeatedly to zoom to the required location to define the site.

Add Trial location 24 ✕

*: denotes a required field.

Please draw the trial location on the map using the polygon object button (draw object button). When you are happy with the shape of the trial, please double click. Then appropriate geometry data will then be filled into this box. *:

Add

Fig. 28: Add Trial Location Window


When the map shows the required area, define the trial area by selecting the  **Create New Polygon Button** and select on the boundary corners of the area. In the following image, the trial location has been defined and is highlighted in a darker yellow:



Fig. 29: Add Trial Location Window - Area Selected

The text box which appears above the map will contain the coordinates for the area that has been selected for the trial location as shown next.

The location field data is also listed in the text area below the map as seen in the image below:

```
POLYGON((149.81012249060802 -30.294504000691564,149.8101962513569 -30.29456421503849,149.81012919612738
-30.2946035859375,149.8100876218894 -30.29456884690914,149.81008359857782
-30.294561899102305,149.81012249060802 -30.294504000691564))
```


Fig. 30: Location Field Data Example

5.5.16 Adding Trial Unit Layouts

A trial unit layout can be added to a trial by There are two ways to add trial unit layouts:

- via CSV format; and
- via KDCCompute method (if configured).

5.5.17 Adding Trial Units Layouts via CSV Format

A trial unit layout can be added to the trial with the CSV method by selecting the  **Add Trial Unit Layout Button** which will open the **Add Trial Layout Window**. The window, along with a table that outlines its fields can be seen below:

Add Trial layout 29
✕

*: denotes a required field.

Trial Unit Layout CSV File*: Choose File No file chosen

Specimen Column*: ▼

Number of Specimens per Unit*: 1 ▼

Auto Column Mapping:

Specimen Number start (Default is 1):

Barcode Column: ▼

Automatically Assign Repeat for Specimen: No ▼

Repeat Column: ▼

Treatment Column: ▼

Trial Unit Note Column: ▼

Unit Position System: Local Position ▼

Trial unit X, Trial unit Y, Trial unit Z and Trial unit EntryId columns must be in between the Unit Position Start and Unit Position End Columns. You cannot reuse the same columns for different fields other than Unit Position Start and End.

Unit Position Start Column*: ▼

Unit Position End Column*: ▼

Trial Unit X Column*: ▼

Trial Unit Y Column*: ▼

Trial Unit Z Column: ▼

Trial Unit EntryId Column*: ▼

Add

Fig. 31: Adding Trial Unit Layouts Window

Table 14: Add Trial Unit Layout Fields

Field	Mandatory	Description
Plant Date	Mandatory	Date the specimen was planted in the trial unit (YYYY-MM-DD format).
Trial Unit Layout File	Mandatory	Browse and select the CSV import file.
Specimen Column	Mandatory	The specimen name column in the input file. It may be automatically provided using the auto column mapping feature or manually entered.
Number of Specimens per Unit	Mandatory	Define the number of copies of the same specimen that will be added per trial unit.
Auto Column Mapping		When a file is chosen this box will be selected if 'Specimen' is found in the header. This can be deselected if it is not the desired column.
Barcode Column		Barcode column in the input file. If this is left blank and a barcode configuration has been created for trial units, a barcode will be automatically generated.
Automatically Assign Repeat for Specimen		Automatically assign repetition number based on reoccurrence of specimen name.
Treatment Column		Treatment column in the input file.
Trial Unit Note Column		Trial unit note column in the input file.
Unit Position System		Type of position label of trial unit to be used.
Unit Position Start Column	Mandatory	The unit position start column in the input file, numbered from zero.
Unit Position End Column	Mandatory	The unit position end column in the input file, numbered from zero.
Trial Unit X	Mandatory	Define the column that reflects X coordinates for a trial unit layout. This column must fall within the unit position start and end column ranges.
Trial Unit Y	Mandatory	Define the column that reflects Y coordinates for a trial unit layout. This column must fall within the unit position start and end column ranges.
Trial Unit Z	Mandatory	Define the column that reflects Z coordinates for a trial unit layout. This column must fall within the unit position start and end column ranges.
Trial Unit EntryID	Mandatory	Define the column that reflects the EntryID for trial unit layout. This column must fall within the unit position start and end column ranges.

Note: X, Y, Z and EntryID columns must all be unique columns.

5.5.18 Adding Trial Unit Layouts via KDCompute

The Add Trial Unit Layout via KDCompute window:

Create Trial Design using Agricolae ✕

*: denotes a required field.

Algorithm Name*:

Design Type*:

Specimen Group (List)*:

Number of Replicates*:

Number of Plot Columns*:



Fig. 32: Add Trial Unit Layout via KDCompute window

Note: KDCompute method requires a working installation of KDCompute attached to your KDManage and specific set up for trial design plugins.

5.5.19 Adding a Keyword to a Trial Unit

Keywords can be added or assigned to trial units.

To add a Keyword to a Trial Unit perform the following:

Step	Action
1.	From the Trial window, at the required Trial, select the Display Trial Layout Action button  .
2.	At the required Trial Unit select the “Add keyword”
3.	Select the Keyword from the dropdown List. Note: Multiple Keywords can be assigned. If the required Keyword is not appearing, new Keywords can be added via the <i>Administrative Settings</i> menu  , top right.

5.6 Trial View Page

When a trial is selected from the **Trials Page**, it will be displayed in a **Trial View Page** (see the image below). The **Trial View Page** provides all details and data of the selected trial including trial units, trial location, traits, etc. There are also tools available such as data curation.

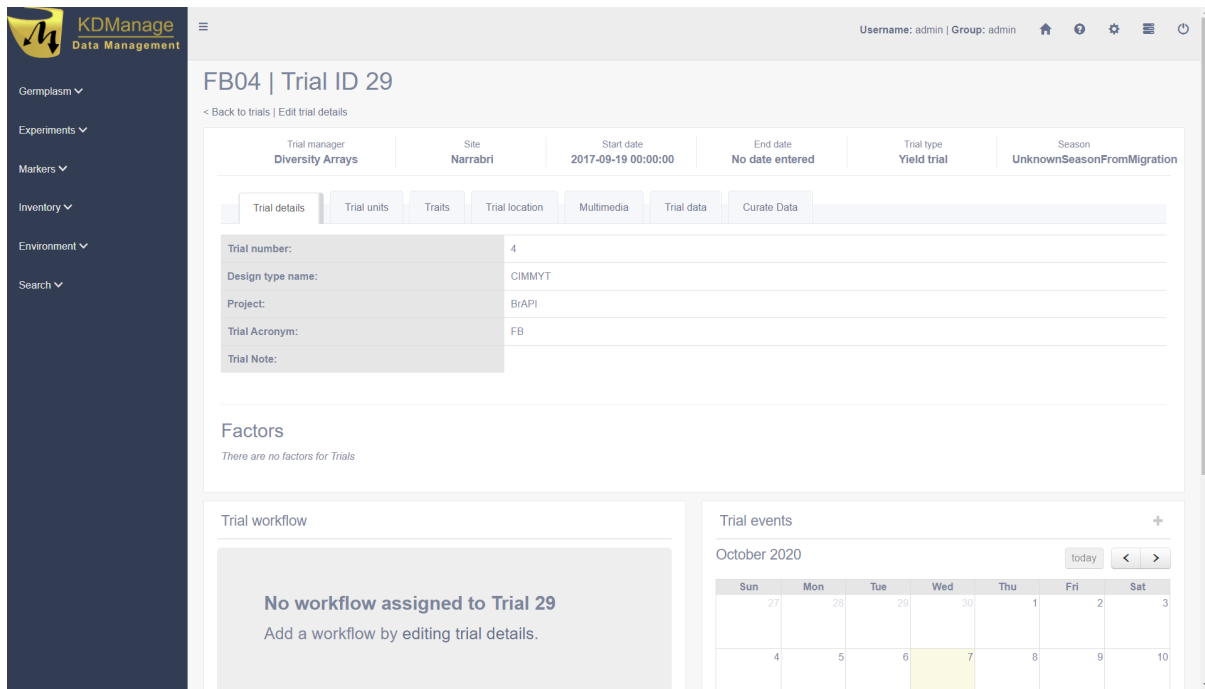


Fig. 33: Trial View Page

A **Trial Workflow Panel** and a **Trial Events Panel** will always be visible on the **Trial View Page**, regardless of the selected tab.

The following sections will outline each of the tabs.

5.6.1 Trial Details Tab

The **Trial Details Tab** is the default tab of the **Trial View Page** (see the image in the above section) which shows details about the selected trial.

To edit trial details select the **Edit Trial Details Button**, below the trial title and ID on the top of the page. This will open the **Update Trial Window** which is pictured below:

Update Trial 29
✕

*: denotes a required field.

Trial Name* :	<input type="text" value="FB04"/>
Trial Number* :	<input type="text" value="4"/>
Trial Type* :	+ Yield trial ▼
Season* :	+ UnknownSeasonFromMigration ▼
Site* :	Narrabri ▼
Project ID:	BrAPI ▼
Current Workflow:	▼
Trial Acronym* :	FB ▼
Design Type* :	+ CIMMYT ▼
Trial Manager* :	Diversity Arrays ▼
Start Date* :	<input type="text" value="2017-09-19 00:00:00"/>
End Date:	<input type="text"/>
Note:	<div style="border: 1px solid #ccc; height: 30px; width: 100%;"></div>
Owner Permission* :	Read/Write/Link ▼
Access Group* :	admin ▼
Access Permission* :	Read/Write/Link ▼
Other Permission* :	Read/Link ▼

Fig. 34: Update Trial Window

5.6.2 Trial Units Tab

Trial units can be added and viewed on the **Trial Unit Tab**.

SIGQDLHXY | Trial ID 705

← Back to trials | Edit trial details

Trial manager: OZTOJBSRDO Tester | Site: QSJLRZZNOC | Start date: 2021-01-25 00:00:00 | End date: No date entered | Trial type: NCJEIAQCKU | Season: MMRJWPQBLG

Trial details | **Trial units** | Traits | Trial location | Multimedia | Trial data | Curate Data

Download field maps | Show all Trial Unit Specimens | Download barcodes

Showing 1 to 10 of 80 entries
Show 10 entries

Barcode	Note	Specimen[0]	Pedigree[0]	TUS Label[0]	Replicate	X (Row)	Y (Column)	Action
10021024061643NU4		Jocelyn_99682	EMPTY/TESTING		1	1	1	Show Trial Unit
10021024061643JR9		Fruttee_99682	EMPTY/TESTING		1	1	2	Show Trial Unit
10021024061643TS4		Full Sal_99682	EMPTY/TESTING		1	1	3	Show Trial Unit
10021024061643ES9		Gemini_99682	EMPTY/TESTING		1	1	4	Show Trial Unit
10021024061643RO3		Geraldine_99682	EMPTY/TESTING		1	1	5	Show Trial Unit
10021024061643EY9		Ginger Meggs_99682	EMPTY/TESTING		1	1	6	Show Trial Unit
10021024061643HD3		Ginger Rogers_99682	EMPTY/TESTING		1	1	7	Show Trial Unit
10021024061643GH0		Gold Bunny_99682	EMPTY/TESTING		1	1	8	Show Trial Unit
10021024061643RA7		Golden Anniversary_99682	EMPTY/TESTING		1	1	9	Show Trial Unit
10021024061643VM1		Golden Emblem_99682	EMPTY/TESTING		1	1	10	Show Trial Unit

Fig. 35: Trial Units Tab

Newly created trials can have trial unit layouts added via CSV or KDCompute methods (see *Adding Trial Unit Layouts*).

After a trial unit layout is added, users may view the table of trial units.

Users can then also download a trial field map in SVG format by selecting the

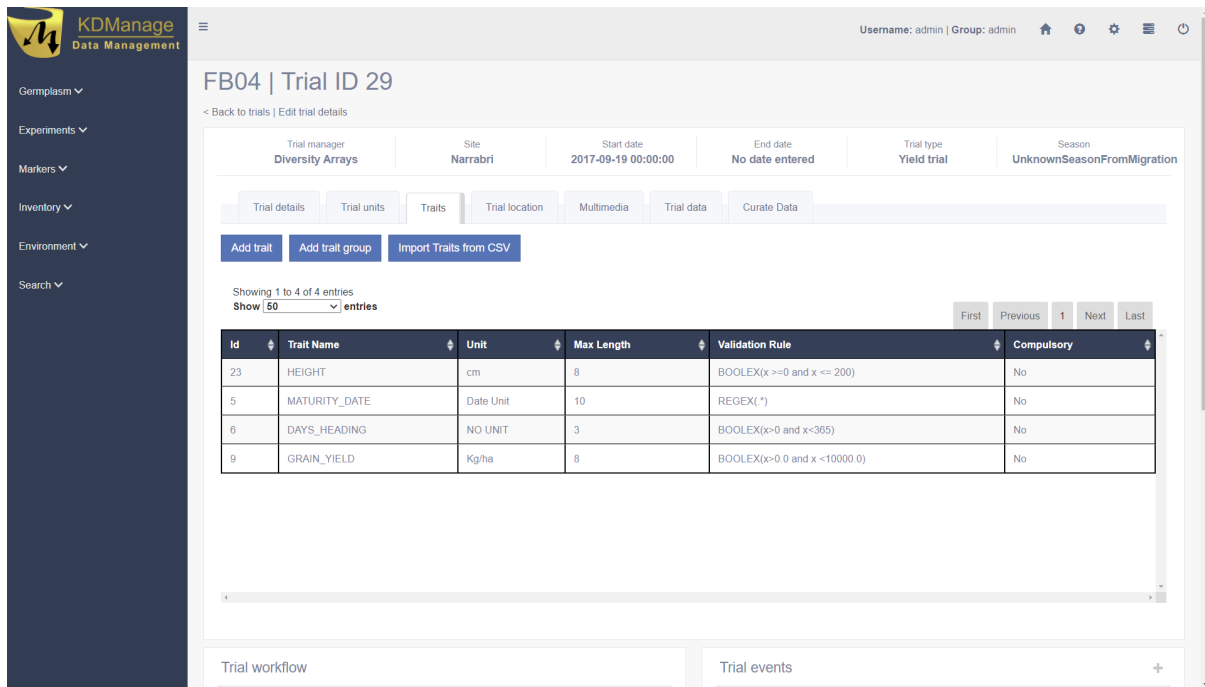
Download field maps

Download Field Maps Button and or a set of printable barcodes by selecting the Download Barcodes Button.

Download barcodes

5.6.3 Traits Tab

Trial traits can be added and viewed on the **Trial Trait Tab**.



The screenshot shows the 'Traits' tab for trial FB04. The page header includes the KDManage logo and navigation menu on the left. The main content area displays the trial details and a table of traits. The table has the following data:

ID	Trait Name	Unit	Max Length	Validation Rule	Compulsory
23	HEIGHT	cm	8	BOOLEX(x >= 0 and x <= 200)	No
5	MATURITY_DATE	Date Unit	10	REGEX{.}	No
6	DAYS_HEADING	NO UNIT	3	BOOLEX(x > 0 and x < 365)	No
9	GRAIN_YIELD	Kg/ha	8	BOOLEX(x > 0.0 and x < 10000.0)	No

Fig. 36: Traits Tab

Trial traits can be added individually or in the *Trait Groups* page.

5.6.4 Trial Location Tab

The trial location can be updated and viewed on the **Trial Location Tab** (see the *Adding a Trial Location* page).

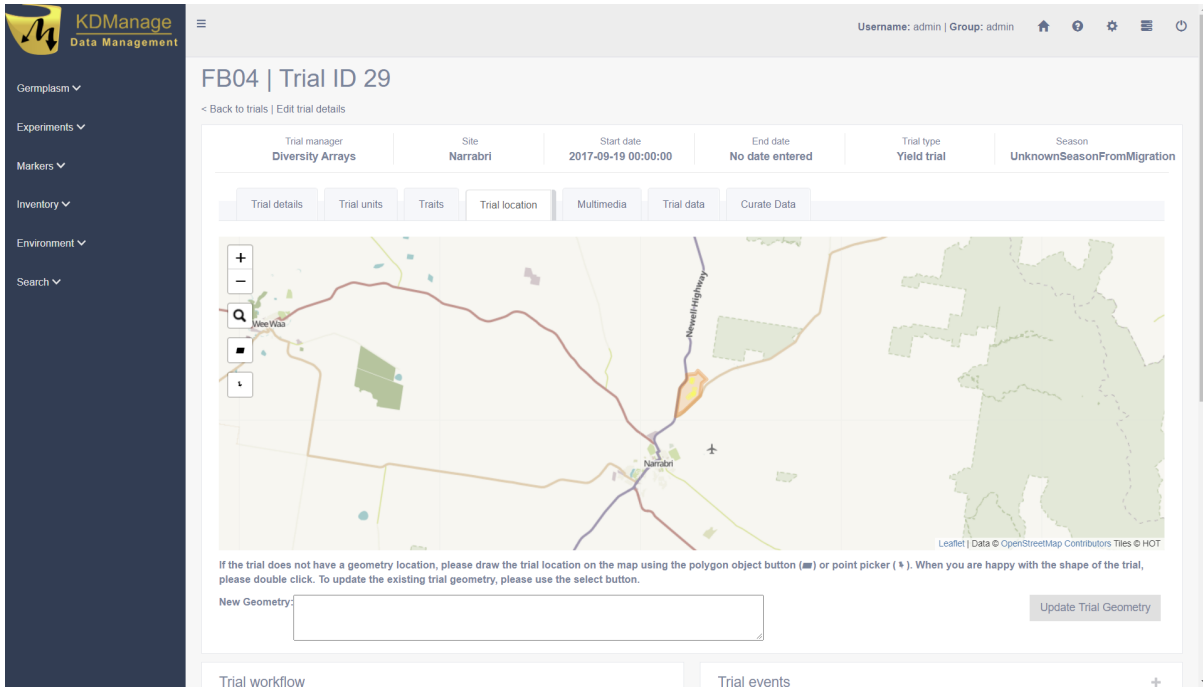


Fig. 37: Trial Location Tab

5.6.5 Multimedia Tab

Trial multimedia can be updated and viewed on the **Trial Multimedia Tab** (see *Uploading a File to a Trial*).

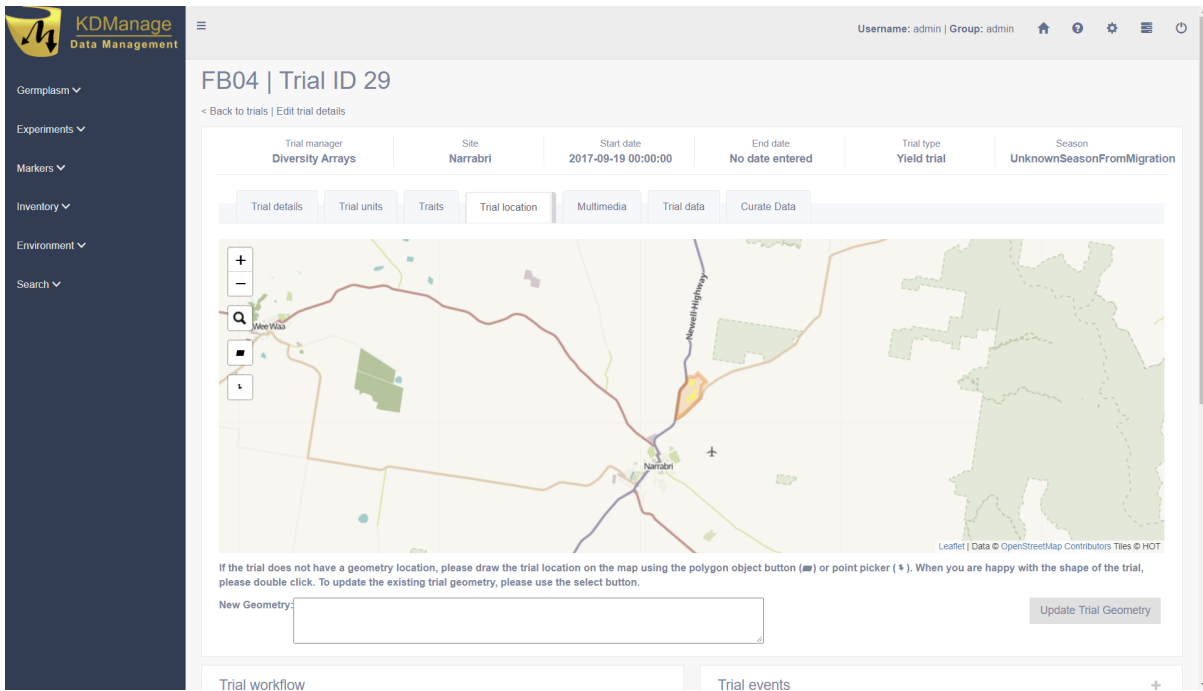


Fig. 38: Multimedia Tab

5.6.6 Trial Data Tab

Trial data can be uploaded, viewed and downloaded in the **Trial Data Tab**.

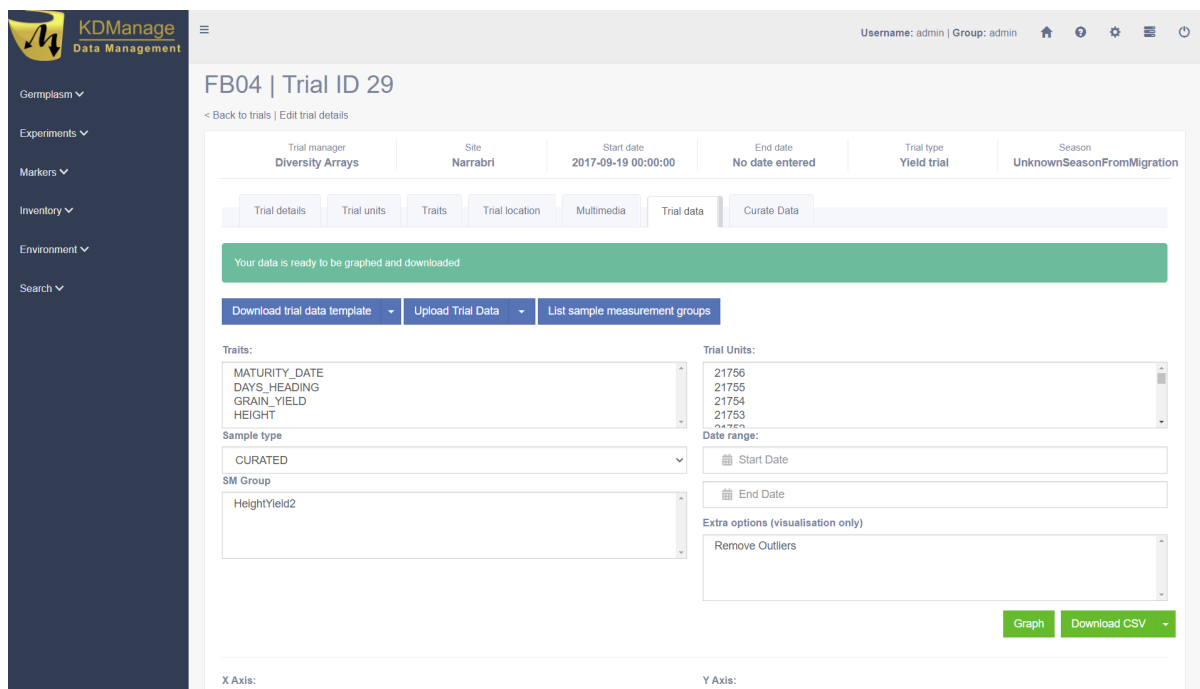


Fig. 39: Trait Data Tab

Trial data can be viewed in a graph which shows selected traits and value:

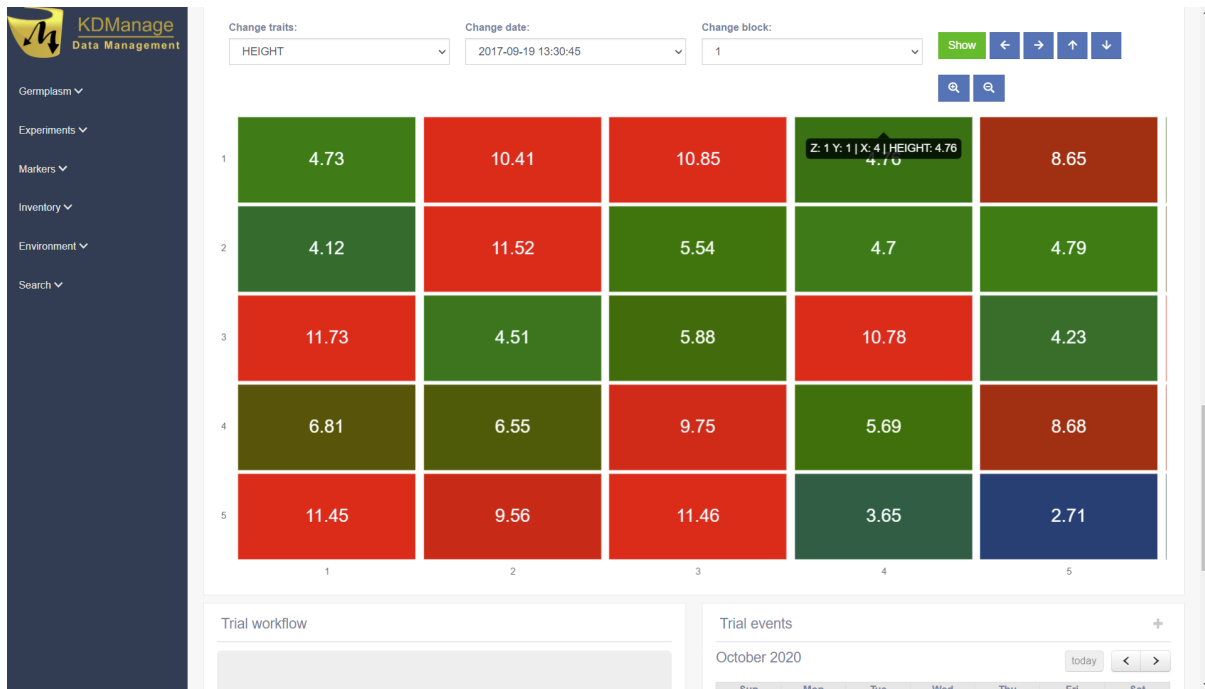


Fig. 40: Trial Data Graph

A trial data map is a heat map based on trial unit dimensions. Red specifies higher values while blue specifies lower values:

The screenshot displays the 'Curate Data' tab for Trial ID 29. At the top, a green banner states 'Your data is ready to be graphed and downloaded.' Below this, there are dropdown menus for 'Traits' (listing MATURITY_DATE, DAYS_HEADING, GRAIN_YIELD, HEIGHT) and 'SM Group*' (set to HeightYield2). A 'Sample Type*' dropdown is set to 'CURATED'. A 'Curate' button is visible on the right. Below the dropdowns, a table shows specimen data with columns for X, Y, EntryId, Specimen, Specimen Number, Barcode, Note, and GRAIN_YIELD:0. The table contains six rows of data. At the bottom, there is a 'Measure Date/Time' field set to '2017-09-19 15:32:22' and an 'Upload Data under Sample Type:' dropdown set to 'CURATED', with an 'Upload Trial Data' button.

X	Y	EntryId	Specimen	Specimen Number	Barcode	Note	GRAIN_YIELD:0
5	2	21	PLOT		10017261152258RS3		5728
5	2	21	FB04-113	0	10017261152258RS3		
10	3	42	PLOT		10017261152258RS6		4084
10	3	42	FB04-108	0	10017261152258RS6		
4	2	20	PLOT		10017261152258II5		5917
4	2	20	FB04-114	0	10017261152258II5		

Fig. 41: Trial Data Map

5.6.7 Curate Data Tab

The **Curate Data Tab** provides options for curating data that has been collected.

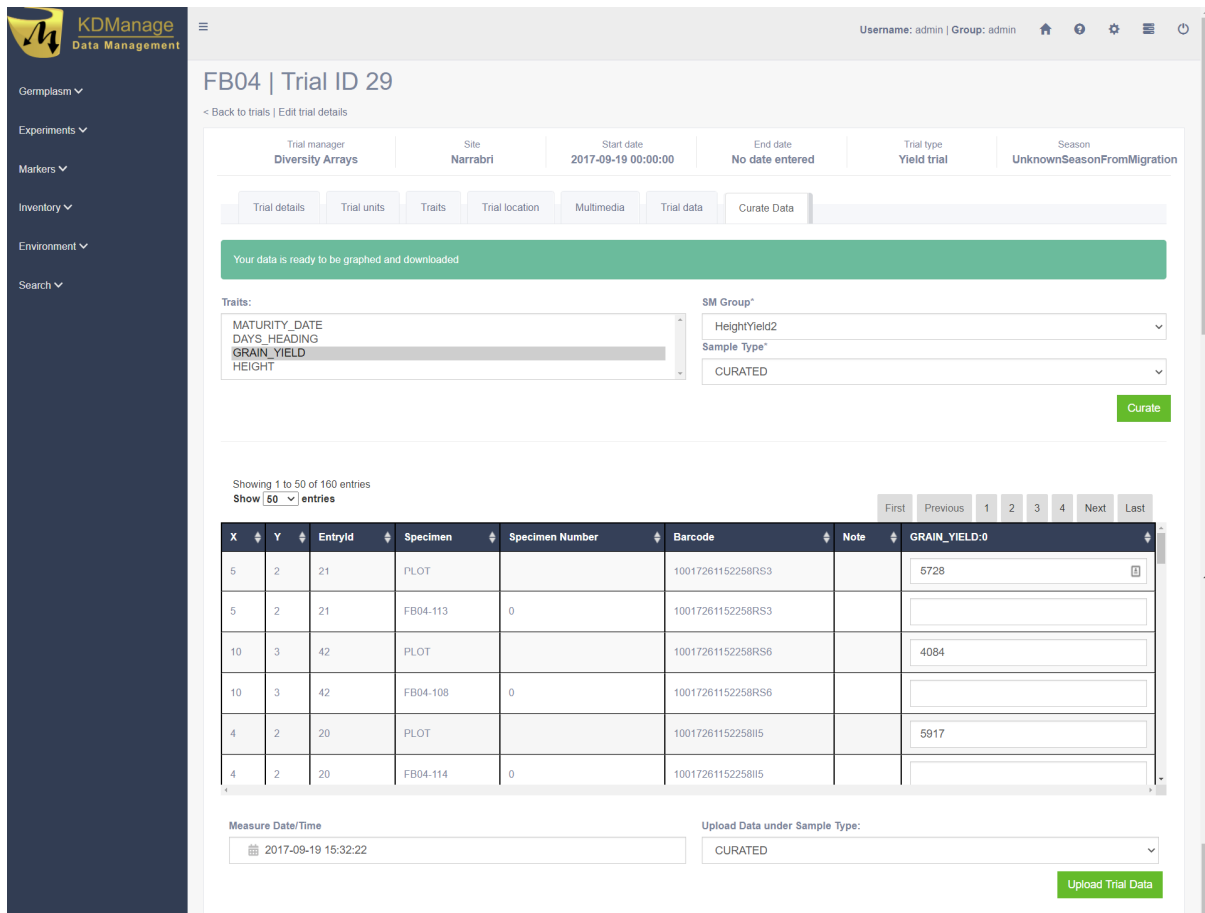


Fig. 42: Curate Data Tab

Existing trial data can be curated and imported as a separate instance in the **Curate Data Tab**.

Tip: Curated data will not always be imported as the same instance. Instances are determined on a per trait basis.

.. _lab-Nursery:

5.7 Nurseries

Nurseries can be defined and set up to allow for new crossings to be added.

The **Nurseries Page** lists defined nurseries which the user/group has permission to view, as shown in the following image:

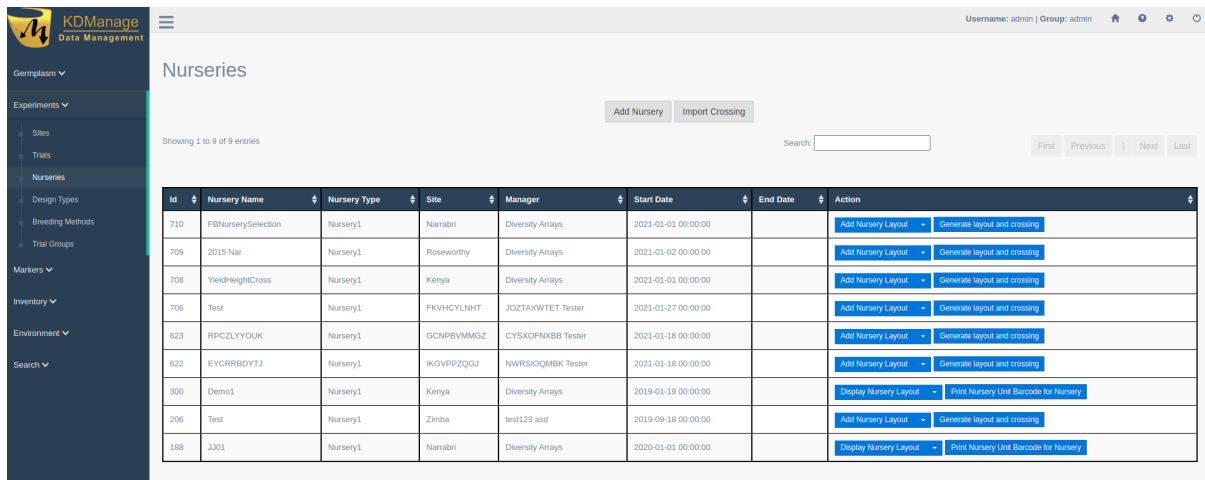


Fig. 43: Nurseries Page

The following table describes the contents of the list in the **Nursery Page**:

Field	Description
ID	A unique system identifier of the nursery.
Trial Name	The user provided name of the nursery.
Nursery Type	The selected nursery type (user defined specific trial <i>types</i> to be nursery types).
Site	The site of the nursery.
Manager	The manager assigned to the nursery (defined in contacts although they are not necessarily a system user).
Start Date	The date the nursery commenced (YYYY-MM-DD format).
End Date	The date the nursery ended (YYYY-MM-DD format).
Action	The actions that can be performed for the nursery. This is described in the following section.

5.7.1 Nursery Actions

The following table lists all the actions that can be performed for the selected nursery in KDManage:

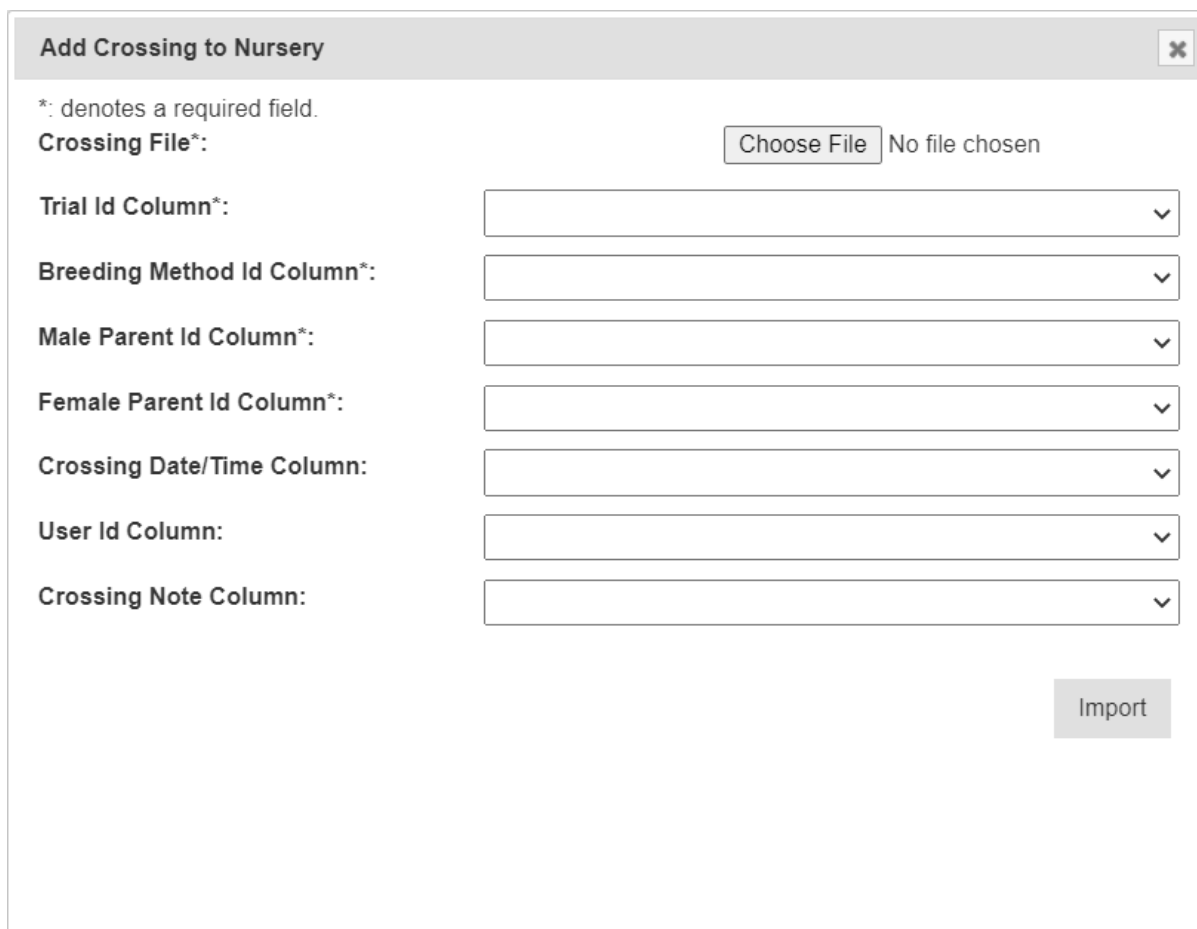
Table 15: Nursery Actions

Action	Description	Parent Button
Generate Layout and Crossing	Automatically generate layout and crossing, if required, from two specimen lists. See <i>Generating Layouts and Crossings</i> .	
Add Nursery Layout	Import a nursery layout for the nursery. See <i>Displaying Trial Unit Layouts</i> .	
Display Nursery Layout	Display the nursery layout for the nursery. See <i>Displaying Trial Unit Layouts</i> .	
Print Nursery Unit Barcode	Export barcodes for nursery trials for printing.	
List Crossings	List Crossing.	Display Nursery Layout
Harvest Crossing	If layout and crossing are present in the nursery, harvest crossing. See <i>Harvest Crossing</i> .	Display Nursery Layout

Note: The presence of action types is dependent upon the nursery state - not all action types will be available for all nurseries.

Importing Crossings

Crossings can be imported (with a CSV file) into nurseries, which can later be harvested to create new genotype and specimen entries. To start importing crossings, select the **Import Crossing Button** which will open the **Import Crossing Window**. The window, along with a table that describes the relevant fields can be found below:



Add Crossing to Nursery [Close]

*: denotes a required field.

Crossing File*: [Choose File] No file chosen

Trial Id Column*: [Dropdown]

Breeding Method Id Column*: [Dropdown]

Male Parent Id Column*: [Dropdown]

Female Parent Id Column*: [Dropdown]

Crossing Date/Time Column: [Dropdown]

User Id Column: [Dropdown]

Crossing Note Column: [Dropdown]

[Import]

Fig. 44: Import Crossings Window

Note: The **Import Crossing Window** will match column names once users select a file to import.

Table 16: Import Crossing Fields

Field	Mandatory	Description
Crossing File	Mandatory	Select the input file for the import.
Trial ID Column	Mandatory	Column number for trial ID (nurseries use a trial ID).
Breeding Method ID Column	Mandatory	Column number for breeding method.
Male Parent ID Column	Mandatory	Column number for male parent ID (Use trial Unit Specimen Id)
Female Parent ID Column	Mandatory	Column number for Female Parent Id (Use Trial Unit Specimen Id)
Crossing Date/Time Column		Column number for date/time.
User ID Column		Column number for user ID.
Crossing Note Column		Column number for Crossing Note

Note: Entries for male and female parent IDs must be trial unit specimen IDs used inside the nursery.

Generating Layouts and Crossings

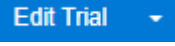
A layout and crossing can be automatically generated from two specimen lists.

Note: Additional crossing and algorithm algorithms can only be added by advanced users.

Table 17: Import Crossing Fields

Field	Mandatory	Description
Male Specimen Group (list)	Mandatory	List of specimens that will be the male in a crossing.
Female Specimen Group (list)	Mandatory	List of specimens that will be the female in a crossing.
Algorithm Name	Mandatory	A choice of algorithm which the layout and crossing will be generated with.
Make Crossing	Mandatory	An option of whether the crossing will be generated following the layout
Breeding Method		If a crossing will be generated, then a breeding method must be defined for crossings.
Replicates	Mandatory	Number of replicates for crossings.

Harvest Crossing

Once a nursery has a layout and a crossing set up, users can harvest from crossing and create new genotype and specimens, with appropriate pedigree entries. To create a harvest crossing, select “Harvest Crossing” (under  dropdown) from the **Action Column** of the relevant nursery. This will bring up the **Harvest Crossing Window** which can be seen in the image below, along with a table that outlines the fields relevant to harvest crossing. Each row refers to a single cross where a new genotype and specimen may be created.

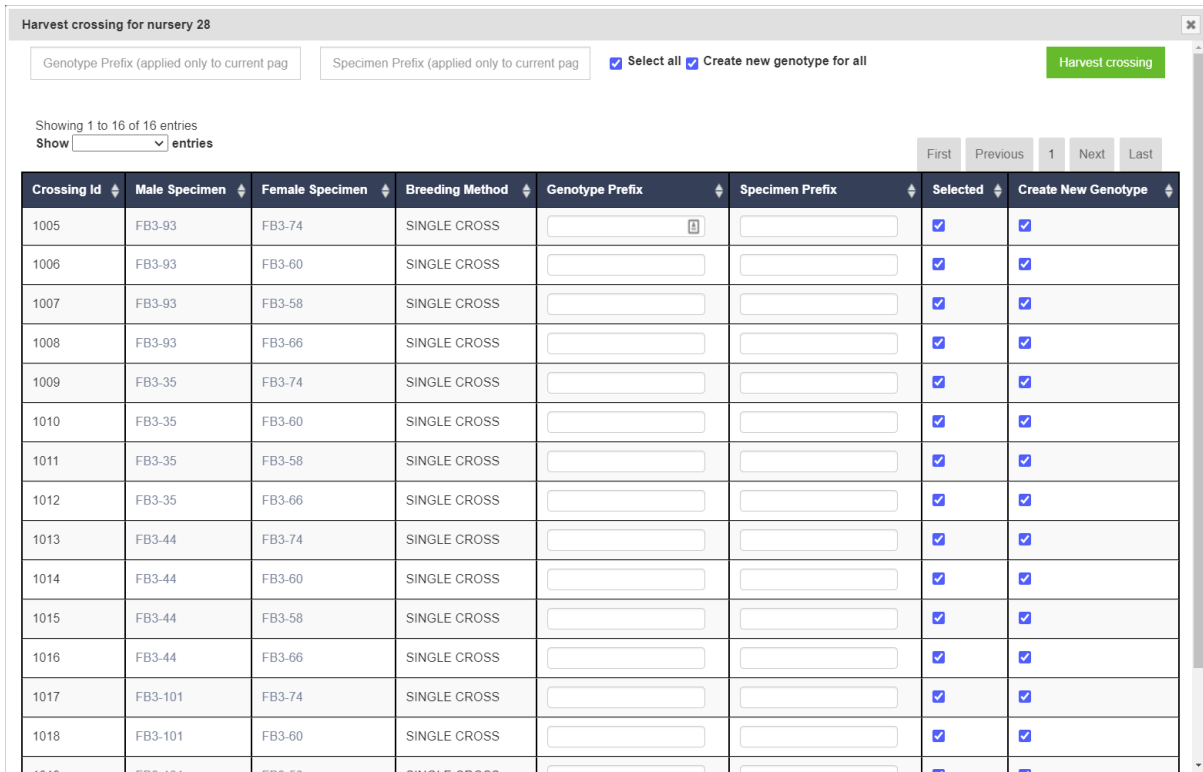


Fig. 45: Harvest Crossing Window

Note: In cases where two specimens have previously been crossed, no genotype will be created and the new specimen will take on the female genotype.

Table 18: Harvest Crossing Fields

Field	Mandatory	Description
Genotype Prefix	Mandatory	The prefix for the newly created genotype. A unique number will be generated and appended to the prefix.
Specimen Prefix	Mandatory	The prefix for the newly created specimen. A unique number will be generated and appended to the prefix.
Selected		If un-ticked, the corresponding crossing will be skipped.
Create New Genotype		If un-ticked, the corresponding crossing will not have a new genotype created.

MARKER MENU

When markers are available for the KDDart implementation and configuration being used, KDDart will display the **Marker Menu** as seen below:

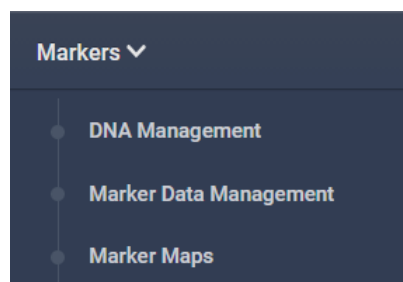


Fig. 1: Marker Menu

The topics in this section are as follows:


1. *Genotyping Marker Process*
2. *DNA Management*
3. *Marker Data Management*
4. *Marker Maps*

6.1 Genotyping Marker Process

The steps for preparing, ordering and storing genotypic analysis data in KDDart are described in the following table:

Note: Bold items within the **Action Column** represent menu/selection text.

Table 1: Genotyping Marker Process

Step	Activity	Action
1.	Define a group of samples for genotyping.	Select KDManage > Marker > Marker Data Management > Add Marker Data Management .
2.	Download file (equivalent to the sample tracking file for the Online Ordering)	Select the  Download Button .
3.	Submit the sample tracking file for the order in the Online Ordering system.	Optional genotyping service (i.e. DArT)
4.	Prepare specification, submit file, sign, pack and ship DNA.	“
5.	Genotyping service performs DNA analysis	“
6.	Genotyping service notification that results are ready	“

There are three choices to download marker datasets, depending on the KDDart configuration:

Table 2: Genotyping Marker Process - KDManage

Step	Activity	Action
1.	Import via KDManage.	Select KDManage -> Marker -> Marker Data Management -> Upload dataset file for Marker Data Management 9

Table 3: Genotyping Marker Process - KDCompute

Step	Activity	Action
1.	Log into the Online Ordering and download the result file to a local/network location.	“
2.	Use KDCompute to upload the result file to the KDCompute server for processing	Select KDCompute -> File Manager -> Upload Files -> Select file and upload
3.	Use KDCompute to import the data into KDDart	Select KDCompute -> Submit a Job -> Import/Export Marker Data -> Import Marker Data -> Complete the form and submit the job
4.	Check job status for successful import	Select KDCompute -> File Manager -> submitted_jobs -> select job number -> download and view file(s)

Table 4: Genotyping Marker Process - KDManage Collect Order via BrAPI

Step	Activity	Action
1.	Retrieve Authentication Token and Order ID from vendors.	<i>This step may vary depending on choice of vendor.</i>
2.	Use Collect Order to import dataset.	Select KDManage -> Marker -> Marker Data Management -> Collect Order

Note: DArT provides an optional genotyping/profiling service.


6.2 DNA Management

The **DNA Management Page** lists DNA plates that have been uploaded to KDDart.

The screenshot shows the KDManage DNA Management page. The page title is "DNA Management". The user is logged in as "admin" with the group "admin". The page displays a table of DNA plates with the following data:

Id	Name	Description	Action
198	PLATE_IGHSGJMHZCRE		List of DNA extracts, Print Plate Barcode
197	PLATE_AGOATKVLRSVM		List of DNA extracts, Print Plate Barcode
196	PLATE_FXZRMSEPOBH		List of DNA extracts, Print Plate Barcode
195	PLATE_DPLHZFYOPEZP		List of DNA extracts, Print Plate Barcode
194	PLATE_CUKRRBDJZHI		List of DNA extracts, Print Plate Barcode
193	PLATE_XWXNTFNKROD		List of DNA extracts, Print Plate Barcode
192	PLATE_ERFHOCQTFXP		List of DNA extracts, Print Plate Barcode
191	PLATE_HROMDULOFWHV		List of DNA extracts, Print Plate Barcode

Fig. 2: Data Management Page

Selecting the  **List Button** for any plate will display a **Plate Window** which lists extracts that are associated with that plate (pictured below).

List of DNA Extracts in Plate 15

Showing 1 to 94 of 94 entries
 Show entries

First Previous 1 Next Last

PlateName	Row	Column	Genotype	Extract
900914336005	A	1	FB-219	2086
900914336005	A	2	FB-220	2076
900914336005	A	3	FB-221	2047
900914336005	A	4	FB-222	2103
900914336005	A	5	FB-223	2104
900914336005	A	6	FB-224	2055
900914336005	A	7	FB-227	2078
900914336005	A	8	FB-228	2123
900914336005	A	9	FB-229	2110
900914336005	A	10	FB-231	2120
900914336005	A	11	FB-236	2077
900914336005	A	12	FB-244	2114
900914336005	B	1	FB-247	2059
900914336005	B	2	FB-253	2128
900914336005	B	3	FB-254	2039

Fig. 3: Plate Window

6.2.1 Adding a DNA Plate

To add a new DNA plate, select the **Add DNA Plate Button** located on the **DNA Management Page**. This will display the **Add DNA Plate Window** as shown in the image below:

Add DNA Plate
✕

*: denotes a required field.

Trial Name:

Please type 2 or more characters to get the drop down list.

Creation Date*:

Plate Layout: No file chosen

CSV file containing plate name, row, column and genotype name columns.

Tissue:

Plate 1 Name*:

Plate 1 Description:

Plate 1 Storage Location:

Plate 1 Tissue*:

	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												

Fig. 4: Add DNA Plate Window

Field descriptions to assist with completing the form are displayed in the following table:

Table 5: Add DNA Plate Fields

Field	Mandatory?	Description
Trial Name	Mandatory	Mandatory: Trial that this plate is associated with. Upon selecting an existing trial, this will display the relevant plates to this trial.
Creation Date	Mandatory	Mandatory: Date the genotyping service was created.
Plate Layout		CSV file containing plate name, row, column and genotype name columns.
Tissue	Mandatory	Mandatory: Tissue used in this plate.

Plates as in the following illustration may be removed using the Remove Plate button at the bottom left. Also, individual cells may be edited or removed as required. The image and table below contain more information:

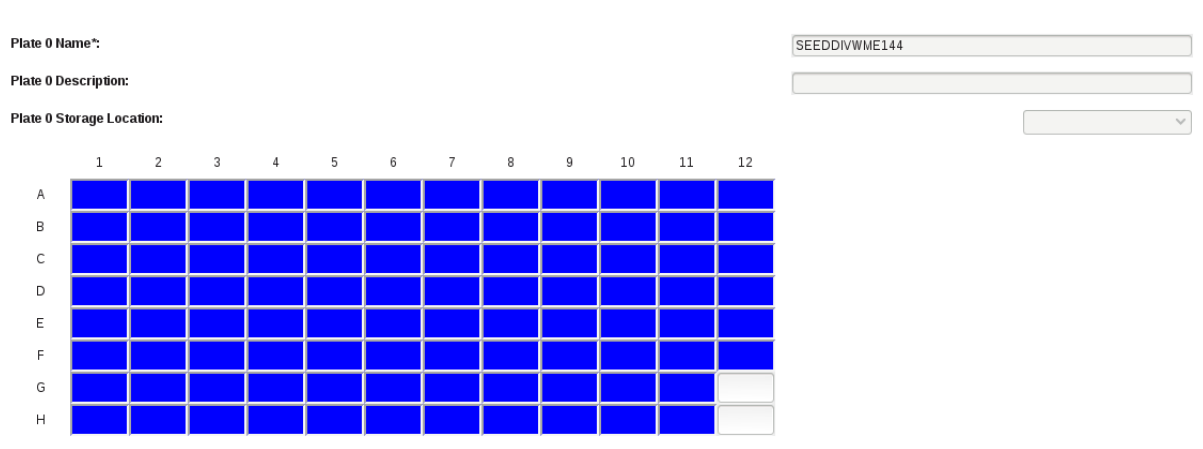


Fig. 5: Add DNA Plate Window - Cells

Table 6: Add DNA Plate Fields - Individual Cells

Field	Mandatory?	Description
Plate 1 Name	Mandatory	Name for this iteration of plate.
Plate 1 Description		Description of the plate.
Plate 1 Storage Location		Location where the plate is stored.
Plate 1 Tissue		Tissue used in these plates.

6.2.2 Editing a Well Plate

Selecting a well will display the **Edit Well Plate Window**, as displayed in the following image, where the well may be edited or removed using the buttons on the window.

Edit Well Plate1_A3
✕

Trial Unit*:

Specimen*:

Tissue: +

Quality:

Remove
Save

Fig. 6: Editing Well Plate Window

Note: Hovering the mouse above a well will display the trial unit position and the specimen name.

6.3 Marker Data Management

The **Marker Data Management Page** lists marker datasets that have been imported to KDDart and provides options for managing them including viewing, editing, and submitting samples.

The screenshot shows the 'Marker Data Management' page. On the left is a navigation sidebar with options like 'Gemplasm', 'Experiments', 'Markers', 'Inventory', 'Environment', and 'Search'. The main content area has a title 'Marker Data Management' and buttons for 'Add Marker Data Management', 'Collect Order', and 'Migrate Data'. Below the title, it says 'Showing 1 to 4 of 4 entries' and includes a search box and pagination controls (First, Previous, 1, Next, Last). The main part of the page is a table with the following data:

Id	Marker Data Management Name	Description	Action
170	Alternative Test		Update Analysis Group Extract List List Datasets Upload Dataset File Submit Samples
169	Test123	Data migrated from migrate_marker_file(1).csv 2022-11-22 00:59:21	Update Analysis Group Extract List List Datasets Upload Dataset File Submit Samples
168	DG19-4810-MigrateTest	Data migrated from Report_DG19-4810_SilicoDART_1.csv 2022-11-21 04:23:16	Update Analysis Group Extract List List Datasets Upload Dataset File Submit Samples
167	Migrate Test 1	Data migrated from migrate_marker_file.csv 2022-11-21 02:20:55	Update Analysis Group Extract List List Datasets Upload Dataset File Submit Samples

Fig. 7: Marker Data Management Page

6.3.1 Adding Marker Data Management

To add a new marker data management genotyping/profiling entry, select the **Add Marker Data Management Button** located on the **Marker Data Management Page** to display the **Add Marker Data Management Window**:

Fig. 8: Add Marker Data Management Window

Field descriptions to assist with completing the form are displayed in the following table:

Field	Mandatory?	Description
Marker Data Management Name	Mandatory	Text string to describe the genotyping service.
Description		Additional description of the genotyping service.
Manager Name		A designated manager for the genotyping service who is defined in KDDart Contacts.
Selected plates	Mandatory	Plates from DNA management selected for this marker data. Drag and drop plates from the Plates List to add specific plates to this marker data.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

Each plate that is selected will be displayed in the window. See the image and table below for more information:

Plate 0 Name*:

Plate 0 Description:

Plate 0 Storage Location:

	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												

Fig. 9: Plate Added to the Add Marker Data Management Window

Table 7: Add Marker Data Management Window - Plate Fields

Field	Mandatory?	Description
Plate 1 Name		Name for this iteration of plate.
Plate 1 Description		Description of the plate.
Plate 1 Storage Location		Location where the plate is stored.

Plates as in the following image may be removed using the **Remove Plate button** at the bottom left of **Plates List**

Note: Hovering the mouse above a well will display the trial Unit position and the specimen name.

6.3.2 Editing a Well Plate

Selecting a well will display the **Edit Well Plate Window** (as displayed in the following image) where the well may be edited or removed using the buttons on the window.

Edit Well Plate0_B3
✕

Extract Id:

Genotype Id:

Genotype Name:

Fig. 10: Edit Well Plate Window

6.3.3 Migrate Marker Data

Migrate marker data and allows plate creation and analysis groups automatically. This also allows easier connection of samples to trial units through Trial unit Barcodes. To start, select **Migrate Data** located on the **Marker Data Management Page** to display **Migrate Data from Marker File** window:

Migrate Data from Marker File
✕

*. denotes a required field.

CSV Data Set File*: migrate_...file.csv

Marker Name Column*:

Sequence Column*:

Meta Data Start Column*:

Meta Data End Column*:

Data Start Column*:

Data End Column*:

Analysis Group Name*:

Data Set Type*: SilicoDArT

Access Group*:

Owner Permission*:

Other Permission*:

Access Permission*:

File Content

ID	0	1	2	3	4	5	6	7	8	9	10	
0	*	*	*	*	*	*	*	*	*	*	*	*
1	*	*	*	*	*	*	*	*	*	*	*	*
2	*	*	*	*	*	*	*	*	*	*	*	*
3	*	*	*	*	*	*	*	*	*	*	*	*
4	CloneID	Sequence	Markername	SNP	Chromosome	mePosition	umOfAligns	allrateREF	allrateSNP	neRatioREF	neRatioSNP	NumofR
5	0-14.A>G	ATCGGAAGAG	999918 F 0			0	0	0.98	0.98	0.67	0.4	654255
6	t G-14.A>G	ATCGGAAGAG	999918 F 0	14.A>G		0	0	0.98	0.98	0.67	0.4	654255
7	0-38.A>G	TAATACTACC	999939 F 0			0	0	1	1	0.18	0.86	175531

Fig. 11: Migrate Data from Marker File

Fill the form accordingly based on the CSV file. Once all the required columns have been filled, select the **Upload** button to proceed with import data.

Note: For referencing the CSV file contents, column and row numbering commences with zero.

Note: All genotype and specimen references must be already created in the database. See

Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

Table 8: Migrate Data Fields

Field	Mandatory?	Description
CSV Data Set File	Mandatory	Browse to locate and select the CSV file to import.
Plate Name Row	Mandatory	The row that contains the plate names.
Item Barcode Row		The row that contains the item barcodes.
Specimen Name Row		The row that contains the specimen names.
Genotype Name Row		The row that contains the genotype names.
Well Position Row		The row that contains the well positions.
Well Row Row		The row that contains the well rows.
Well Column Row		The row that contains the well columns.
Header Row	Mandatory	The row that contains the headers.
Marker Name Column	Mandatory	The column that contains the marker names.
Sequence Column	Mandatory	The column that contains the sequences.
Meta Data Start Column	Mandatory	The first column in the CSV file containing meta data for import.
Meta Data End Column	Mandatory	The last column in the CSV file containing meta data for import.
Data Start Column	Mandatory	The first column in the CSV file containing data for import.
Data End Column	Mandatory	The last column in the CSV file containing data for import.
Analysis Group Name	Mandatory	Given analysis group name.
Data Set Type	Mandatory	The type of dataset, as defined in type definitions.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

6.3.4 Upload Dataset File

To upload a new dataset to a marker data management group, select **Upload Dataset File** in the **Actions Column** for the required group. This will display the **Upload Dataset File Window**. The window and a table that describes the related fields can be found below:

Upload Dataset File for Marker Data Management 9 ✕

*: denotes a required field.

CSV Data Set File*: **Sequence Column*:**

Plate Name Row*: **Meta Data Start Column*:**

Well Row Position Row*: **Meta Data End Column*:**

Well Column Position Row*: **Data Start Column*:**

Header Row*: **Data End Column*:**

Marker Name Column*: **Data Set Type*:** +

File Content												
ID	0	1	2	3	4	5	6	7	8	9	10	11
0	*	*	*	*	*	*	*	*	*	*	*	*
1	*	*	*	*	*	*	*	*	*	*	*	*
2	*	*	*	*	*	*	*	*	*	*	*	*
3	*	*	*	*	*	*	*	*	*	*	*	*
4	CloneID	Sequence	Markername	SNP	Chromosome	mePosition	umOfAligns	allrateREF	allrateSNP	neRatioREF	neRatioSNP	NumofRefs
5	t,G-38:A>G	TAATACTACC	999939[F]0	38:A>G		0	0	1	1	0.18	0.86	17531914
6	l0-32:G>C	CAACAGAGGA	999968[F]0			0	0	0.89	0.89	0.49	0.65	436170212
7	t,C-32:G>C	CAACAGAGGA	999968[F]0	32:G>C		0	0	0.89	0.89	0.49	0.65	436170212
8	l0-66:A>C	ACAAAGCATA	999941[F]0			0	0	0.75	0.75	0.07	0.93	053191489
9	t,C-66:A>C	ACAAAGCATA	999941[F]0	66:A>C		0	0	0.75	0.75	0.07	0.93	053191489

Fig. 12: Edit Well Plate Window

Note: For referencing the CSV file contents, column and row numbering commences with zero.

Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

Field	Description
CSV Data Set File	Browse to locate and select the appropriate CSV file for import.
Plate Name Row	The row that contains the plate names.
Well Row Position Row	The row that contains the well row positions.
Well Column Position Row	The row that contains the well column positions.
Header Row	The row that contains the headers.
Marker Name Column	The column that contains the marker names.
Sequence Column	The column that contains the sequences.
Meta Data Start Column	The first column in the CSV file containing meta data for import.
Meta Data End Column	The last column in the CSV file containing meta data for import.
Data Start Column	The first column in the CSV file containing data for import.
Data End Column	The end column in the CSV file containing data for import.
Data Set Type	The type of dataset, as defined in type definitions.

6.3.5 Upload Alternative Format Dataset File

To upload an alternative format of dataset file, where samples are organised in rows, to an analysis group, select **Upload Alternative Format Dataset File** (under **Upload Dataset File** dropdown) in the Action Column for the required group. This will display **Upload Dataset File for Marker Data Management** window that shown below:

Upload Dataset File for Marker Data Management 99
✖

*: denotes a required field.
 CSV Data Set File*: markerda...00 .csv Marker Name Column*:
 Metadata for Marker*: metadata500.csv Sequence Column*:
 Plate Name Column*: Marker Metadata Start Column*:
 Well Position Column*: Marker Metadata End Column*:
 Sample Id*: Data Set Type*: SilicoDArT
 Data Start Column*:
 Data End Column*:

File Content												
ID	0	1	2	3	4	5	6	7	8	9	10	11
0	Plate	llPosition	Sample	ryMarker1	ryMarker2	ryMarker3	ryMarker4	ryMarker5	ryMarker6	ryMarker7	ryMarker8	ryMarker9
1	platetest4	A1	mac1	A	0.07	ZZ11	iled score	1	0	1	0	2
2	platetest4	A2	mac2	G	4.33	ZZ33	alid score	0	1	0	0	1
3	platetest4	A3	mac3	A	8.6	FF11	missing	0	1	1	1	1
4	platetest4	A4	mac4	T	4.81	HH12	iled score	0	1	0	1	2
5	platetest4	A5	mac5	G	1.42	KA11	alid score	1	1	1	1	1
6	platetest4	A6	mac6	A	2.9	AA44	missing	1	1	1	0	2
7	platetest4	A7	mac7	A	8.01	TT23	alid score	1	1	1	0	0
8	platetest4	A8	mac8	A	0.07	ZZ11	iled score	1	0	1	0	2
9	platetest4	A9	mac9	G	4.33	ZZ33	alid score	0	1	0	0	1

Fig. 13: Upload Dataset File for Marker Data Management

Number the cells in the form and click on **Upload** button once all the required columns have been filled. This will continue the process to upload dataset file.

Note: For referencing the CSV file contents, column and row numbering commences with zero.

Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

Table 9: Upload Alternative Format Dataset File Fields

Field	Mandatory	Description
CSV Data Set File	Mandatory	Browse to locate and select the marker data CSV file to import.
Metadata for Marker	Mandatory	Browse to locate and select the marker metadata CSV file to import.
Plate Name Column	Mandatory	The column that contains the plate names.
Well Position Column	Mandatory	The column that contains the well positions.
Sample Id	Mandatory	The column that contains the sample Id. This is usually made up of genotype names.
Data Start Column	Mandatory	The first column in the CSV file containing data for import.
Data End Column	Mandatory	The last column in the CSV file containing data for import.
Marker Name Column	Mandatory	The column that contains the marker names.
Sequence Column	Mandatory	The column that contains the sequences.
Marker Metadata Start Column	Mandatory	The first column in the CSV file containing meta data for import.
Marker Metadata End Column	Mandatory	The last column in the CSV file containing meta data for import.
Data Set Type	Mandatory	The type of dataset, as defined in type definitions.

6.3.6 Collecting an Order

To collect a completed order and create relevant data points, select the **Collect Order Button** located on the **Marker Data Management Page**. This will display the **Collect Order Window** which is pictured below, along with a table that describes the relevant fields:

Collect Order
✕

*: denotes a required field.

BrAPI Genotyping Vendor Base URL*:

Order Id*:

Authentication Token*:

Source Field for Sample Id*:

Owner Permission*:

Access Group*:

Access Permission*:

Other Permission*:

Fig. 14: Collect Order Window

Note: This feature requires system administrator set up, including the creation of relevant types and KDManage system configuration.

Field	Mandatory?	Description
BrAPI Genotyping Vendor Base URL	Mandatory	Select the vendor BrAPI URL.
Order ID	Mandatory	Full Order ID of completed order for import.
Authentication Token	Mandatory	Authentication token from genotyping vendor.
Source Field for Sample ID	Mandatory	KDDart entity that will be created or linked to sample ID.
Access Fields	Mandatory	Access and permissions. See the <i>Access Settings and Permissions</i> topic.

6.3.7 Printing Barcodes for Marker Data

To download a set of barcodes for the Marker Data Management group, select “Print Barcodes” (under **Extract List** dropdown) in the **Action Column** for the required group in the **Marker Data Management Page**.

6.3.8 List Marker Datasets of Group

To list all datasets in a group, select **List Datasets** in the **Actions Column** for the required group in the **Marker Data Management Page**.

Id	Data Set Type	Description	Marker Name Field	Marker Sequence	Action
86	DataSetType - 06699510638		CloneID	Sequence	Visualise Data Download dataset

Fig. 15: List Datasets Window

6.3.9 Visualising a Dataset with a Heatmap

To visualise a dataset with a heatmap, select **Visualise Data** in the **Action Column** of the **List Datasets Window** (for the required marker dataset of a group). This will open the **Marker Data Window** as seen in the image below:

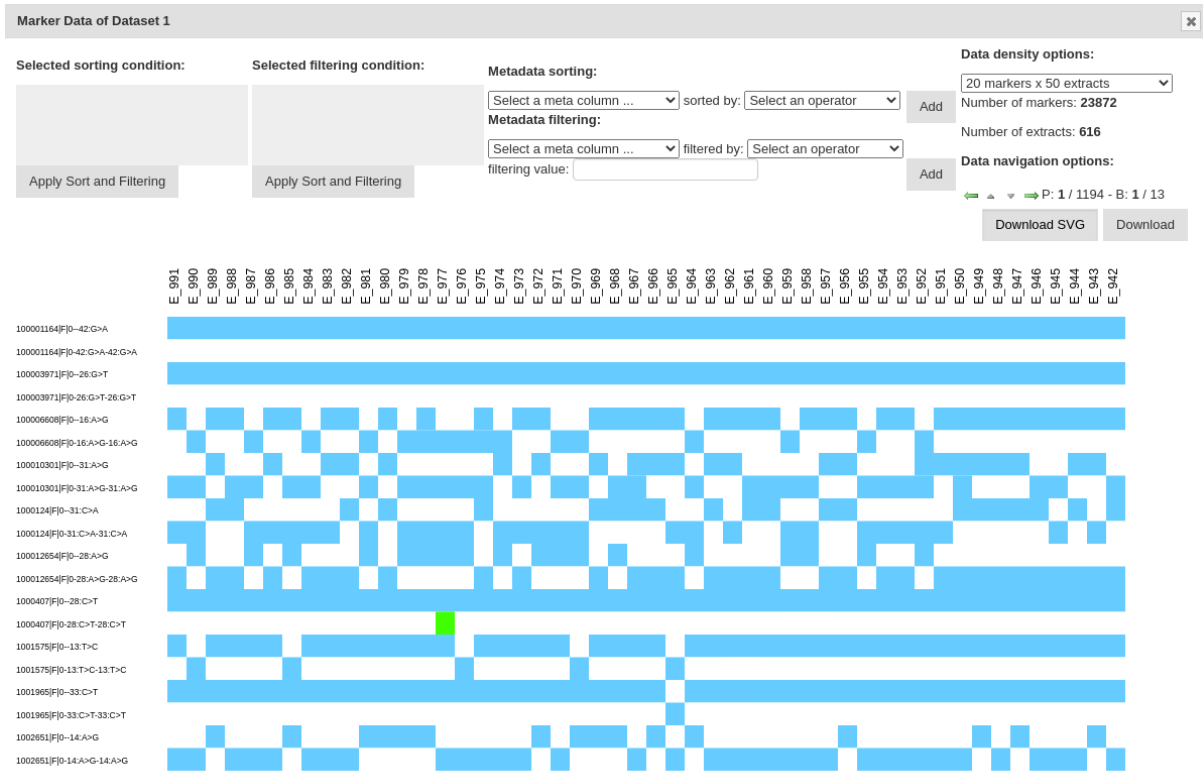


Fig. 16: Marker Data Window

Data can be further filtered and sorted to retrieve more specific data. Visualised data can also be downloaded as an SVG file for further use.

Individual sample/marker squares can also be selected to reveal more information about a sample.

6.3.10 Downloading a Dataset

To download a dataset, select  **Download dataset** **Download Data** in the **Action Column** of the **List Datasets Window** (for the required marker dataset of a group). This will open the **Download Dataset Window** as seen in the image below:

Fig. 17: Download Dataset Window

Table 10: Download Dataset Fields

Field	Description
Format Type	The format that the dataset will be downloaded in. In standard installations, this will either be CSV or Flapjack. Extra formats can be added with extra development.
Marker Meta-data Field List	Chosen marker metadata fields to include in the download. Leave blank to include all.
List of DNA Extracts	Chosen DNA Extracts to include in the download. Leave blank to include all.
List of Marker	Chosen markers to include in the download. Leave blank to include all.
Marker list from CSV	Upload a CSV of markers to filter from.
Extract list from CSV	Upload a CSV of extracts to filter from. Use genotype names.

Data can be further filtered and sorted to retrieve more specific data.

6.3.11 Submitting Samples to a Genotyping Vendor

If KDManage has been configured with a vendor ID, users will be able to submit samples to the vendor from analysis group plates. To submit, select **Submit Samples** **Submit Samples** in the **Actions Column** for the required analysis group. That will display the **Sample Submissions Window** which is shown below, along with a table that explains its fields:

Fig. 18: Download Dataset Window

Table 11: Sample Submission to Genotyping Vendor Fields

Field	Description
BrAPI Genotyping Vendor Base URL	The URL for genotyping vendors. These must be configured by a system administrator.
Source Field for Sample ID	How samples will be identified.
Authentication Token	Authentication token from vendor.

6.3.12 Downloading Genotyping Results from a Vendor

If KDManage has been configured with a vendor ID, users will be able to download genotyping results to the vendor for an analysis group. To submit, select “Download Genotyping result” (under **Submit Samples** dropdown) in the **Action Column** for the required analysis group.

6.4 Marker Maps

The **Marker Maps Page** lists marker maps that have been created within KDDart.

The screenshot shows the 'Marker Map' page in the KDManage application. The page features a sidebar with navigation options like 'Germplasm', 'Experiments', 'Markers', 'DNA Management', 'Marker Data Management', 'Marker Maps', 'Inventory', 'Environment', and 'Search'. The main content area displays a table of marker maps. The table has the following data:

Id	Map Name	Operator	Action
10	VEJMIKVVYAO	admin	Import Marker Map Position List Marker Map Positions
9	TOFZHDQXIA	admin	Import Marker Map Position List Marker Map Positions
8	MarkerMap_94794659821	admin	Import Marker Map Position List Marker Map Positions
7	MarkerMap_39805468997	admin	Import Marker Map Position List Marker Map Positions
6	MarkerMap_97658868224	admin	Import Marker Map Position List Marker Map Positions
5	MarkerMap_69162967912	admin	Import Marker Map Position List Marker Map Positions
4	FOPRZNTKYW	admin	Import Marker Map Position List Marker Map Positions

Fig. 19: Marker Map Page

6.4.1 Adding Marker Maps

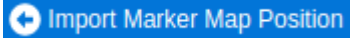
To add a new marker map, select the **Add Marker Map Button** located in the **Marker Map Page** to open the **Add Marker Map Window**. An image of the window and a table explaining the related fields can be found below:

Fig. 20: Add Marker Map Window

Table 12: Add Marker Map Fields

Field	Mandatory	Description
Map Name	Mandatory	Text string to describe the marker map.
Map type	Mandatory	The type of marker map, as defined in type definitions.
Map Software		Name of software used to create map.
Model Reference Information		Model reference information for physical maps.
Map Description		General description of the map.
Map Parameters	Mandatory	Map parameters (also software parameters) used for creation.

6.4.2 Importing a Marker Map Position

To add a new marker map position, select the  **Import Marker Map**. This will open the **Import Marker Map Position Window** which is pictured below, along with a table that details related fields:

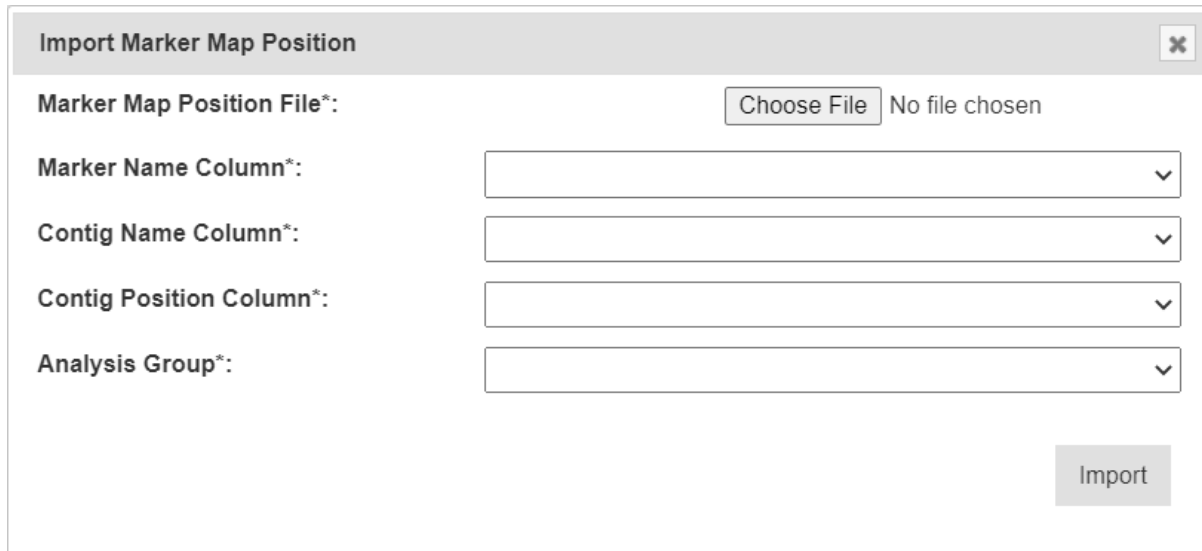


Fig. 21: Import Marker Map Position Window

Note: For referencing the CSV file contents, column and row numbering commences with zero.

Table 13: Import Marker Map Fields

Field	Description
Marker Map Position File	Browse to locate and select the appropriate CSV file for import.
Marker Name Column	The column that contains the marker names. Markers must match the ones contained in the selected analysis group.
Contig Name Column	The column that contains the contig names
Contig Position Column	The column that contains the contig positions
Analysis Group	The analysis group associated with uploaded marker map positions. The analysis group must have a least one dataset.

Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

INVENTORY MENU

The KDManage **Inventory menu** provides tools that you can use to manage inventory items and locations, including performing stocktakes or adding/removing items. The tools available in the **Inventory** are listed below:

- *Storage locations*;
- *Items*; and
- *Inventory Management*.

The items are listed in order of dependency.

7.1 Storage Locations

Storage locations are the **Inventory** elements used for organising item storage for trials and nurseries. Storage locations are typically for grain storage; however, this is not a limitation. See the image and table below for an example and information on the fields for each storage location:

ID	Storage Location	Storage details	Items Count	Action
34	Test Room 4	Test Storage Barcode auto-generate	1	Update Storage location Show children storage Delete Storage
33	Test Room 3	Test Storage Barcode auto-generate - fail	0	Update Storage location Show children storage Delete Storage
32	Test Room 2	Testing - parent storage	1	Update Storage location Show children storage Delete Storage
31	Test Room 1	Testing 1	0	Update Storage location Show children storage Delete Storage
30	Cool Room 2	Secondary seed storage	1056	Update Storage location Show children storage Delete Storage
29	Cool Room 1	Secondary seed storage	1064	Update Storage location Show children storage Delete Storage
28	Cool Room 2 Shelf 1	Secondary seed storage location	1056	Update Storage location Show children storage Delete Storage
27	Cool Room 1 Shelf 1	Primary seed storage location	1055	Update Storage location Show children storage Delete Storage

Fig. 1: Storage Locations

Table 1: Storage Location Fields

Field	Mandatory	Description
Storage Barcode		A barcode to identify the storage location.
Storage Location	Mandatory	Main name to identify the storage location.
Storage Parent ID		The ID of the parent of the storage location (e.g. <i>North Pole Building 1</i> can be the parent of <i>North Pole Building 1 Room A</i>).
Storage Details		A detailed storage description. This is flexible as it can be a text description.
Storage Note		Extra notes, comments, or extra details about the storage locations.

7.1.1 Filtering Storage Locations

Each storage location may have a single parent, which creates a hierarchical structure that can be explored by viewing the children of a single parent location. The following image shows some storage locations filtered to display *parent locations*. Select the **Show All Storage Locations** button/**Show Only Parent Storage Locations** button to switch this filtered view off/on.

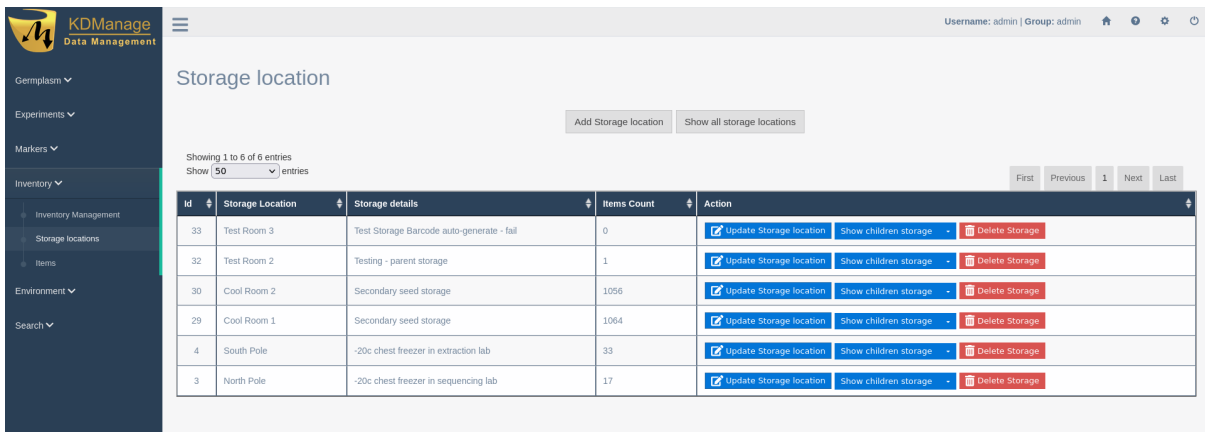


Fig. 2: Filtered Storage Locations - Parent Storage


7.1.2 Adding a Storage Location

You can add both parent and child storage locations to the **Inventory**. Follow the steps below to add a new storage location:

Fig. 3: Adding a Storage Location

Table 2: Adding a Storage Location

Step	Action
1.	Expand Inventory in the main left-hand menu, then select Storage Locations which will display a window as in the above illustration.
2.	Select the Add Storage Location button . This will display the Add Storage Location window (as seen in the above image).
3.	Complete the mandatory Storage location field, as well as any other fields you want to include. Note <ul style="list-style-type: none"> • All fields can be updated later if required. • To create a storage parent: do not provide a storage parent id, the application will auto-recognise it as a storage parent. • To create a storage child: provide a parent id, and it will auto-recognise it as a child
4.	Select the Add button to create the storage location.

Tip: Selecting  **Update Storage location** for a storage item will open the **Update Storage Location window**, which is identical to the **Add Storage Location window**, except the purpose is to update an existing storage location rather than create a new one.

7.1.3 Viewing Storage Trees

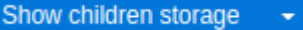
A *storage tree* shows the relationship between a parent storage location and its children. Select the  **Show Children Storage button** in the **Action column** of a storage location to view its storage tree in a **Storage Tree window** (as seen in the image below). The following example illustrates an expanded view showing all the children storage locations of the selected parent storage location.



Fig. 4: Storage Tree

From the example above, selecting the **i** **Info button** next to the location will display an **Update Storage Location window** which facilitates easier viewing and updating of storage locations.

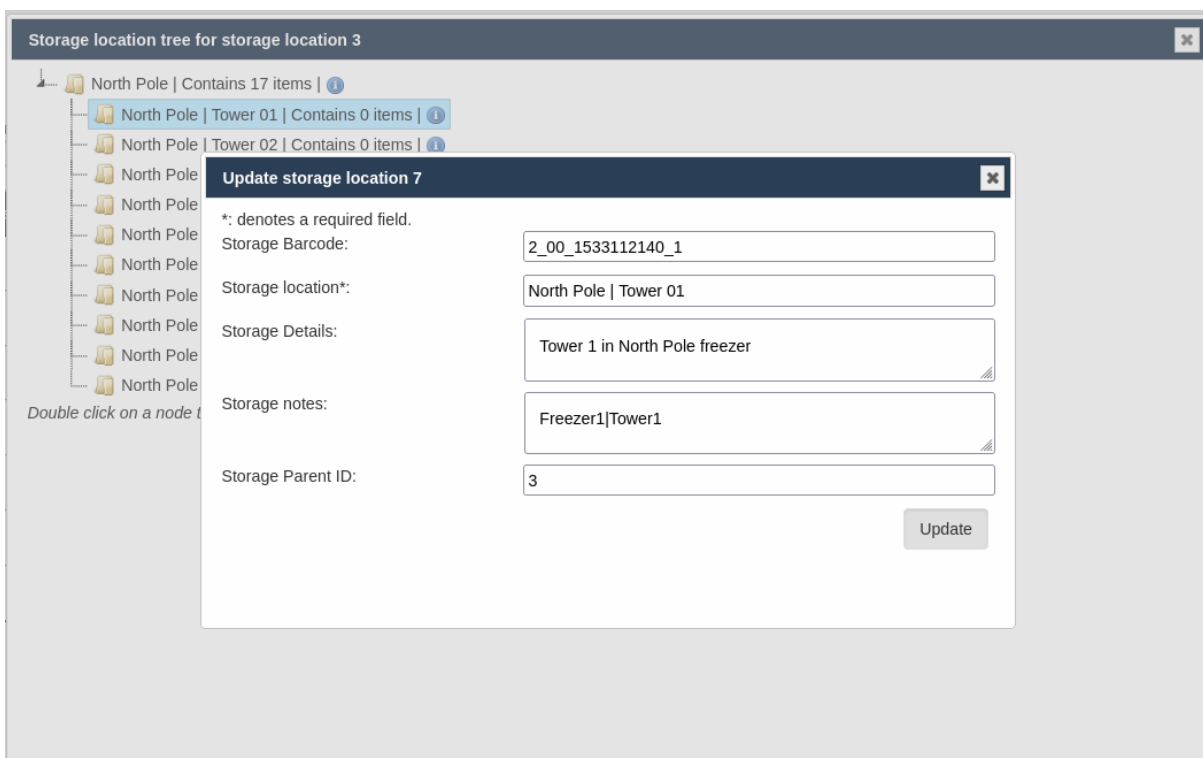


Fig. 5: Updating a Storage Location from a Storage Tree

7.2 Items

Items are the elements of the **Inventory** that represent the various stock and samples that you can use in future experiments or for post-experiment operations and analysis.

Each item is generally associated with a specimen, which may or may not be used in a trial. This reflects how different samples can be extracted or harvested from the specimens used in experiments.

This table describes the fields for an item:

Table 3: Item Fields

Field	Description
Trial Unit Specimen ID	The ID of the trial unit specimen that the item was harvested from.
Specimen ID	Material-specimen that the item is from.
Item Source ID	ID of the contact (who is the external source).
Container Type	The container type for item.
Scale	The device used to take measurements.
Storage Location	Id of the storage location where the item is stored.
Item Type	Material-item type (e.g. seed).
Item State	A description of the state of the item (e.g. damaged, thrown away, active, etc.)
Item Barcode	The barcode on the item container.
Amount	The number of the items in container.
Unit	The unit of the item if it is known (refer to the <i>Units</i> topic).
Date Added	Material-date and time that the item was added to the database. This field only displays in Item-related functions of Inventory Management page. but no user's action required
Last Measured Date	The date and time that the item was last measured.
Last Measured User	The user who last updated the item.
Item Operation	If the item is derived from other items by taking sample or grouping (mixing) it can be defined here.
Item Note	Comments for the item.
Item Log type	The item log type that will be added to the log of new items and original item.
Item Log Message	Message that user wants to add to Item Log. This field only displays in Item-related functions of Inventory Management page.
Last Updated	Material-date and time that the item was last updated. KDManage fill this field out automatically as user update item. This field only displays in Update Item Window of Items page. but no user's action required

7.2.1 Adding a New Item

New items can be created and added to the **Inventory** by performing the following steps:

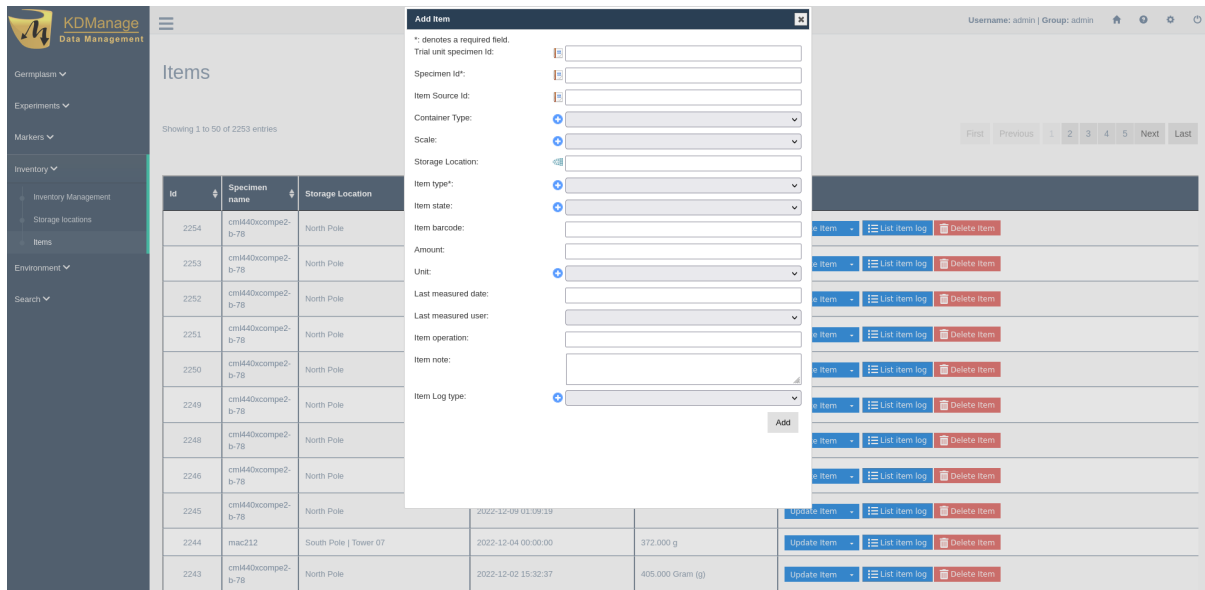




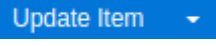


Fig. 6: Adding a New Item

Table 4: Adding a New Item

Step
<ol style="list-style-type: none"> From the Items page in the Inventory, select the Add Item button. This will display the Add Item window. Fill out all necessary fields in the Add Item window. The below list provides some more information on how to add data for the different fields: <ul style="list-style-type: none"> The <i>Specimen ID</i> and <i>Item Type</i> fields are mandatory. Whilst <i>Trial Unit Specimen ID</i> is not a mandatory field, if used, the <i>Specimen ID</i> must match the <i>Specimen ID</i> of the <i>Trial Unit Specimen</i>. All fields can also be updated later if required. Some fields have a  List button which allows the user to choose pre-existing elements from the database to be added in the item information with the  Grab button. The  Add button allows users to add elements for some fields to be used for the item. The <i>Storage Location</i> has the  Storage Tree button so that an existing storage location can be chosen for the item. If required, add an <i>Item Log Type</i> to add an “Addition” Item log for a newly created item. Select the Add button to create the item.

It is often impractical to add items individually. A more practical method is to import items from a CSV which is described in the *Importing an Existing Item* section.

Tip: Selecting the  **Update Item** for a storage item will open the **Update Item window**, which is the same to the **Add Item window**, except an extra field of Last Updated and the purpose is to update an existing item rather than create a new one. The picture below shows how the Add Item Window looks.

Update item 2251
✕

*: denotes a required field.

Trial unit specimen Id:	<input type="text"/>
Specimen Id*:	<input type="text" value="1232"/>
Item Source Id:	<input type="text"/>
Container Type:	<input type="text" value=""/>
Scale:	<input type="text" value=""/>
Storage Location:	<input type="text" value="3"/>
Item type*:	<input type="text" value="Seed bag"/>
Item state:	<input type="text" value=""/>
Item barcode:	<input type="text"/>
Amount:	<input type="text" value="210.000"/>
Unit:	<input type="text" value="g"/>
Last measured date:	<input type="text" value="2022-12-09 16:30:26"/>
Last measured user:	<input type="text" value=""/>
Item operation:	<input type="text"/>
Item note:	<input style="height: 40px;" type="text"/>
Item Log type:	<input type="text" value=""/>
Last Updated (automatically filled in)*:	<input type="text" value="2022-12-09 16:30:26"/>

Fig. 7: Update an Item

7.2.2 Importing an Existing Item

Importing items allows a large number of items from a CSV file to be added in bulk. These items are usually sourced from a harvest method.

Item CSV Preparation

An Item CSV file must be prepared correctly to ensure a seamless import. This means ensuring the correct:

- *Types*;
- *Device Registrations*;
- *Units*; and
- *Storage Locations*.

The following *types* can be used:

- Item type (mandatory);
- Item state type (optional); and
- Item container type (optional).

If a *barcode configuration* (refer to the [Barcode Configurations](#) topic), has been created for *items* and the barcode column is not given, then barcodes can be automatically generated for new items.

Use the IDs in columns of the CSV. When importing a CSV, the first row will not be added as KDManage will assume these are the *headings* of each column.

You may name these columns to the correct fields, to which the Import tool will automatically assign the columns to the correct fields.

The full column names that can be used are:

- TrialUnitSpecimenId,
- SpecimenId,
- ItemSourceId,
- ContainerType,
- ScaleId,
- StorageId,
- ItemTypeId,
- ItemStateId,
- ItemBarcode,
- Amount,
- Unit,
- DateAdded,
- MeasuredByUser, and
- ItemNote.

A single erroneous row will stop the process.

The following example shows a small item input CSV file.

```

SPECIMENID,TRIALUNITSPECIMEN,ITEMTYPEID,DATEADDED,UNITID,AMOUNT,ITEMSOURCEID,STORAGEID,ITEMNOTE,ITEMSTATEID,SCALEID,CONTAINERTYPEID,ITEMBARCODE
19,18629,98,2017-02-17,11,500,1,31,Test 1,103,1,99,BARCODE123456
20,18630,98,2017-02-17,11,500,1,31,Test 2,103,1,99,fBARCODE123457
14,18631,98,2017-02-17,11,500,1,31,Test 3,103,1,99,BARCODE123458
22,18632,98,2017-02-17,11,500,1,31,Test 4,103,1,99,BARCODE123459
23,18633,98,2017-02-17,11,500,1,31,Test 5,103,1,99,BARCODE123450
5,18634,98,2017-02-17,11,500,1,31,Test 6,103,1,99,BARCODE123461
    
```

Fig. 8: Example Item CSV Import File

Note: IDs of entities are used in the columns of the CSV.

Steps for Importing an Existing Item CSV

If an item CSV has been prepared and you are ready to import the items, then see the images and steps below for information on how to do that:

Import Items
✕

*: denotes a required field.

Item CSV File*: Browse... No file selected.

Specimen Name Column*:

Item Type Column*:

Unit Column*:

Amount Column*:

Storage Location Column:

Storage Location Barcode Column:

Barcode Column:

Item State Column:

Automatically generate empty barcodes:

Start Item Factor Column:


End Item Factor Column:

Item Log Type: +

Import

Fig. 9: Importing Items

Table 5: Import CSV

Step	
1.	From the Items tool in the Inventory menu , select the Import Items button to display the Import Items window (as seen in the image above).
2.	Select the Choose File button to open a window to select a file from your local machine. The columns will be automatically mapped to fields if the uploaded CSV has the headings specified in the <i>Item CSV Preparation</i> section. If not, you must specify the column name for each field. Leave a field empty if it is not required to be uploaded, but all mandatory fields must be included (fields with * is mandatory).
3.	If required, add a new item log type with the  Add button , or select an existing one from the dropdown menu to create a new item log for all newly created items. Only items with unique barcodes will have an item log created. Note: Select “Yes” from Automatically generate empty barcode dropdown if the barcode column is not given.
4.	Select the Import button to finalise the import of the items file. The items will now be listed in the Items tool .

7.3 Inventory Management

Inventory Management is a tool that provides management options for the **Inventory**. These options include bulk stocktake, split, merge, and other operations.

The image below shows **Inventory Management** with the **Inventory Management panel** (currently on the **Storage tab**) where items can be searched for by their storage location. The **Barcode tab** provides a search tool for searching items by their barcodes. The **CSV Search tab** provides a search tool for items which were created by provided csv file.

Below the **Inventory Management Search panel** is the **Items panel** which contains the items listed according to selections in the **Storage tab** or **Barcode tab**.

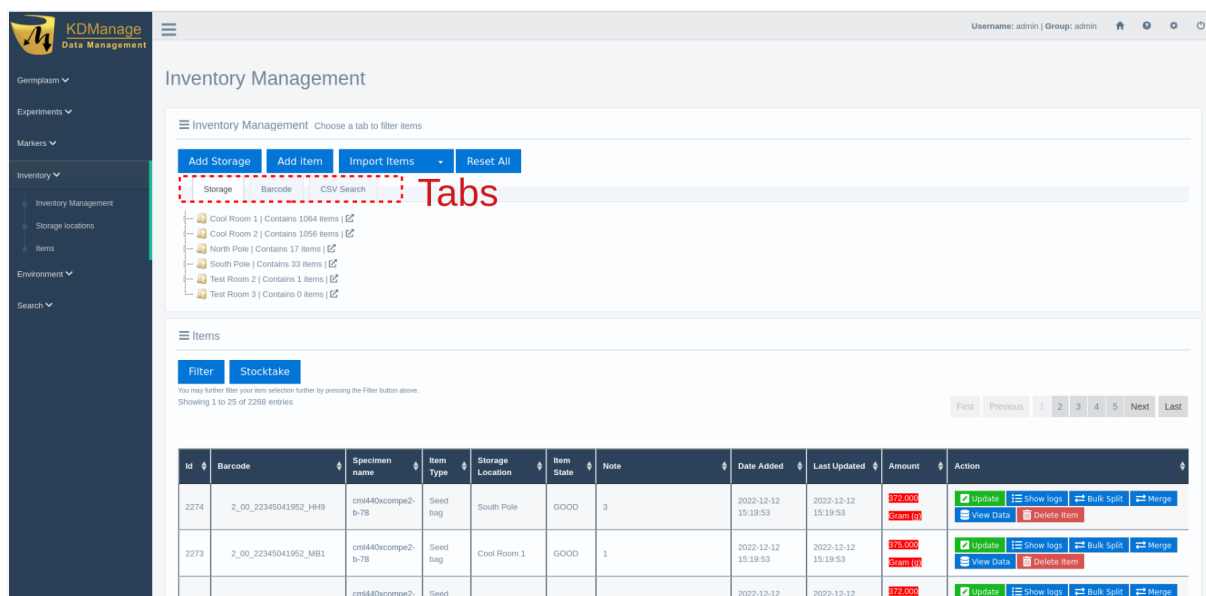


Fig. 10: Inventory Management

You can add storage locations and items by selecting the **Add Storage** and **Add Item buttons**. You can also import items by selecting the **Import Items button**. These three actions are all outlined in the above sections (*Adding a Storage Location*, *Adding a New Item*, and *Importing an Existing Item*) as they are identical to the actions available in the **Storage Location tool** and the **Items tool**.

Other actions available in **Inventory Management** are listed in the sections below.

7.3.1 Importing Items in Inventory Management

Importing items in the **Inventory Management tool** differs from previously described methods as it allows for more user-friendly data entry. In addition, instead of users requiring to use KDDart database IDs, these methods allow for named references.

Item CSV Preparation for Inventory Management

An Item CSV file must be prepared correctly to ensure a seamless import. This means ensuring the correct:

- *Types*;
- *Units*; and
- *Storage Locations*.

If users wish to link items to specific specimens in a Trial, *Trial Unit Barcodes* should be used (see *Adding Trial Unit Layouts*).

Specimen names can be used in imports but must already exist in the database (see *Specimen*).

Import Item ✕

Item Factor Columns can only be added to existing items. This requires items to be imported first and then using the same CSV, update the existing items with the Item Factor columns.

Item CSV File*: No file selected.

Specimen Name Column:

Item Type Column:

Unit Column:

Amount Column:

Storage Location Column:

Storage Barcode Column:

Item State Column:

Barcode Column:

Item Note Column:

Automatically generate barcodes:

Set the Item Type Log type. Note: only item logs will be added for items with barcodes. If barcode configuration have been set for Items, then barcodes will be automatically generated.

Item Log Type:

Update Existing Items*:

Override Last Measured Date Lock:

Fig. 11: Item Import with Specimen Names

Import Item
✕

Item CSV File*: Browse... No file selected.

Trial Unit Barcode Column*:

Specimen Number Column:

Item Type Column*:

Unit Column*:

Amount Column*:

Storage Location Column:

Storage Barcode Column:

Item State Column:

Barcode Column:

Item Note Column:

Automatically generate barcodes:

Set the Item Type Log type. Note: only item logs will be added for items with barcodes. If barcode configuration have been set for Items, then barcodes will be automatically generated.

Item Log Type: +

Update Existing Items*:

Override Last Measured Date Lock:

Import Item

Fig. 12: Item Import with Trial Unit Barcodes

The following *types* can be used:

- Item type (mandatory);
- Item state type (optional);

If a *barcode configuration* (refer to the [Barcode Configurations](#) topic), has been created for *items* and the barcode column is not given. In that case, barcodes can be automatically generated for new items.

The following example shows a small item input CSV file.

```

Specimen,Amount,Type,unit,StorageBarcode,StorageLocationName
Specimen1,43.78,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen2,1.91,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen3,65.21,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen4,66.89,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen5,42.44,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen6,1.08,Seed,g,2_00_1533112918_8,South Pole | Tower 09
    
```

Fig. 13: Example Item CSV Import File

Warning: An invalid row will stop the import process.

7.3.2 Filtering Items

Any selections from the **Inventory Management** panel can be filtered in the **Items** panel.

Items in Cool Room 1 | Storage Id 29

Filter Stocktake

You may further filter your item selection further by pressing the Filter button above.

Item filter

Item Id (separate multiple ids with commas) Specimen Id (separate multiple ids with commas)

Item type Item state

Search Trial name Trial Id Search Storage location Storage Id Include items in children storage locations

Barcodes (separate multiple barcodes with commas)

Operator Amount Unit


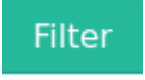
Reset Filter

Showing 1 to 25 of 2360 entries

First Previous 1 2 3 4 5 Next Last

Fig. 14: Filtering Inventory Items

Table 6: Filtering Inventory Items

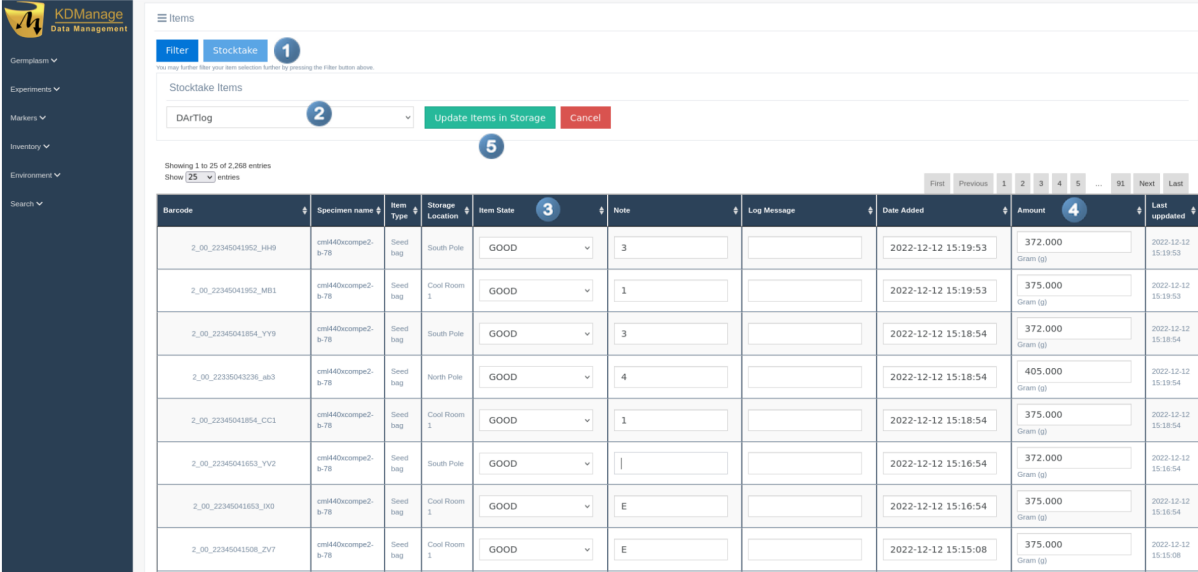
Step	Action
1.	Select the Filter button  from the Items panel to display filtering options.
2.	Enter one or more filter parameters such as an item type, item ID, or trial name.
3.	Select the green Filter button  to complete the filter. All relevant items will be shown in the list below.
4.	More filter parameters can be applied by repeating steps 2-3 and results can be cleared by selecting the Reset button .

7.3.3 Conducting a Stocktake



After choosing a set of items, users may click on the **Stocktake button** to begin a bulk stocktake. This allows users to update amounts and item states in bulk.

After making updates, users may choose the Item Log Type to track changes in each Item’s log.



The screenshot shows the 'Items' section of the KDManage application. At the top, there are 'Filter' and 'Stocktake' buttons. Below them is a 'Stocktake Items' form with a dropdown menu set to 'DARtlog' and an 'Update Items in Storage' button. A table below the form displays a list of items with columns: Barcode, Specimen name, Item Type, Storage Location, Item State, Note, Log Message, Date Added, Amount, and Last updated. The table contains 8 rows of data.

Barcode	Specimen name	Item Type	Storage Location	Item State	Note	Log Message	Date Added	Amount	Last updated
2_00_22345041952_H49	cm1440xcomp2-b-78	Seed bag	South Pole	GOOD	3		2022-12-12 15:19:53	372.000 Gram (g)	2022-12-12 15:19:53
2_00_22345041952_MB1	cm1440xcomp2-b-78	Seed bag	Cool Room 1	GOOD	1		2022-12-12 15:19:53	375.000 Gram (g)	2022-12-12 15:19:53
2_00_22345041954_YY9	cm1440xcomp2-b-78	Seed bag	South Pole	GOOD	3		2022-12-12 15:18:54	372.000 Gram (g)	2022-12-12 15:18:54
2_00_22335043236_ab3	cm1440xcomp2-b-78	Seed bag	North Pole	GOOD	4		2022-12-12 15:18:54	405.000 Gram (g)	2022-12-12 15:19:54
2_00_22345041954_CC1	cm1440xcomp2-b-78	Seed bag	Cool Room 1	GOOD	1		2022-12-12 15:18:54	375.000 Gram (g)	2022-12-12 15:18:54
2_00_22345041953_YV2	cm1440xcomp2-b-78	Seed bag	South Pole	GOOD	1		2022-12-12 15:16:54	372.000 Gram (g)	2022-12-12 15:16:54
2_00_22345041953_0D	cm1440xcomp2-b-78	Seed bag	Cool Room 1	GOOD	E		2022-12-12 15:16:54	375.000 Gram (g)	2022-12-12 15:16:54
2_00_22345041958_ZV7	cm1440xcomp2-b-78	Seed bag	Cool Room 1	GOOD	E		2022-12-12 15:15:08	375.000 Gram (g)	2022-12-12 15:15:08

Fig. 15: Conducting a Stocktake

Table 7: Conducting a Stocktake

Step	Action
1.	When items have been listed, select the Stocktake button (1) from the Items panel .
2.	Choose an item log from the Item Log Dropdown menu at (2).
3.	For each item, select an <i>item state</i> from the Item State column at (3).
4.	If required, edit the <i>amount</i> for each item from the Amount column at (4).
5.	When all items have been updated, select the Update Items in Storage button (at (5)) to finalise the stocktake.

7.3.4 Updating an Item

Individual items can be updated by selecting the Update Button within the Action Column. This will display the Update Item Window as seen in the image below where any details can be updated.

Update Item
✕

*: denotes a required field.

Trial unit specimen Id:	<input type="text"/>
Specimen Id*:	<input type="text" value="1232"/>
Item Source Id:	<input type="text"/>
Container Type:	<input type="text" value=""/>
Scale:	<input type="text" value=""/>
Storage Location:	<input type="text" value="4"/>
Item type*:	<input type="text" value="Seed bag"/>
Item state:	<input type="text" value="GOOD"/>
Item barcode:	<input type="text" value="2_00_22345041952_HH9"/>
Amount:	<input type="text" value="372.000"/>
Unit:	<input type="text" value="Gram (g)"/>
Date added*:	<input type="text" value="2022-12-12 15:19:53"/>
Last measured date:	<input type="text"/>
Last measured user:	<input type="text" value=""/>
Item operation:	<input type="text"/>
Item note:	<input style="height: 30px;" type="text" value="3"/>
Item Log type:	<input type="text" value=""/>
Item Log Message:	<input type="text"/>

Fig. 16: Updating an Item

7.3.5 Show Logs

If any item has an associated log, it can be accessed by selecting the **Show Logs button**, which is located in the **Action column** of the **Items panel**.

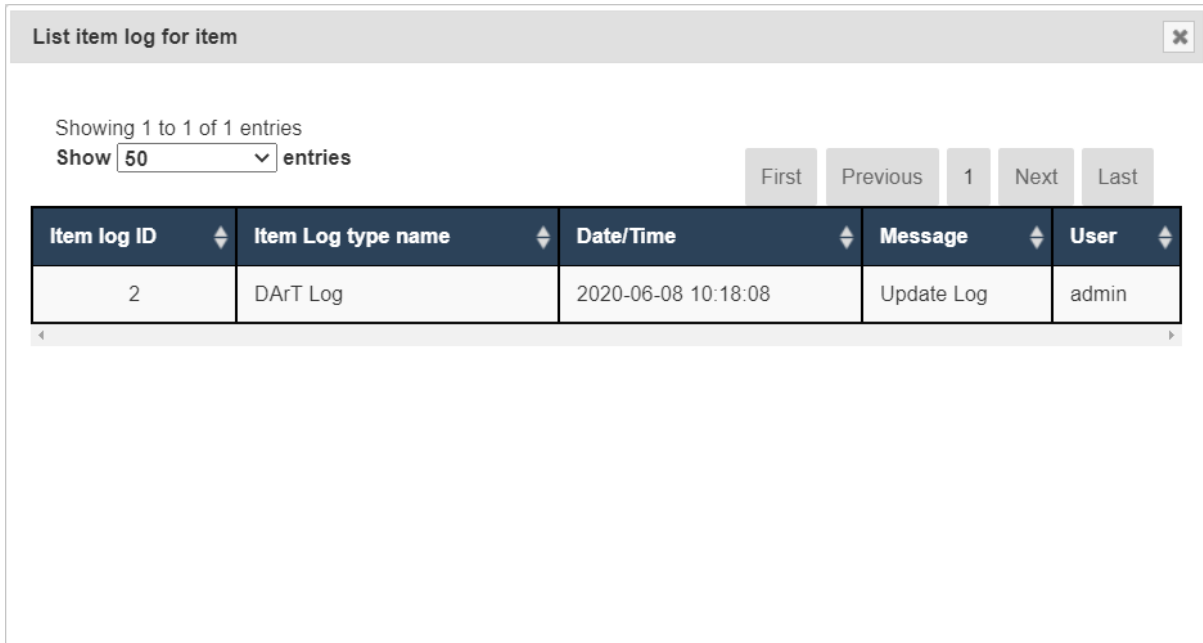


Fig. 17: Showing Item Logs

7.3.6 Splitting an Item

Single items can be split to create multiple new items. An example of this might be if a seed bag is split into two bags.

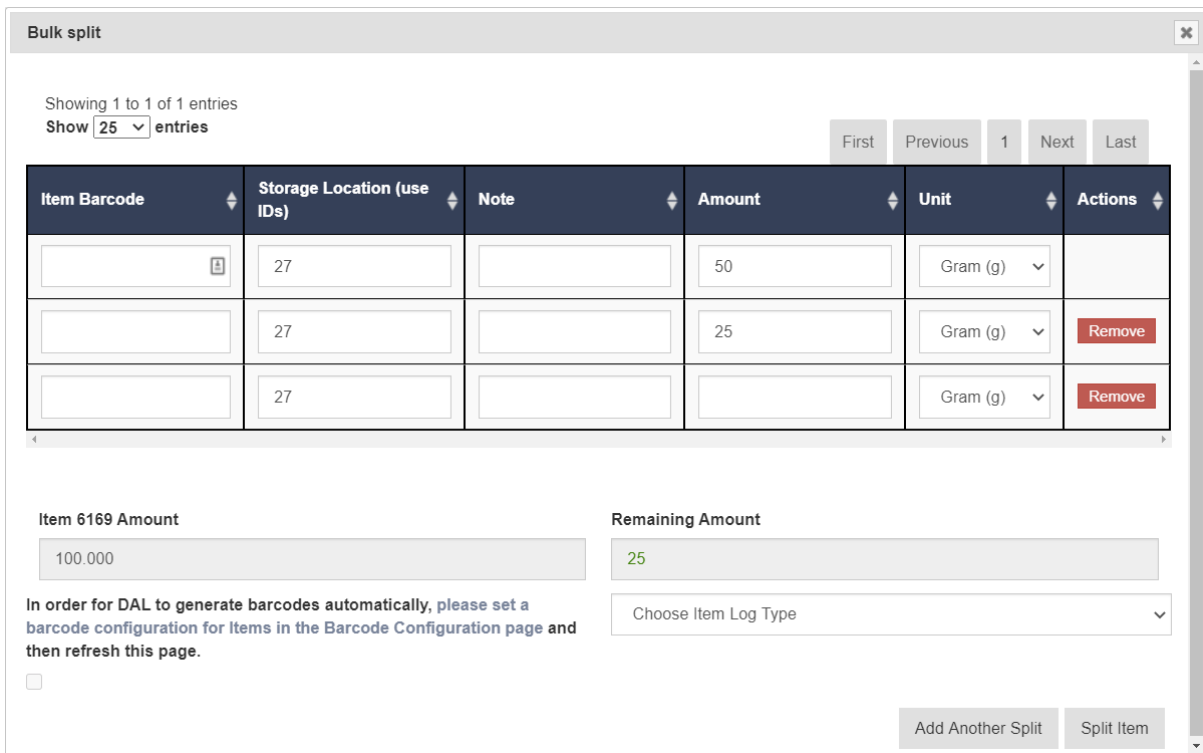



Fig. 18: Splitting an Item

Table 8: Splitting an Item

Step	Action
1.	When items have been listed, choose an item to be split and select the  Bulk Split button. This will open the Split window where splitting options can be selected (see the table below for more information).
2.	Enter a barcode for the new item (if required). Select Automatically generate Barcodes checkbox if required. There is a link for the Barcode Configuration page which enables users to generate barcodes automatically. Continue with the other parameters for the new item which are a storage location ID, note (if required), and weight. Adjust the unit from the dropdown menu if required.
3.	More than one new items can be created at the same time. If you want to split into more than one item, select the Add Another Split button to create a new row for a new item. Continue by creating as many items as required.
4.	As you split the existing into more items, watch the Remaining Amount field , which shows the amount of the existing item remaining.
5.	Choose an item log option from the Choose Item Log Dropdown menu if required.
6.	Select the Split Item button to confirm the item split and the creation of new items.

The two tables below contain information about the fields contained in the **Split Item window**. The first table (the fields in **1** in the image) are for newly created items from an item split, and the second table outlines the fields for updating the existing item that is being split.

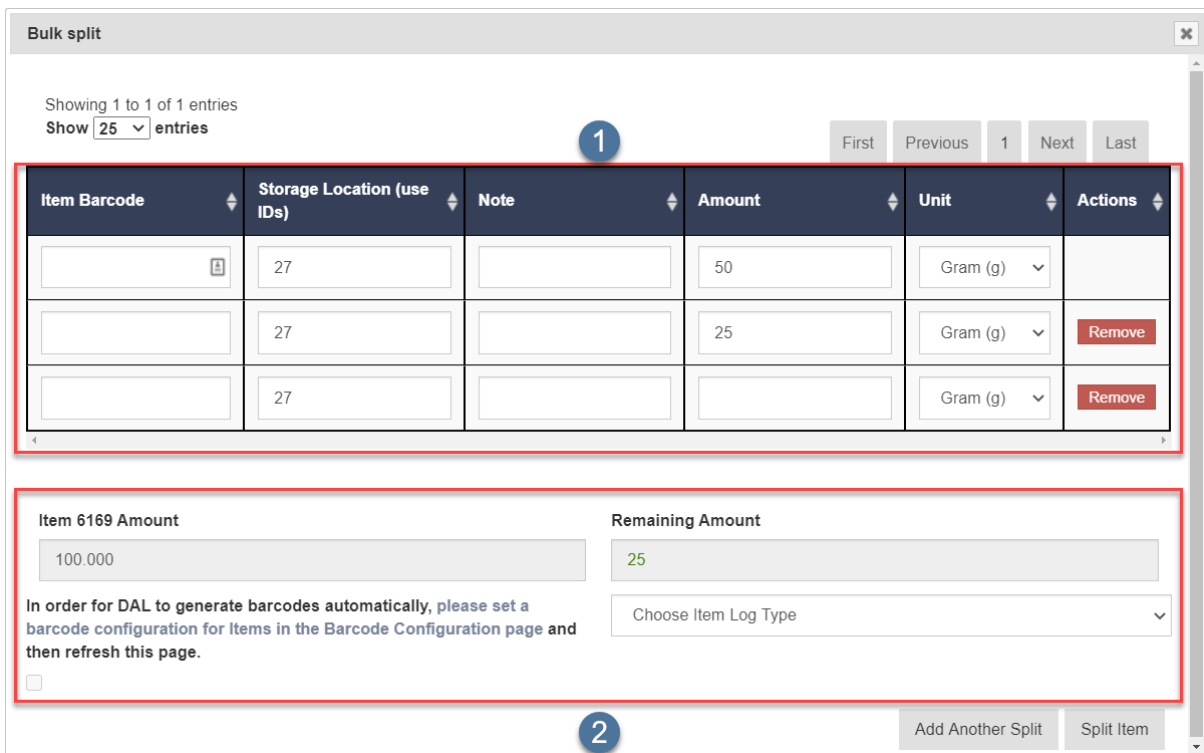


Fig. 19: Splitting an Item - New and Existing Item Fields

Table 9: Newly Split Items

Field	Manually	Description
Item Barcode		A barcode to identify the item.
Storage Location (use IDs)		The ID of the storage location that new item will be stored in.
Note		Note attached to the item.
Amount	Manually	New amount. The total split amount cannot exceed the original item amount.
Unit		Unit of the new item (such as grams). By default, this will be the original item unit.

Table 10: Existing Item

Field	Manually	Description
Item Amount		The amount of the original item that is remaining after splitting.
Remaining Amount		The remaining amount of the original item calculated from the rows above. The remaining amount cannot be below 0.
Barcode Generate Check-box		New items will have their barcode generated if a barcode configuration has been specified. If a row has a barcode filled in manually, the manual barcode will overwrite the automatically generated barcode.
Item Log		The item log type that will be added to the log of new items and original item.

Note: Item splitting is a two-step process. Firstly, the new items will be created. Secondly, the original item will be updated if the new items are successfully added. This means if there is a connection interruption to DAL, the original item amount update may fail, and the user will need to update the original item manually.

7.3.7 Merging Items

Items of the same specimen and item type can be merged to create a new item with a specified amount. See the images and tables below for instructions and more information:

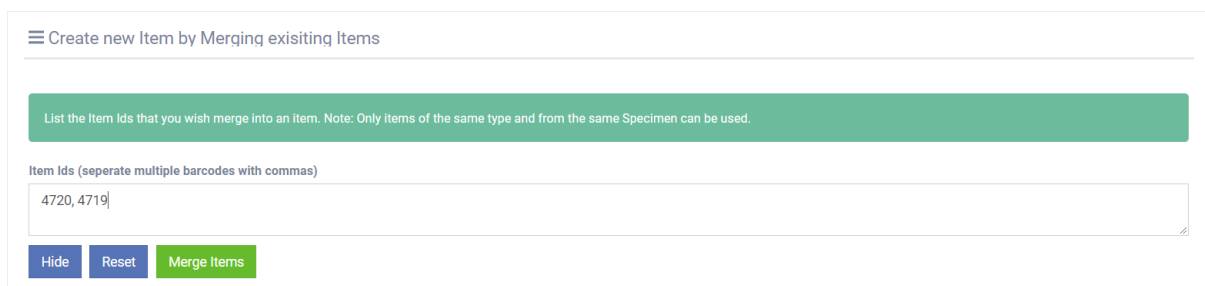


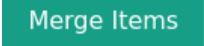


Fig. 20: Merge Items Panel

Table 11: Merging Items (1/2)

Step	Action
1.	When items have been listed, choose an item to be split and select the  Bulk Split button. This will display the item ID in the Merge Items panel as seen in the image above.
2.	Enter the item ID of any additional items in the Merge Items panel and separate each ID with a comma. Alternatively, user can select  for each item that is included in the merge.
3.	After all items have been chosen, select the Merge Items button  to display the Merge Items window , as seen in the image below.

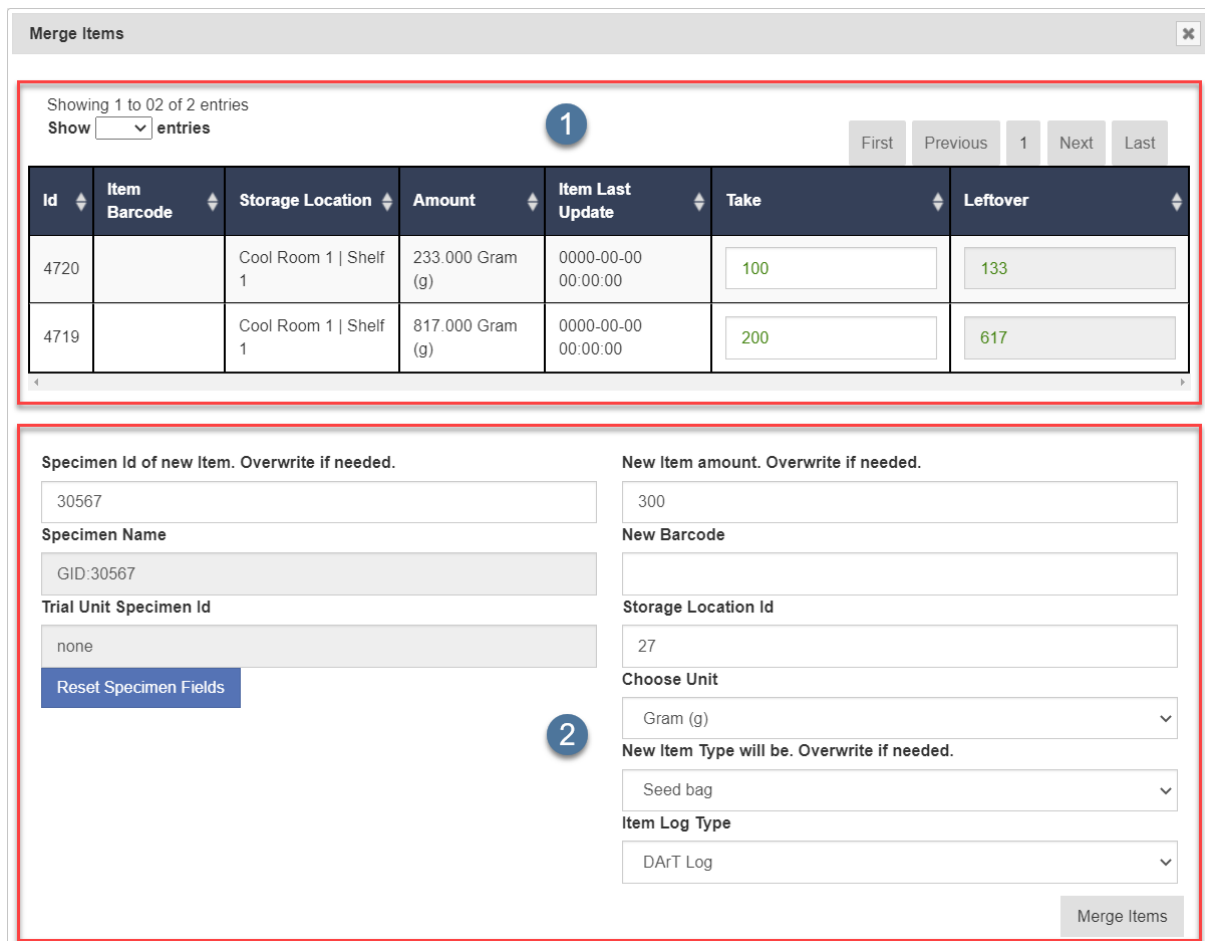


Fig. 21: Merge Items Window

Table 12: Merging Items (2/2)

Step	
1.	All items selected to be merged will be listed in the Merge Item rows (as seen in the image above). From the Take column , enter an amount from each item that will be taken to merge into a new item. In the example above, 100 grams of seeds have been taken from 4720, and 200 grams have been taken from 4719.
2.	The fields below the Merge Item rows present options for the creation of the new item that will result from the item merge. A new specimen ID will be automatically created, but it can be overwritten to create a new one if need be. Continue to fill in other details as required.
3.	Select the Merge Items button to complete the item merge. The newly merged item will now be available in Inventory .

Merge Items
✕

Showing 1 to 02 of 2 entries
 Show entries

First Previous 1 Next Last

Id	Item Barcode	Storage Location	Amount	Item Last Update	Take	Leftover
4720		Cool Room 1 Shelf 1	233.000 Gram (g)	0000-00-00 00:00:00	<input style="width: 80%;" type="text" value="100"/>	<input style="width: 80%;" type="text" value="133"/>
4719		Cool Room 1 Shelf 1	817.000 Gram (g)	0000-00-00 00:00:00	<input style="width: 80%;" type="text" value="200"/>	<input style="width: 80%;" type="text" value="617"/>

Specimen Id of new Item. Overwrite if needed.

Specimen Name

Trial Unit Specimen Id

Reset Specimen Fields

New Item amount. Overwrite if needed.

New Barcode

Storage Location Id

Choose Unit

New Item Type will be. Overwrite if needed.

Item Log Type

Fig. 22: Merge Items Window - New and Existing Item Fields

The two tables below contain information about the fields contained in the **Merge Items window**. The first table (the fields in **1** in the image) are for items to be merged and the second table outlines the fields for creating a new item from the merge.

Table 13: Existing Items

Field	Mandatory	Description
Take		The numerical amount that is to be taken from an item and put into a newly merged item.
Storage Location		A name to identify the storage location.
Leftover		The numerical amount that is leftover after a merge.

Table 14: Newly Merged Item

Field	Mandatory	Description
Specimen ID	Mandatory	Specimen Id of the new item. Normally taken from the merged items. This can be changed but is not recommended.
New Item Amount		The given amount for the new item. This is calculated by the taken amounts above but can be overwritten manually.
New Barcode		The new barcode of the new item. This is not automatically generated.
Storage Location ID		Storage location ID of the new item. Normally in the same storage of the first item in the merge list but can be overwritten manually.
Unit		Unit of the new item.
Item Type	Mandatory	The item type of the new item. This will normally be the same item type as the merged items but can be overwritten manually.
Item Log Type		The item log type that will be added to the log of existing items and new item.

ENVIRONMENT MENU

The KDManage **Environment Menu** contains tools for environmental data. These tools are located within the **Layers Page**.

8.1 Layers Page

Layers refers to the data group that handles environmental data. A layer can cover multiple locations and include multiple attributes for data collection. The **Layers Page** is pictured below:

ID	Site Name	Site Type	Acronym	Manager Name	Start Date	End Date	Action
27	ZDYGDQXAJ	RICFOLGTV	TEST	CUECHCHQFM Tester			Update Site Show Maps for Site Delete Site
26	PODBJLQKC	XNCSNOSKI	TEST	HDMYJHMKEN Tester			Update Site Show Maps for Site Delete Site
7	Test Maca	Breeding station	Test	Diversity Arrays			Update Site Show Maps for Site Delete Site
6	GermanyTest	University	Test	Diversity Arrays			Update Site Show Maps for Site Delete Site
5	Zimba	Breeding station	ZWE	Diversity Arrays			Update Site Show Maps for Site Delete Site
4	Kenya	Breeding station	KEN	Diversity Arrays			Update Site Show Maps for Site Delete Site
3	Tlalizapan	Breeding station	TZ	Diversity Arrays			Update Site Show Maps for Site Delete Site
2	Roseworthy	Breeding station	Rose	Diversity Arrays			Update Site Show Maps for Site Delete Site
1	Narrabri	Breeding station	Narra	Diversity Arrays			Update Site Show Maps for Site Delete Site

Fig. 1: Layers Page

The following table describes the contents of the **Layers Page**:

Table 1: Elements of the Layers Page

Field	Description
ID	A unique system identifier of the layer.
Layer Name	The user provided name of the layer.
Create Date/Time	Create Date/Time of Layer
Action	Provides actions for the relevant layer. See the section below for more information.

The image below is an example of a layer at a site called ‘Narrabri’:

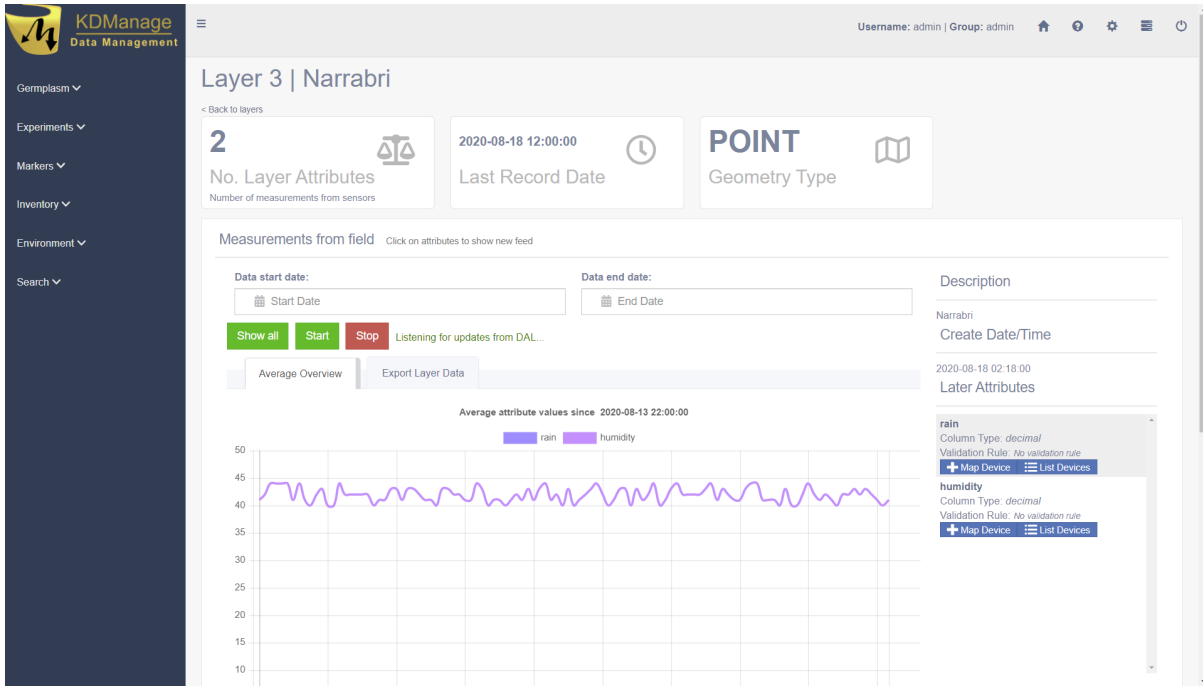


Fig. 2: Layer Example

8.1.1 Layer Actions

The following table lists all the actions that can be performed for the selected Layer in KDManage.

Table 2: Layer Actions

Action	Description	Parent button
View Layer	View layer in a single page. Selecting the layer name from the Layer Name Column will also open the layer in a single page.	
Download	Add a layer attribute (such as rain or humidity) to the layer.	
Edit	List all layer attributes in layer.	View layer
Import Layer Data	Import layer attribute data from a CSV file.	Add a layer attribute to Layer
Export Layer Data	Export layer attribute data to various file formats.	

Note: The presence of action types is dependant upon the *layer state* - not all action types will be available for all layers.

8.1.2 Adding Layers

To add a layer, select the **Add Layer Button** which will display the **Add Layer Window**.

The following image shows the **Add Layer Window**, displaying the description fields:

Fig. 3: Add Layer Window

The fields for the **Add Layer Window** are described in the following table:

Table 3: Add Layer Window Fields

Field	Mandatory?	Description
Layer Name	Mandatory	The name of the layer. A naming convention is suggested (e.g. a concatenation of site, type, date, number).
Layer Alias		An alias for Layers
Layer Type	Mandatory	Either layer, layer2d or layering. These three values refer to the base name of the real layer.
Layer Metadata		Metadata for layers
Is editable?	Mandatory	Flag for whether layer can be edited.
Geometry Type	Mandatory	For internal layers, this is the type of the geometry and have to match OGC standards (POINT, MULTIPOINT, POLYGON .. etc)
Description		Description of the layer.
Access Fields	Mandatory	<i>Access Settings and Permissions</i>

8.1.3 Add Layer Attribute to a Layer

Layer attributes define the measurements that are collected in a layer such as *humidity*. Users can define the size, type, unit name and any validation rule they require.

Fig. 4: Add Layer Attribute Window

The fields for the **Add Layer Attribute Window** are described in the following table:

Field	Mandatory?	Description
Unit	Mandatory	Unit of uploaded data (refer to the <i>Units</i> topic).
Attribute Column Name	Mandatory	Name of attribute e.g. rain.
Attribute Column Type	Mandatory	Type of attribute.
Attribute Column Size	Mandatory	Data size of attribute data.
Validation Rule		Validation rule.
Attribute Column Unit Name	Mandatory	Unit name of column.

8.1.4 Import Data to a Layer

While most environmental data will be uploaded via applications like KDSens, users can upload data via CSV through KDManage.

For each layer attribute, users will need to include a column in uploaded CSV.



Fig. 5: Import Layer Data Window

The fields for the **Import Layer Data Window** are described in the following table:

Field	Mandatory?	Description
Layer data file	Mandatory	File of layer data to be imported.
Geometry Column	Mandatory	The column in the CSV that contains the geometry of each data point.
Time Stamp	Mandatory	The column in the CSV that contains the timestamp of each data point.
All Layer Attributes in Layer Columns	Mandatory	Each layer attribute (<i>RAIN</i> and <i>HUMIDITY</i> in the above example) will appear as a field and users will need to specify each column in the CSV for each layer attribute. Users may not skip any of the layer attributes.

8.2 Layers Page

Single layers can be viewed as a single view which includes a live feed of the average attribute values from a set time.

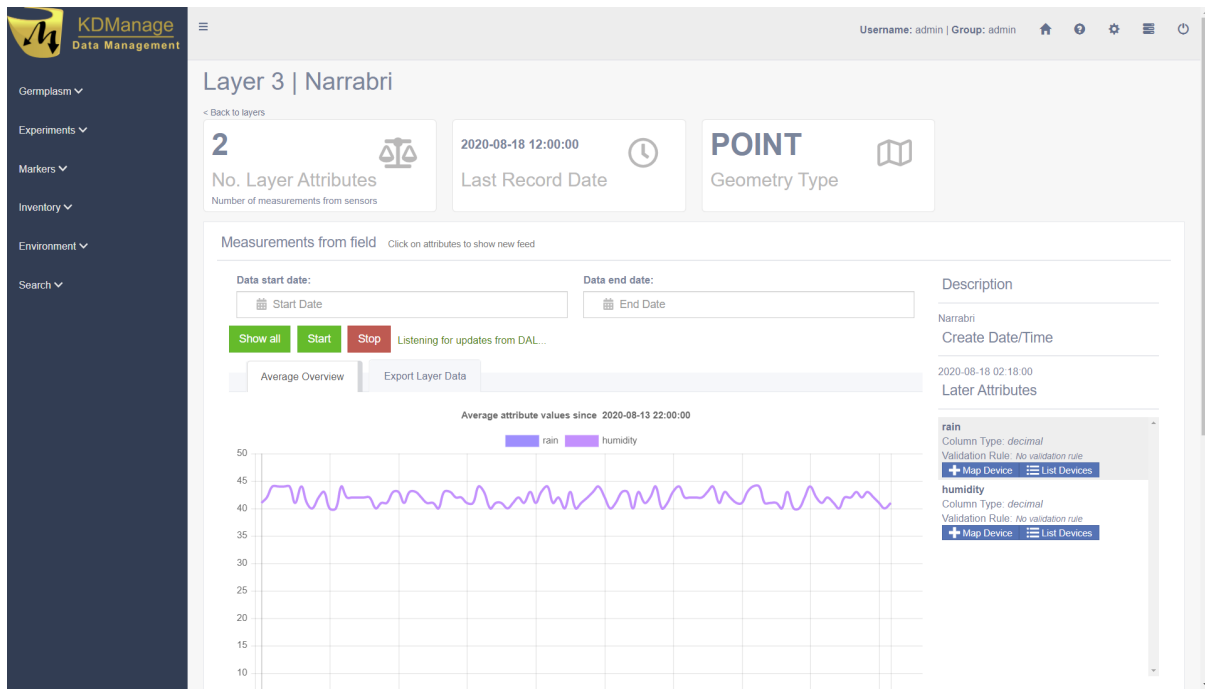




Fig. 6: Layer Example

The live feed of the layer data can be started by pressing the  **Start Button** and stopped by pressing the  **Stop Button**.

8.2.1 Map Device to Attribute

Devices can be mapped to an attribute. This connects a device (usually a sensor) to a layer attribute which specifies the device that is collecting data for an attribute.

To map a device to an attribute, select the **Map Device Button** for the appropriate attribute as seen in the image below:

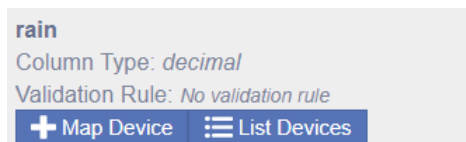


Fig. 7: Mapping a Device

That will open the **Map Device Window** as seen in the image below:

Fig. 8: Map Device Window

The fields for the **Map Device Window** are described in the following table:

Table 4: Map Device Window Fields

Field	Mandatory?	Description
Device Id	Mandatory	ID for device. This is not to be confused with Device Register ID.
Parameter	Mandatory	Name of parameter from the device for that attribute.
Is Active	Mandatory	Flag to determine whether mapping is active.

SEARCH MENU

The KDManage **Search Tool** enables users to search for various entries across the different data sets which are:











- Trial data (all four data sets combined);
- Inventory data;
- Ancestor data;
- Genotype trait data; and
- Genotype specimen data.

KDManage features two search methods which are described in the following sections:

- *Standard Search*
- *CSV Search*

9.1 Standard Search





A *Standard Search* allows users to search through data that is already available in KDManage, with a table for each of the data sets that are listed in the above section. An example of a typical search table for trial data can be seen in the image below:

Trial Data - Advanced Combined Search								
		Genotype Id	Genotype Name	Average Trait Value	Trait Unit Name	Trait Name	Trial Name	Site Name
+		7249513	FB04-117	5140.2		GRAIN_YIELD	FB04	Narrabri
+		7249513	FB04-117	7.768		HEIGHT	FB04	Narrabri
+		7249512	FB04-116	4947.2		GRAIN_YIELD	FB04	Narrabri
+		7249512	FB04-116	8.51		HEIGHT	FB04	Narrabri
+		7249511	FB04-115	5317.4		GRAIN_YIELD	FB04	Narrabri
+		7249511	FB04-115	8.696		HEIGHT	FB04	Narrabri
+		7249510	FB04-114	5220.0		GRAIN_YIELD	FB04	Narrabri
+		7249510	FB04-114	5.916		HEIGHT	FB04	Narrabri
+		7249509	FB04-113	5326.8		GRAIN_YIELD	FB04	Narrabri
+		7249509	FB04-113	5.812		HEIGHT	FB04	Narrabri

Page 1 of 1,193 | 10 | View 1 - 10 of 11,922

Fig. 1: Search Table for Trial Data

Table 1: Searching Data with the Standard Search

Step	Action
1.	Navigate to the Standard Search Page in KDManage. There should be a set of tables (like the image above) - one for each of the data sets.
2.	Select the  Search Button to open the Search Window as illustrated in the image below.
3.	Choose the search parameters and then select the  Search Button to display results in the browser.
4.	To edit the search, select the  Search Button to display the Search Window again. Additional search parameters can be added or removed here with the + Add Button or - Remove Button . You can also edit existing parameters here or select the Reset Button to clear all search parameters.
5.	When the search has been finalised, you can also select the  Download Button to download the search data as a CSV file.

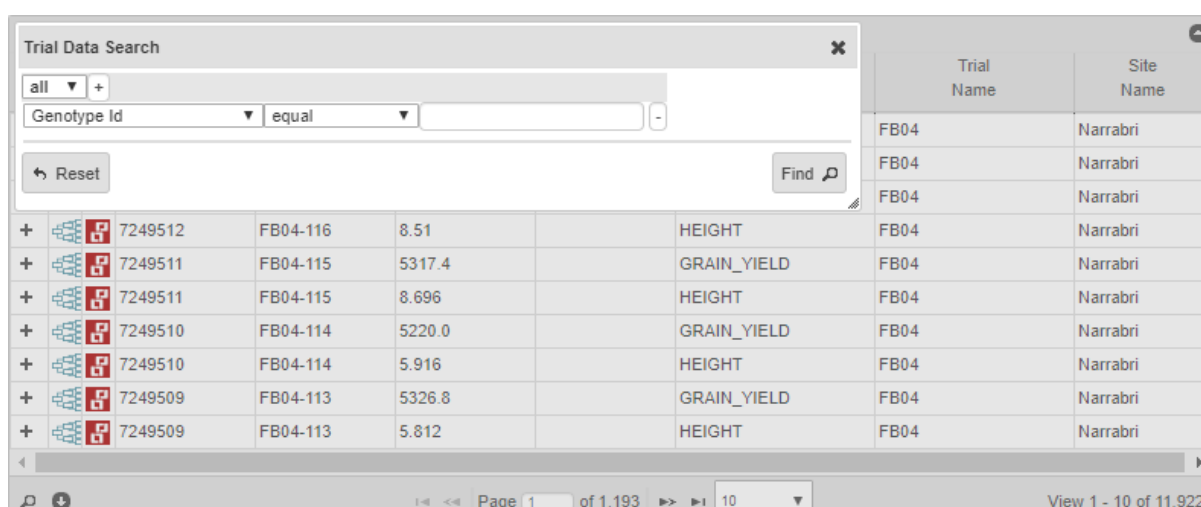



Fig. 2: Search Filter Example

Note: CSV results are limited to 50,000 entries.

9.1.1 The Pedigree Tree

Depending on the table being used, table rows can be expanded for more information. This is illustrated in the image below which shows the **Pedigree Tree** for a genotype in the ancestor data by selecting the  **Pedigree Button**.

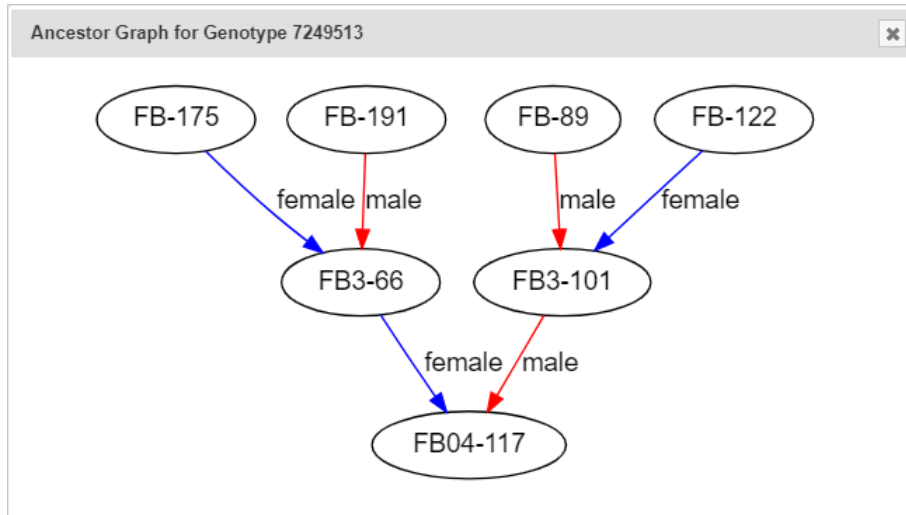


Fig. 3: Pedigree Tree

9.2 CSV Search


A search can also be performed on a single CSV column. The CSV search is similar to the standard search except results are filtered to match a column from an uploaded CSV file. A small section of an example CSV file is shown below:

K	L	M	N	O
entity_name	TraitId	GenotypeName	GenotypeId	SpecimenId
geno_avg_trait_val	9	GID:3567668	3567668	3567668
geno_avg_trait_val	9	GID:5398338	5398338	5398338
geno_avg_trait_val	9	GID:5525159	5525159	5525159
geno_avg_trait_val	9	GID:5592544	5592544	5592544
geno_avg_trait_val	9	GID:5686308	5686308	5686308
geno_avg_trait_val	9	GID:5686524	5686524	5686524
geno_avg_trait_val	9	GID:5686525	5686525	5686525
geno_avg_trait_val	9	GID:5686537	5686537	5686537
geno_avg_trait_val	9	GID:5686545	5686545	5686545
geno_avg_trait_val	9	GID:5686575	5686575	5686575
geno_avg_trait_val	9	GID:5686616	5686616	5686616
geno_avg_trait_val	9	GID:5686762	5686762	5686762
geno_avg_trait_val	9	GID:5686789	5686789	5686789

Fig. 4: Example of CSV Search File

Note: Column names must match the column names of data tables.

Table 2: Searching Data with the CSV Search

Step	Action
1.	Navigate to the Standard Search Page in KDManage and uploading a file by selecting the Choose File Button and selecting a file from your local machine.
2.	<p>Select a column and then a data set from the dropdown menus that appear (as seen in the below image), then select the Search Button.</p>  <p style="text-align: center;">Fig. 5: CSV Search Options</p>
3.	The results table has the same functionality as a standard search. The image below demonstrates CSV search results for <i>GenotypeID</i> .

Genotype Specimen Data								
Genotype Id	Genotype Name	Specimen Name	Pedigree	Genotype Note				
🔍 + Page 1 of 0 10 No records to view								
Inventory Data								
Genotype Id	Item Type Name	Storage Location	Unit Name	Amount	Date Added			
+ 7247652			Gram (g)	725.0	2016-06-15T14:20:00Z			
+ 7247652			Gram (g)	833.0	2016-06-15T14:20:00Z			
+ 7247652					2016-07-18T16:48:10Z			
+ 7247649			Gram (g)	716.0	2016-06-15T14:20:00Z			
+ 7247649			Gram (g)	431.0	2016-06-15T14:20:00Z			
+ 7247649					2016-09-14T10:49:44Z			
+ 7247648			Gram (g)	560.0	2016-06-15T14:20:00Z			
+ 7247648			Gram (g)	624.0	2016-06-15T14:20:00Z			
+ 7247648					2016-09-14T10:49:44Z			
+ 7247646			Gram (g)	649.0	2016-06-15T14:20:00Z			
🔍 + Page 1 of 45 10 View 1 - 10 of 450								
Trial Data - Advanced Combined Search								
	Genotype Id	Genotype Name	Average Trait Value	Trait Unit Name	Trait Name	Trial Name	Site Name	
+ 🌱 📄	7247652	95-ZIZ09	99.5		DAYS_HEADING	Narrabri 2010	Narrabri	
+ 🌱 📄	7247652	95-ZIZ09	147.5		DAYS_MATURITY	Narrabri 2010	Narrabri	
+ 🌱 📄	7247652	95-ZIZ09	6877.5		GRAIN_YIELD	Narrabri 2010	Narrabri	
+ 🌱 📄	7247652	95-ZIZ09	101.1		HEIGHT	Narrabri 2010	Narrabri	
+ 🌱 📄	7247652	95-ZIZ09	3399.6375		GRAIN_YIELD	CIMMYT BIG WHEAT	Narrabri	
+ 🌱 📄	7247649	92-ZIZ09	98.0		DAYS_HEADING	Narrabri 2010	Narrabri	
+ 🌱 📄	7247649	92-ZIZ09	145.0		DAYS_MATURITY	Narrabri 2010	Narrabri	
+ 🌱 📄	7247649	92-ZIZ09	6061.0		GRAIN_YIELD	Narrabri 2010	Narrabri	
+ 🌱 📄	7247649	92-ZIZ09	94.4		HEIGHT	Narrabri 2010	Narrabri	
+ 🌱 📄	7247649	92-ZIZ09	3097.8374		GRAIN_YIELD	CIMMYT BIG WHEAT	Narrabri	
🔍 + Page 1 of 71 10 View 1 - 10 of 709								
Genotype Trait Data			Trait Name			Trait Value		
🔍 + Page 1 of 0 10 No records to view								
Ancestor Data								
Genotype Id	Genotype Name	Ancestor Name	Level	Type				
🔍 + Page 1 of 0 10 No records to view								

Fig. 6: CSV Search Results

Note: At the bottom of the results in the example above, the empty table *Genotype Trait Data* show that no records were found to match entries in the CSV file.