KDManage Documentation

Release 1.10.0

DArT Team

Jun 28, 2024

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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.

CHAPTER

ONE

INTRODUCTION TO KDMANAGE

This help provides an introduction to the KDManage 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 KDManage 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 KDManage 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, KDManage has an important role within the Applications Layer

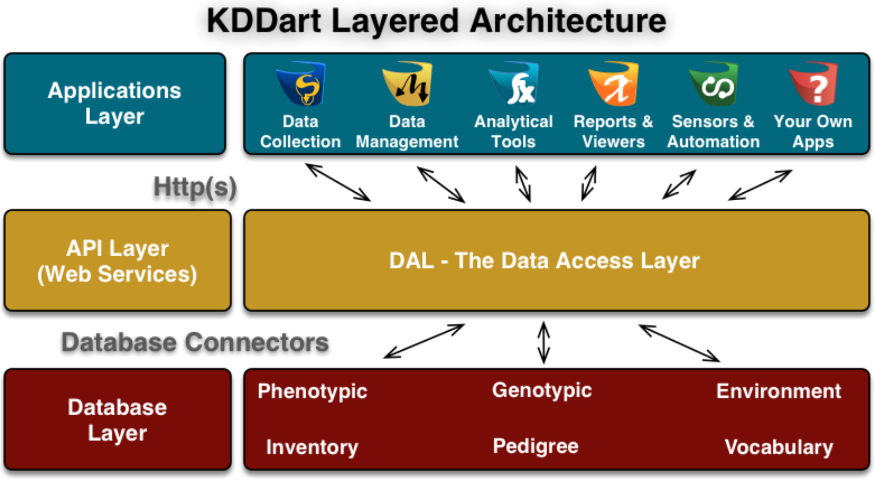


Fig. 1: The KDDart System Architecture

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 exisiting 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.

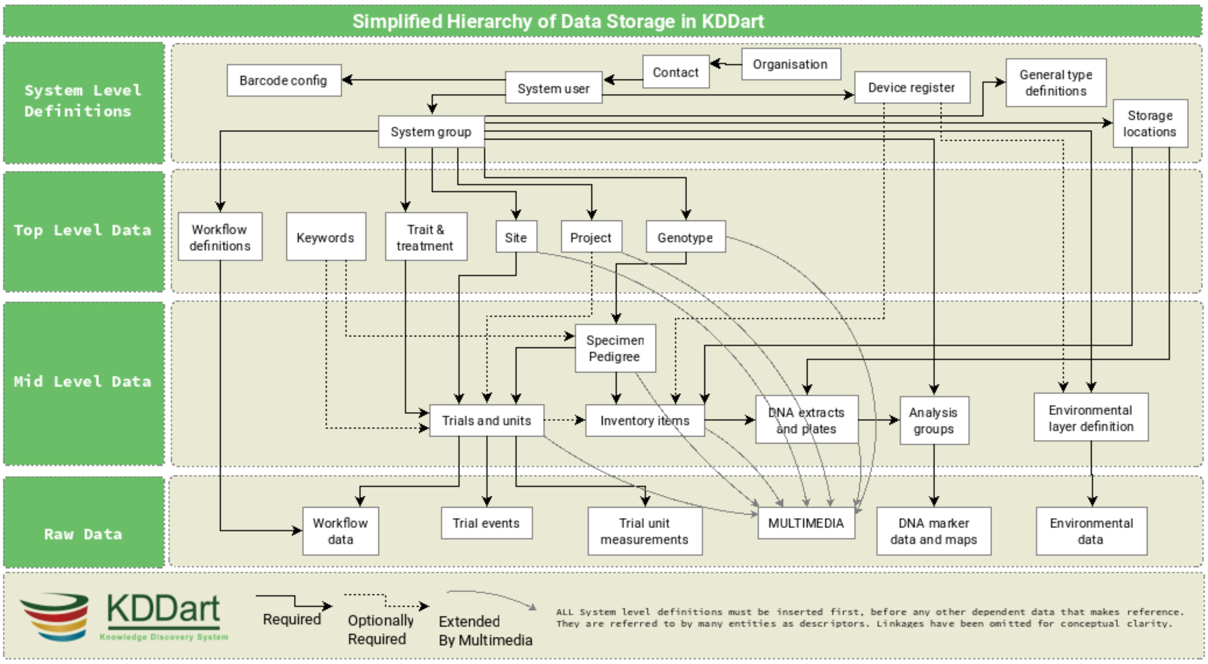


Fig. 2: Simplified hierarchical view of KDDart data dependencies

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 entires 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 onit.

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.

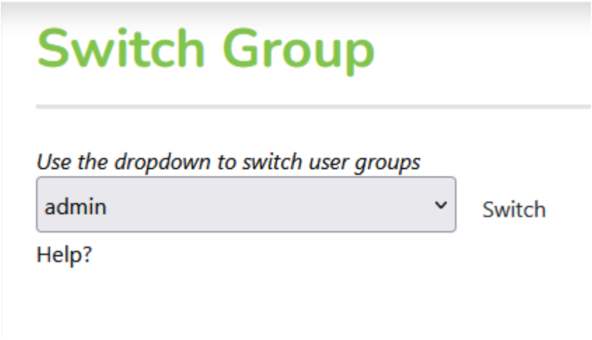
1.7 Login and Switch Group

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.

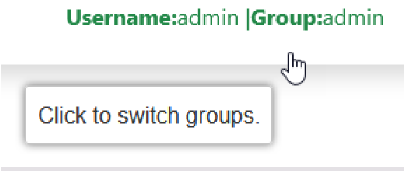


Switch Group

Use the dropdown to switch user groups

Fig. 3: KDManage switch Group selection after login

If you have already logged in and selected a group, select the **Group button** in the **Admin bar** to navigate to the **Switch Group page**.



Username:admin |**Group:**admin

Click to switch groups.

Fig. 4: KDManage Switch Group

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 a 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.

Owner Permission*:

Access Group*:

Access Permission*:

Other Permission*:

Fig. 5: 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 *not* 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.

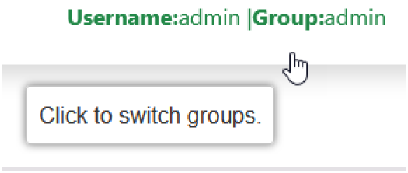


Fig. 6: Admin Bar

Automatic logoff from KDDart may occur following a period of inactivity if the timeout has not been programatically 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 it's 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

CHAPTER

TWO

NEW FEATURES IN V1.10.0

KDManage v1.10.0 marks the beginning of the a major release that includes:

1. Support for DAL v2.7.0
2. Major colour and interface rebrand

2.1 Support for DAL v2.7.0

There will be more features added through future versions of KDManage v1.10.x releases.

- Trial Units can now have multiple treatments.
- Trial Units can now have Trial Factors declared on them.
- Taxonomy object introduced. This can further classify Genotypes.

2.2 Major colour and interface rebrand

- Major rebrand of KDManage towards OneDart suite.
- KDManage v1.10.0 now uses Bootstrap v5.0.2

CHAPTER
THREE

ADMINISTRATIVE SETTINGS

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

Username:admin |**Group:**admin

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*

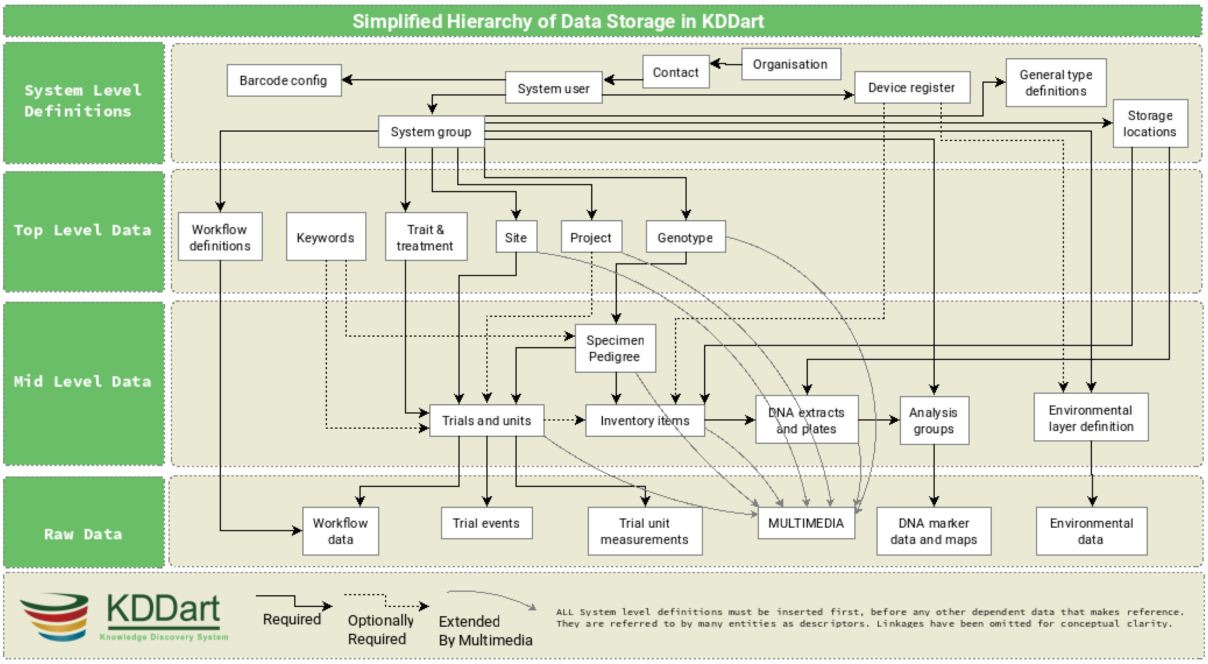
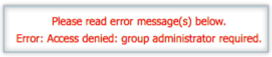


Fig. 2: Simplified Hierarchical View of KDDart Data Dependencies

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

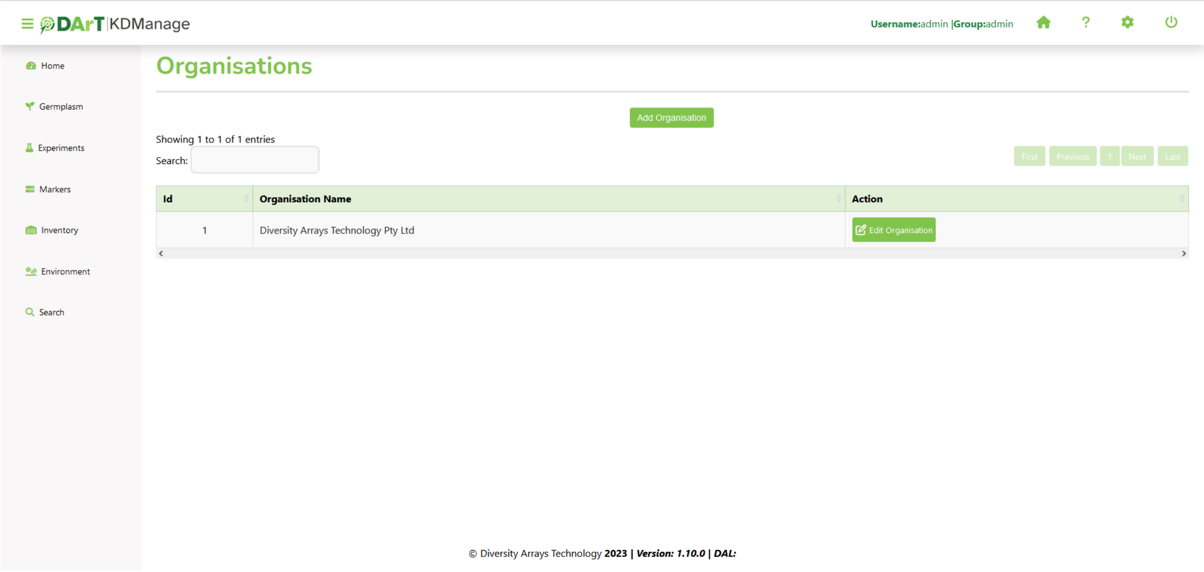


Please read error message(s) below.
Error: Access denied: group administrator required.

Fig. 3: Access Denied Error Message

3.2 Organisations

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



Showing 1 to 1 of 1 entries

Search:

Id	Organisation Name	Action
1	Diversity Arrays Technology Pty Ltd	Edit Organisation

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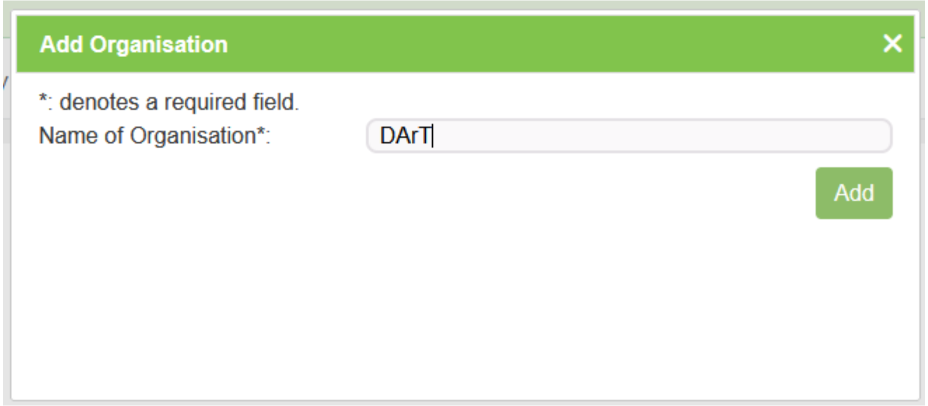
Fig. 4: Organisation Page

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



*: denotes a required field.

Name of Organisation*: DArT

Fig. 5: Adding a New Organisation

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

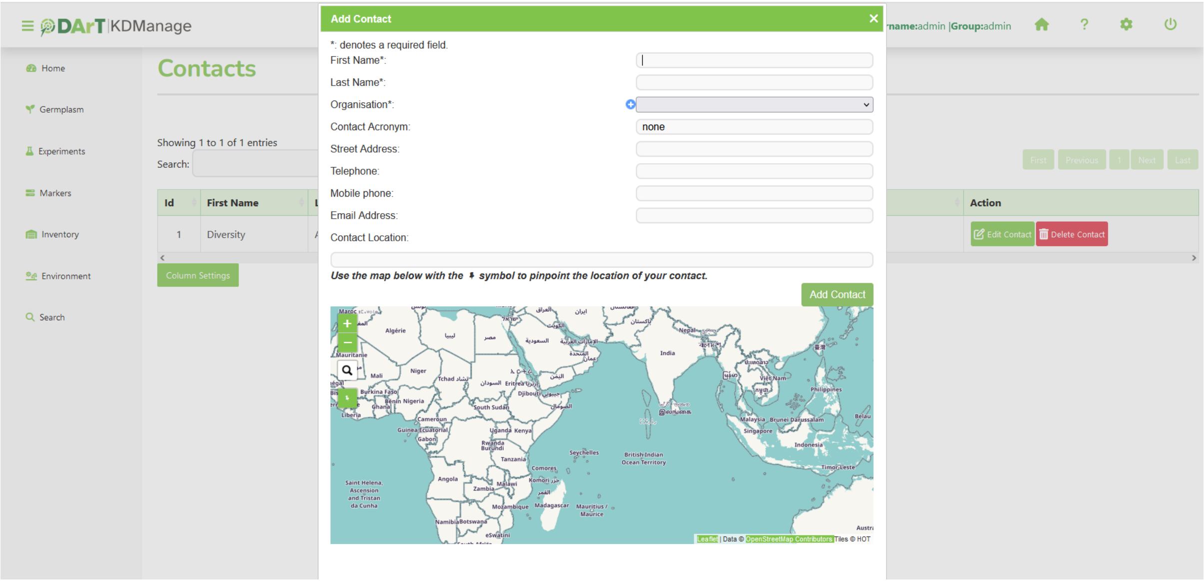
3.3 Contacts

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.



Showing 1 to 1 of 1 entries

Id	First Name	Action
1	Diversity	Edit Contact Delete Contact

*: denotes a required field.

First Name*:

Last Name*:

Organisation*:

Contact Acronym: none

Street Address:

Telephone:

Mobile phone:

Email Address:

Contact Location:

Use the map below with the symbol to pinpoint the location of your contact.

Fig. 6: Adding a New Contact

Table 2: Adding a New Item

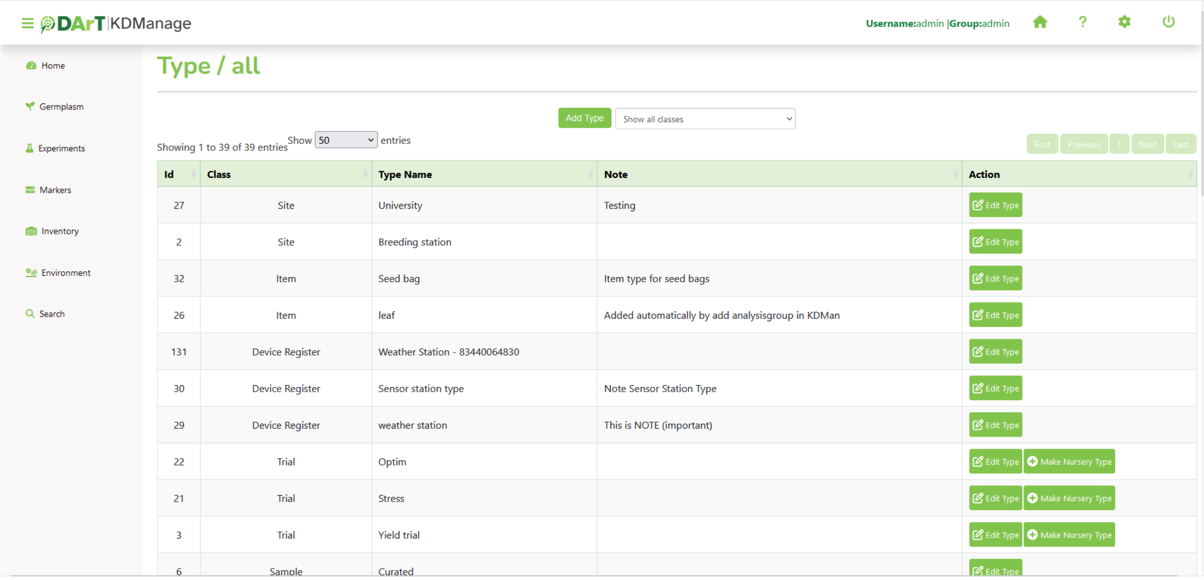
Step	Action
1.	Select the **Add Contact Button** to display the **Add Contact Window**.
2.	Enter all known details about the contact. The *first name*, *last name*, and *organisation* fields are all mandatory.
3.	Select the **Marker Button** from the map and place it on the place that the contact is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



Username:admin |Group:admin

Type / all

Show all classes

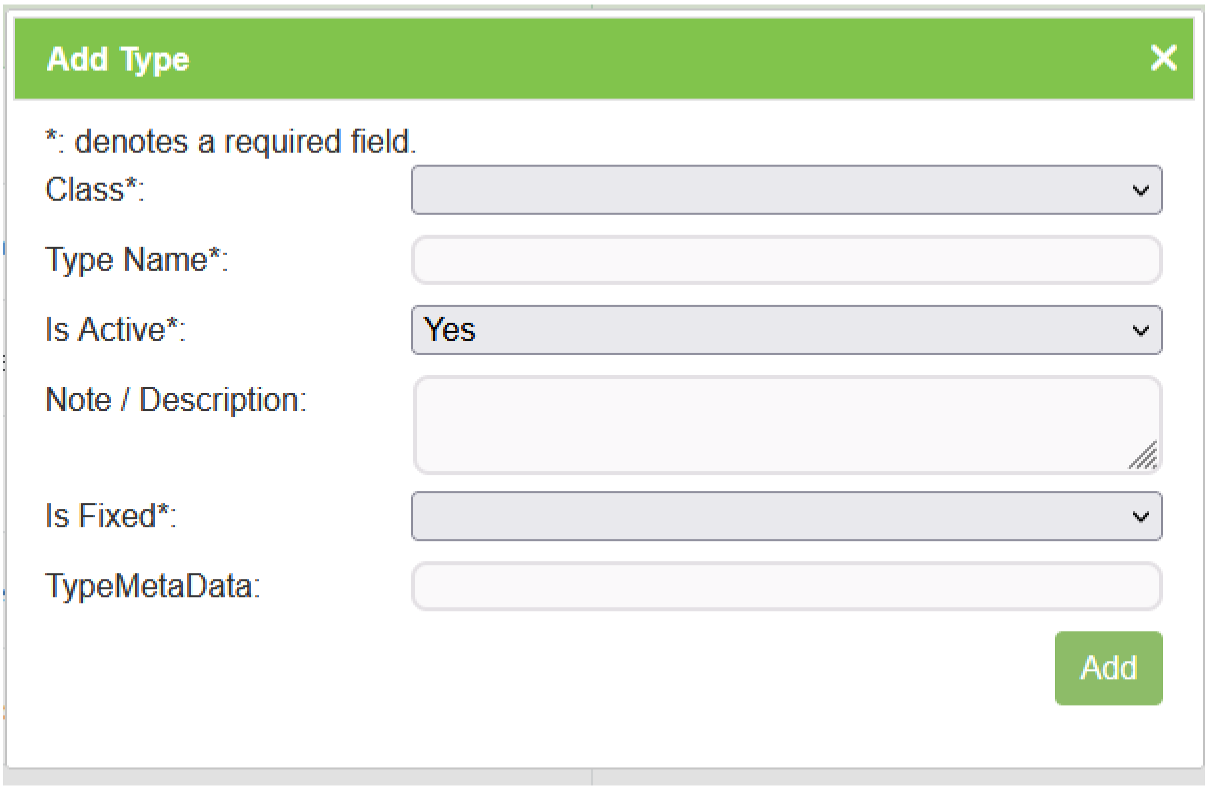
Showing 1 to 39 of 39 entries Show 50 entries

Id	Class	Type Name	Note	Action
27	Site	University	Testing	Edit Type
2	Site	Breeding station		Edit Type
32	Item	Seed bag	Item type for seed bags	Edit Type
26	Item	leaf	Added automatically by add analysisgroup in KDMan	Edit Type
131	Device Register	Weather Station - 83440064830		Edit Type
30	Device Register	Sensor station type	Note Sensor Station Type	Edit Type
29	Device Register	weather station	This is NOTE (important)	Edit Type
22	Trial	Optim		Edit Type Make Nursery Type
21	Trial	Stress		Edit Type Make Nursery Type
3	Trial	Yield trial		Edit Type Make Nursery Type
6	Sample	Curated		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.



Is Active*: Yes

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.

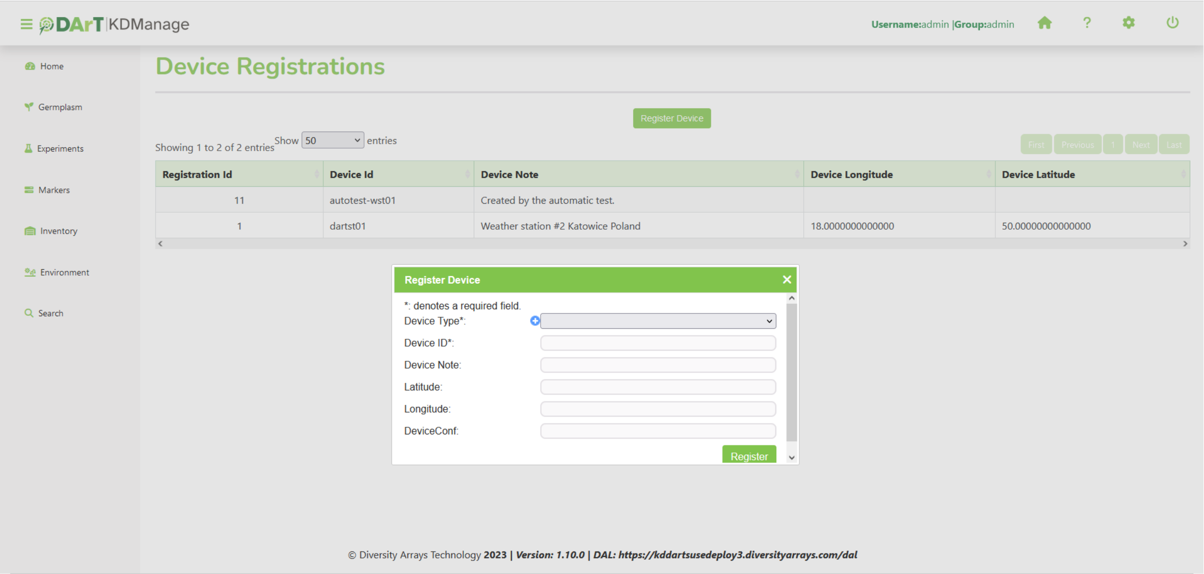
3.5 Device Registrations

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:



Showing 1 to 2 of 2 entries

Registration Id	Device Id	Device Note	Device Longitude	Device Latitude
11	autotest-wst01	Created by the automatic test.		
1	dartst01	Weather station #2 Katowice Poland	18.0000000000000	50.00000000000000

*: denotes a required field.
Device Type*:
Device ID*:
Device Note:
Latitude:
Longitude:
DeviceConf:

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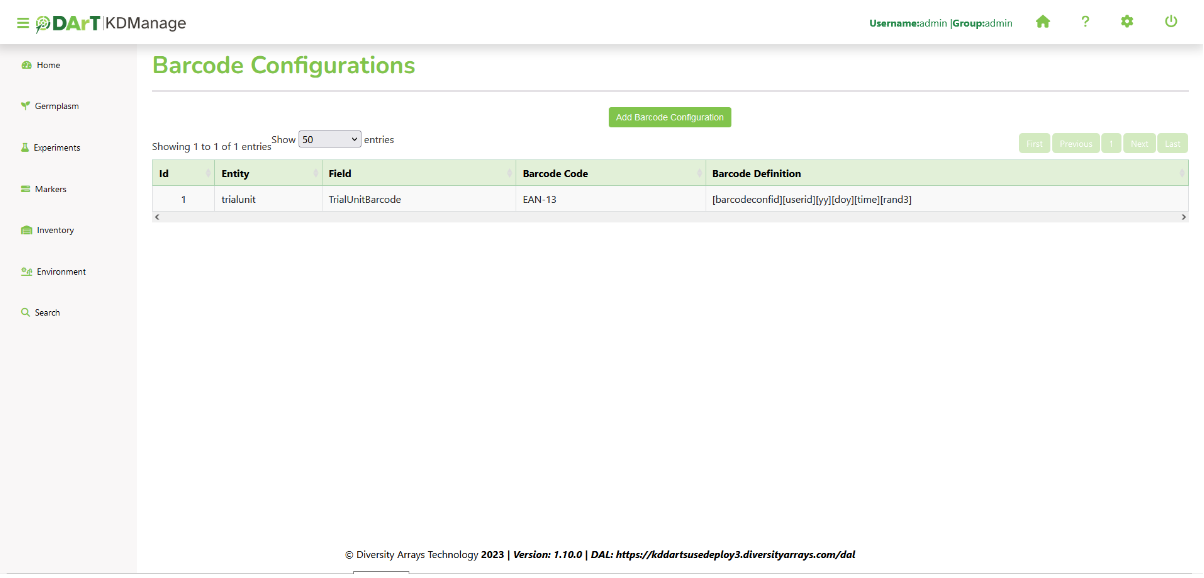
Fig. 9: Registering a Device

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.



Showing 1 to 1 of 1 entries

Id	Entity	Field	Barcode Code	Barcode Definition
1	trialunit	TrialUnitBarcode	EAN-13	[barcodeconfid][userid][yy][doy][time][rand3]

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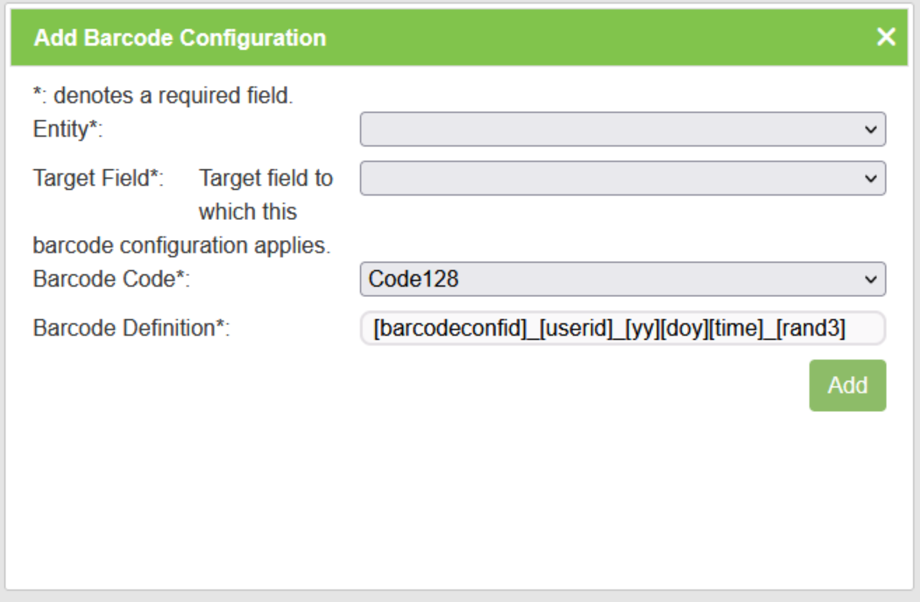
Fig. 10: Barcode Configuration Page

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:



*: denotes a required field.

Entity*:

Target Field*: Target field to which this barcode configuration applies.

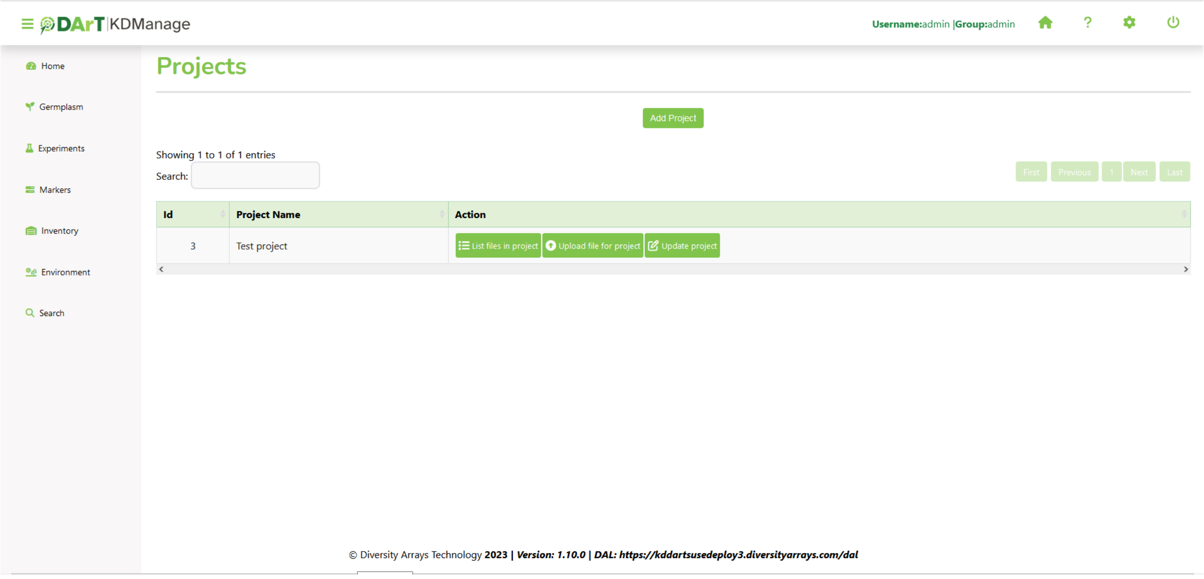
Barcode Code*: Code128

Barcode Definition*: [barcodeconfid]_[userid]_[yy][doy][time]_[rand3]

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**.



Username:admin |**Group:**admin

Projects

Showing 1 to 1 of 1 entries

Search:

Id	Project Name	Action
3	Test project	List files in project Upload file for project Update project

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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**:

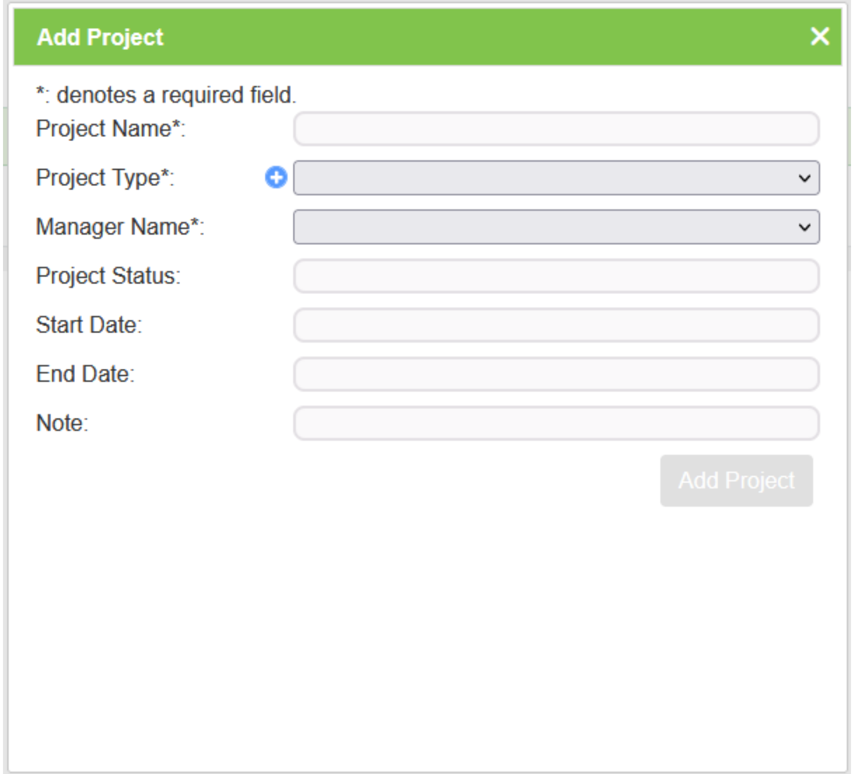
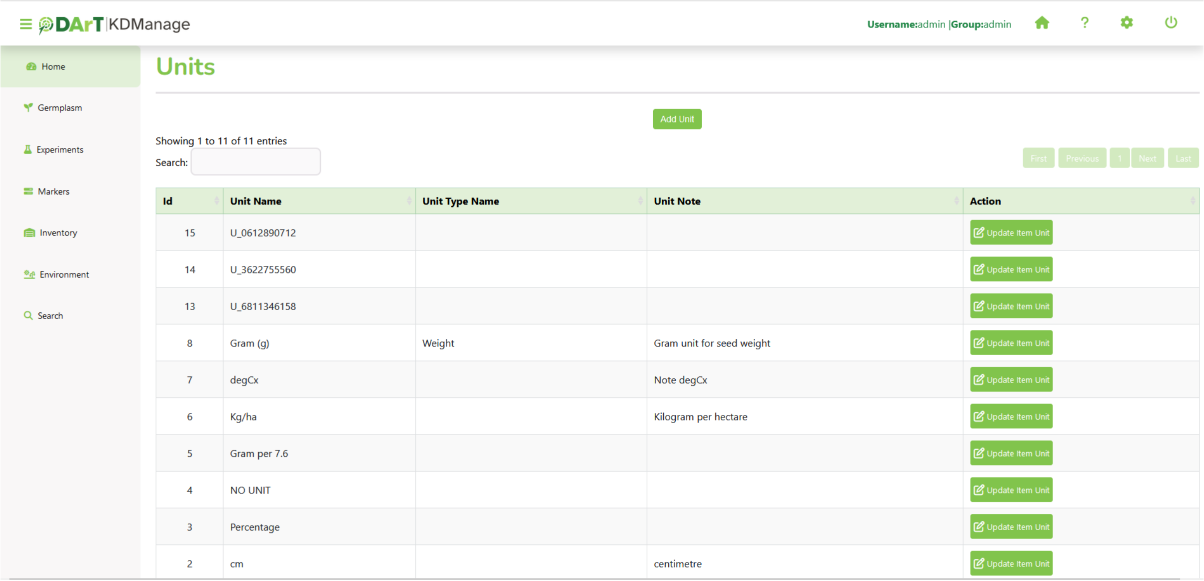


Fig. 13: Adding a New Project

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**:

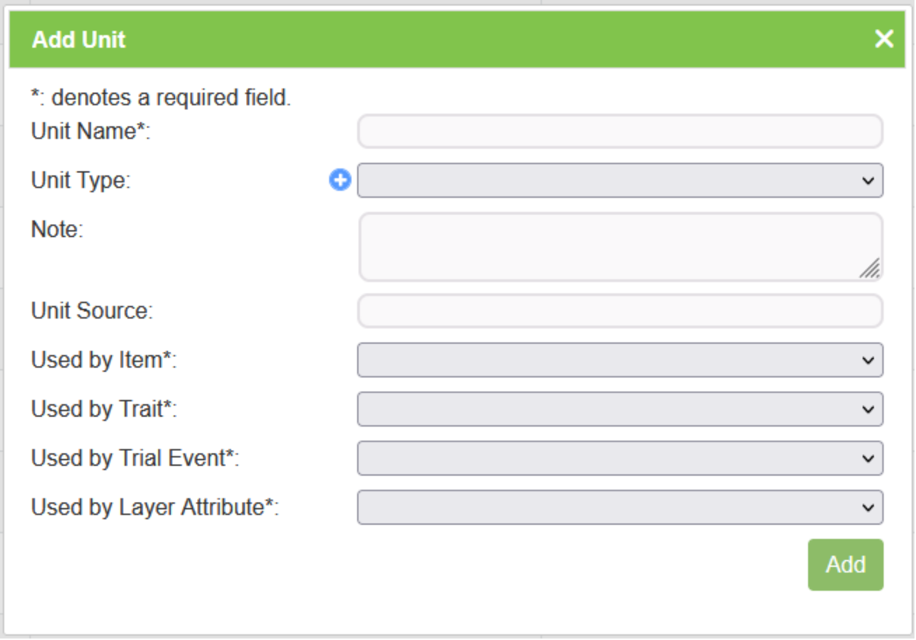


Showing 1 to 11 of 11 entries

Id	Unit Name	Unit Type Name	Unit Note	Action
15	U_0612890712			Update Item Unit
14	U_3622755560			Update Item Unit
13	U_6811346158			Update Item Unit
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

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).

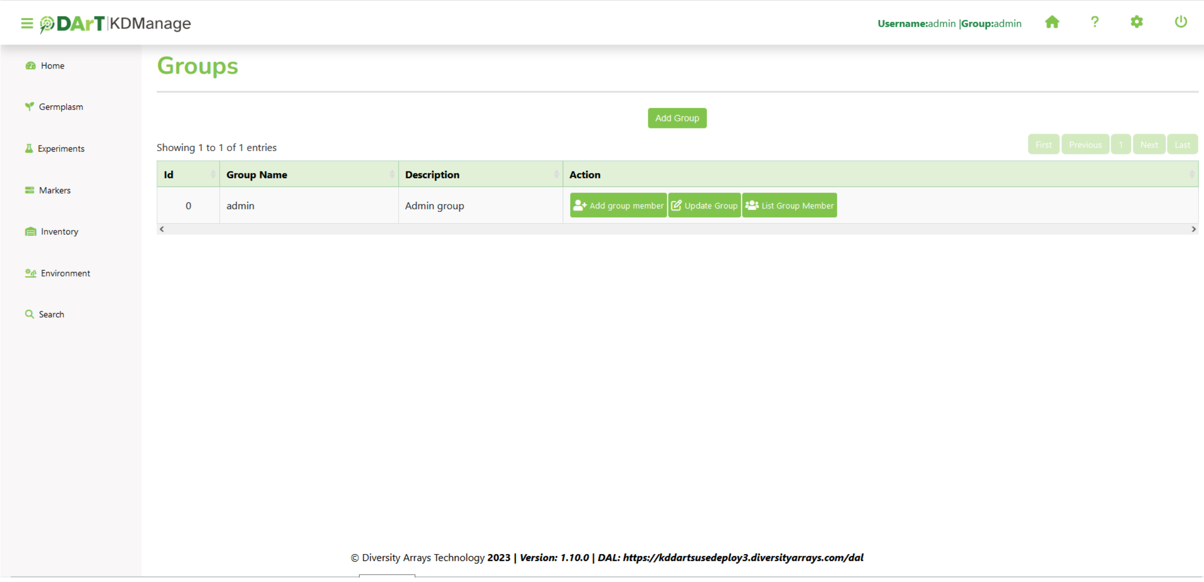


*: denotes a required field.

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.



Showing 1 to 1 of 1 entries

Id	Group Name	Description	Action
0	admin	Admin group	Add group member Update Group List Group Member

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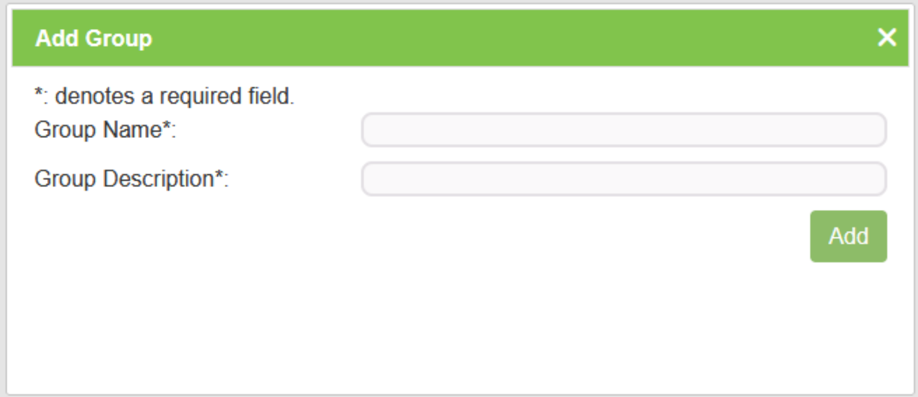
Fig. 16: The Groups Page



*: denotes a required field.

Group Name*:

Group Description*:

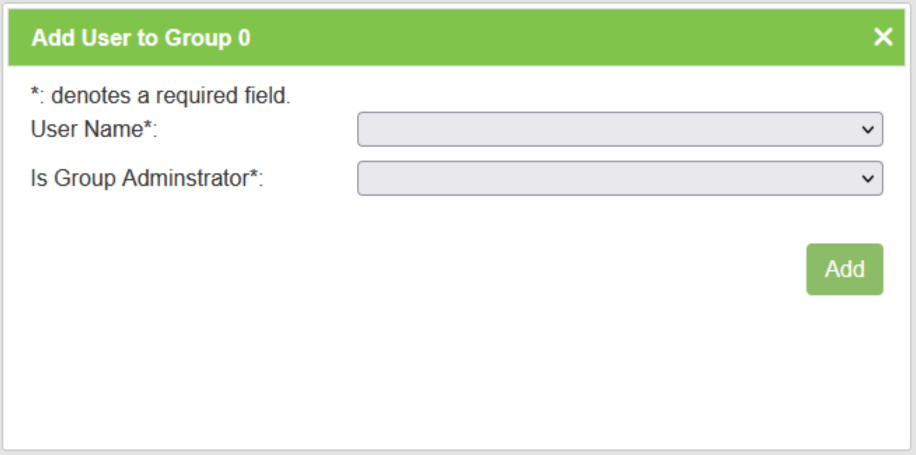
Fig. 17: Adding a New Group

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	Action
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:



Add User to Group 0

*: denotes a required field.

User Name*:

Is Group Adminstrator*:

Fig. 18: Assigning a User to a Group

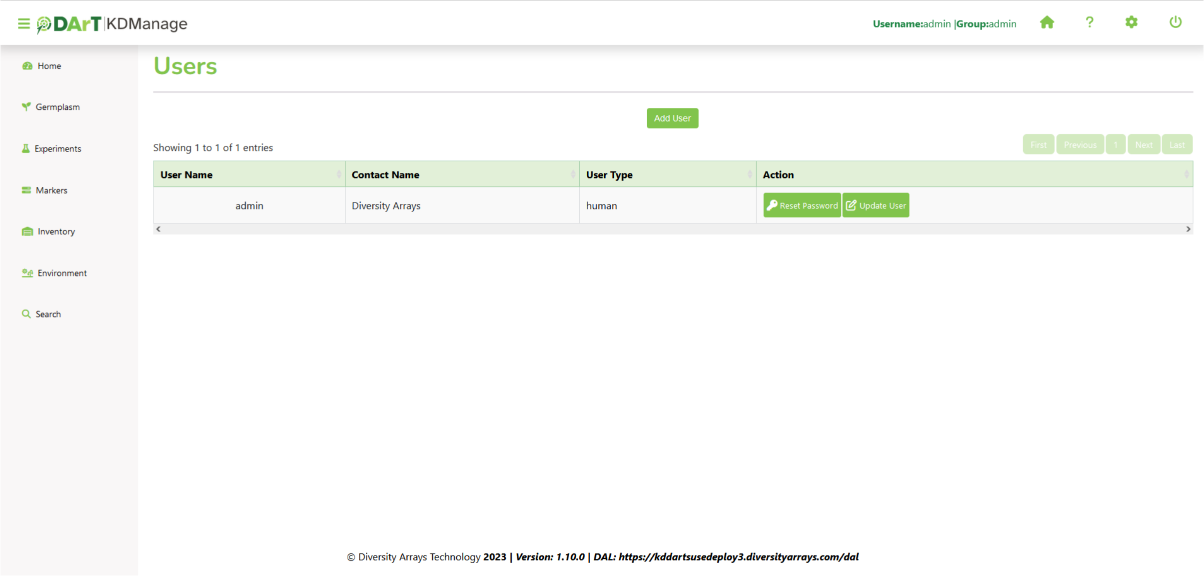
Table 4: Assigning a User to a Group

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:



Users

Showing 1 to 1 of 1 entries

User Name	Contact Name	User Type	Action
admin	Diversity Arrays	human	Reset Password Update User

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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:

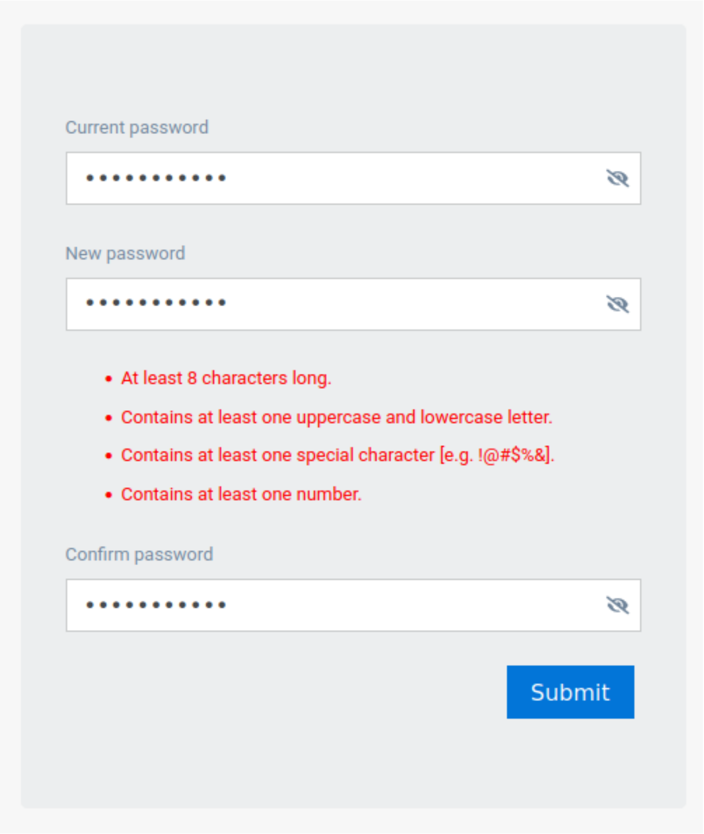
Table 5: Assigning a User to a Group

Task	**Admin and a 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

3.11 User Passwords

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

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



- 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.

Fig. 20: Password reset page

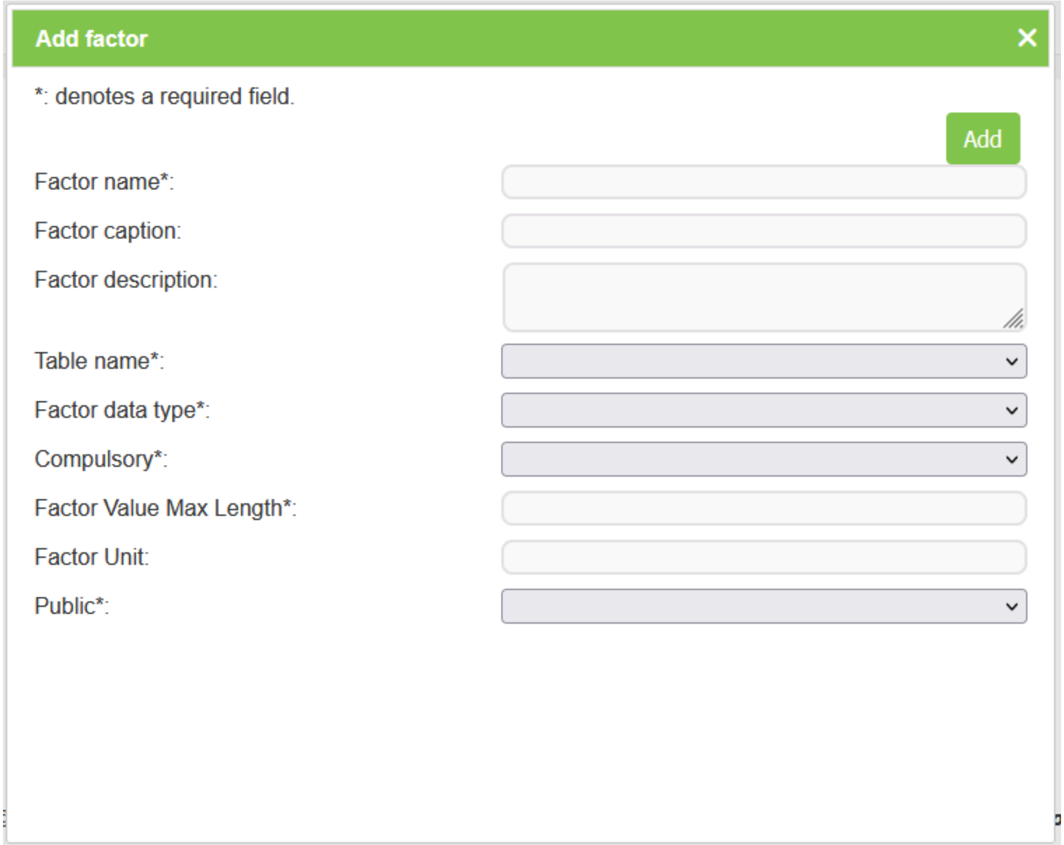
3.12 Factors

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:



Add factor

*: denotes a required field.

Factor name*:
Factor caption:
Factor description:
Table name*:
Factor data type*:
Compulsory*:
Factor Value Max Length*:
Factor Unit:
Public*:

Fig. 21: Adding a New Factor

Table 6: Adding a New Factor

Step	Action
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:

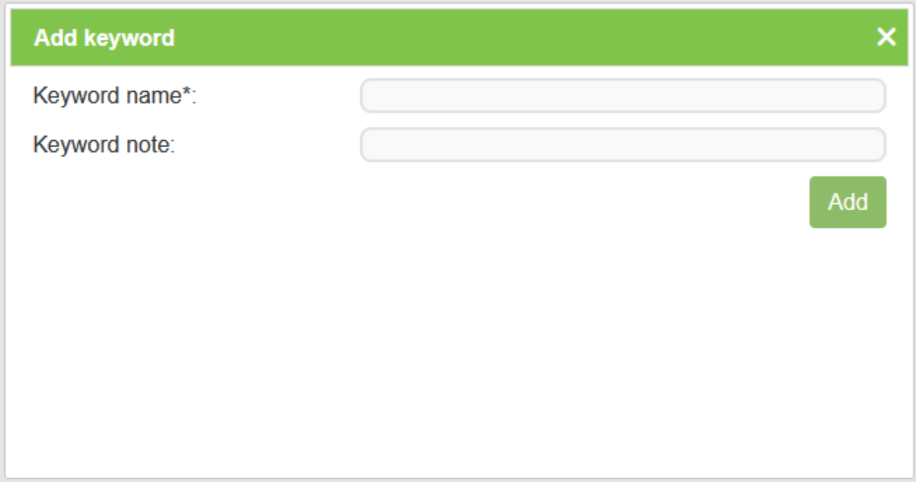
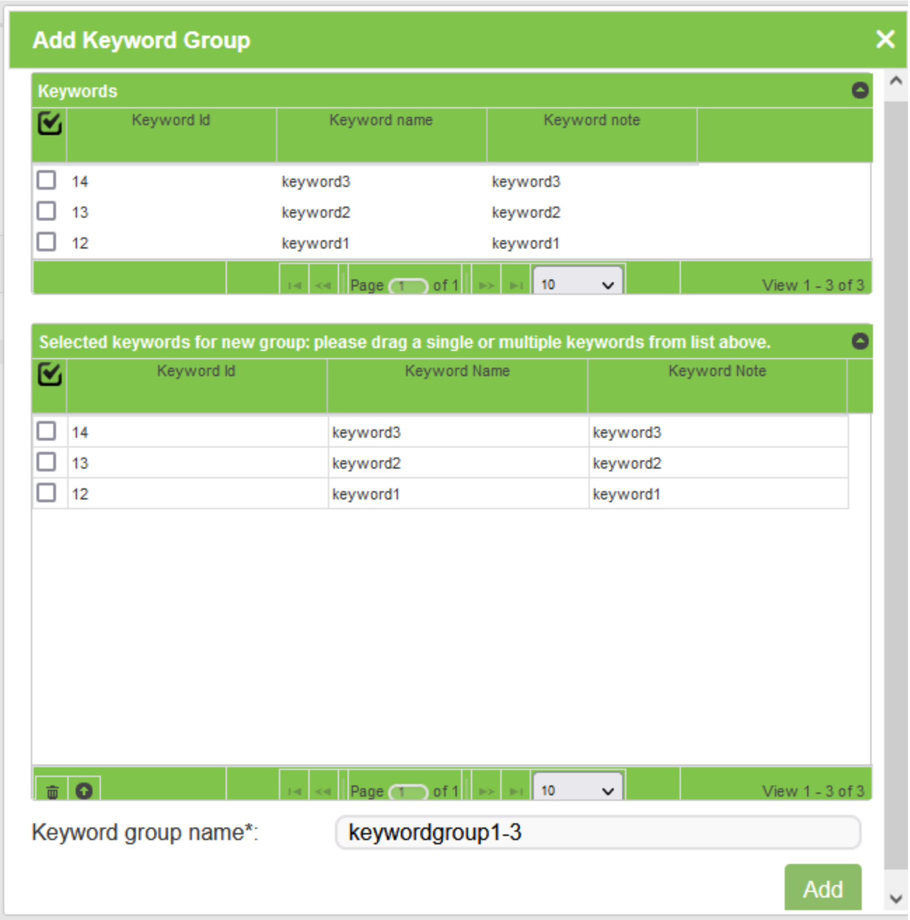


Fig. 22: Adding a New Keyword

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
☐	14	keyword3	keyword3
☐	13	keyword2	keyword2
☐	12	keyword1	keyword1

☑	Keyword Id	Keyword Name	Keyword Note
☐	14	keyword3	keyword3
☐	13	keyword2	keyword2
☐	12	keyword1	keyword1

Keyword group name*: keywordgroup1-3

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:

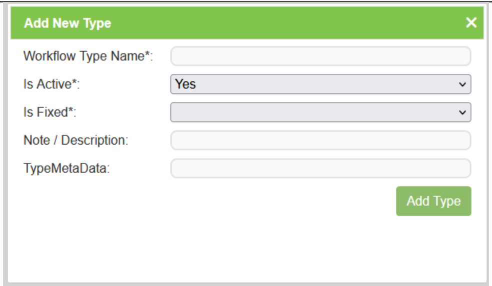
1. Create a workflow type
2. Create a workflow
3. Create the workflow definition
4. Assign a workflow to a trial/nursery

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.

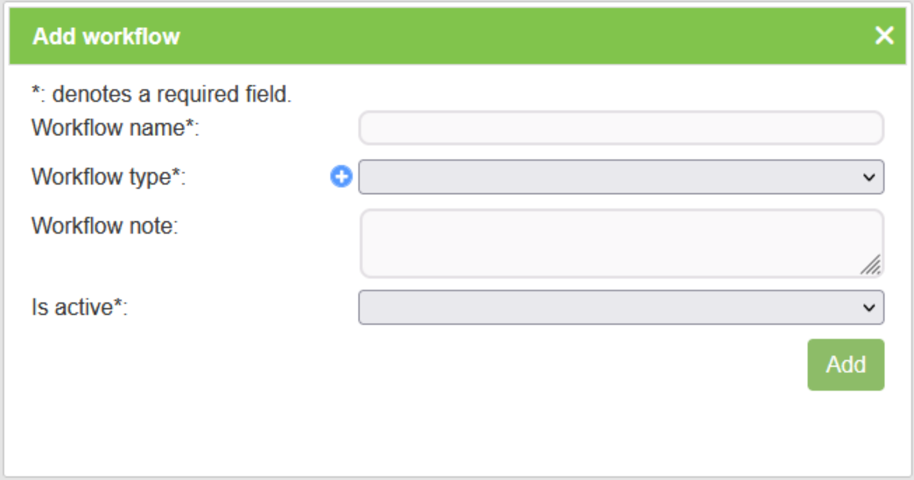
To add a new workflow type, follow these instructions:

Table 8: Creating a Workflow Type

Step	Action
1.	Select the ⚙ **Administrative Settings Button** at top right of any KDManage page, then select the *Types* option from the list.
2.	Select the **Add Type Button**. This will display the **Add Type Window**.
3.	At *Class*, select *Workflow Type*.
	 Add New Type Workflow Type Name*: Is Active*: Yes Is Fixed*: Note / Description: TypeMetaData: Fig. 24: Add a New Class: Workflow Type
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:



*: denotes a required field.

Workflow name*:

Workflow type*:

Workflow note:

Is active*:

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 Step button** for the workflow that you want to add a definition to. This will display the **Add Step to Workflow Window**.
2.	Enter the *step name*, *step order* and optional *step note*.
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 Definitions button**.

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 *Experiments*, then *Trials* to navigate to the **Trials Page**.
2.	At the required trial, select the **Edit Trial button** in the **Action Column** to display the **Update Trial Window**
3.	At the *Current Workflow* 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 **Edit Trial button** 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.

CHAPTER

FOUR

GERMPLASM MENU

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

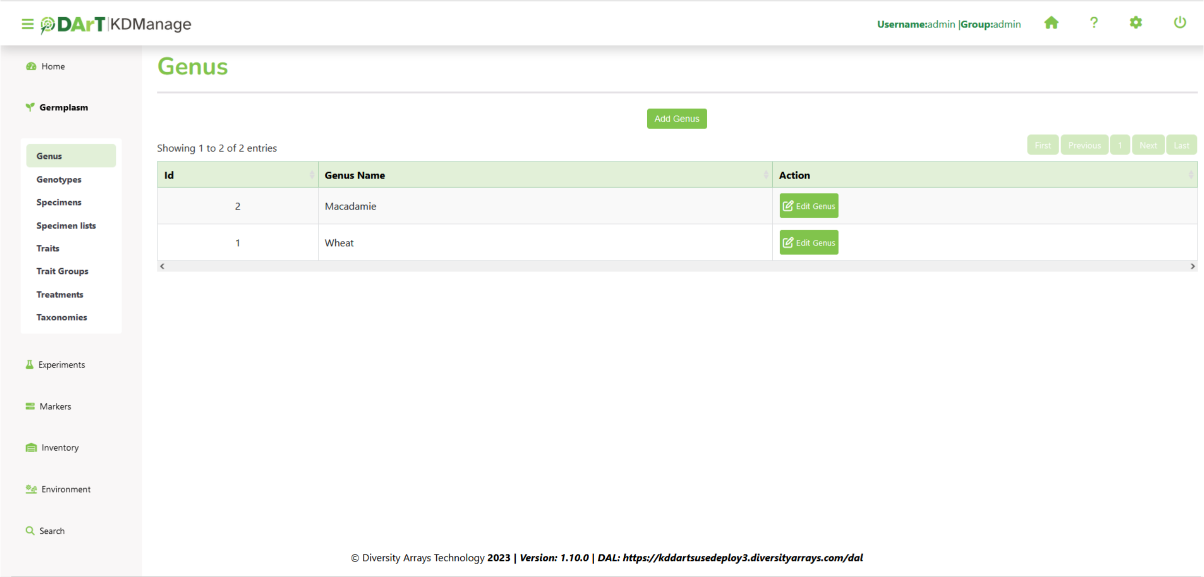
The following pages of the **Germplasm Menu** illustrate the *order of dependency*:

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.



Showing 1 to 2 of 2 entries

Id	Genus Name	Action
2	Macadamie	Edit Genus
1	Wheat	Edit Genus

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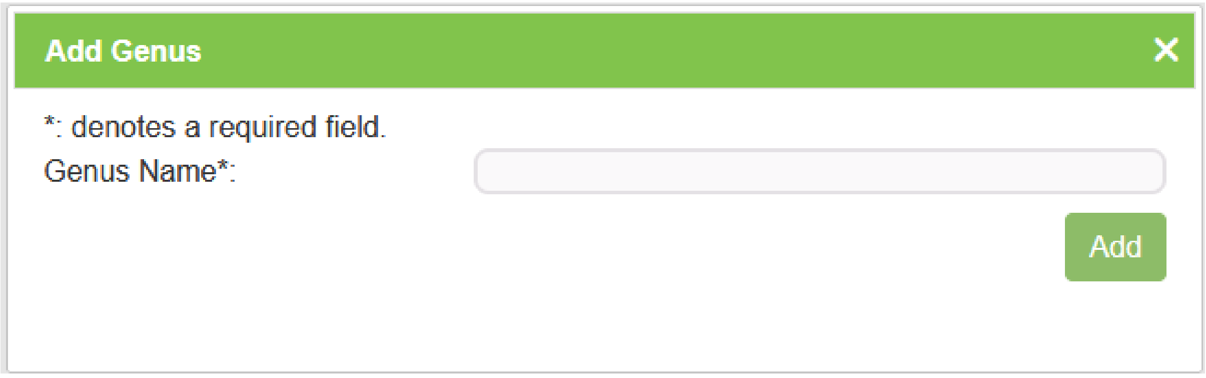
Fig. 1: Genus Page

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:



*: denotes a required field.

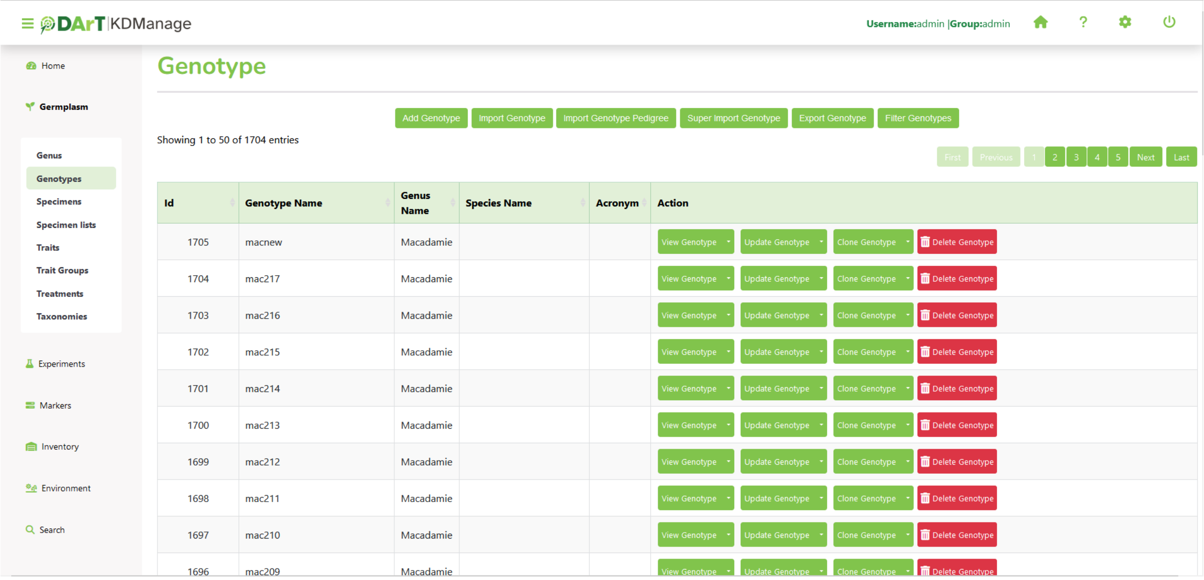
Genus Name*:

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.



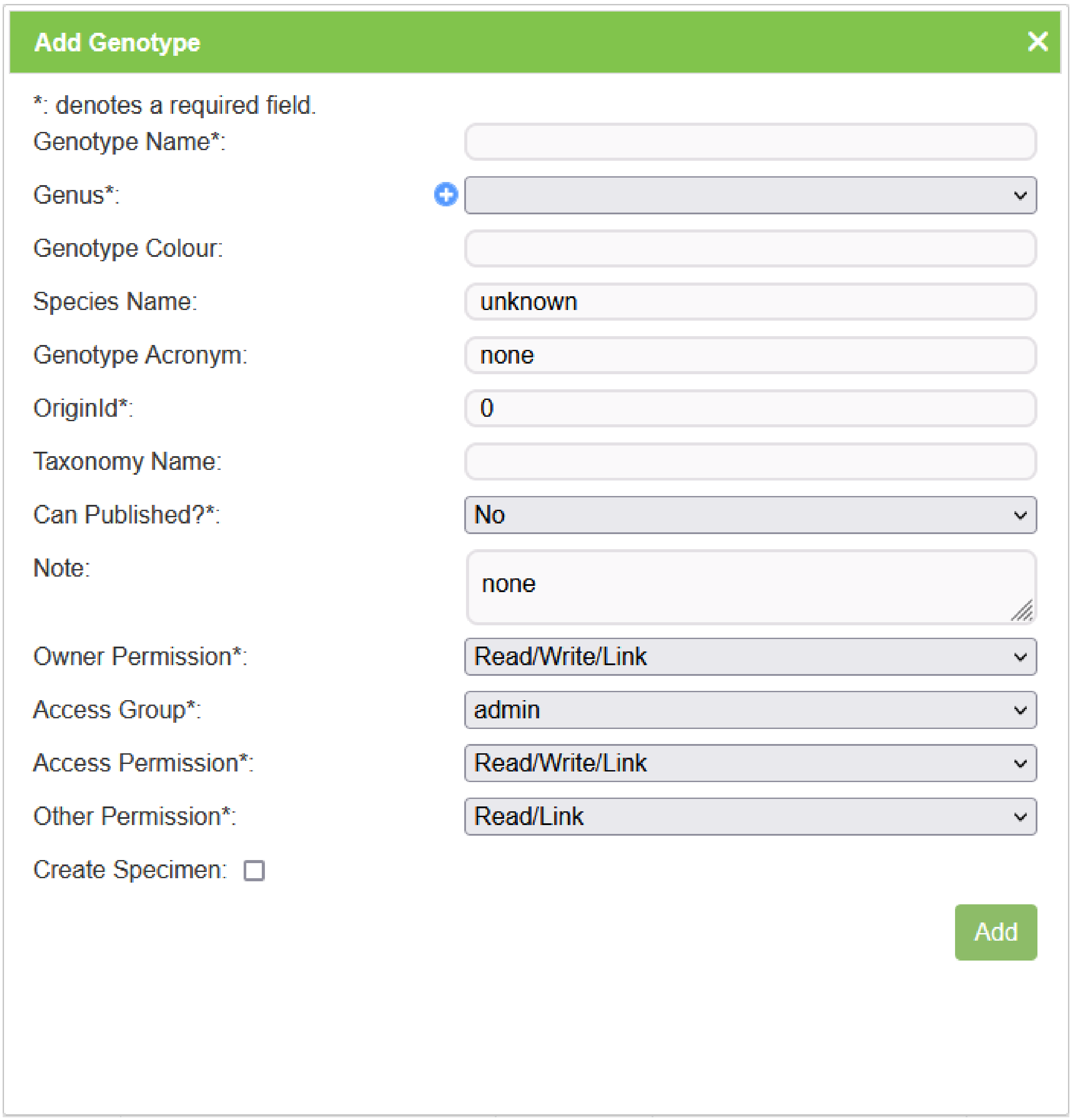
Showing 1 to 50 of 1704 entries

Id	Genotype Name	Genus Name	Species Name	Acronym	Action
1705	macnew	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1704	mac217	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1703	mac216	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1702	mac215	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1701	mac214	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1700	mac213	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1699	mac212	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1698	mac211	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1697	mac210	Macadamie			View Genotype Update Genotype Clone Genotype Delete Genotype
1696	mac209	Macadamie			View Genotype Update Genotype Clone 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:



*: denotes a required field.

Genotype Name*:	
Genus*:	
Genotype Colour:	
Species Name:	unknown
Genotype Acronym:	none
OriginId*:	0
Taxonomy Name:	
Can Published?*:	No
Note:	none
Owner Permission*:	Read/Write/Link
Access Group*:	admin
Access Permission*:	Read/Write/Link
Other Permission*:	Read/Link
Create Specimen:	☐

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 gennotype 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 *Access Settings and Permissions* 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:

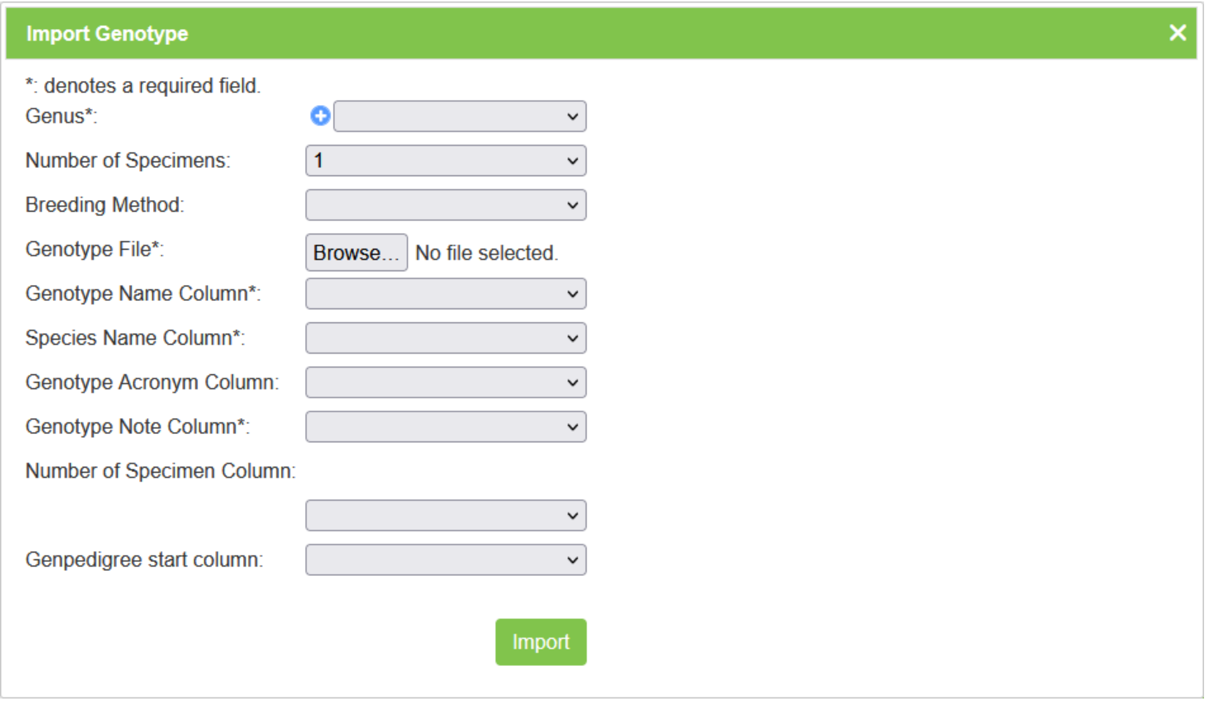
Table 2: Genotype Actions

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 explict 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

*: denotes a required field.

Genus*:	
Number of Specimens:	1
Breeding Method:	
Genotype File*:	No file selected.
Genotype Name Column*:	
Species Name Column*:	
Genotype Acronym Column:	
Genotype Note Column*:	
Number of Specimen Column:	
Genpedigree start column:	

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

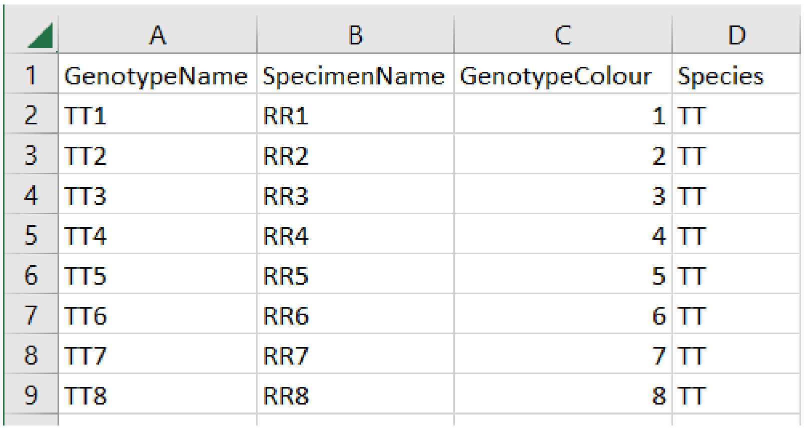
Group	Privilege
Owner (Group used for import)	Read & Write
Access	Read & Link
Public	Read & Link

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:



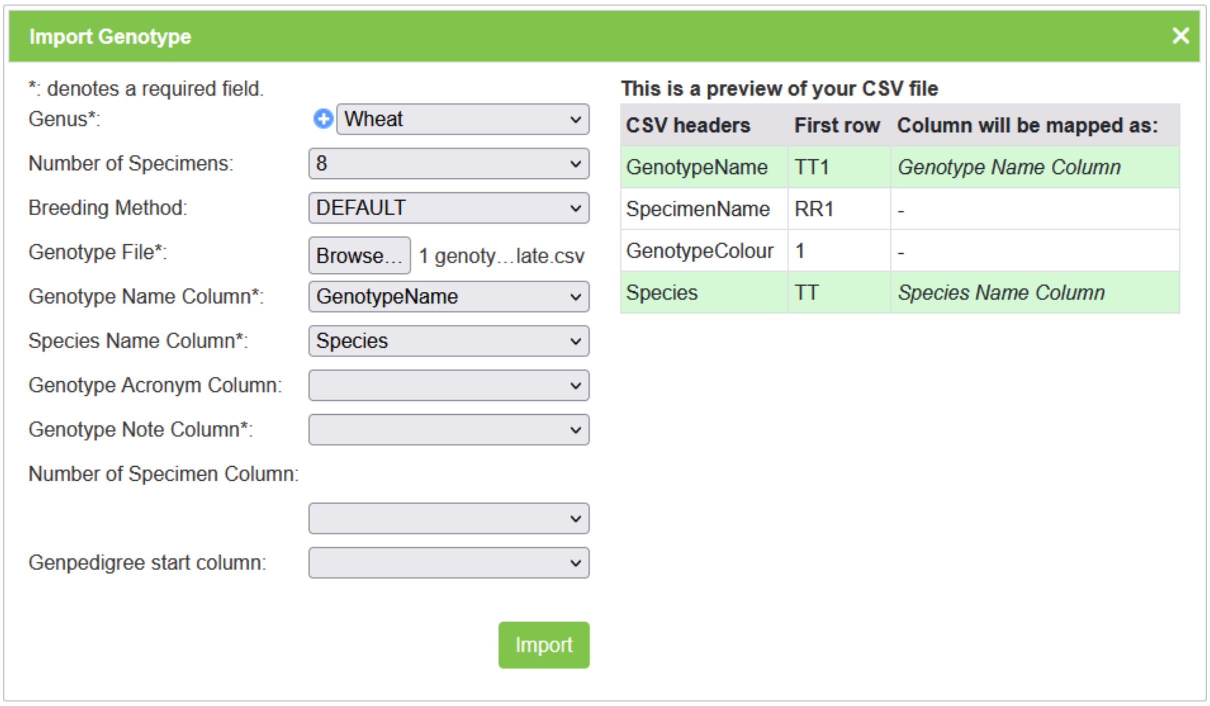
	A	B	C	D
1	GenotypeName	SpecimenName	GenotypeColour	Species
2	TT1	RR1	1	TT
3	TT2	RR2	2	TT
4	TT3	RR3	3	TT
5	TT4	RR4	4	TT
6	TT5	RR5	5	TT
7	TT6	RR6	6	TT
8	TT7	RR7	7	TT
9	TT8	RR8	8	TT

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.

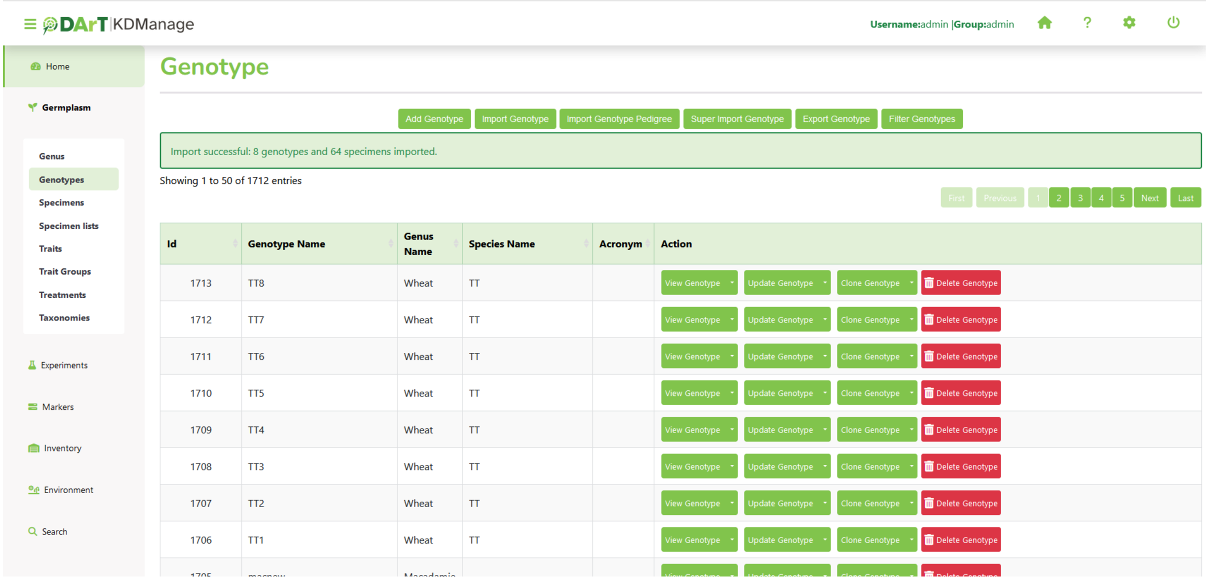
Genus*:	Wheat
Number of Specimens:	8
Breeding Method:	DEFAULT
Genotype File*:	Browse... 1 genoty...late.csv
Genotype Name Column*:	GenotypeName
Species Name Column*:	Species
Genotype Acronym Column:	
Genotype Note Column*:	
Number of Specimen Column:	
Genpedigree start column:	

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
GenotypeName	TT1	*Genotype Name Column*
SpecimenName	RR1	-
GenotypeColour	1	-
Species	TT	*Species Name Column*

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:



Import successful: 8 genotypes and 64 specimens imported.

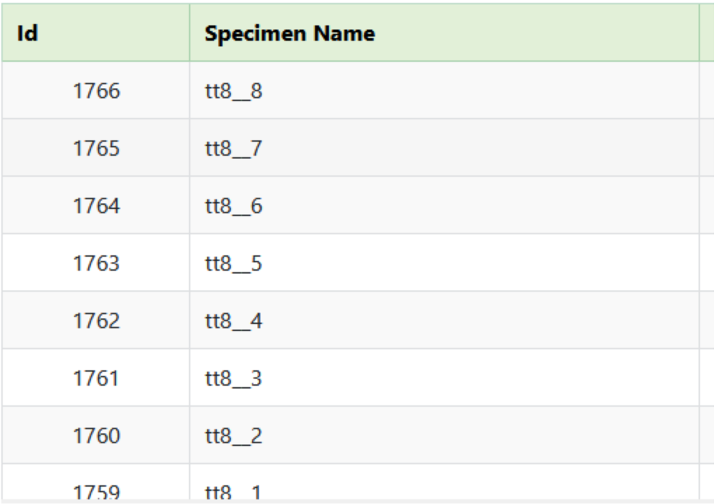
Showing 1 to 50 of 1712 entries

Id	Genotype Name	Genus Name	Species Name	Acronym	Action
1713	TT8	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1712	TT7	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1711	TT6	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1710	TT5	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1709	TT4	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1708	TT3	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1707	TT2	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype
1706	TT1	Wheat	TT		View Genotype · Update Genotype · Clone Genotype · Delete Genotype

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).

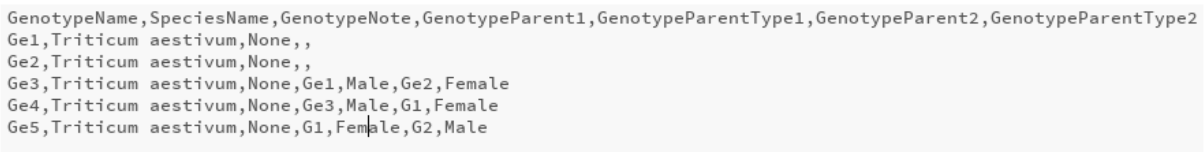


Id	Specimen Name
1766	tt8__8
1765	tt8__7
1764	tt8__6
1763	tt8__5
1762	tt8__4
1761	tt8__3
1760	tt8__2
1759	tt8__1

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*:

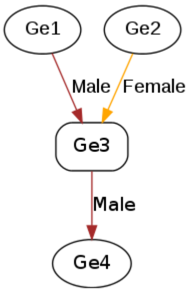
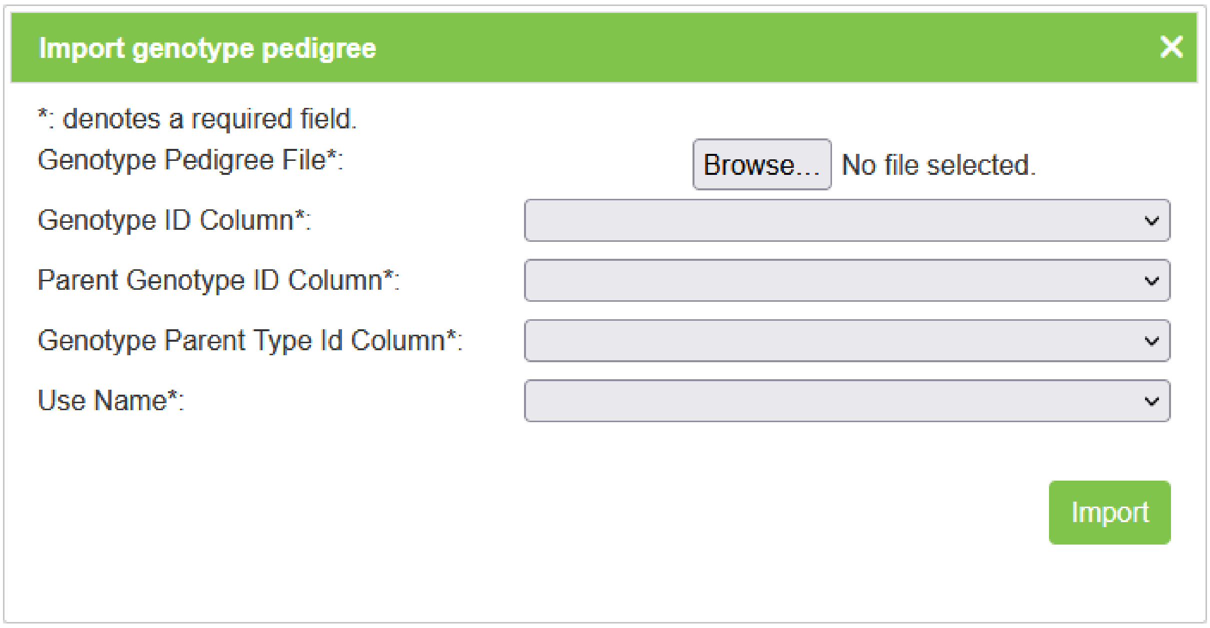


Fig. 11: Imported Genpedigree Example

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*: No file selected.

Genotype ID Column*:

Parent Genotype ID Column*:

Genotype Parent Type Id Column*:

Use Name*:

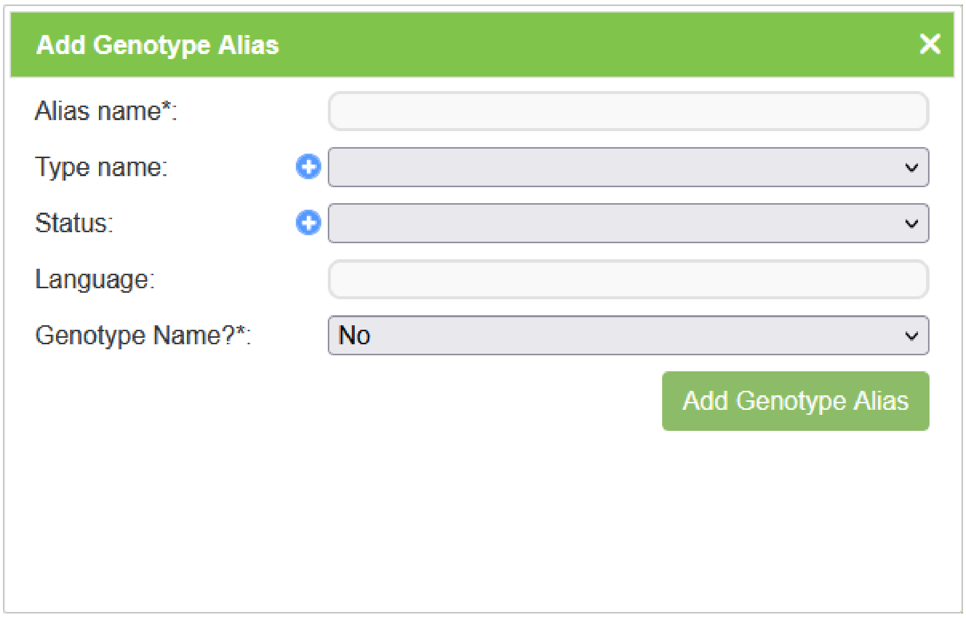
Fig. 12: Import Genotype Pedigree Window

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 *children* genotypes.
Parent Genotype ID Column	Mandatory	Column number for parent genotype ID. These are the *parent* 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 the **Update Genotype button** and the *Add Genotype Alias option* to display the **Add Genotype Alias Window**. The window and a table that explain the related fields can be found below:



Add Genotype Alias

Alias name*:

Type name:

Status:

Language:

Genotype Name?*: No

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.

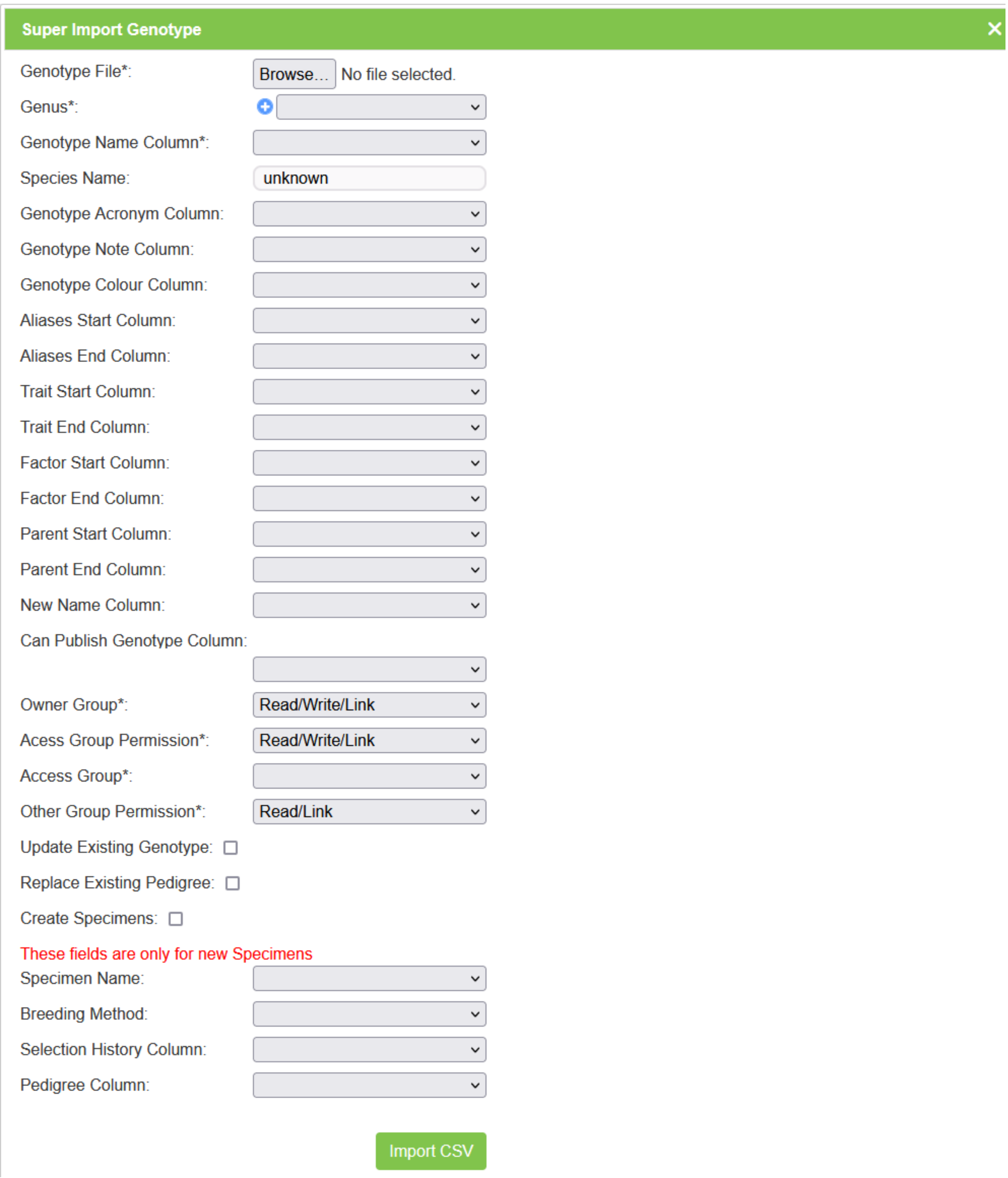
Prerequisite: Before the Genotype Super Import can be used, a .csv file containing the relevant data must be prepared. This .csv file should contain the columns listed within the Genotype Super Import Form.

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.



Super Import Genotype

Genotype File*: Browse... No file selected.
Genus*:
Genotype Name Column*:
Species Name: unknown
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:
Parent Start Column:
Parent End Column:
New Name Column:
Can Publish Genotype Column:
Owner Group*: Read/Write/Link
Acess Group Permission*: Read/Write/Link
Access Group*:
Other Group Permission*: Read/Link
Update Existing Genotype: ☐
Replace Existing Pedigree: ☐
Create Specimens: ☐

These fields are only for new Specimens

Specimen Name:
Breeding Method:
Selection History Column:
Pedigree Column:

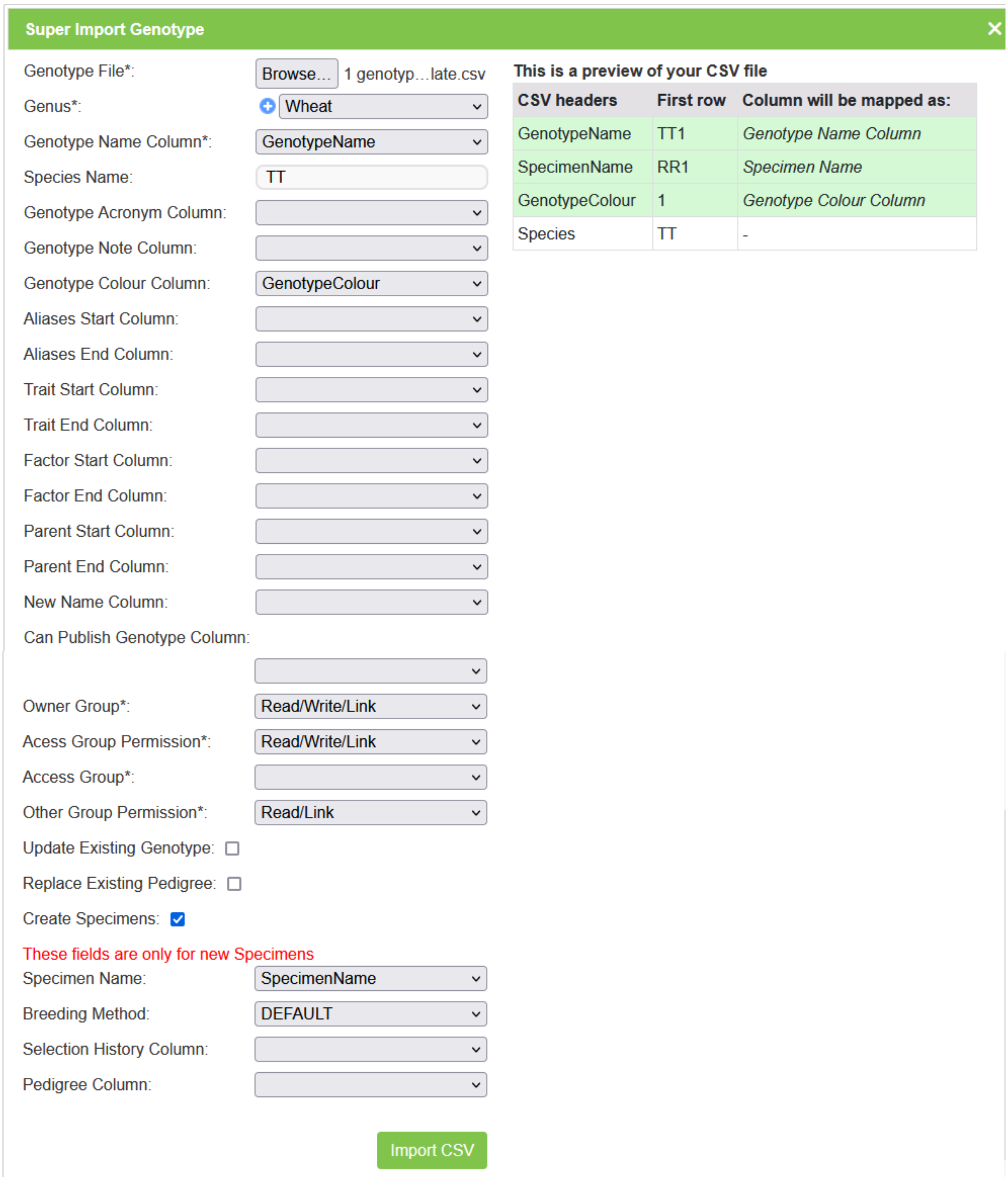
Fig. 14: Genotype Super Import Window

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.
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 al the columns of the .csv file.



Super Import Genotype

Genotype File*: 1 genotyp…late.csv
Genus*: Wheat
Genotype Name Column*: GenotypeName
Species Name: TT
Genotype Acronym Column:
Genotype Note Column:
Genotype Colour Column: GenotypeColour
Aliases Start Column:
Aliases End Column:
Trait Start Column:
Trait End Column:
Factor Start Column:
Factor End Column:
Parent Start Column:
Parent End Column:
New Name Column:
Can Publish Genotype Column:
Owner Group*: Read/Write/Link
Acess Group Permission*: Read/Write/Link
Access Group*:
Other Group Permission*: Read/Link
Update Existing Genotype: ☐
Replace Existing Pedigree: ☐
Create Specimens: ☑

These fields are only for new Specimens
Specimen Name: SpecimenName
Breeding Method: DEFAULT
Selection History Column:
Pedigree Column:

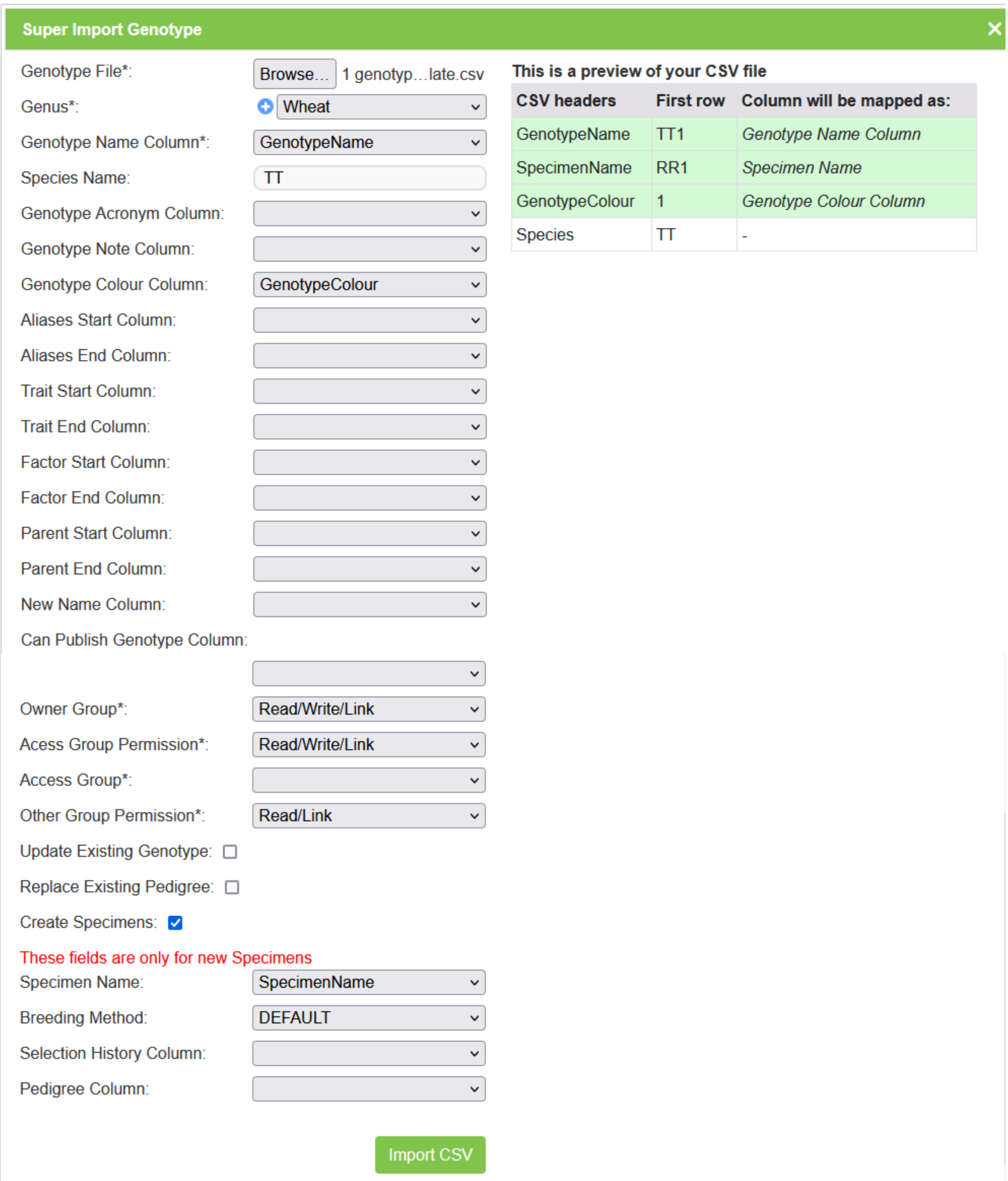
This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
GenotypeName	TT1	*Genotype Name Column*
SpecimenName	RR1	*Specimen Name*
GenotypeColour	1	*Genotype Colour Column*
Species	TT	-

Fig. 15: Genotype Super Import Example

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.



Genotype File*: Browse… 1 genotyp…late.csv
Genus*: Wheat
Genotype Name Column*: GenotypeName
Species Name: TT
Genotype Acronym Column:
Genotype Note Column:
Genotype Colour Column: GenotypeColour
Aliases Start Column:
Aliases End Column:
Trait Start Column:
Trait End Column:
Factor Start Column:
Factor End Column:
Parent Start Column:
Parent End Column:
New Name Column:
Can Publish Genotype Column:
Owner Group*: Read/Write/Link
Acess Group Permission*: Read/Write/Link
Access Group*:
Other Group Permission*: Read/Link
Update Existing Genotype: ☐
Replace Existing Pedigree: ☐
Create Specimens: ☑

These fields are only for new Specimens
Specimen Name: SpecimenName
Breeding Method: DEFAULT
Selection History Column:
Pedigree Column:

This is a preview of your CSV file

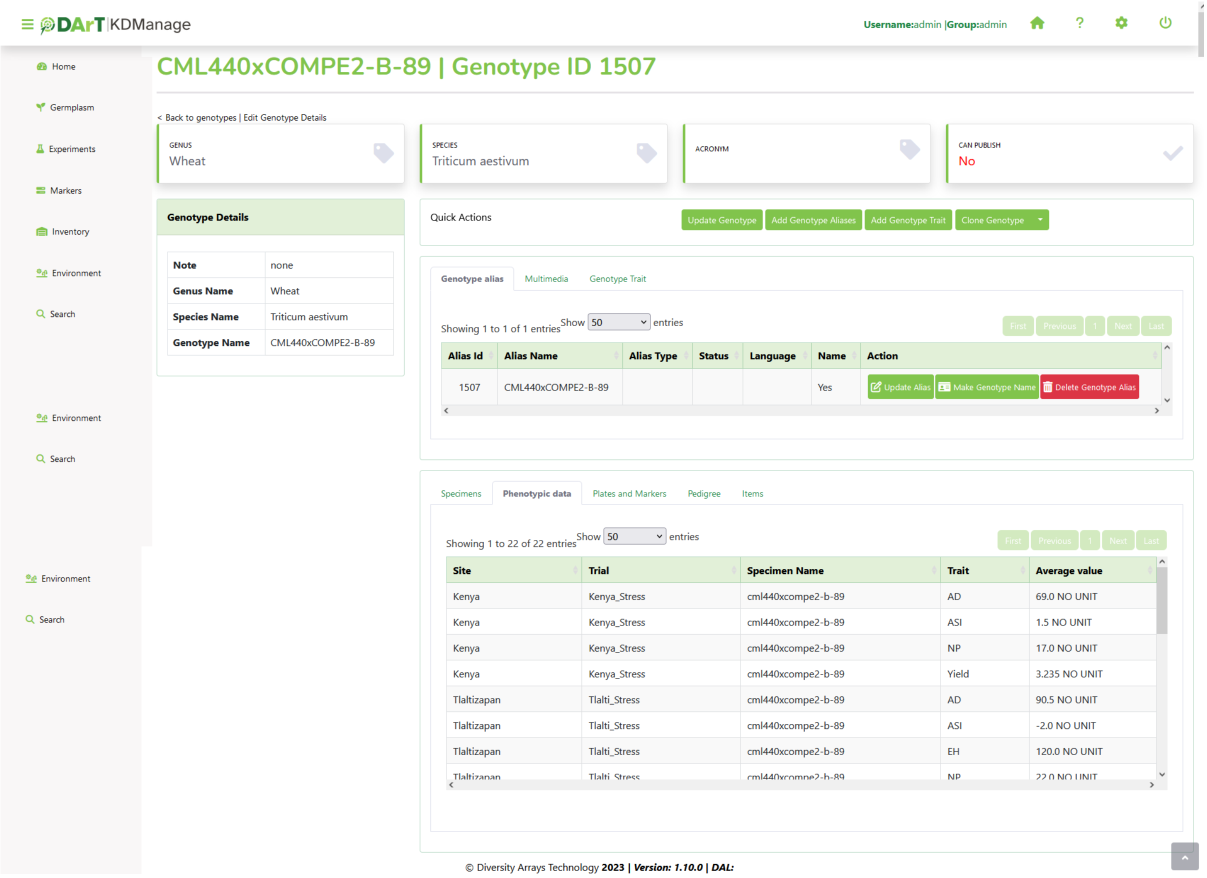
CSV headers	First row	Column will be mapped as:
GenotypeName	TT1	*Genotype Name Column*
SpecimenName	RR1	*Specimen Name*
GenotypeColour	1	*Genotype Colour Column*
Species	TT	-

Fig. 16: Genotype Super Import Invalid Example

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.

4.2.6 Genotype Data Page

Select the **View Genotype button** for any genotype to reach the **Genotype Data Page**. This page provides the data/details about each genotype that is contained in your KDDart instance.



CML440xCOMPE2-B-89 | Genotype ID 1507

< Back to genotypes | Edit Genotype Details

GENUS
Wheat

SPECIES
Triticum aestivum

ACRONYM

CAN PUBLISH
No

Genotype Details

Note	none
Genus Name	Wheat
Species Name	Triticum aestivum
Genotype Name	CML440xCOMPE2-B-89

Showing 1 to 1 of 1 entries Show 50 entries

Alias Id	Alias Name	Alias Type	Status	Language	Name	Action
1507	CML440xCOMPE2-B-89				Yes	Update Alias Make Genotype Name Delete Genotype Alias

Showing 1 to 22 of 22 entries Show 50 entries

Site	Trial	Specimen Name	Trait	Average value
Kenya	Kenya_Stress	cml440xcompe2-b-89	AD	69.0 NO UNIT
Kenya	Kenya_Stress	cml440xcompe2-b-89	ASI	1.5 NO UNIT
Kenya	Kenya_Stress	cml440xcompe2-b-89	NP	17.0 NO UNIT
Kenya	Kenya_Stress	cml440xcompe2-b-89	Yield	3.235 NO UNIT
Tlaltizapan	Tlalti_Stress	cml440xcompe2-b-89	AD	90.5 NO UNIT
Tlaltizapan	Tlalti_Stress	cml440xcompe2-b-89	ASI	-2.0 NO UNIT
Tlaltizapan	Tlalti_Stress	cml440xcompe2-b-89	EH	120.0 NO UNIT
Tlaltizapan	Tlalti_Stress	cml440xcompe2-b-89	NP	22.0 NO UNIT

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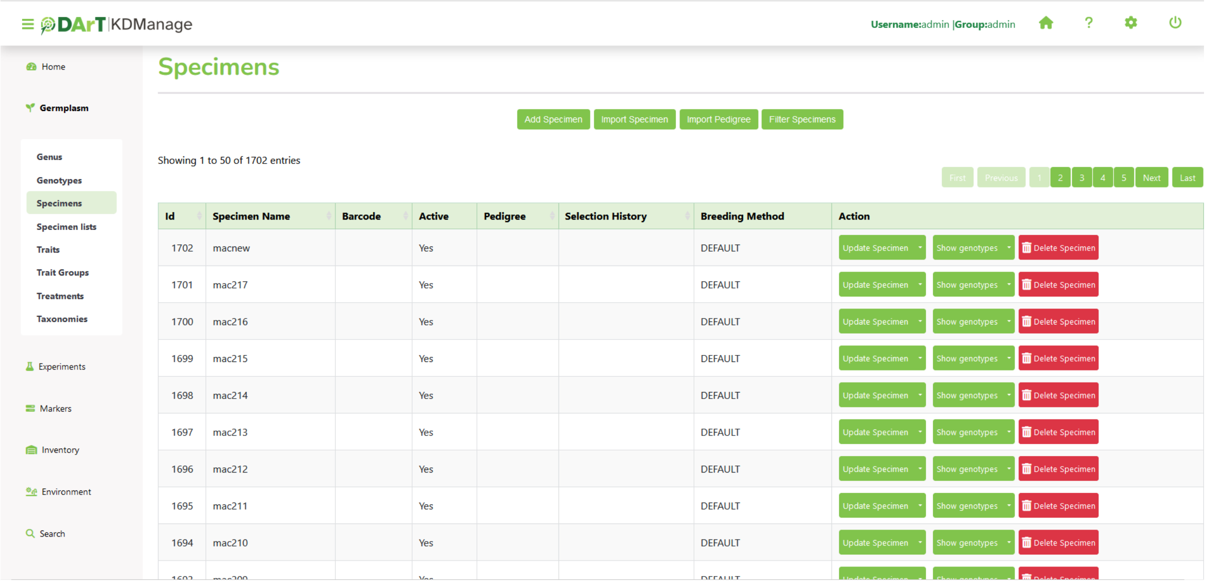
Fig. 17: Genotype Data Page

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.

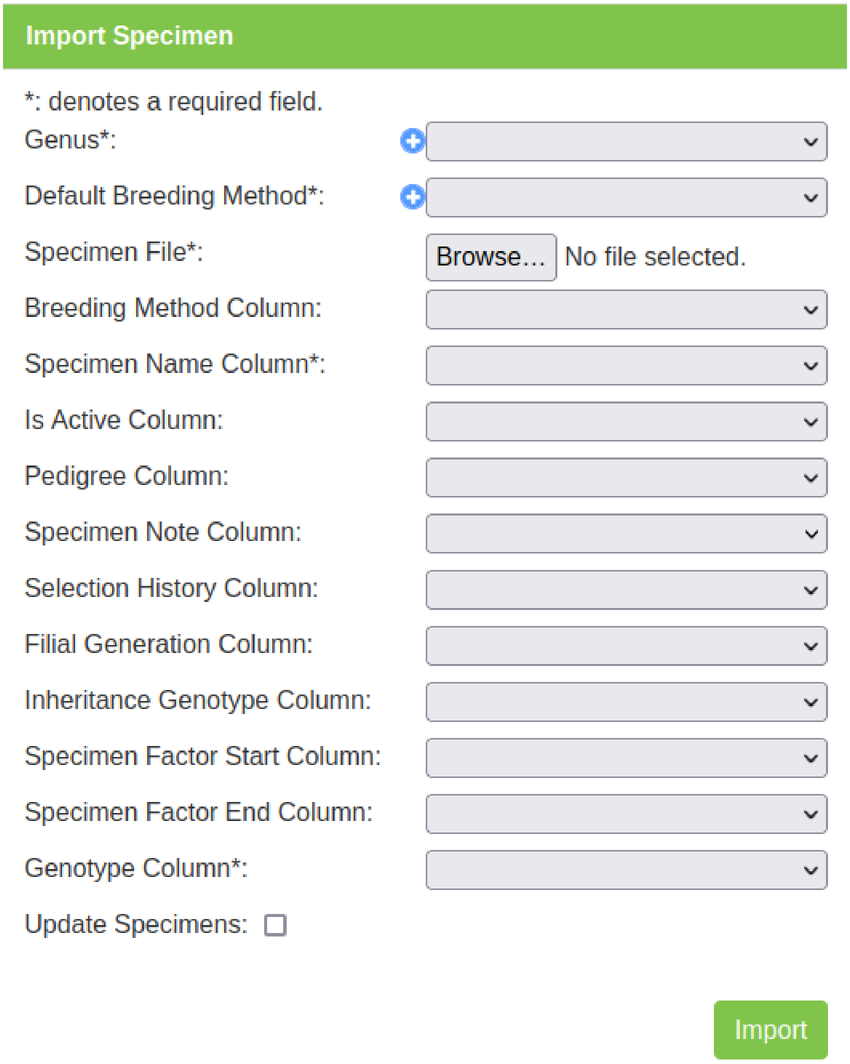


Showing 1 to 50 of 1702 entries

Id	Specimen Name	Barcode	Active	Pedigree	Selection History	Breeding Method	Action
1702	macnew		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1701	mac217		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1700	mac216		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1699	mac215		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1698	mac214		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1697	mac213		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1696	mac212		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1695	mac211		Yes			DEFAULT	Update Specimen Show genotypes Delete Specimen
1694	mac210		Yes			DEFAULT	Update Specimen Show genotypes 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*:

Default Breeding Method*:

Specimen File*: Browse… No file selected.

Breeding Method Column:

Specimen Name Column*:

Is Active Column:

Pedigree Column:

Specimen Note Column:

Selection History Column:

Filial Generation Column:

Inheritance Genotype Column:

Specimen Factor Start Column:

Specimen Factor End Column:

Genotype Column*:

Update Specimens: ☐

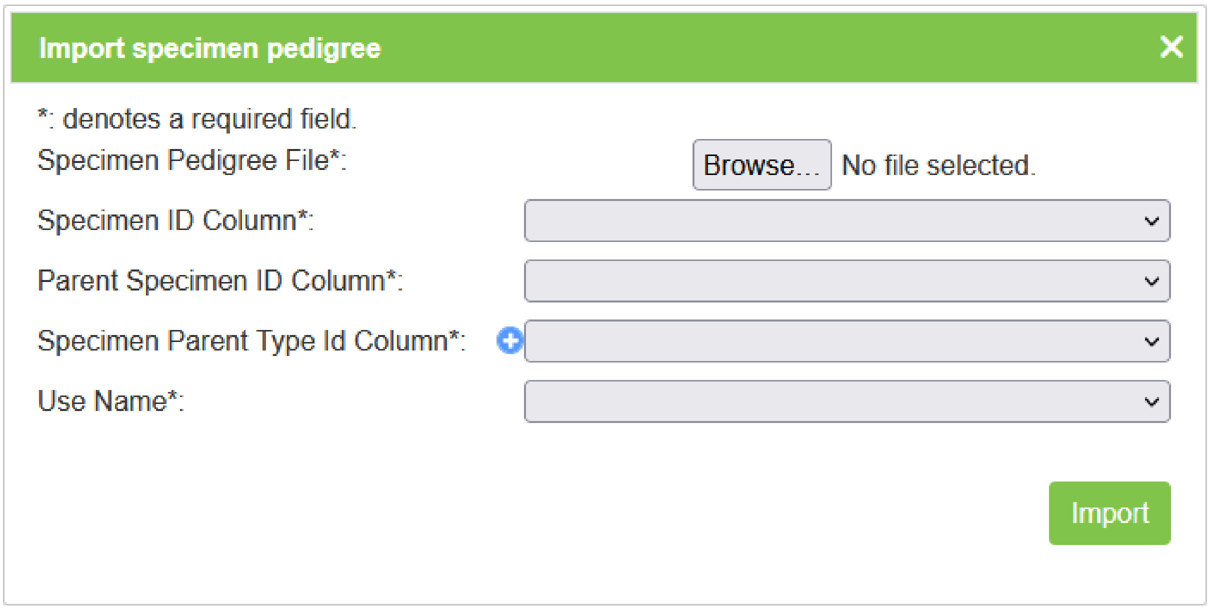
Fig. 19: Import Specimen Window

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 *selfed*, 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:



*: denotes a required field.

Specimen Pedigree File*:

Specimen ID Column*:

Parent Specimen ID Column*:

Specimen Parent Type Id Column*:

Use Name*:

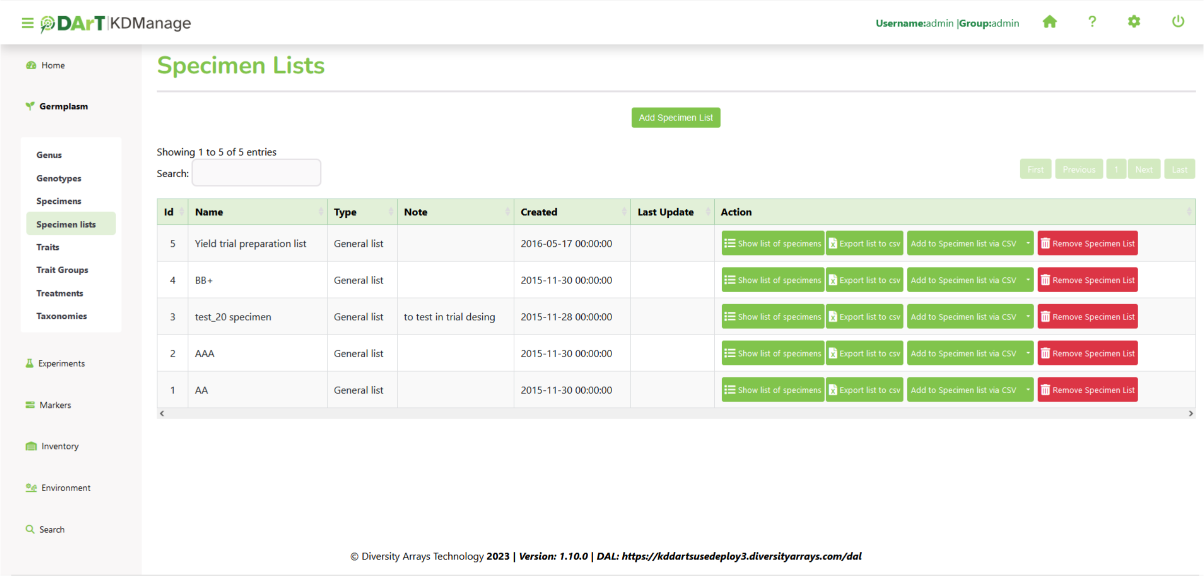
Fig. 20: Import Pedigree Window

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 *children* genotypes.
Parent Specimen ID Column	Mandatory	Column number for parent specimen ID. These are the *parent* 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:



Specimen Lists

Showing 1 to 5 of 5 entries

Search:

Id	Name	Type	Note	Created	Last Update	Action
5	Yield trial preparation list	General list		2016-05-17 00:00:00		Show list of specimens Export list to csv Add to Specimen list via CSV Remove Specimen List
4	BB+	General list		2015-11-30 00:00:00		Show list of specimens Export list to csv Add to Specimen list via CSV Remove Specimen List
3	test_20 specimen	General list	to test in trial desing	2015-11-28 00:00:00		Show list of specimens Export list to csv Add to Specimen list via CSV Remove Specimen List
2	AAA	General list		2015-11-30 00:00:00		Show list of specimens Export list to csv Add to Specimen list via CSV Remove Specimen List
1	AA	General list		2015-11-30 00:00:00		Show list of specimens Export list to csv Add to Specimen list via CSV Remove Specimen List

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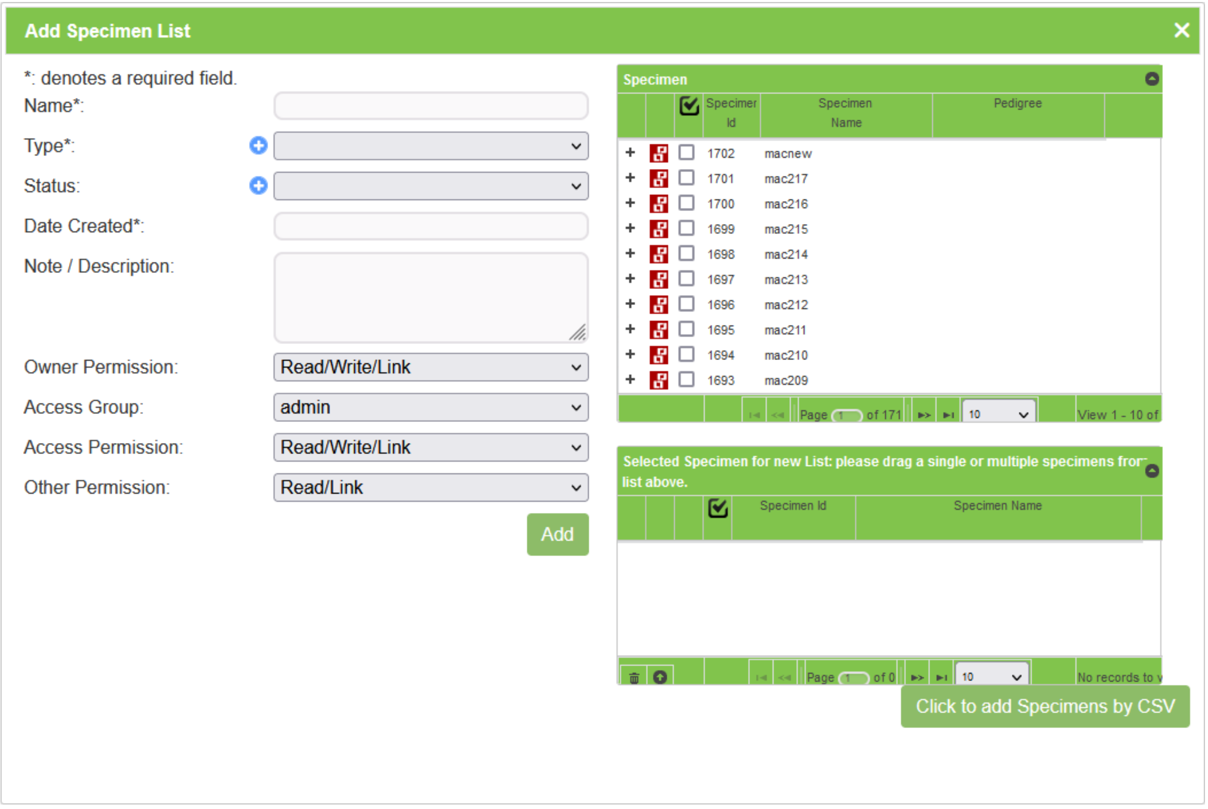
Fig. 21: Specimen Lists Page

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: Read/Write/Link

Access Group: admin

Access Permission: Read/Write/Link

Other Permission: Read/Link

Specimen

Specimen Id	Specimen Name	Pedigree
1702	macnew	
1701	mac217	
1700	mac216	
1699	mac215	
1698	mac214	
1697	mac213	
1696	mac212	
1695	mac211	
1694	mac210	
1693	mac209	

Page 1 of 171 10 View 1 - 10 of

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

Specimen Id	Specimen Name

Page 1 of 0 10 No records to v

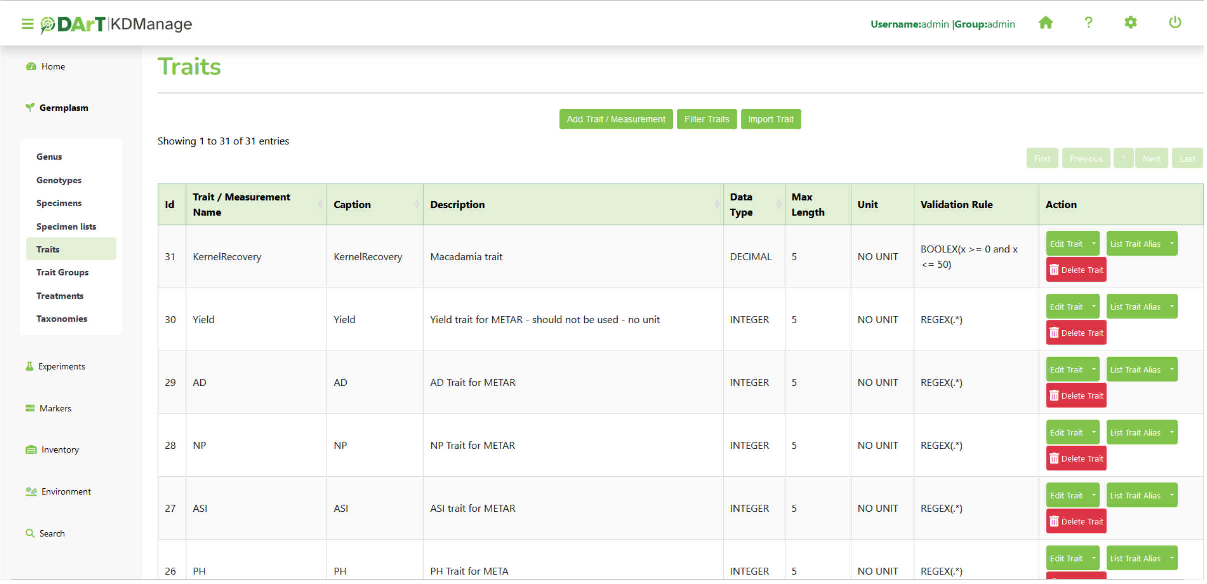
Fig. 22: Add Specimen List Window

Table 10: Add Specimen List Fields

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

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.



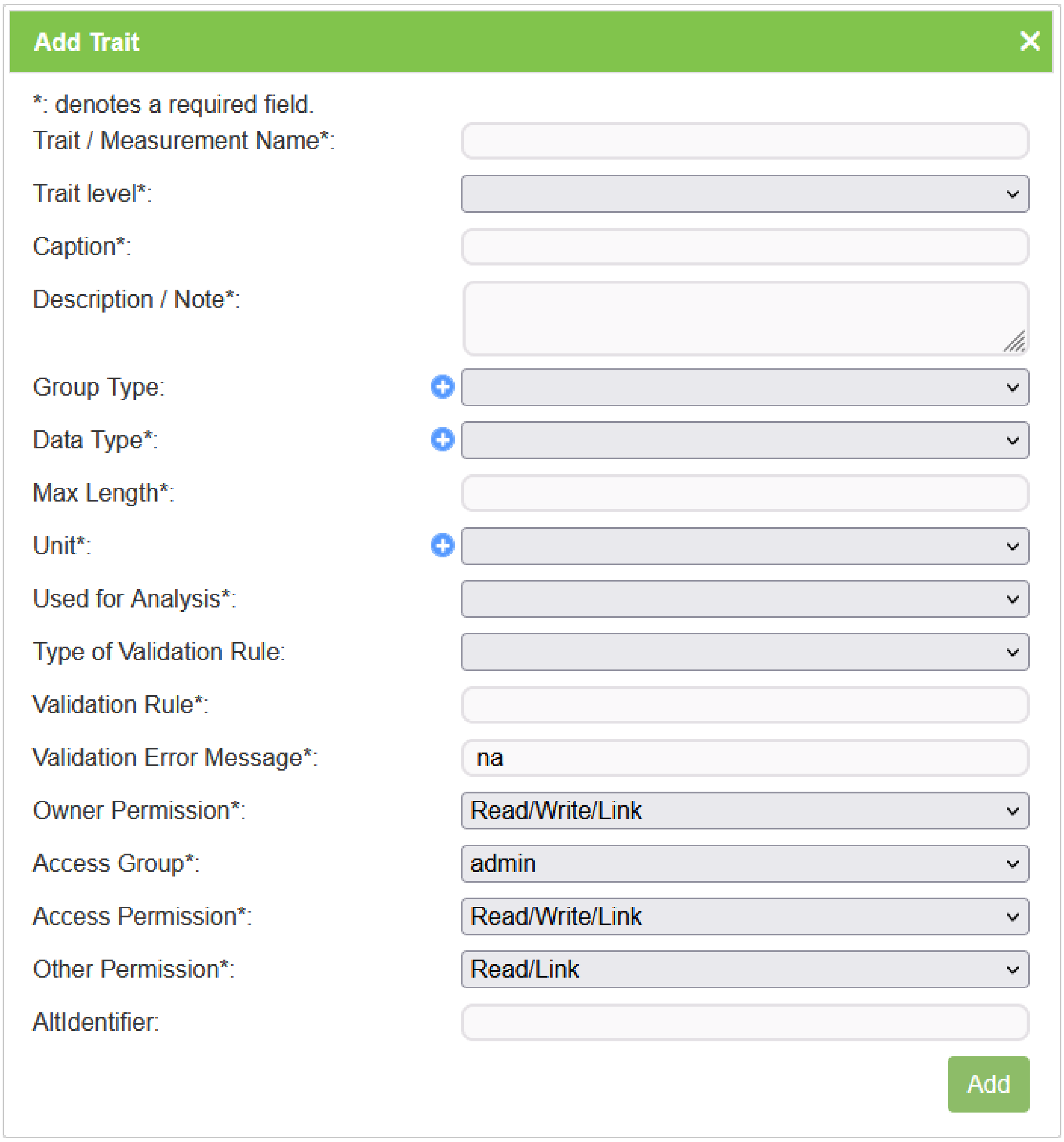
Showing 1 to 31 of 31 entries

Id	Trait / Measurement Name	Caption	Description	Data Type	Max Length	Unit	Validation Rule	Action
31	KernelRecovery	KernelRecovery	Macadamia trait	DECIMAL	5	NO UNIT	BOOLEX(x >= 0 and x <= 50)	Edit Trait List Trait Alias Delete Trait
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
29	AD	AD	AD Trait for METAR	INTEGER	5	NO UNIT	REGEX(.*)	Edit Trait List Trait Alias Delete Trait
28	NP	NP	NP Trait for METAR	INTEGER	5	NO UNIT	REGEX(.*)	Edit Trait List Trait Alias Delete Trait
27	ASI	ASI	ASI trait for METAR	INTEGER	5	NO UNIT	REGEX(.*)	Edit Trait List Trait Alias Delete Trait
26	PH	PH	PH Trait for META	INTEGER	5	NO UNIT	REGEX(.*)	Edit Trait List Trait Alias

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:



*: denotes a required field.

Trait / Measurement Name*:

Trait level*:

Caption*:

Description / Note*:

Group Type:

Data Type*:

Max Length*:

Unit*:

Used for Analysis*:

Type of Validation Rule:

Validation Rule*:

Validation Error Message*: na

Owner Permission*: Read/Write/Link

Access Group*: admin

Access Permission*: Read/Write/Link

Other Permission*: Read/Link

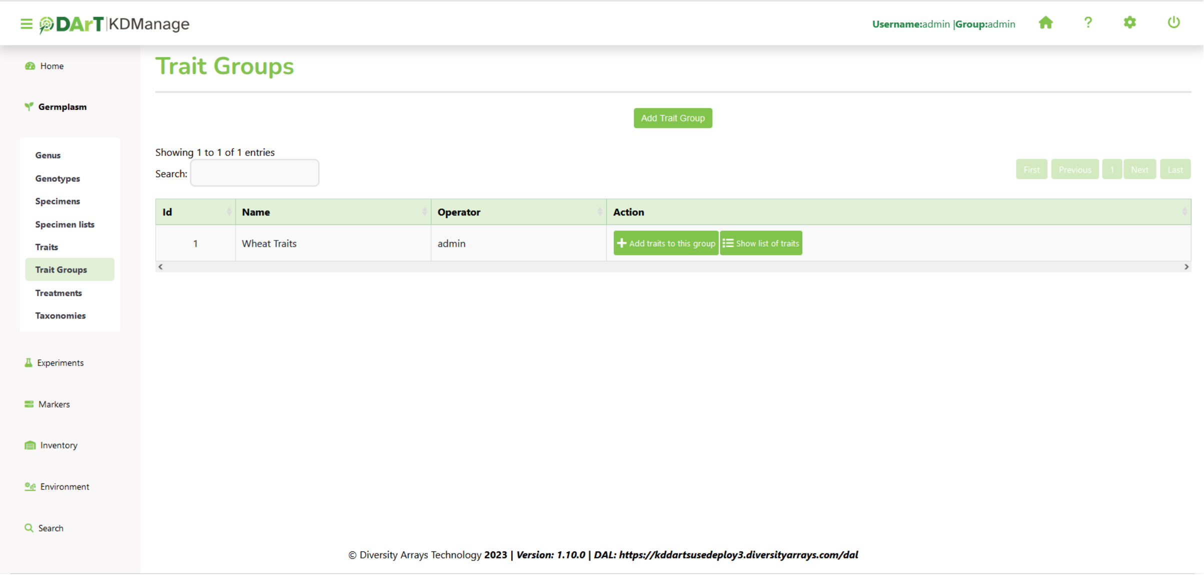
AltIdentifier:

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 *Trait Data Type* in **Types** (see Types section in *Administrative Settings*)
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 *Access Settings and Permissions* 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:



Showing 1 to 1 of 1 entries

Id	Name	Operator	Action
1	Wheat Traits	admin	Add traits to this group Show list of traits

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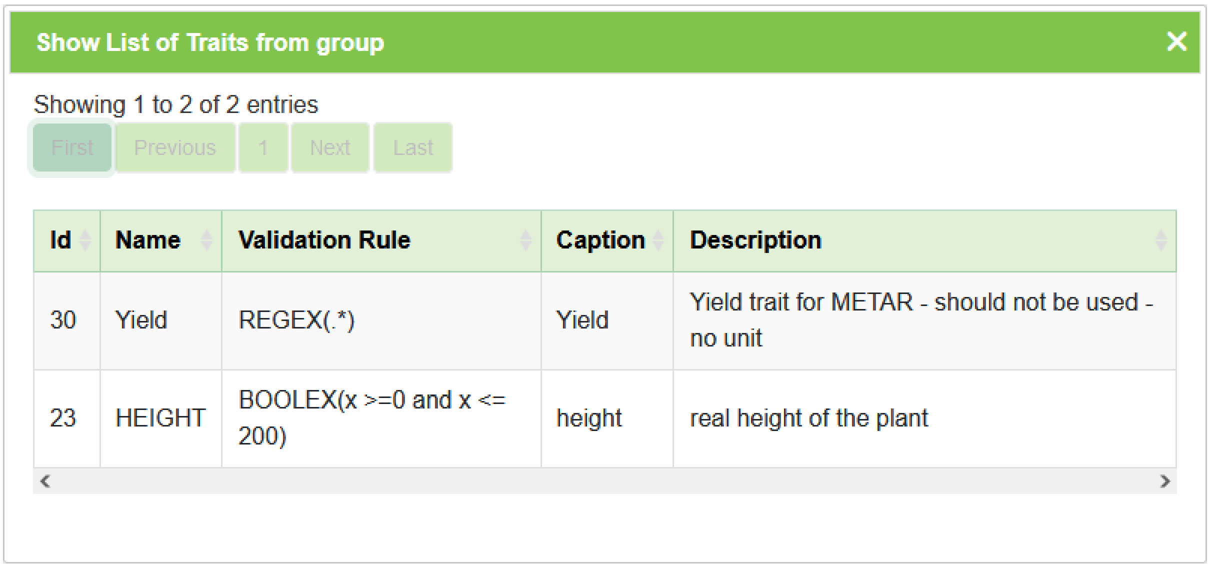
Fig. 25: Trait Groups Page

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

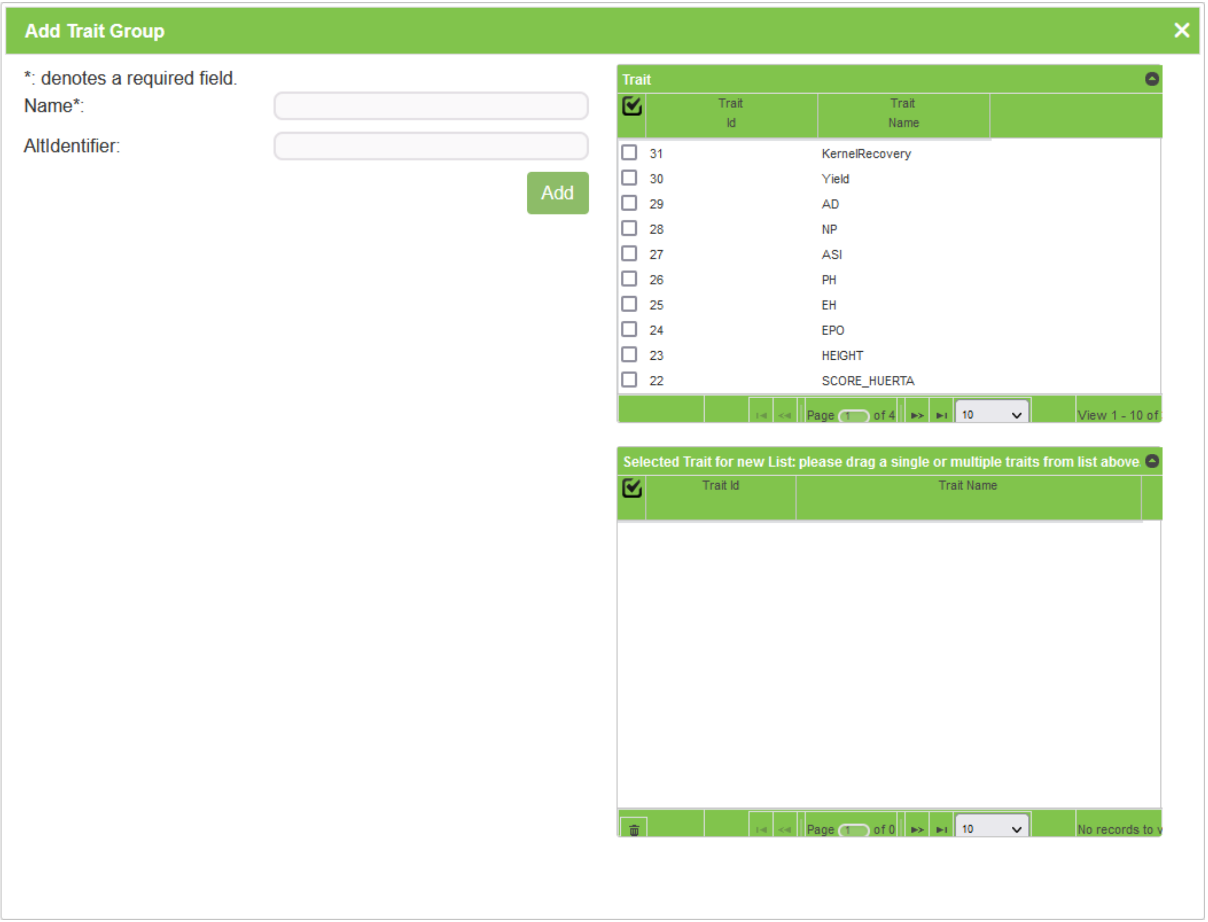


Showing 1 to 2 of 2 entries

Id	Name	Validation Rule	Caption	Description
30	Yield	REGEX(.*)	Yield	Yield trait for METAR - should not be used - no unit
23	HEIGHT	BOOLEX(x >=0 and x <= 200)	height	real height of the plant

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.



Add Trait Group

*: denotes a required field.

Name*:

AltIdentifier:

Trait

☑	Trait Id	Trait Name
☐	31	KernelRecovery
☐	30	Yield
☐	29	AD
☐	28	NP
☐	27	ASI
☐	26	PH
☐	25	EH
☐	24	EPO
☐	23	HEIGHT
☐	22	SCORE_HUERTA

Selected Trait for new List: please drag a single or multiple traits from list above

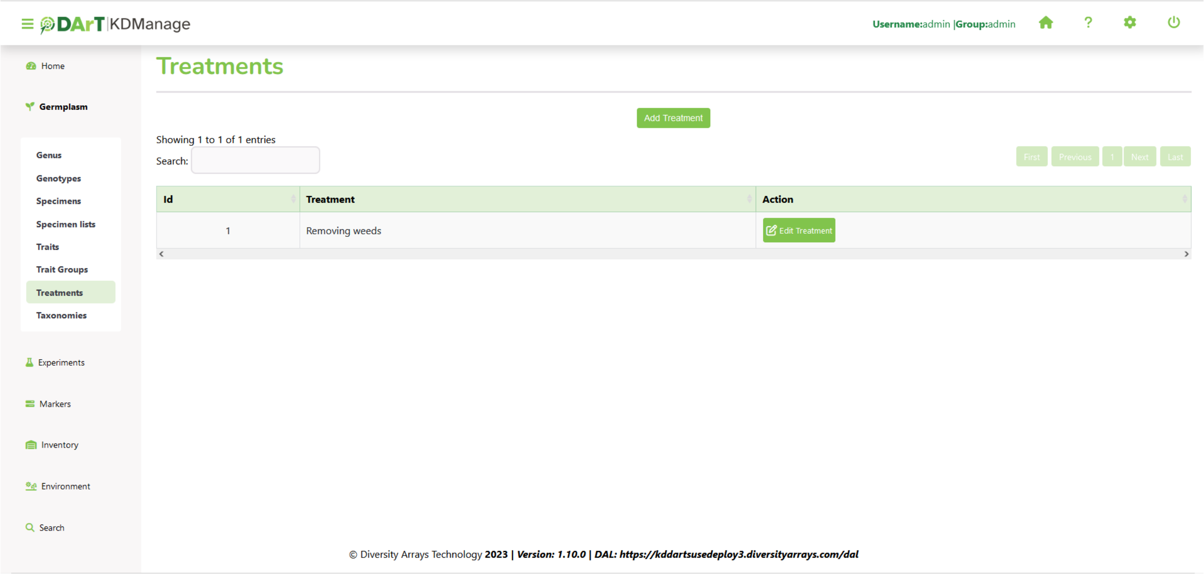
☑	Trait Id	Trait Name

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.



Showing 1 to 1 of 1 entries

Id	Treatment	Action
1	Removing weeds	Edit Treatment

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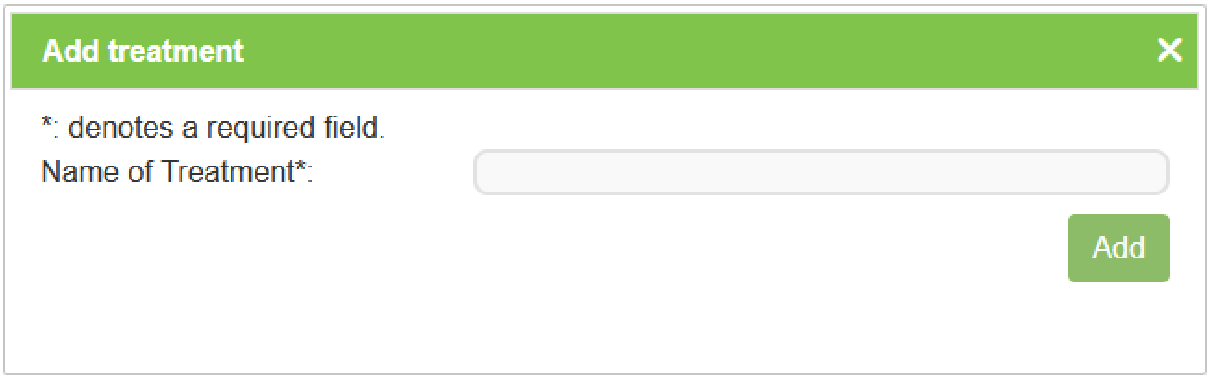
Fig. 28: Treatments Page

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



*: denotes a required field.

Name of Treatment*:

Fig. 29: Add Treatments Window

CHAPTER
FIVE

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.

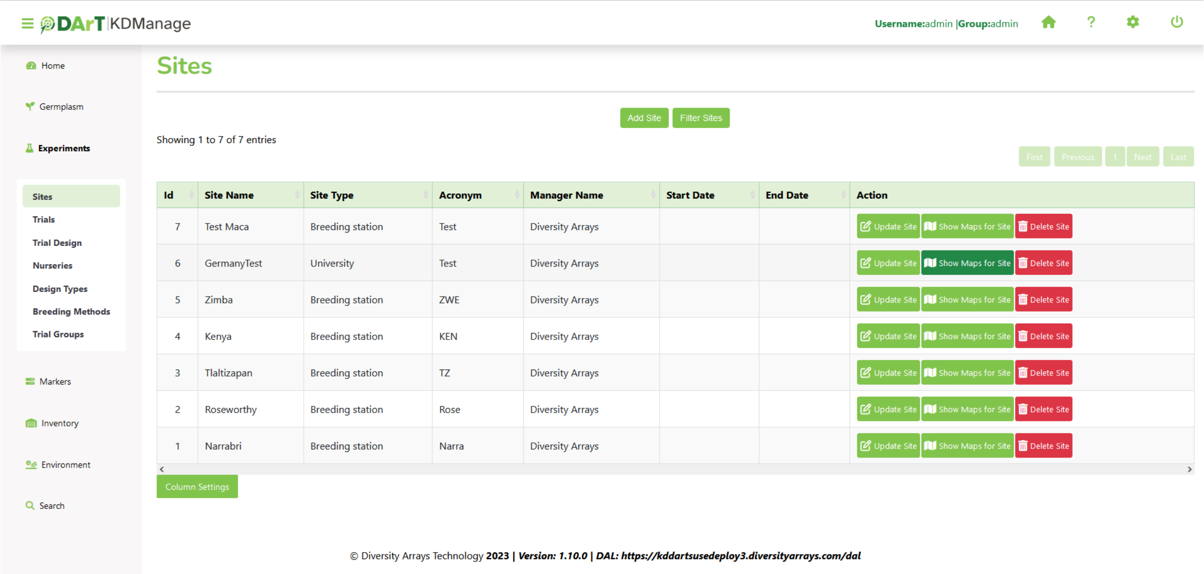
The following items of the **Experiment Menu** illustrate the *order of dependency*:

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.



Sites

Showing 1 to 7 of 7 entries

Id	Site Name	Site Type	Acronym	Manager Name	Start Date	End Date	Action
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	Tlaltizapan	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

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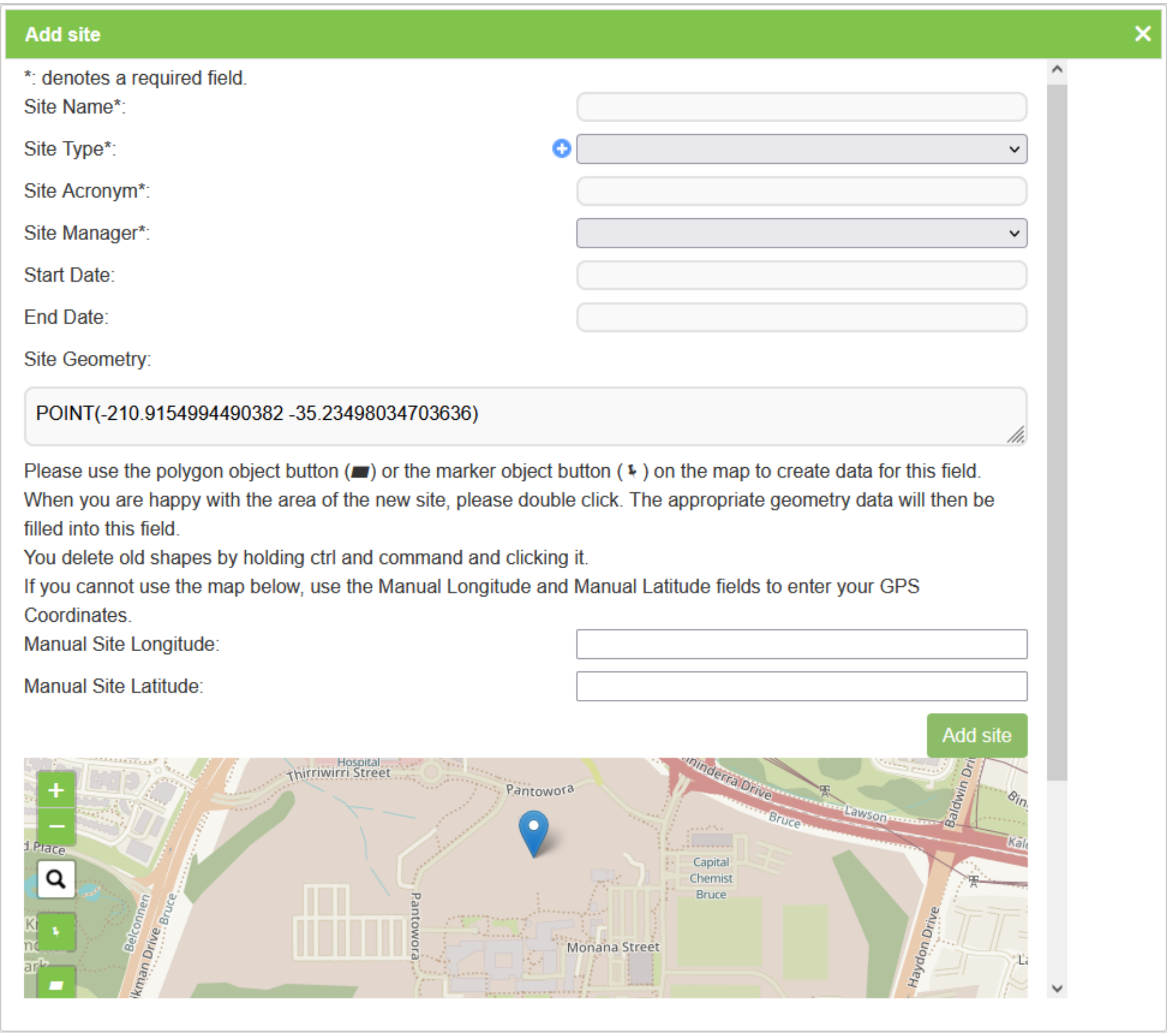
Fig. 1: Sites Page

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 it's fields can be found below:



Add site

*: denotes a required field.

Site Name*:

Site Type*:

Site Acronym*:

Site Manager*:

Start Date:

End Date:

Site Geometry:

POINT(-210.9154994490382 -35.23498034703636)

Please use the polygon object button (▰) or the marker object button (↓) on the map to create data for this field.
When you are happy with the area of the new site, please double click. The appropriate geometry data will then be filled into this field.
You delete old shapes by holding ctrl and command and clicking it.
If you cannot use the map below, use the Manual Longitude and Manual Latitude fields to enter your GPS Coordinates.

Manual Site Longitude:

Manual Site Latitude:

Fig. 2: Add Sites Window

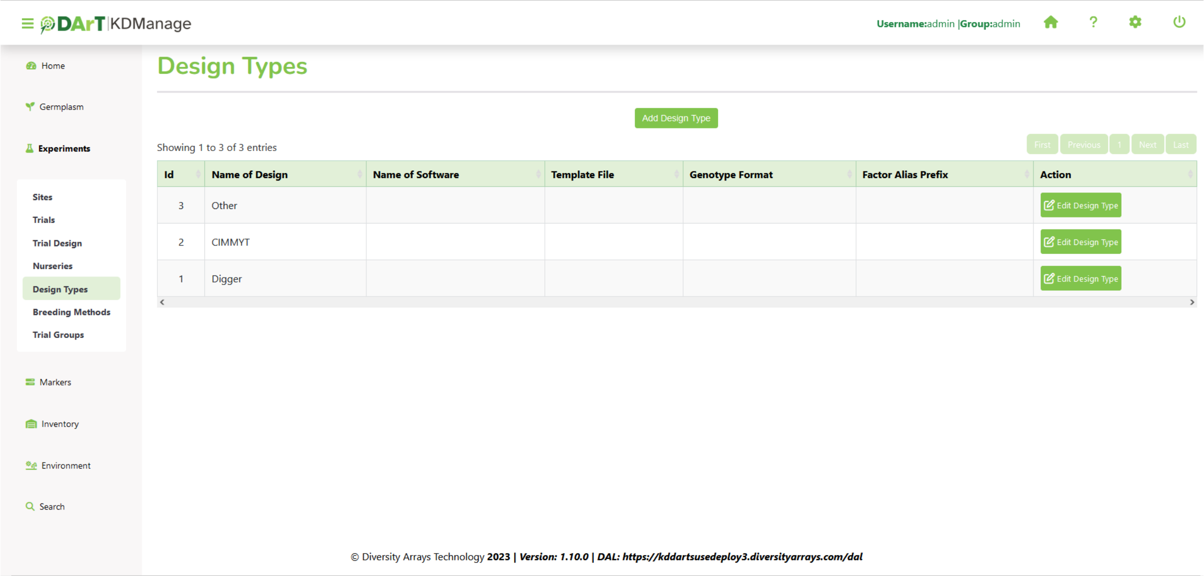
Table 1: Add Site Fields

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.



Design Types

Showing 1 to 3 of 3 entries

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

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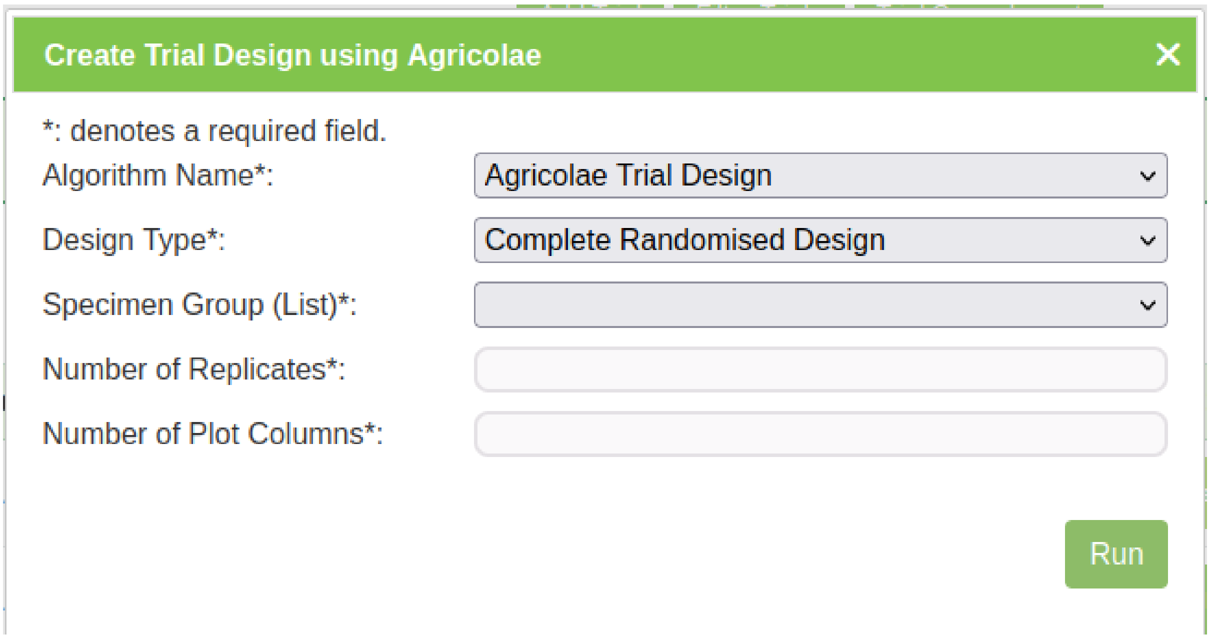
Fig. 3: Design Types Page

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:



Create Trial Design using Agricolae

*: denotes a required field.

Algorithm Name*: Agricolae Trial Design

Design Type*: Complete Randomised Design

Specimen Group (List)*:

Number of Replicates*:

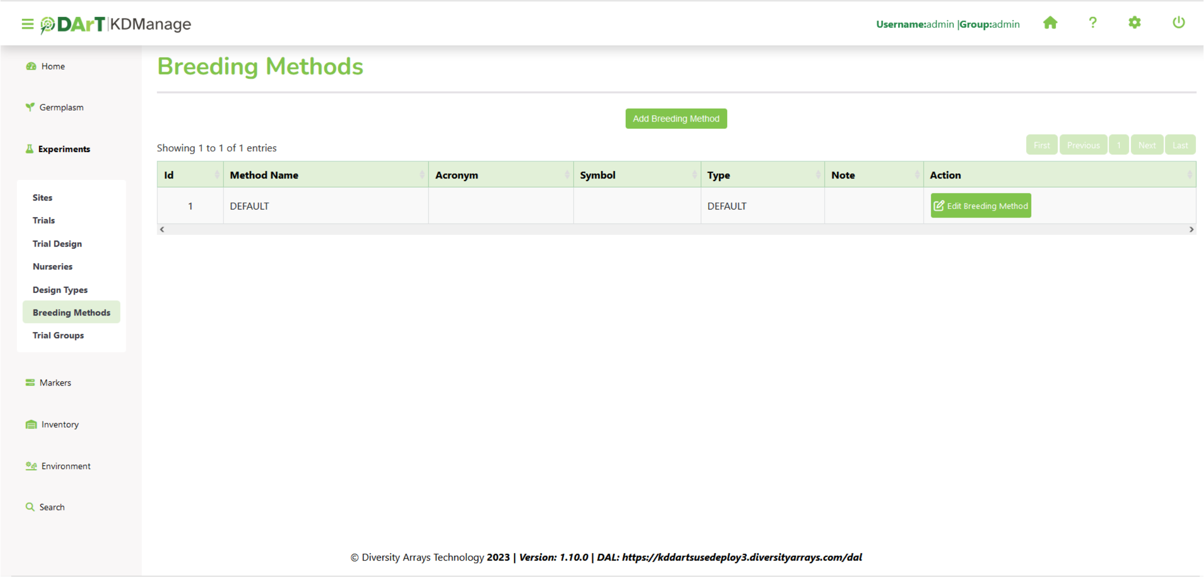
Number of Plot Columns*:

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.



Breeding Methods

Showing 1 to 1 of 1 entries

Id	Method Name	Acronym	Symbol	Type	Note	Action
1	DEFAULT			DEFAULT		Edit Breeding Method

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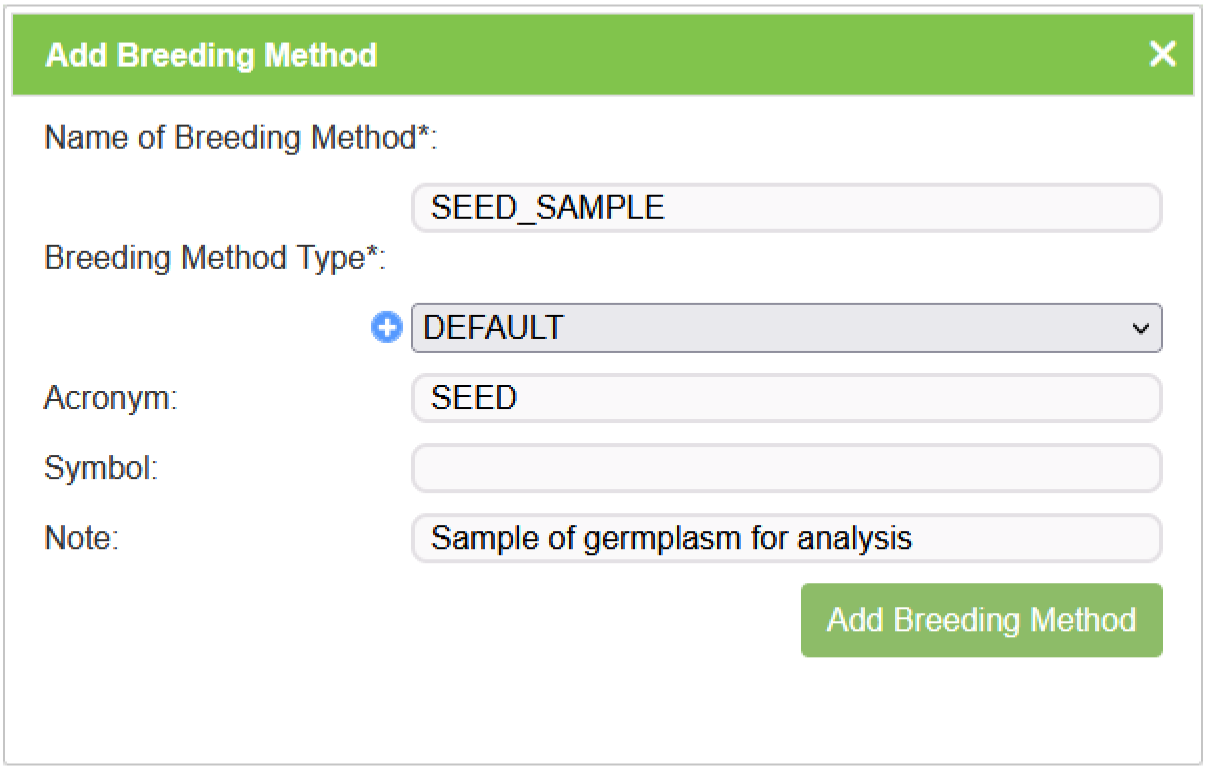
Fig. 5: Breeding Methods Page

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:



Name of Breeding Method*: SEED_SAMPLE

Breeding Method Type*: DEFAULT

Acronym: SEED

Symbol:

Note: Sample of germplasm for analysis

Fig. 6: Add Breeding Method Window

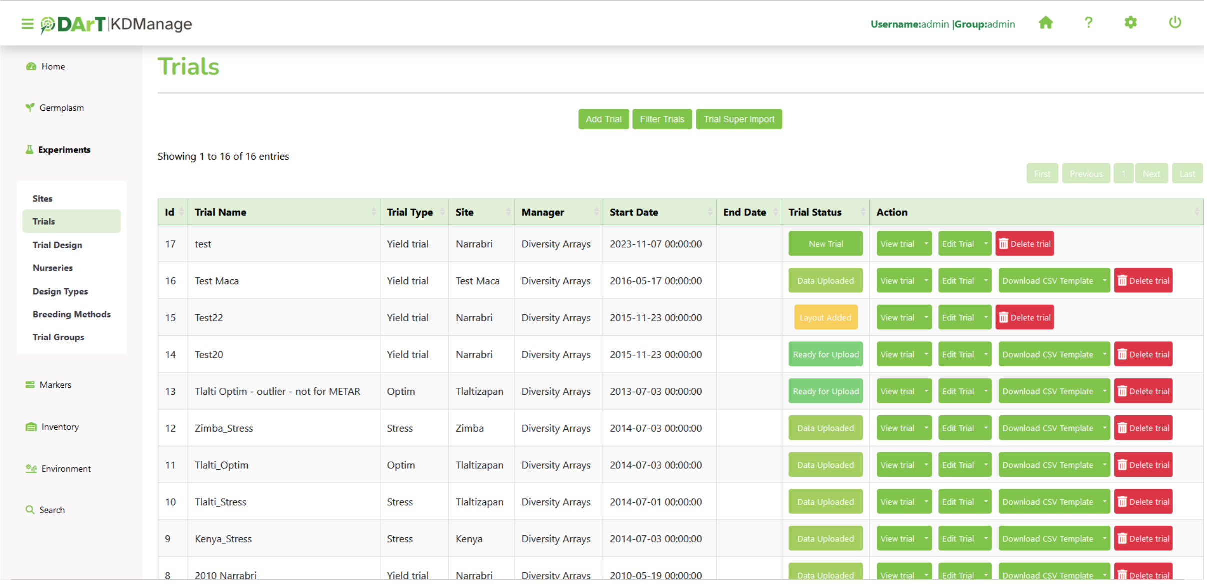
Field	Mandatory?	Description
Name of Breeding Method	Mandatory	Name of the breeding methodology.
Breeding Method Type	Mandatory	Type of breeding method. A new breeding method type can be created by selecting the **Add Button**.
Acronym	Acronym for the name of the breeding method.	
Symbol	Symbol to represent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



Showing 1 to 16 of 16 entries

Id	Trial Name	Trial Type	Site	Manager	Start Date	End Date	Trial Status	Action
17	test	Yield trial	Narrabri	Diversity Arrays	2023-11-07 00:00:00		New Trial	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	Tlalti Optim - outlier - not for METAR	Optim	Tlaltizapan	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
11	Tlalti_Optim	Optim	Tlaltizapan	Diversity Arrays	2014-07-03 00:00:00		Data Uploaded	View trial Edit Trial Download CSV Template Delete trial
10	Tlalti_Stress	Stress	Tlaltizapan	Diversity Arrays	2014-07-01 00:00:00		Data Uploaded	View trial Edit Trial Download CSV Template Delete trial
9	Kenya_Stress	Stress	Kenya	Diversity Arrays	2014-07-03 00:00:00		Data Uploaded	View trial Edit Trial Download CSV Template Delete trial
8	2010 Narrabri	Yield trial	Narrabri	Diversity Arrays	2010-05-19 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.

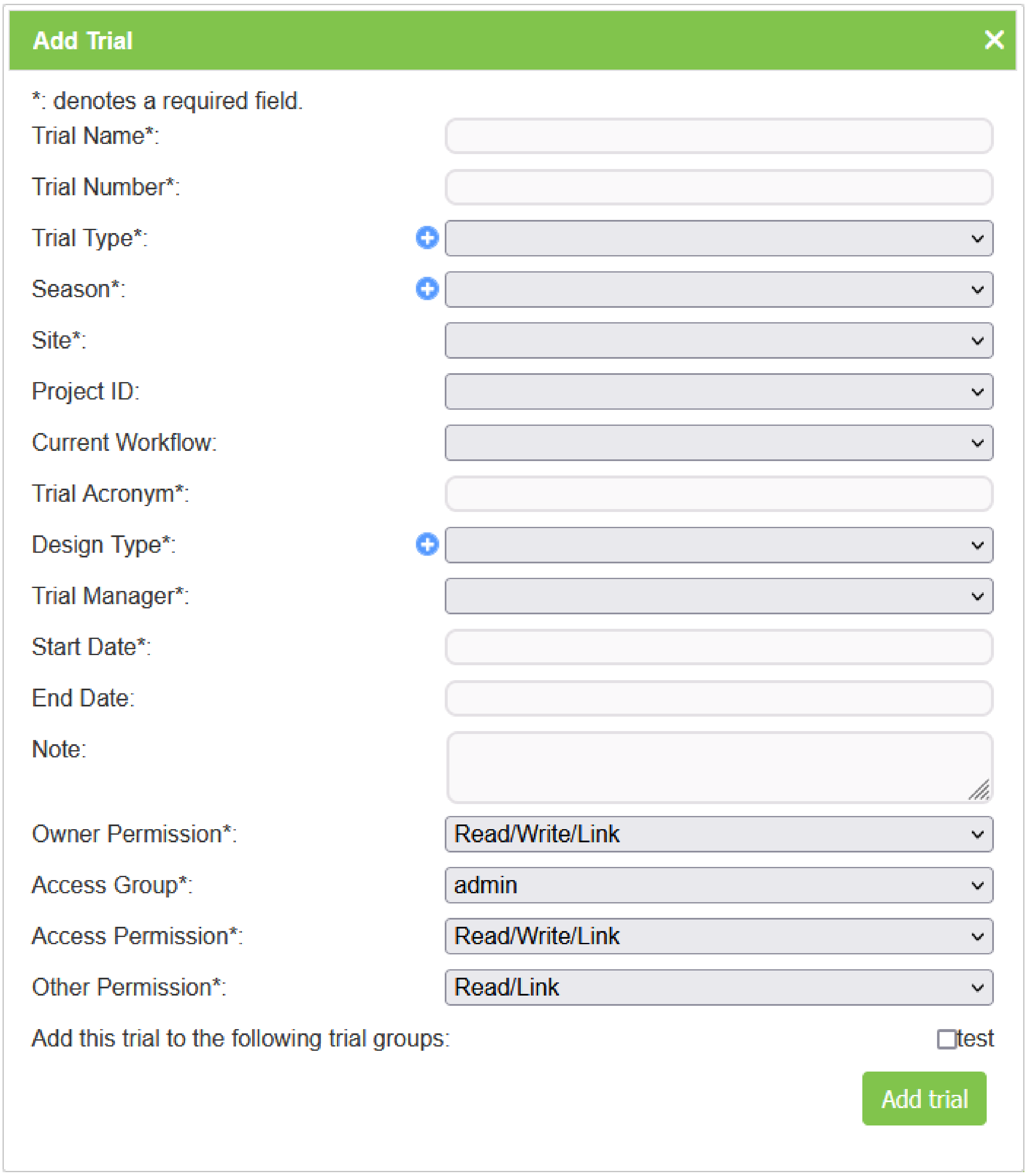
Action	Description	Parent Button
Add Trait to Trial	Add a trait to the trial.	Edit Trial
Download	Download trial data.	Download CSV Template
Edit Trial	Edit the trial.	
Download CSV Template	Down the CSV template for the trial.	
List Trait for Trial	List the traits for the selected trial.	View Trial
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*:

Trial Number*:

Trial Type*:

Season*:

Site*:

Project ID:

Current Workflow:

Trial Acronym*:

Design Type*:

Trial Manager*:

Start Date*:

End Date:

Note:

Owner Permission*: Read/Write/Link

Access Group*: admin

Access Permission*: Read/Write/Link

Other Permission*: Read/Link

Add this trial to the following trial groups: ☐ test

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 *Access Settings and Permissions* 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.

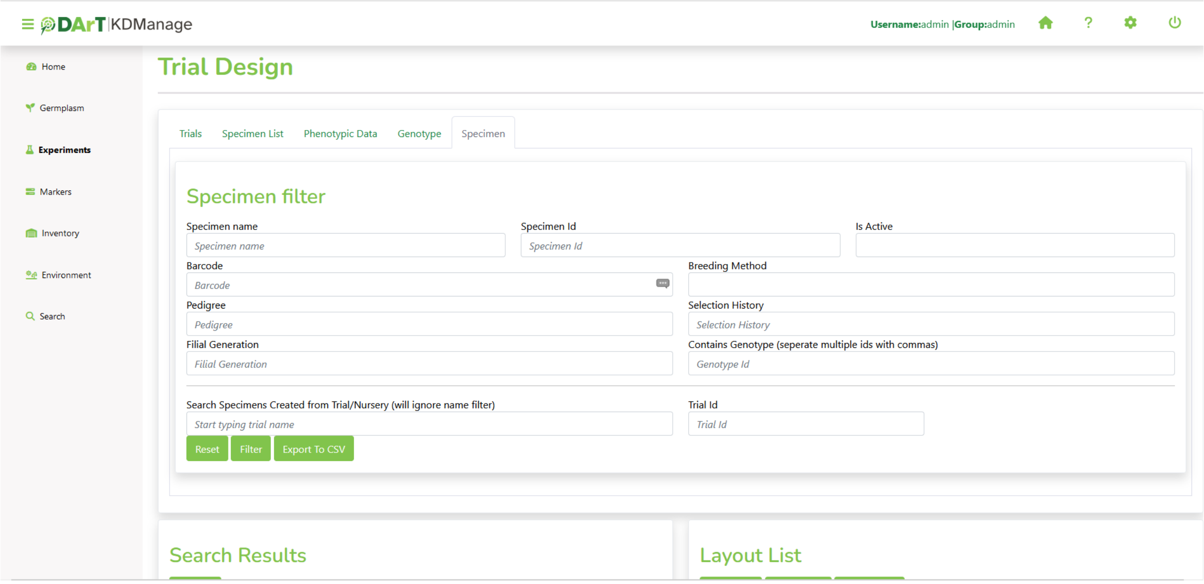
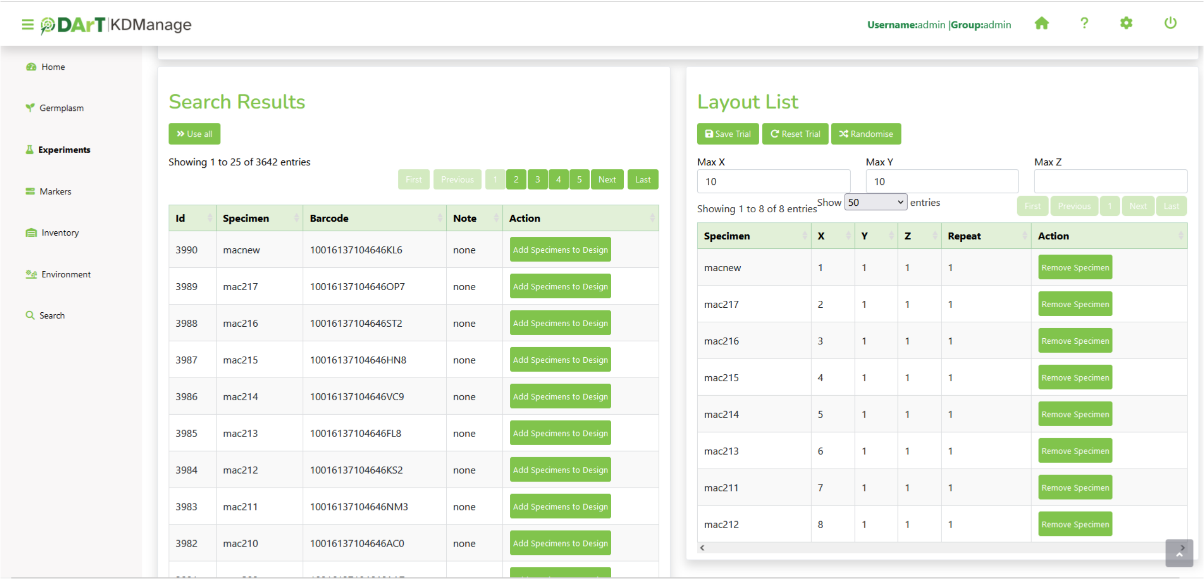


Fig. 9: Trial Design Page

To add the data to map, select from the search results (scroll down, underneath the filters) 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**.



Showing 1 to 25 of 3642 entries

Id	Specimen	Barcode	Note	Action
3990	macnew	10016137104646KL6	none	Add Specimens to Design
3989	mac217	10016137104646OP7	none	Add Specimens to Design
3988	mac216	10016137104646ST2	none	Add Specimens to Design
3987	mac215	10016137104646HN8	none	Add Specimens to Design
3986	mac214	10016137104646VC9	none	Add Specimens to Design
3985	mac213	10016137104646FL8	none	Add Specimens to Design
3984	mac212	10016137104646KS2	none	Add Specimens to Design
3983	mac211	10016137104646NM3	none	Add Specimens to Design
3982	mac210	10016137104646AC0	none	Add Specimens to Design

Max X: 10
Max Y: 10
Max Z:

Showing 1 to 8 of 8 entries Show 50 entries

Specimen	X	Y	Z	Repeat	Action
macnew	1	1	1	1	Remove Specimen
mac217	2	1	1	1	Remove Specimen
mac216	3	1	1	1	Remove Specimen
mac215	4	1	1	1	Remove Specimen
mac214	5	1	1	1	Remove Specimen
mac213	6	1	1	1	Remove Specimen
mac211	7	1	1	1	Remove Specimen
mac212	8	1	1	1	Remove Specimen

Fig. 10: 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

Select Z: 1 Select Orientation: topleft Map Size: 10x10

macnew	mac217	mac216	mac215	mac214	mac213	mac211	mac212	macnew	mac217
mac216	mac214	mac210	mac209	mac208	mac207	mac206	mac205	mac204	mac203
mac202	mac201	mac200	mac199	mac198	mac197	mac196	mac195	mac194	Empty

Fig. 11: 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).
Orientation	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:

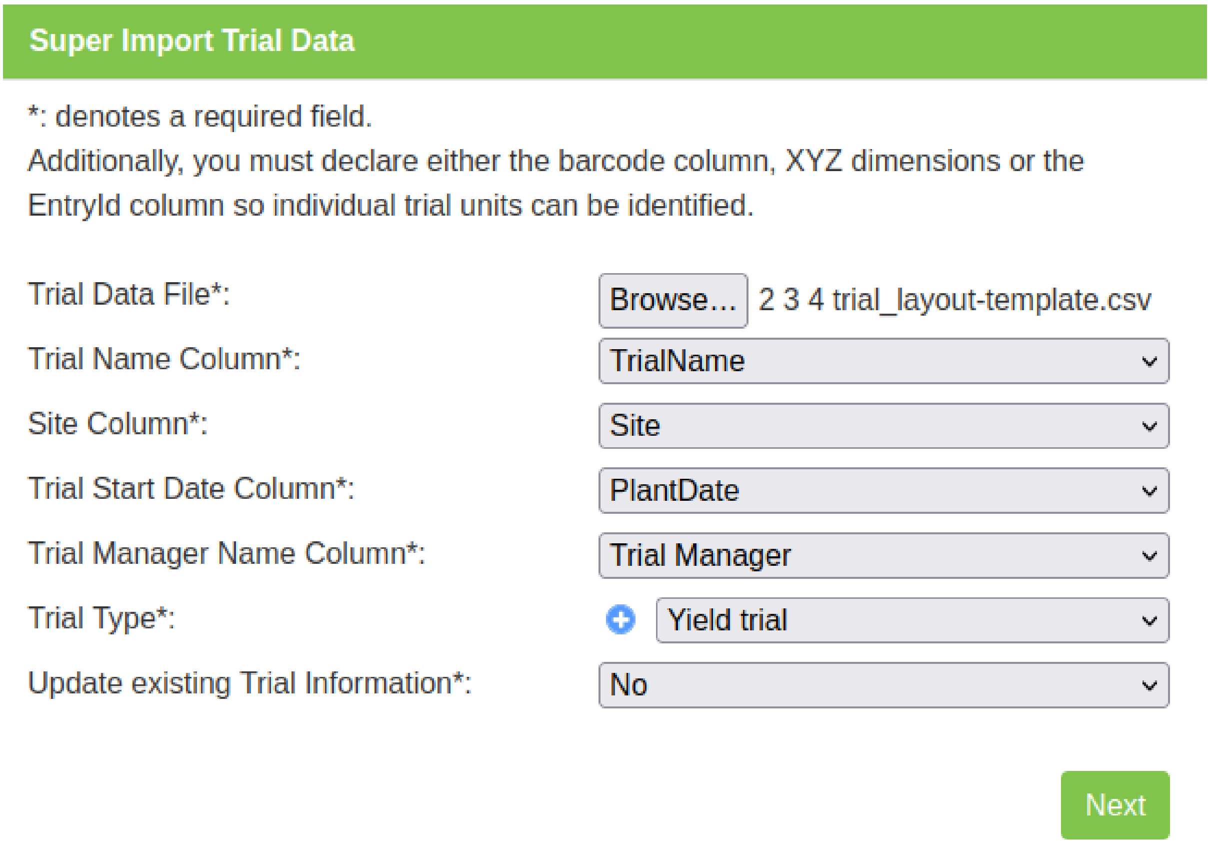
- **Allow creation of Specimens/Genotypes** - determines whether specimens and genotypes that don’t exist should be created.
- **Update existing Trial Information** - determines whether an existing trial should be updated with given information.
- **Update existing Trial Units/Plots** - determines whether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



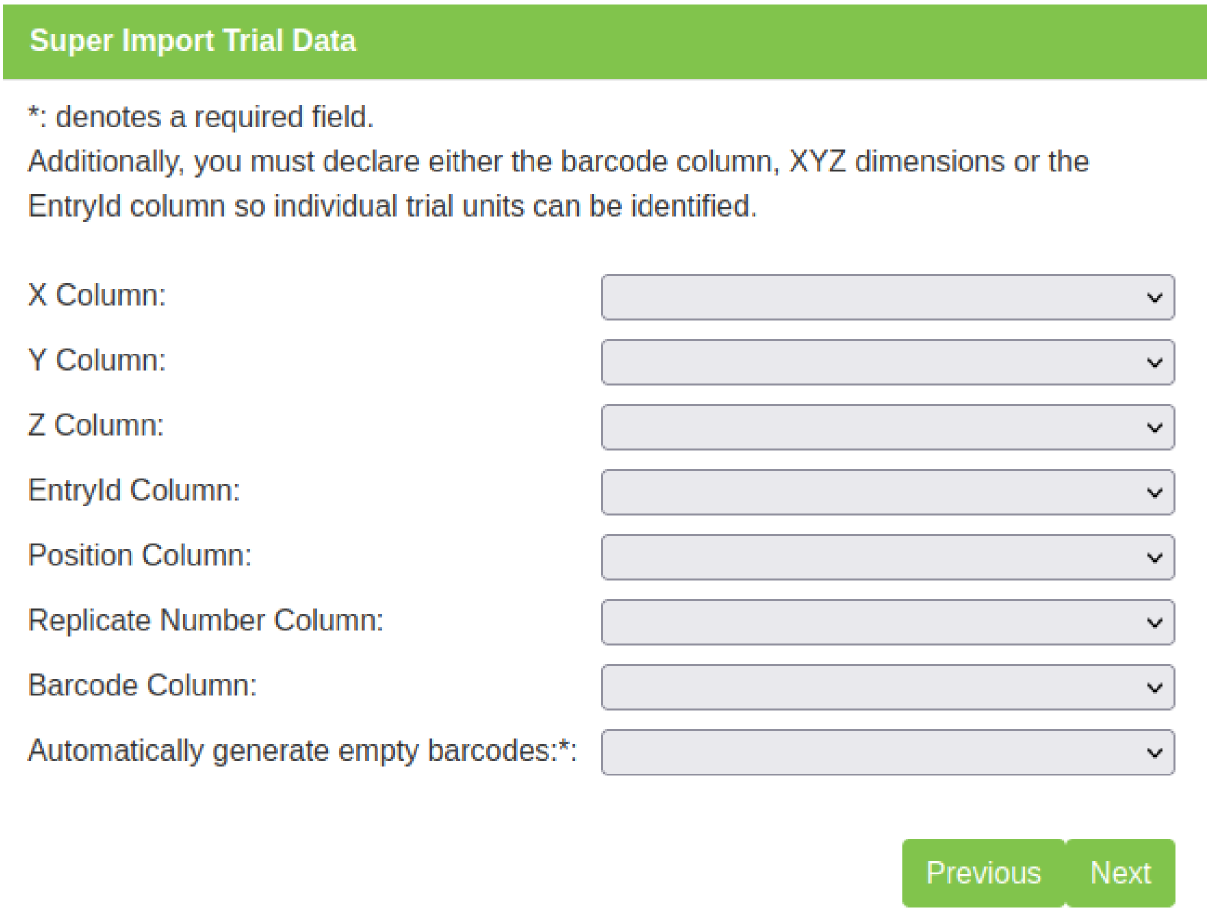
*: denotes a required field.

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

Trial Data File*:	2 3 4 trial_layout-template.csv
Trial Name Column*:	TrialName
Site Column*:	Site
Trial Start Date Column*:	PlantDate
Trial Manager Name Column*:	Trial Manager
Trial Type*:	Yield trial
Update existing Trial Information*:	No

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.

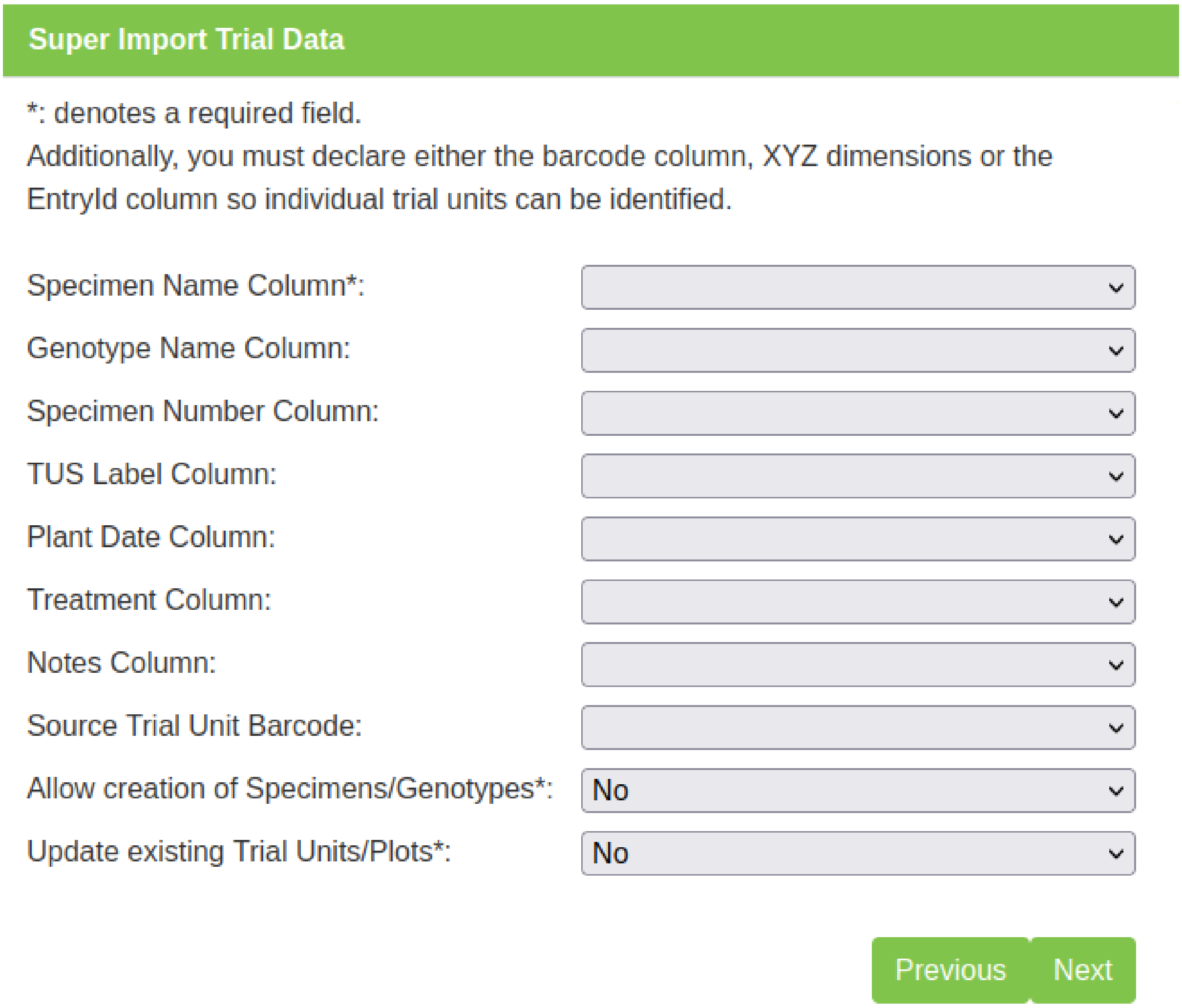
Field	Mandatory	Description
X Column	(!)	One of the trial dimension columns as part of XYZ which will be added to new trials, to create new trial units and to identify existing trial units.
Y Column	(!)	One of the trial dimension columns as part of XYZ which will be added to new trials, to create new 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.

continues on next page

Table 5 – continued from previous page

Field	Mandatory	Description
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



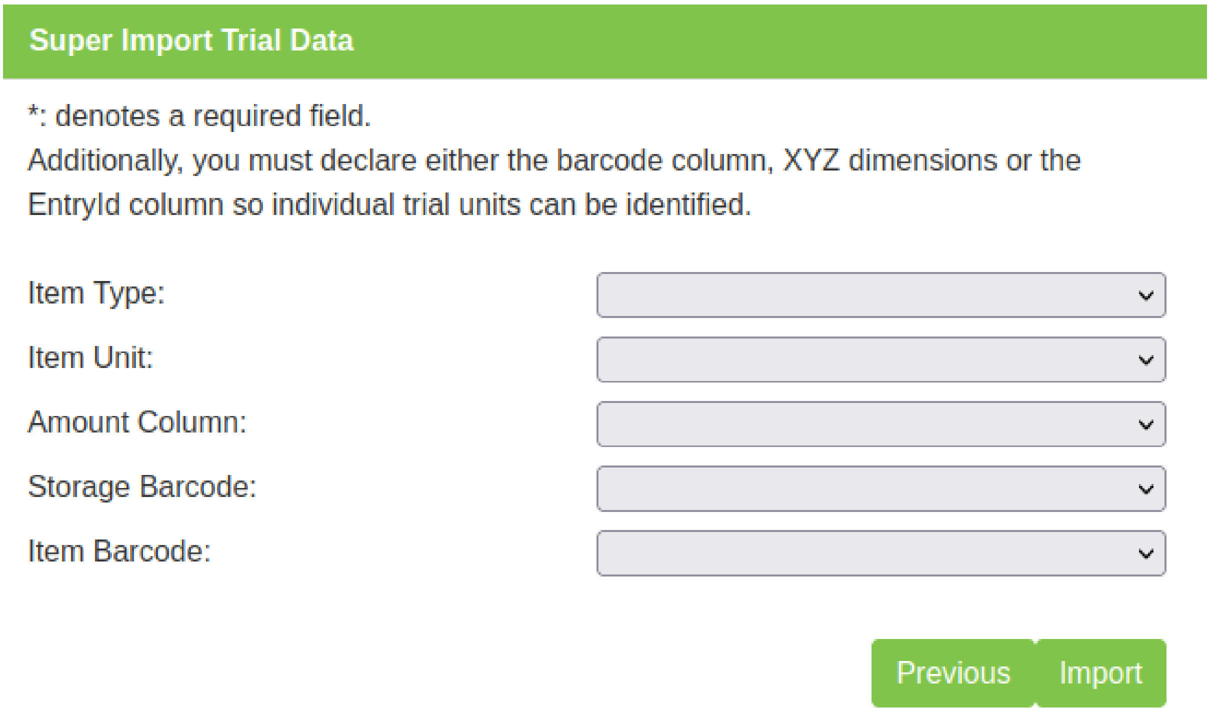
Super Import Trial Data

*: 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*:	No
Update existing Trial Units/Plots*:	No

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.
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:

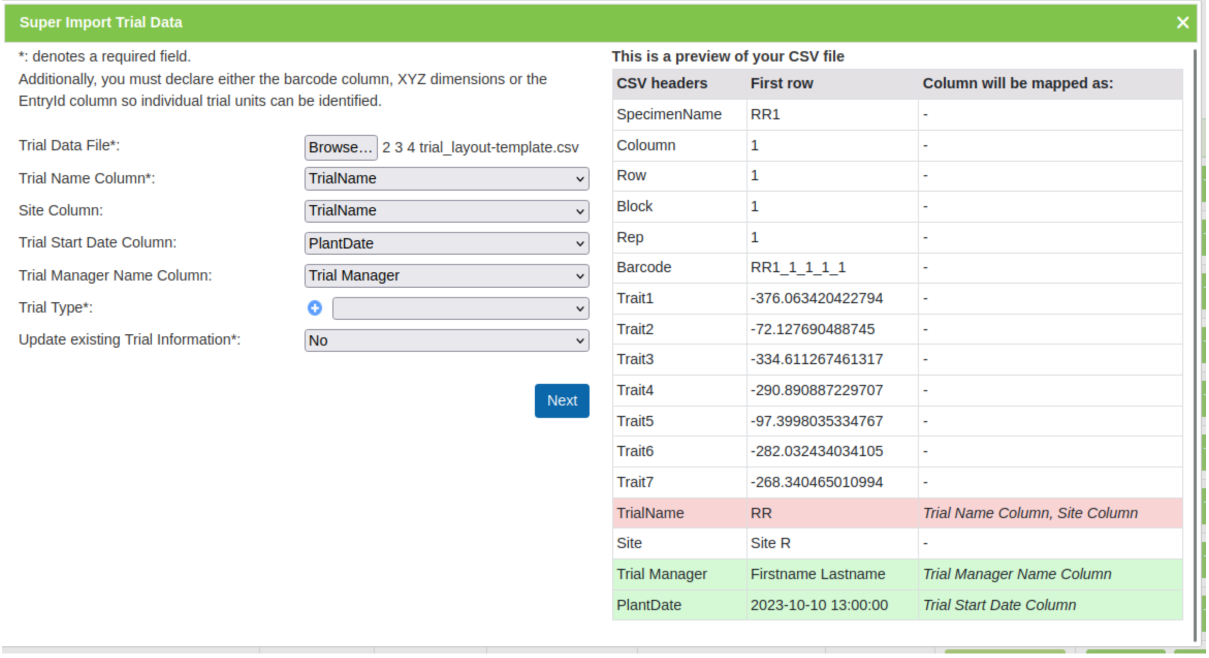
Storage Barcode:

Item Barcode:

Field	Mandatory	Description
Item Type		The column that contains the Item Type for each item. Also, a flag to determine whether ths 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.

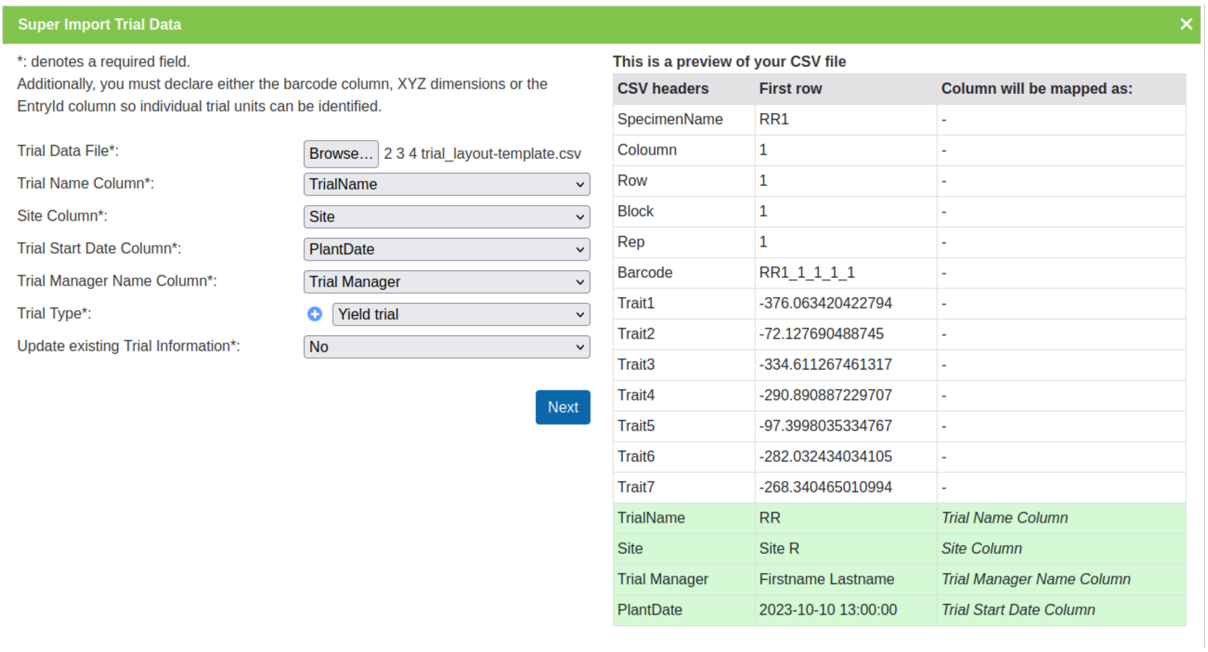
Trial Data File*: Browse... 2 3 4 trial_layout-template.csv
Trial Name Column*: TrialName
Site Column: TrialName
Trial Start Date Column: PlantDate
Trial Manager Name Column: Trial Manager
Trial Type*:
Update existing Trial Information*: No

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
SpecimenName	RR1	-
Coloumn	1	-
Row	1	-
Block	1	-
Rep	1	-
Barcode	RR1_1_1_1_1	-
Trait1	-376.063420422794	-
Trait2	-72.127690488745	-
Trait3	-334.611267461317	-
Trait4	-290.890887229707	-
Trait5	-97.3998035334767	-
Trait6	-282.032434034105	-
Trait7	-268.340465010994	-
TrialName	RR	*Trial Name Column, Site Column*
Site	Site R	-
Trial Manager	Firstname Lastname	*Trial Manager Name Column*
PlantDate	2023-10-10 13:00:00	*Trial Start Date Column*

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

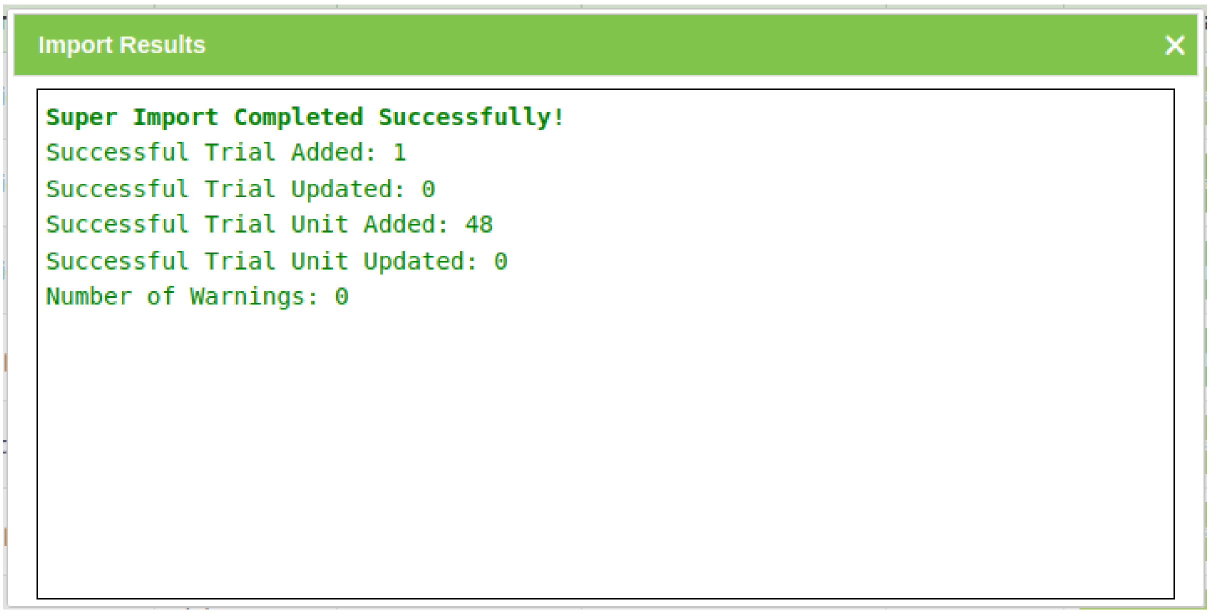
*: denotes a required field.
Additionally, you must declare either the barcode column, XYZ dimensions or the EntryId column so individual trial units can be identified.

Trial Data File*: 2 3 4 trial_layout-template.csv
Trial Name Column*: TrialName
Site Column*: Site
Trial Start Date Column*: PlantDate
Trial Manager Name Column*: Trial Manager
Trial Type*: Yield trial
Update existing Trial Information*: No

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
SpecimenName	RR1	-
Coloumn	1	-
Row	1	-
Block	1	-
Rep	1	-
Barcode	RR1_1_1_1_1	-
Trait1	-376.063420422794	-
Trait2	-72.127690488745	-
Trait3	-334.611267461317	-
Trait4	-290.890887229707	-
Trait5	-97.3998035334767	-
Trait6	-282.032434034105	-
Trait7	-268.340465010994	-
TrialName	RR	*Trial Name Column*
Site	Site R	*Site Column*
Trial Manager	Firstname Lastname	*Trial Manager Name Column*
PlantDate	2023-10-10 13:00:00	*Trial Start Date Column*

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.



Import Results

```
Super Import Completed Successfully!
Successful Trial Added: 1
Successful Trial Updated: 0
Successful Trial Unit Added: 48
Successful Trial Unit Updated: 0
Number of Warnings: 0
```

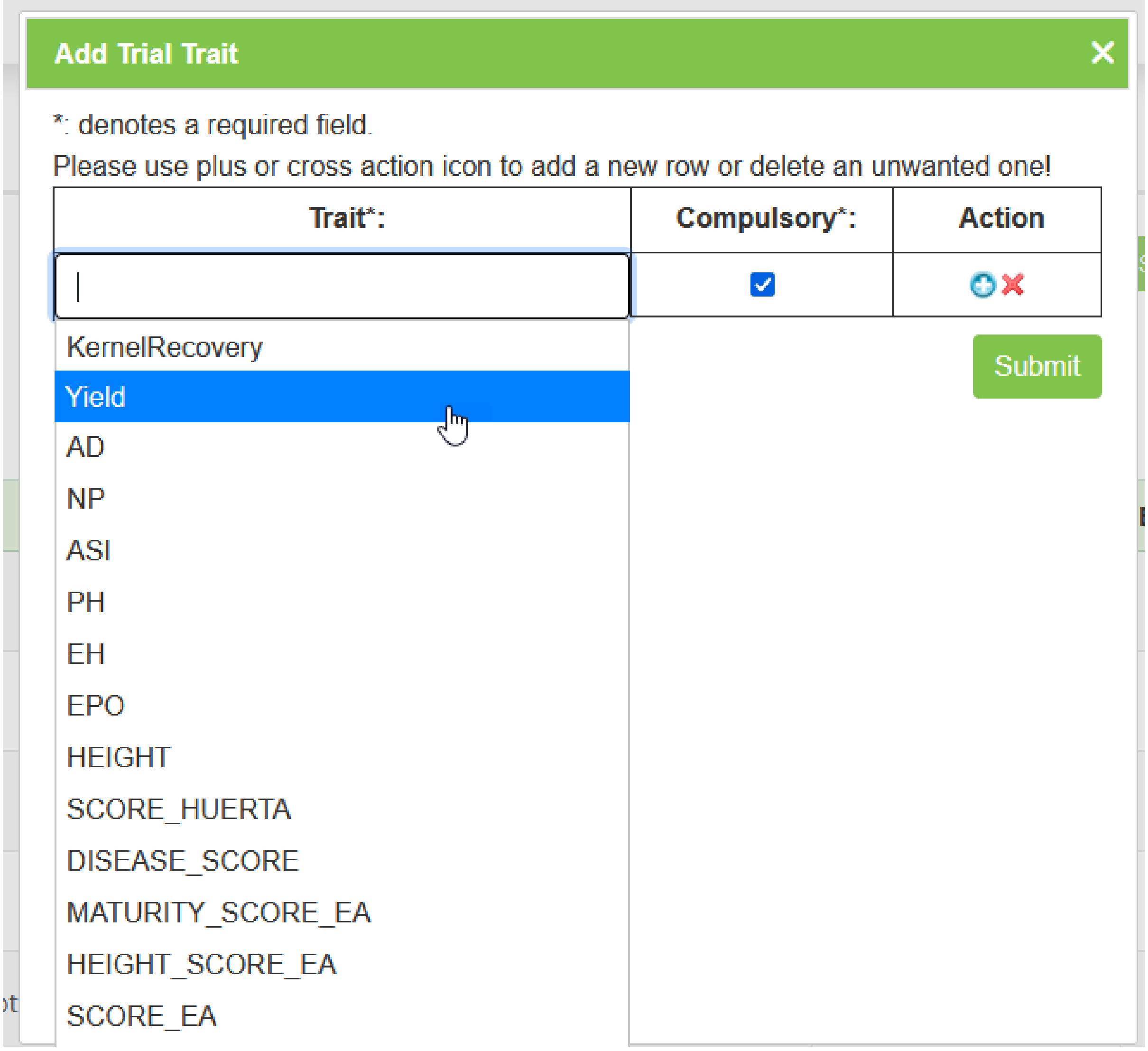
The general statistics are displayed at the top, while all the warnings will are printed in yellow below.

5.5.2 Add Traits to a Trial

Selecting **Add a Trait to Trial** (under **Edit Trial 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
	☑	⊕ ✕

Fig. 12: Add Trial Trait Window

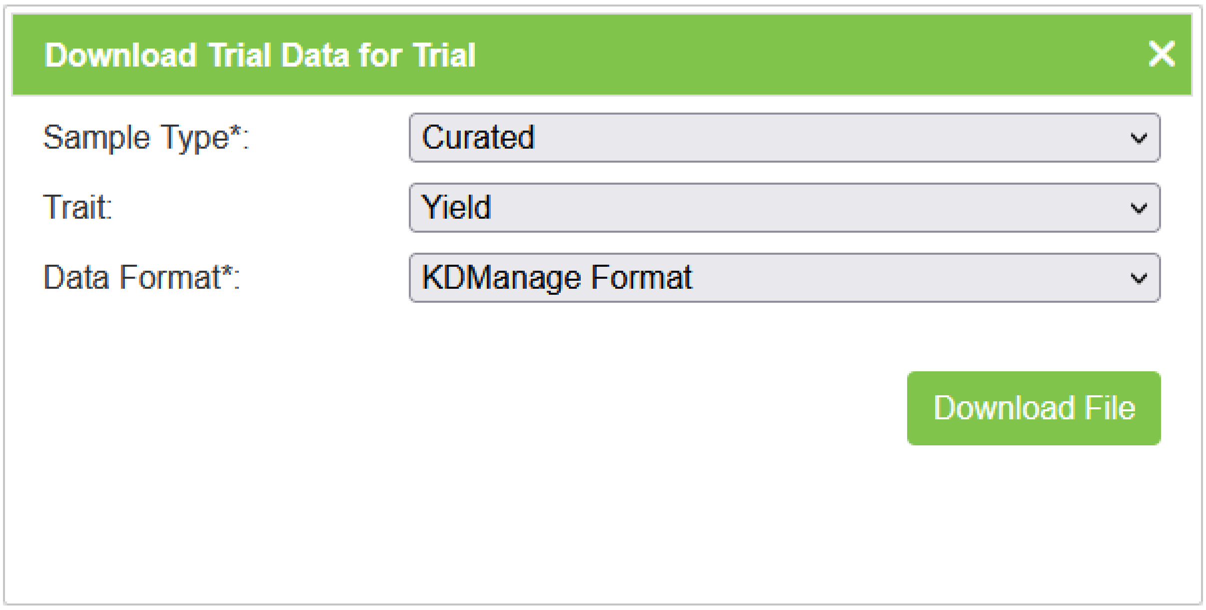
The trait is selected from a list of predefined traits (refer to the *Traits* topic).

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 the **Edit Trial dropdown**) from the **Action Column**.

5.5.3 Downloading Trial Data

To download trial data in CSV format, select the **Download CSV Template button** for the required trial and then the **Download Trial Data** option. 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

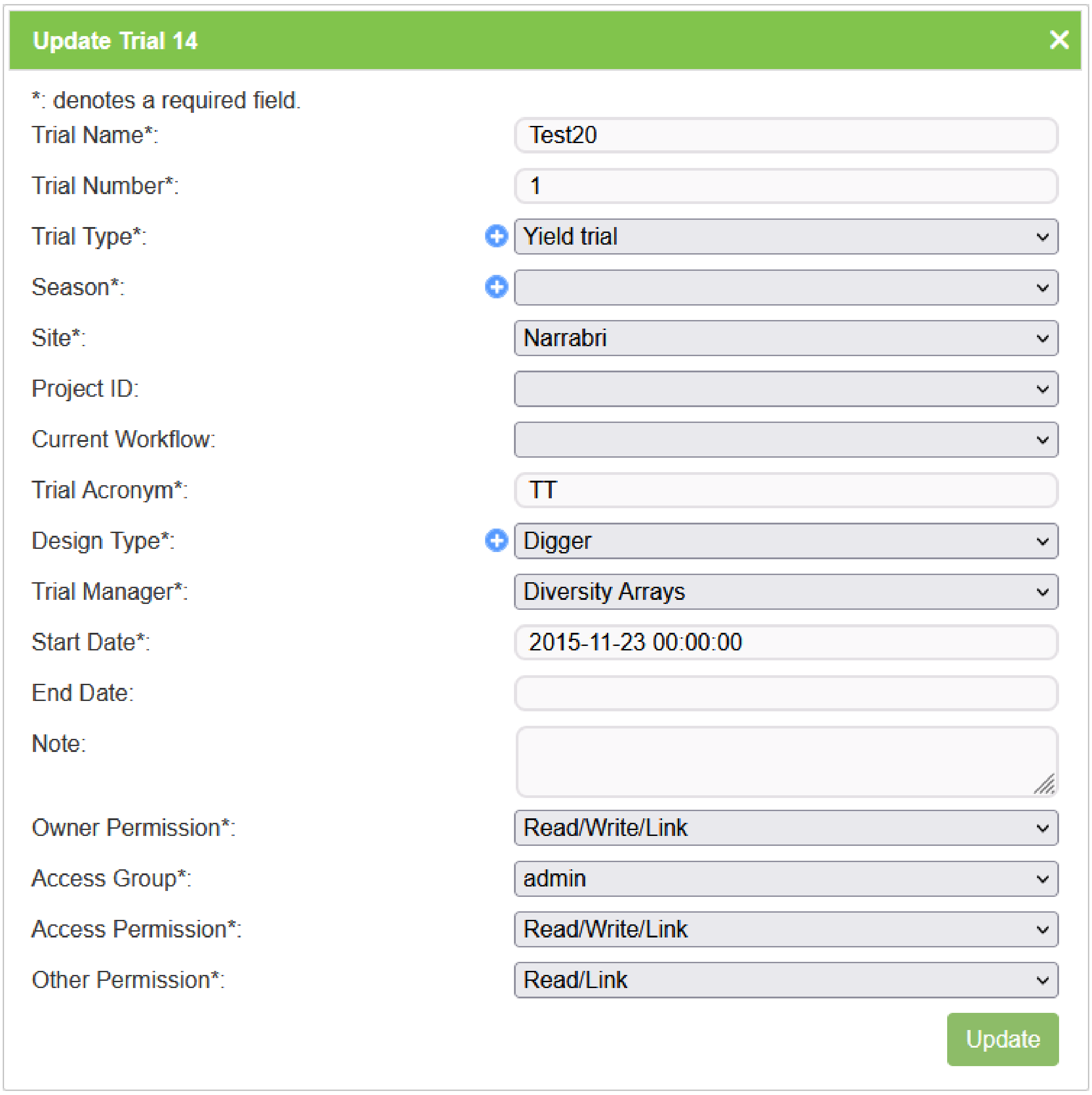
Trait: Yield

Data Format*: KDManage Format

Fig. 13: Download Trial Data Window

5.5.4 Editing Trials

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



Update Trial 14

*: denotes a required field.

Trial Name*:	Test20
Trial Number*:	1
Trial Type*:	Yield trial
Season*:	
Site*:	Narrabri
Project ID:	
Current Workflow:	
Trial Acronym*:	TT
Design Type*:	Digger
Trial Manager*:	Diversity Arrays
Start Date*:	2015-11-23 00:00:00
End Date:	
Note:	
Owner Permission*:	Read/Write/Link
Access Group*:	admin
Access Permission*:	Read/Write/Link
Other Permission*:	Read/Link

Fig. 14: 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

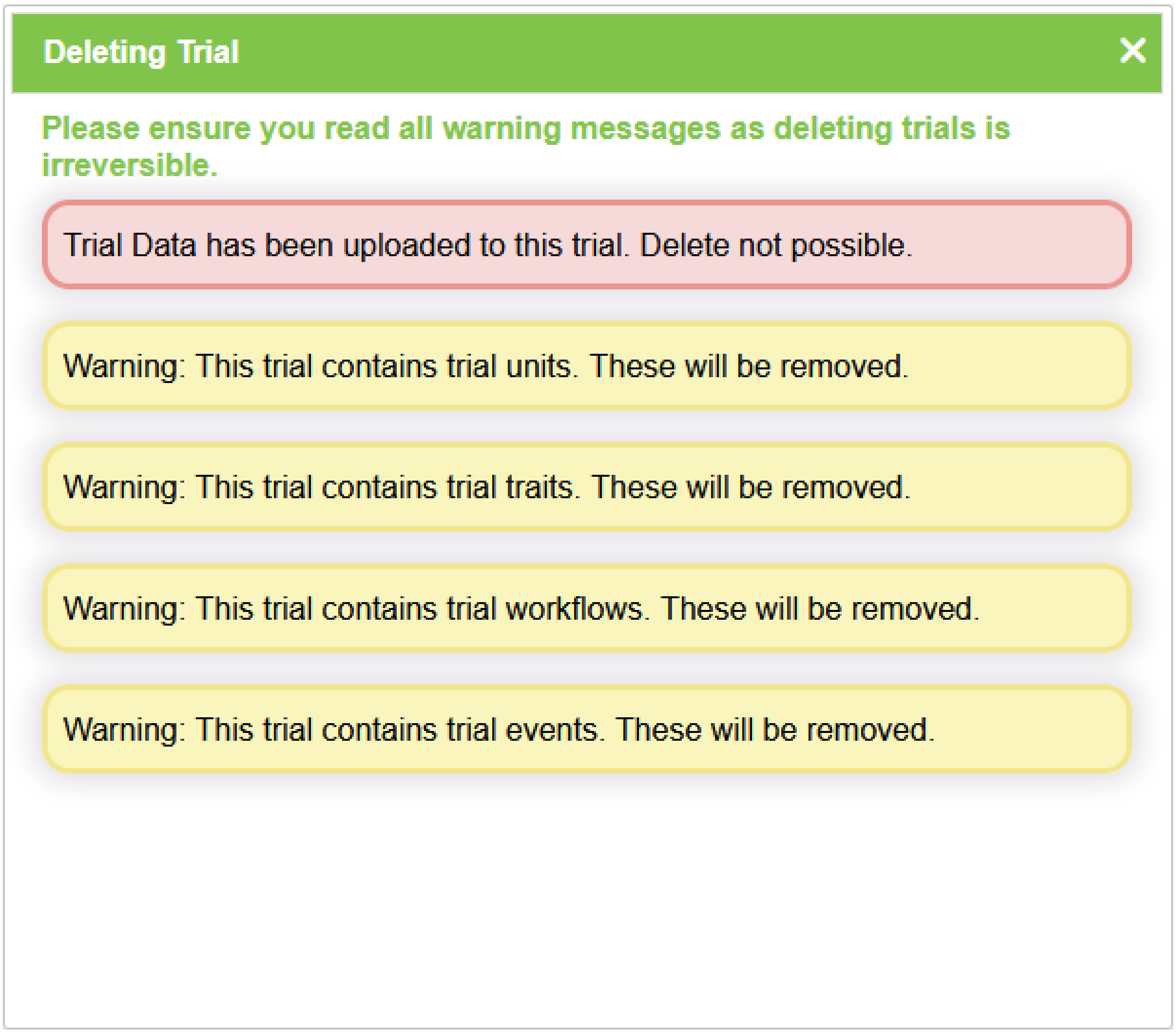
KDManage can be used to delete trials from a KDDart database by selecting the ||kdmanage-button-deletetrial|| **Delete Button** for the relevant trial.

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:



Deleting Trial

Please ensure you read all warning messages as deleting trials is irreversible.

Trial Data has been uploaded to this trial. Delete not possible.

Warning: This trial contains trial units. These will be removed.

Warning: This trial contains trial traits. These will be removed.

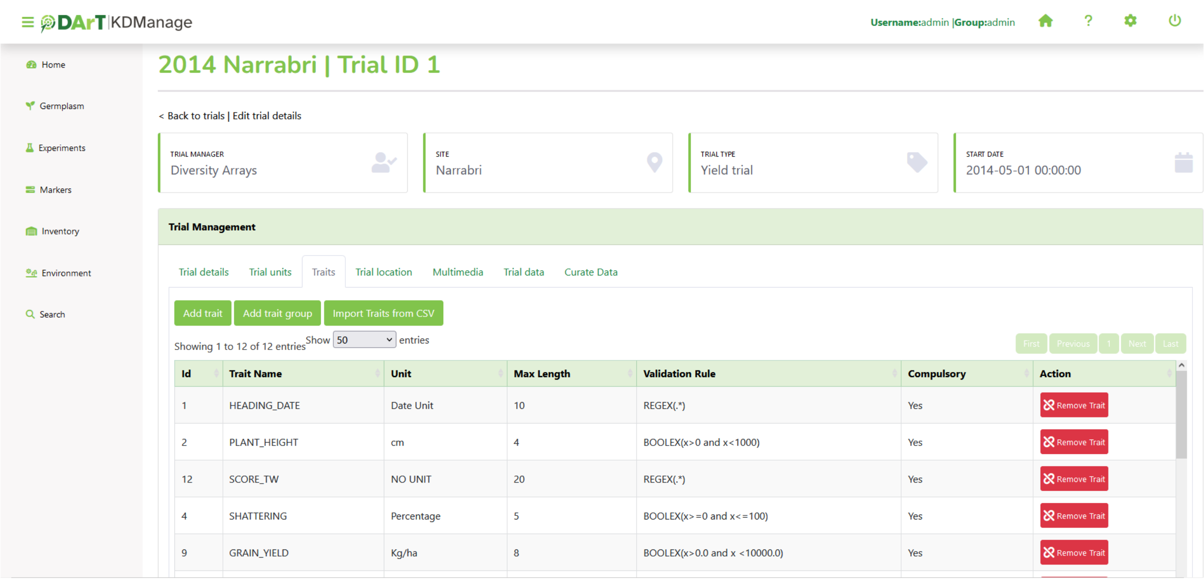
Warning: This trial contains trial workflows. These will be removed.

Warning: This trial contains trial events. These will be removed.

Fig. 15: Delete a Trial

5.5.6 List Traits

To display the traits for a trial, select the **View Trial button** and then the **Traits tab**.



2014 Narrabri | Trial ID 1

TRIAL MANAGER Diversity Arrays

SITE Narrabri

TRIAL TYPE Yield trial

START DATE 2014-05-01 00:00:00

Showing 1 to 12 of 12 entries

Id	Trait Name	Unit	Max Length	Validation Rule	Compulsory	Action
1	HEADING_DATE	Date Unit	10	REGEX(.*)	Yes	Remove Trait
2	PLANT_HEIGHT	cm	4	BOOLEX(x>0 and x<1000)	Yes	Remove Trait
12	SCORE_TW	NO UNIT	20	REGEX(.*)	Yes	Remove Trait
4	SHATTERING	Percentage	5	BOOLEX(x>=0 and x<=100)	Yes	Remove Trait
9	GRAIN_YIELD	Kg/ha	8	BOOLEX(x>0.0 and x <10000.0)	Yes	Remove Trait

Fig. 16: Traits List

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 proceeding 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 proceeding column.

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

Plot data: [TRAITNAME]:[INSTANCENUMBER] Sub-plot data: [TRAITNAME]:[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

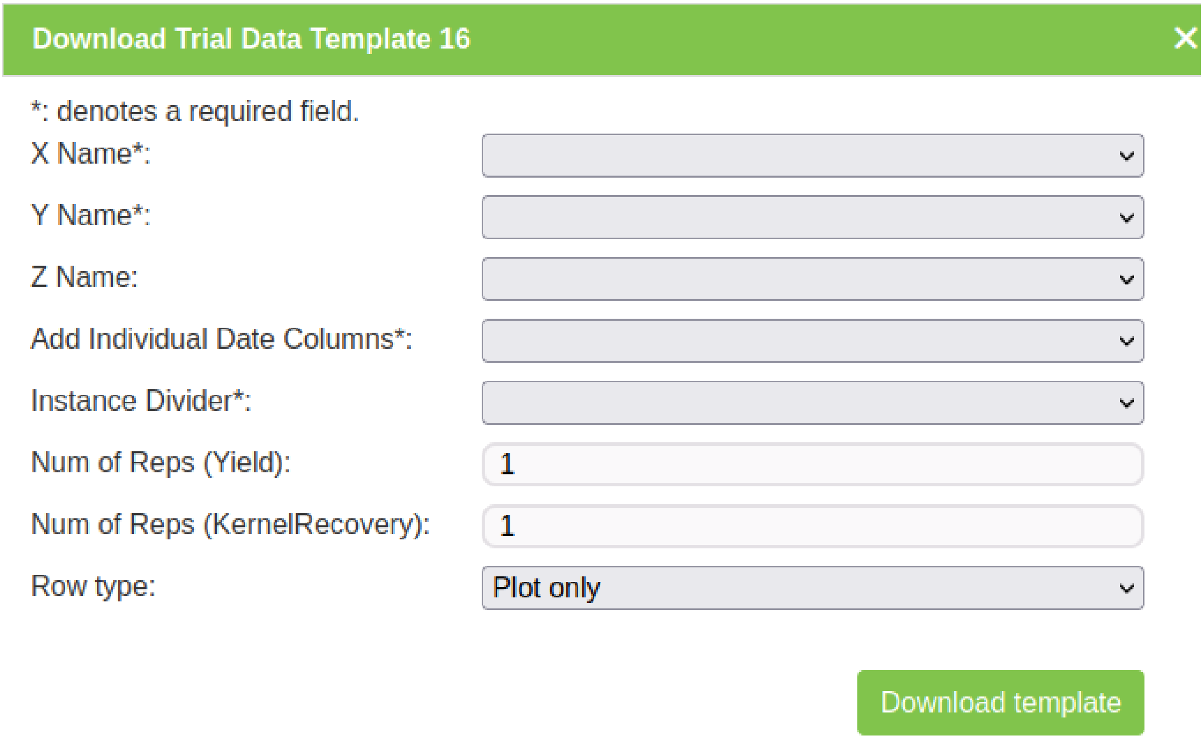
This is also called the *sample measurement format* and is the format that uses the Database ID identities (including TrialUnitId, TrialUnitSpecimenId and TraitId) to directly upload data to the database. This is only recommended for advanced users as it requires a good understanding of the KDDArT database 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 16

*: denotes a required field.

X Name*:

Y Name*:

Z Name:

Add Individual Date Columns*:

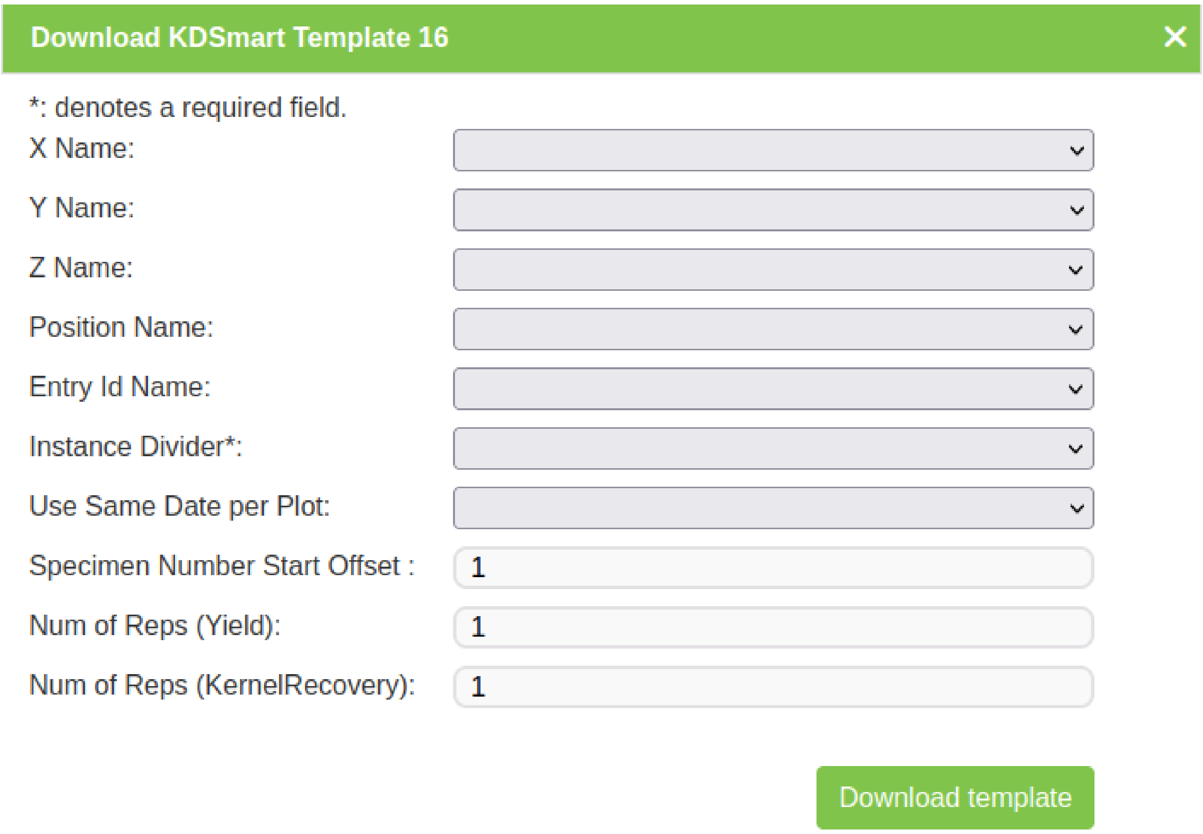
Instance Divider*:

Num of Reps (Yield): 1

Num of Reps (KernelRecovery): 1

Row type: Plot only

Fig. 17: Exporting a KDManage CSV Format Template



*: 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 : 1
Num of Reps (Yield): 1
Num of Reps (KernelRecovery): 1

Fig. 18: Exporting a KDSmart CSV Format Template

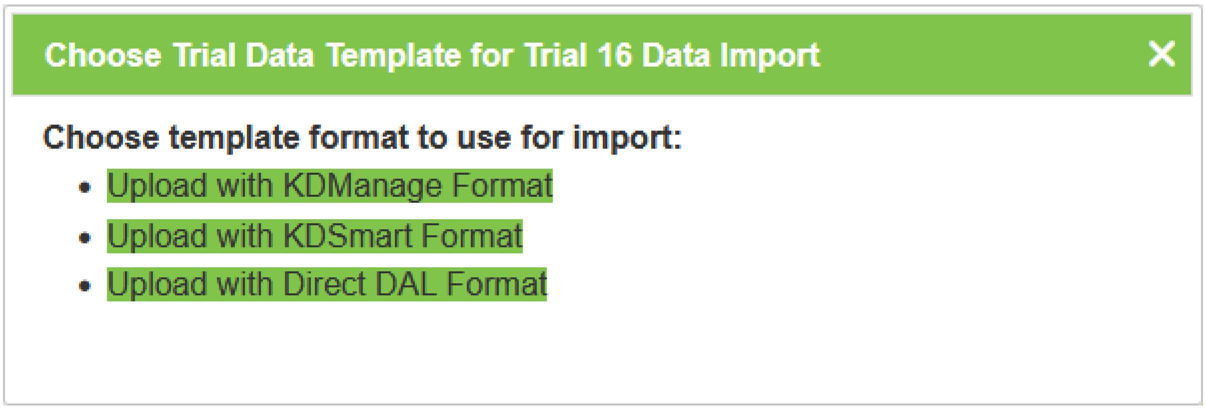
For the KDManage format, users will be given the choice to add date/time columns per trait instance per plot/sub-plot row.

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.

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.



Choose Trial Data Template for Trial 16 Data Import

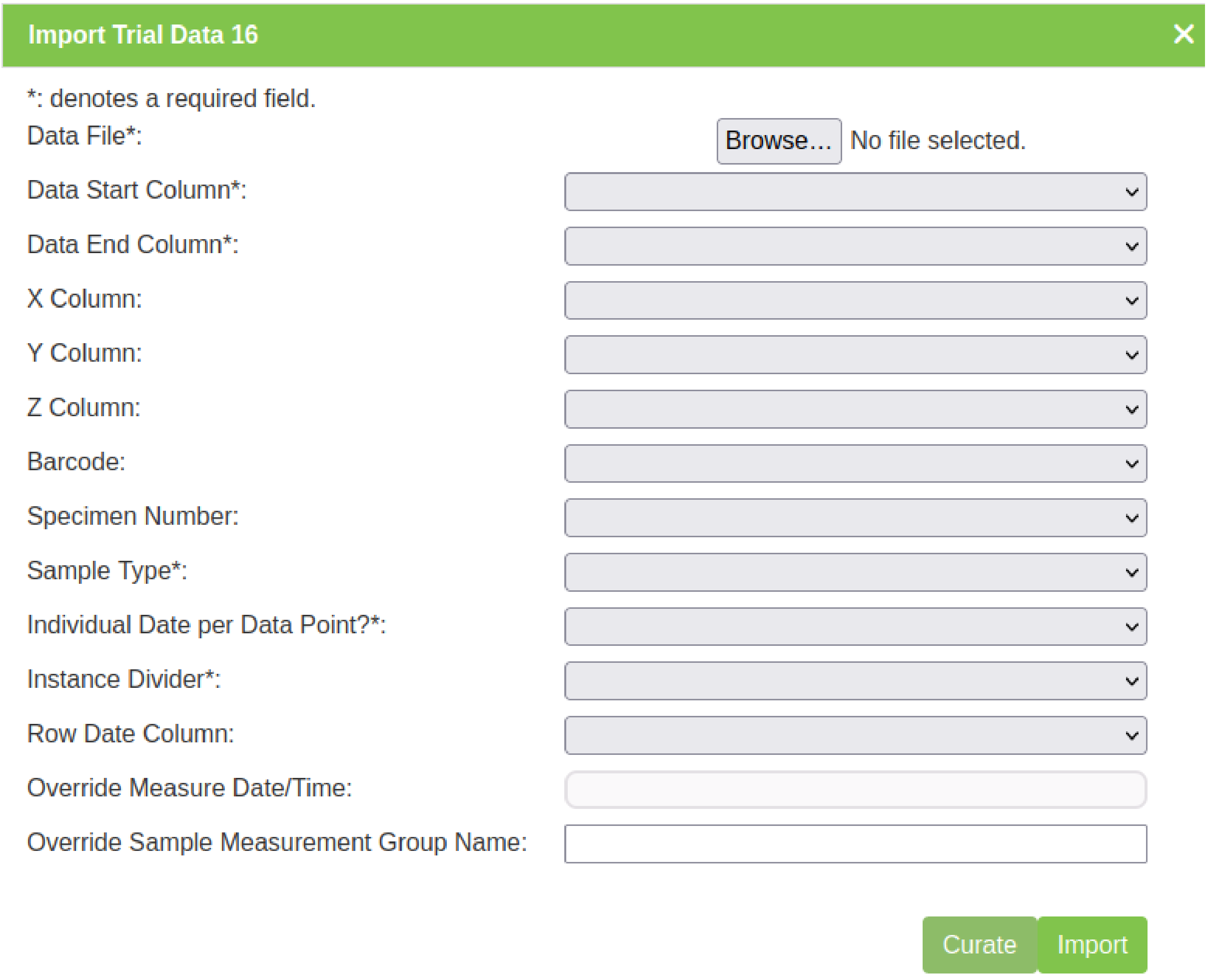
Choose template format to use for import:

- Upload with KDManage Format
- Upload with KDSmart Format
- Upload with Direct DAL 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.



Import Trial Data 16

*: denotes a required field.

Data File*: No file selected.

Data Start Column*:

Data End Column*:

X Column:

Y Column:

Z Column:

Barcode:

Specimen Number:

Sample Type*:

Individual Date per Data Point?*:

Instance Divider*:

Row Date Column:

Override Measure Date/Time:

Override Sample Measurement Group Name:

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**:

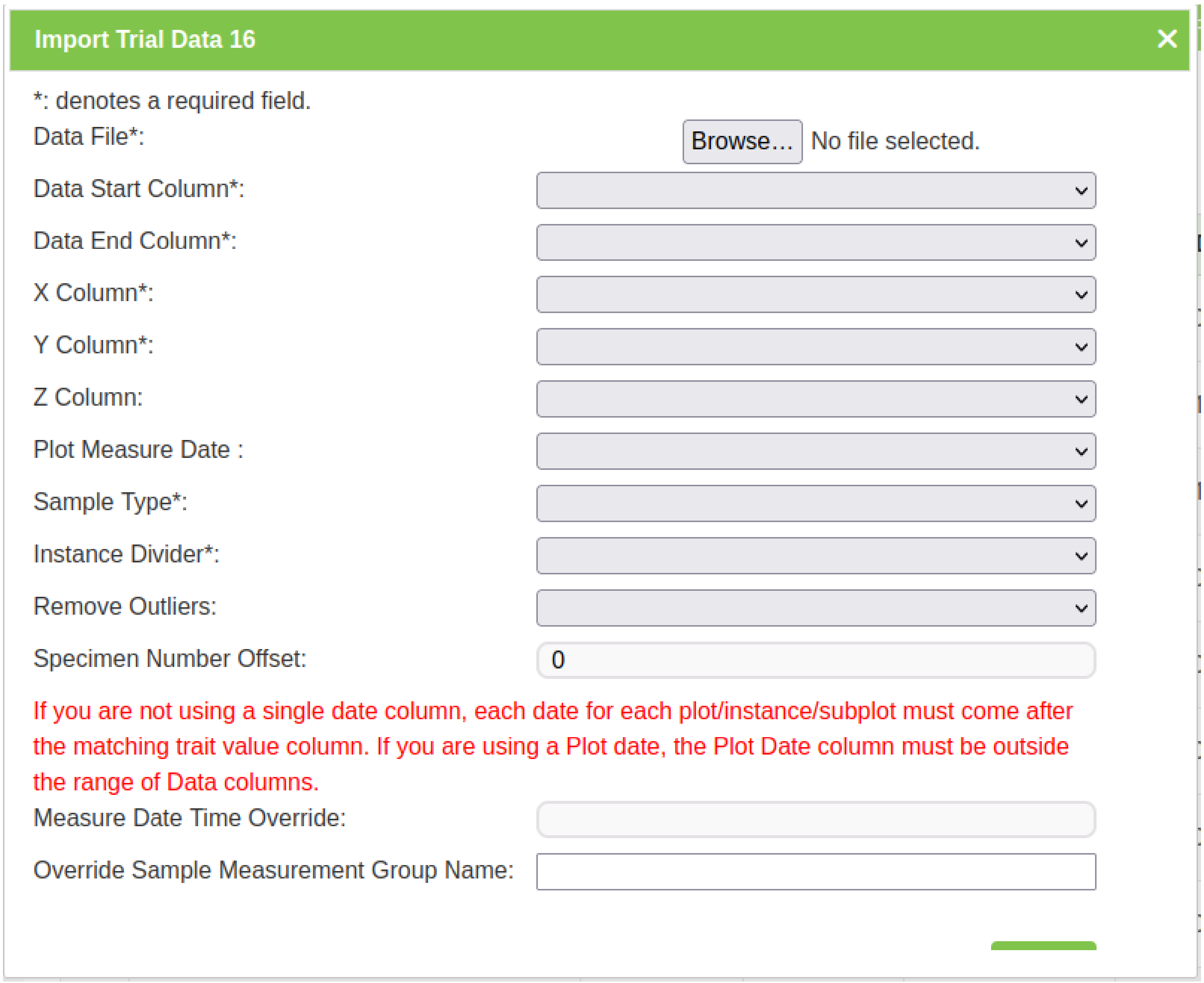
Table 8: Import KDManage Trial Data Format Fields

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 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.



*: denotes a required field.
Data File*:
Data Start Column*:
Data End Column*:
X Column*:
Y Column*:
Z Column:
Plot Measure Date :
Sample Type*:
Instance Divider*:
Remove Outliers:
Specimen Number Offset: 0

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.

Measure Date Time Override:
Override Sample Measurement Group Name:

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**:

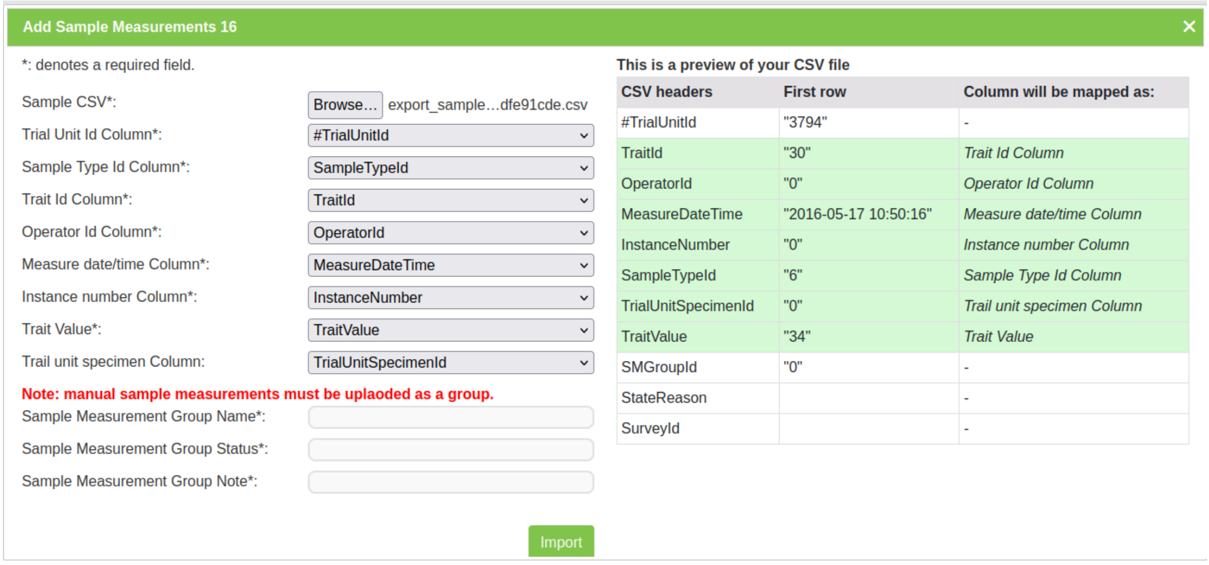
Table 9: Import KDSmart Trial Data Format Fields

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:



Add Sample Measurements 16

*: denotes a required field.

Sample CSV*: export_sample…dfe91cde.csv
Trial Unit Id Column*: #TrialUnitId
Sample Type Id Column*: SampleTypeId
Trait Id Column*: TraitId
Operator Id Column*: OperatorId
Measure date/time Column*: MeasureDateTime
Instance number Column*: InstanceNumber
Trait Value*: TraitValue
Trail unit specimen Column: TrialUnitSpecimenId

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

Sample Measurement Group Name*:
Sample Measurement Group Status*:
Sample Measurement Group Note*:

This is a preview of your CSV file

CSV headers	First row	Column will be mapped as:
#TrialUnitId	"3794"	-
TraitId	"30"	*Trait Id Column*
OperatorId	"0"	*Operator Id Column*
MeasureDateTime	"2016-05-17 10:50:16"	*Measure date/time Column*
InstanceNumber	"0"	*Instance number Column*
SampleTypeId	"6"	*Sample Type Id Column*
TrialUnitSpecimenId	"0"	*Trail unit specimen Column*
TraitValue	"34"	*Trait Value*
SMGroupId	"0"	-
StateReason		-
SurveyId		-

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 *List Traits*)
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.

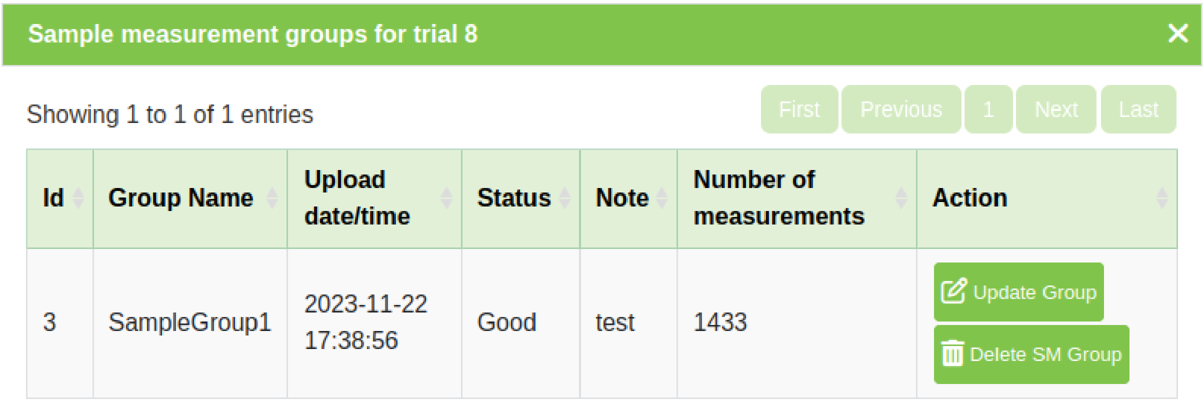
If required, sample measurements can also be uploaded and added to a new sample measurement group.

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:


Sample measurement groups for trial 8

Showing 1 to 1 of 1 entries

Id	Group Name	Upload date/time	Status	Note	Number of measurements	Action
3	SampleGroup1	2023-11-22 17:38:56	Good	test	1433	Update Group Delete SM Group

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.

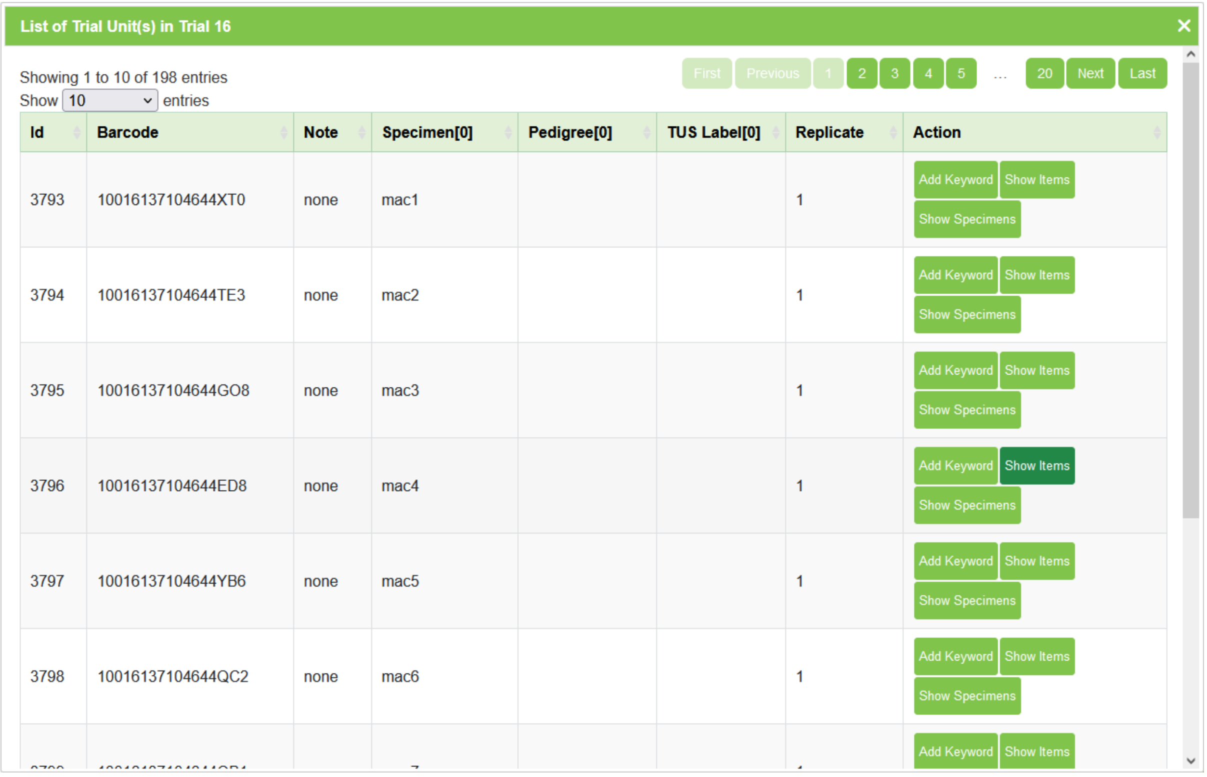
Table 12: Sample Measurement Group Actions

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 the **View Trial dropdown** in the **Action Column** to display the **List of Trial Units Window**:



List of Trial Unit(s) in Trial 16

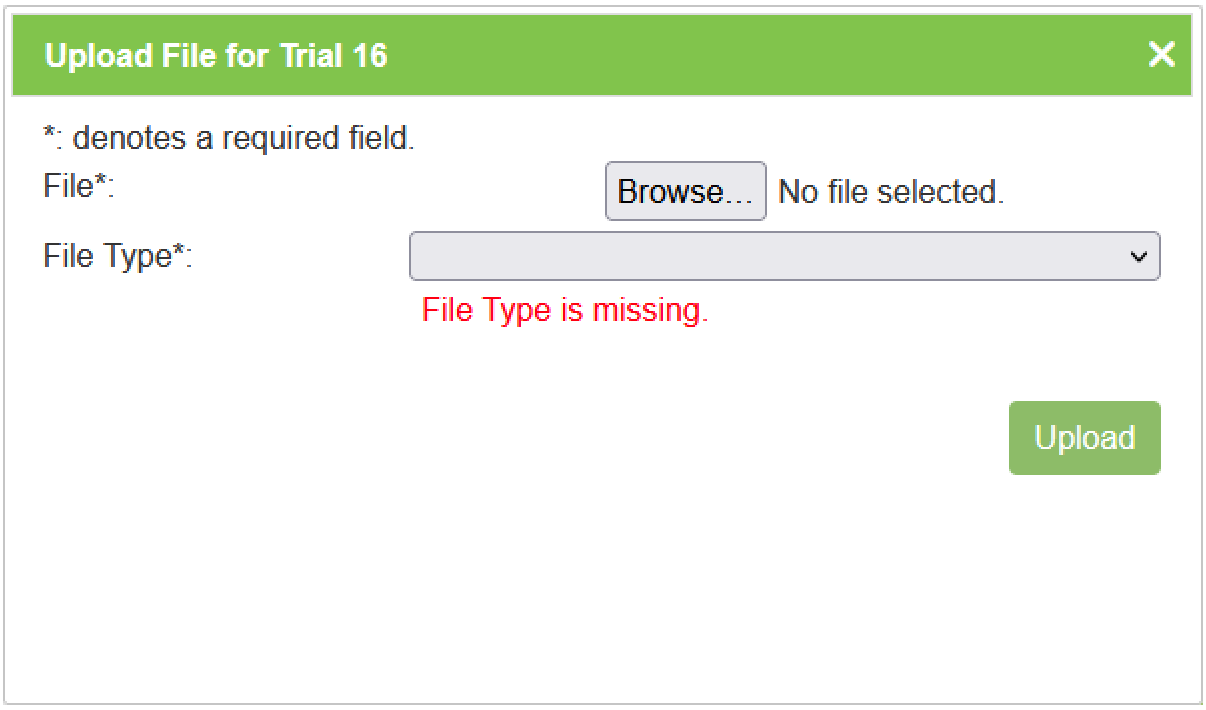
Showing 1 to 10 of 198 entries
Show 10 entries

Id	Barcode	Note	Specimen[0]	Pedigree[0]	TUS Label[0]	Replicate	Action
3793	10016137104644XT0	none	mac1			1	Add Keyword Show Items Show Specimens
3794	10016137104644TE3	none	mac2			1	Add Keyword Show Items Show Specimens
3795	10016137104644GO8	none	mac3			1	Add Keyword Show Items Show Specimens
3796	10016137104644ED8	none	mac4			1	Add Keyword Show Items Show Specimens
3797	10016137104644YB6	none	mac5			1	Add Keyword Show Items Show Specimens
3798	10016137104644QC2	none	mac6			1	Add Keyword Show Items Show Specimens
							Add Keyword Show Items

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 the **View Trial dropdown button**)in the **Action Column** to display the **Upload File Window** (below image). File types are defined in the *Types* page.



Upload File for Trial 16

*: denotes a required field.

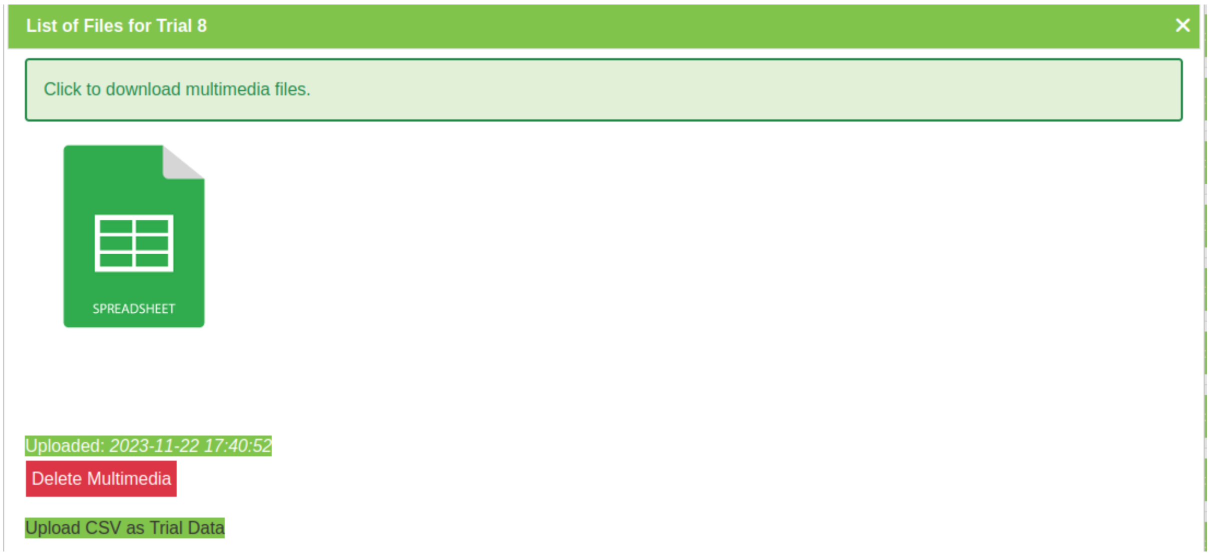
File*: No file selected.

File Type*:

File Type is missing.

Fig. 25: Upload File Window

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



List of Files for Trial 8

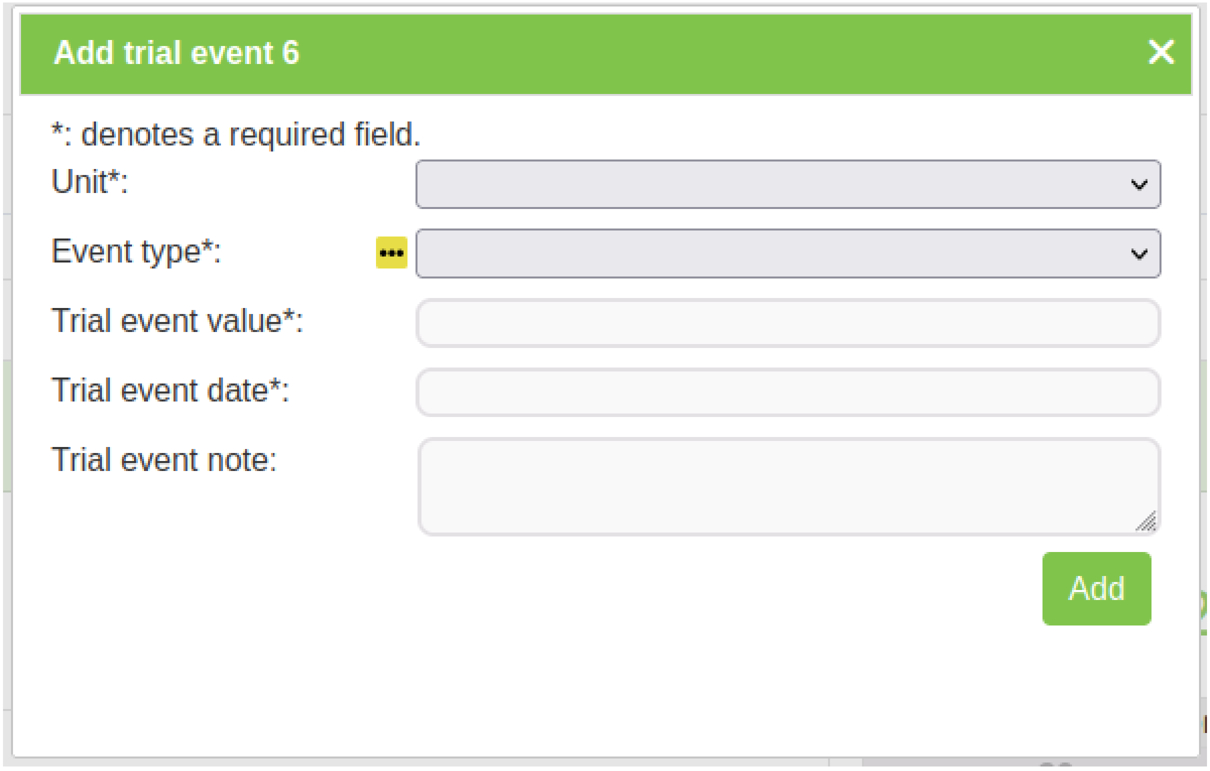
Click to download multimedia files.

Uploaded: *2023-11-22 17:40:52*

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**.



Add trial event 6

*: denotes a required field.

Unit*:

Event type*:

Trial event value*:

Trial event date*:

Trial event note:

Fig. 27: Add Trial Event Window

Table 13: Add Trial Event Fields

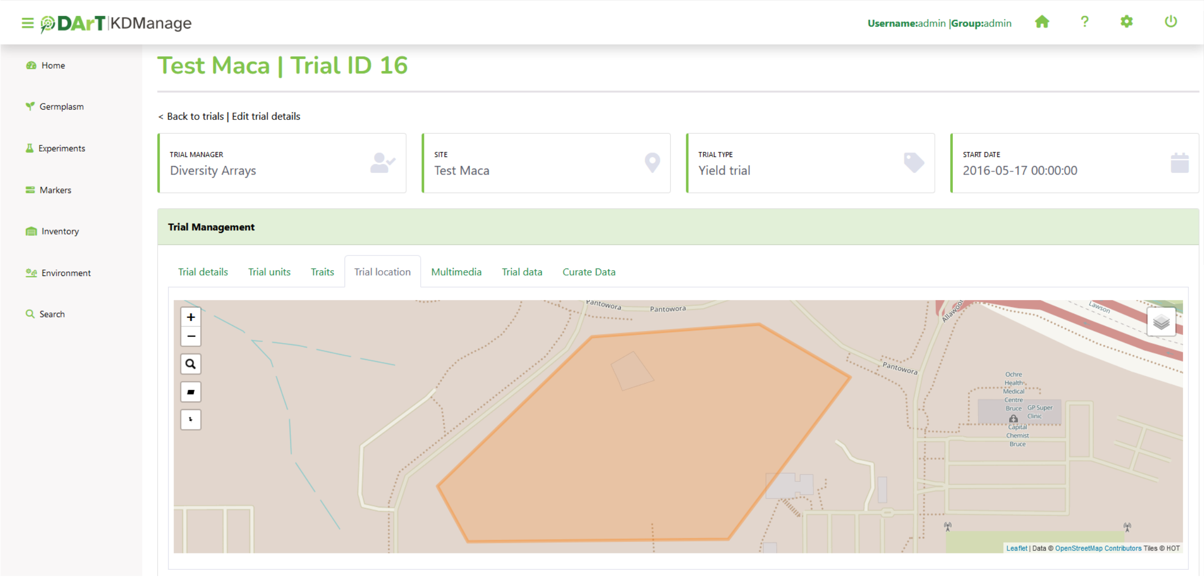
Field	Mandatory	Description
Unit	Mandatory	Unit of trial event.
Event Type	Mandatory	The type of event, as defined in type definitions.
Trial Event Value	Mandatory	Value of trial event.
Trial Event Date	Mandatory	Date of trial event.
Trial Event Note		Note of trial event.

5.5.15 Adding a Trial Location

Once a site has been added to a trial, a geographic location can also be added.

Note: Please note that a trial must have a site with geometry before a location can be added. See the *Site* section for more information.

To add a trial location, first go to the **Trial Location tab**.



Test Maca | Trial ID 16

TRIAL MANAGER Diversity Arrays

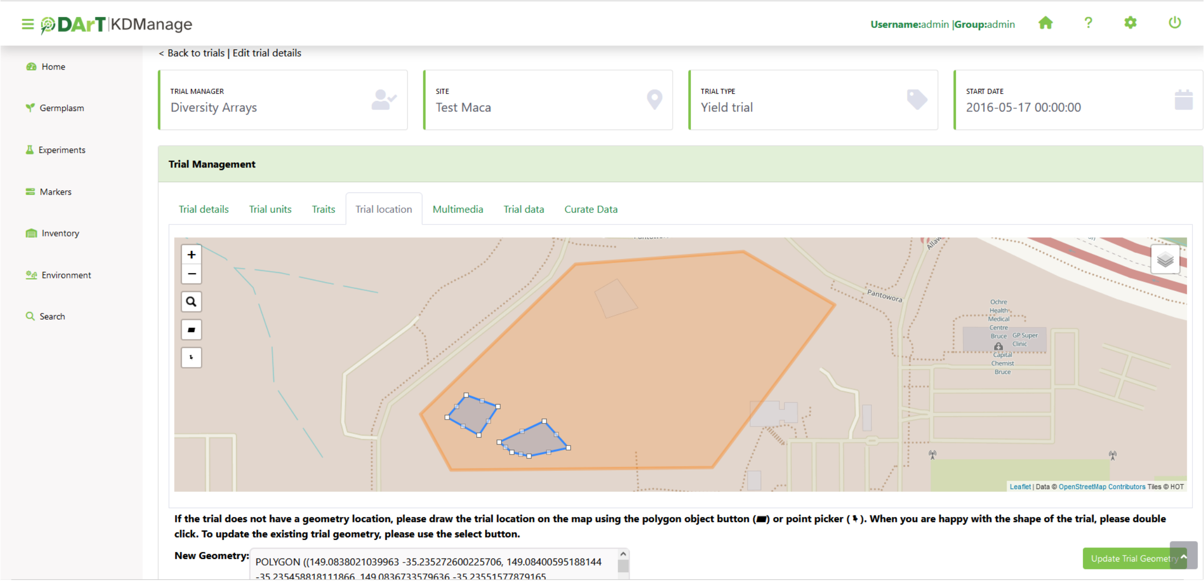
SITE Test Maca

TRIAL TYPE Yield trial

START DATE 2016-05-17 00:00:00

Fig. 28: Add Trial Location Window

When the map shows the required are, 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:



TRIAL MANAGER
Diversity Arrays

SITE
Test Maca

TRIAL TYPE
Yield trial

START DATE
2016-05-17 00:00:00

If the trial does not have a geometry location, please draw the trial location on the map using the polygon object button (▰) or point picker ( ). When you are happy with the shape of the trial, please double click. To update the existing trial geometry, please use the select button.

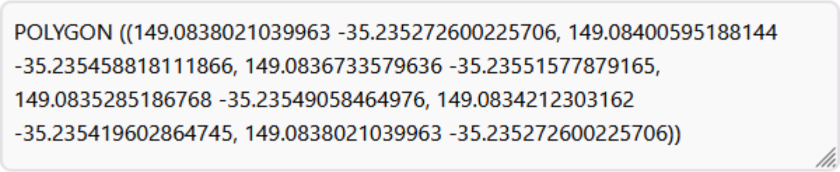
New Geometry: POLYGON ((149.0838021039963 -35.235272600225706, 149.08400595188144 -35.235458818111866, 149.0836733579636 -35.23551577879165

Fig. 29: Add Trial Location Window - Area Selected

Note: Double-click on the last point of a polygon to set the points and complete the shape.

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 ((149.0838021039963 -35.235272600225706, 149.08400595188144 -35.235458818111866, 149.0836733579636 -35.23551577879165, 149.0835285186768 -35.23549058464976, 149.0834212303162 -35.235419602864745, 149.0838021039963 -35.235272600225706))

Fig. 30: Location Field Data Example

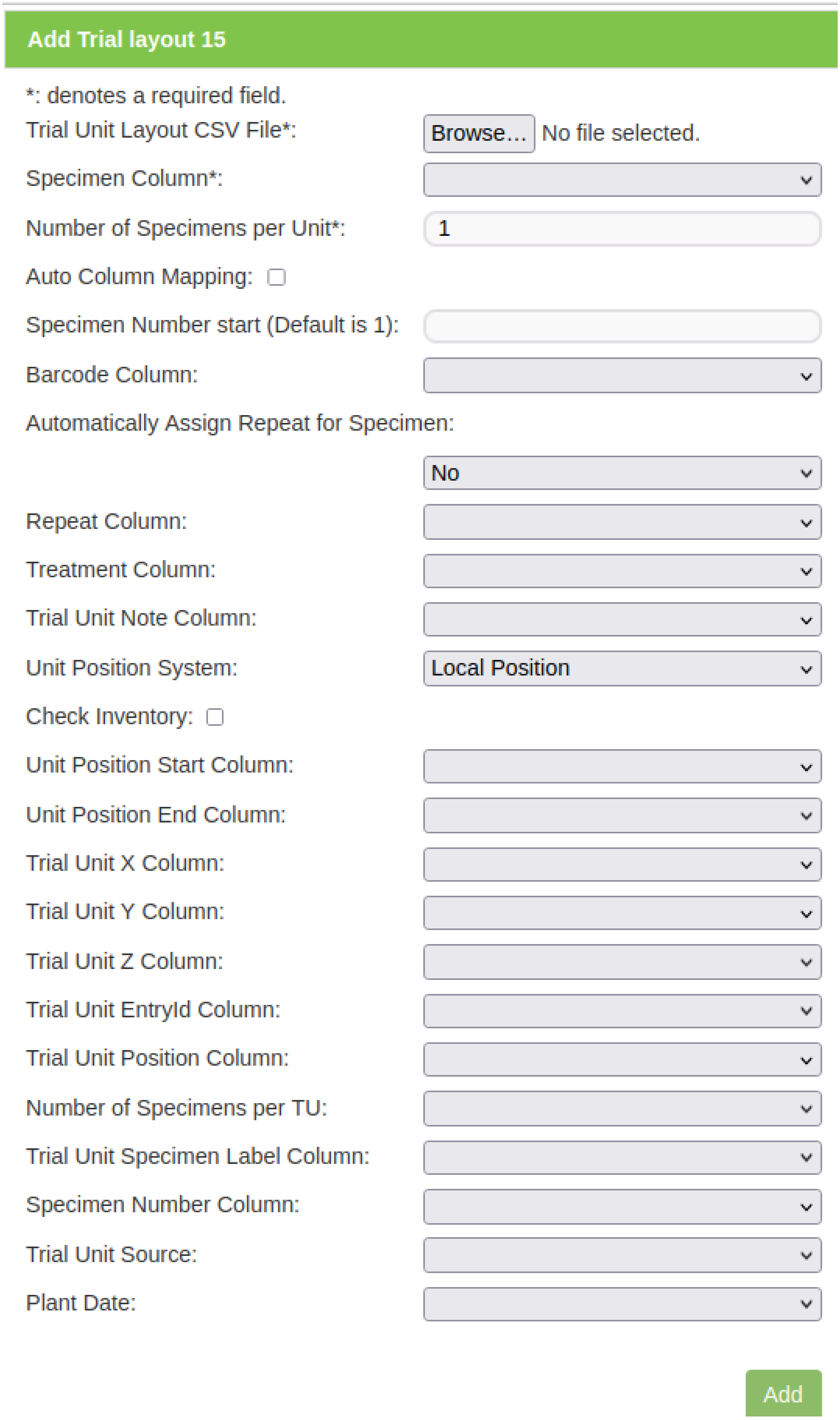
5.5.16 Adding Trial Unit Layouts

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 KDCompute 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 15

*: denotes a required field.

Trial Unit Layout CSV File*: No file selected.

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

Check Inventory: ☐

Unit Position Start Column:

Unit Position End Column:

Trial Unit X Column:

Trial Unit Y Column:

Trial Unit Z Column:

Trial Unit EntryId Column:

Trial Unit Position Column:

Number of Specimens per TU:

Trial Unit Specimen Label Column:

Specimen Number Column:

Trial Unit Source:

Plant Date:

Fig. 31: Adding Trial Unit Layouts Window

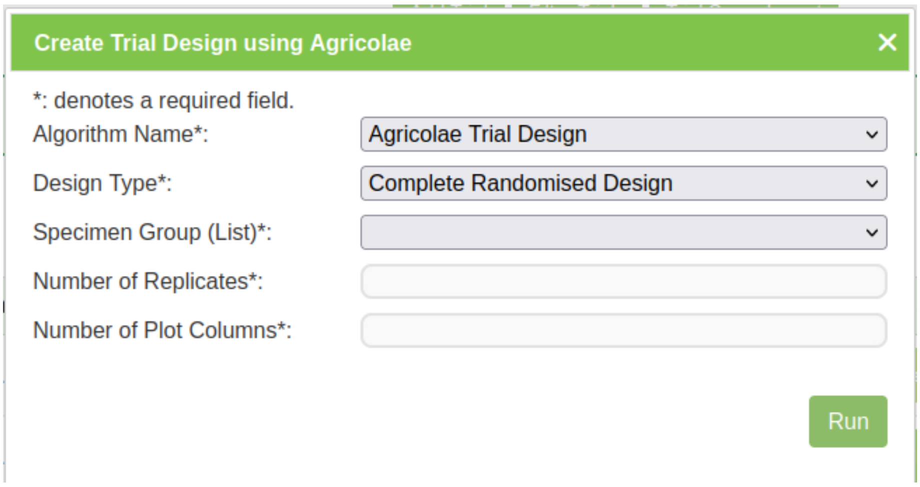
Table 14: Add Trial Unit Layout Fields

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:



*: denotes a required field.
Algorithm Name*: Agricolae Trial Design
Design Type*: Complete Randomised Design
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

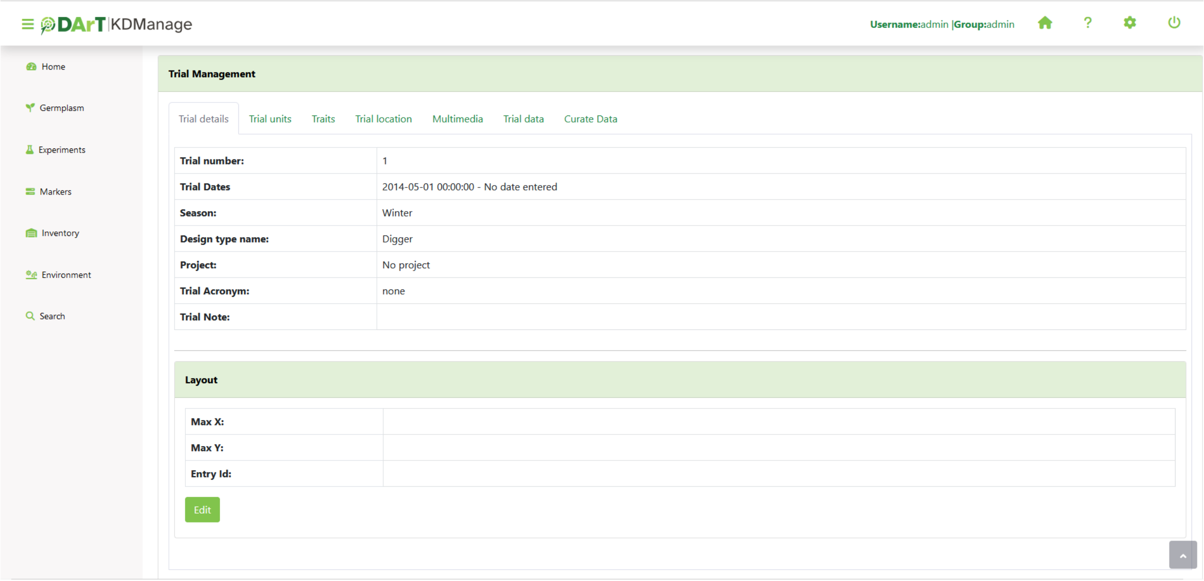
Keywords can be added or assigned to trial units.

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 *Administrative Settings* 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.



Trial number:	1
Trial Dates	2014-05-01 00:00:00 - No date entered
Season:	Winter
Design type name:	Digger
Project:	No project
Trial Acronym:	none
Trial Note:	

Max X:	
Max Y:	
Entry Id:	

Fig. 33: Trial View Page

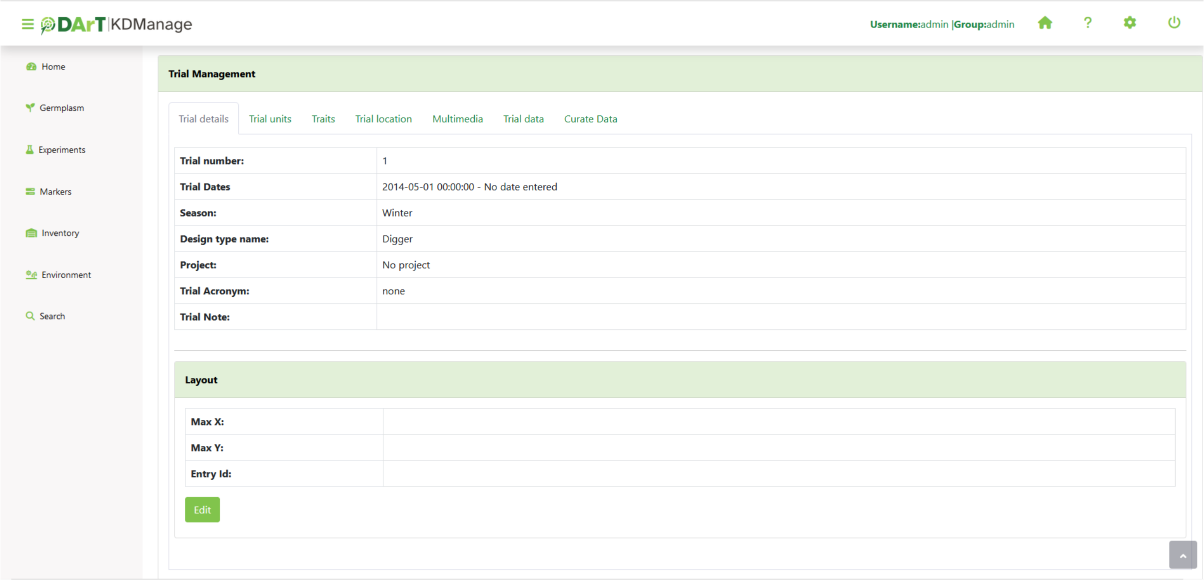
A **Trial Workflow Panel** and a **Trial Events Panel** will always be visible on the **Trial View Page**, regardless of the selected tab.

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:



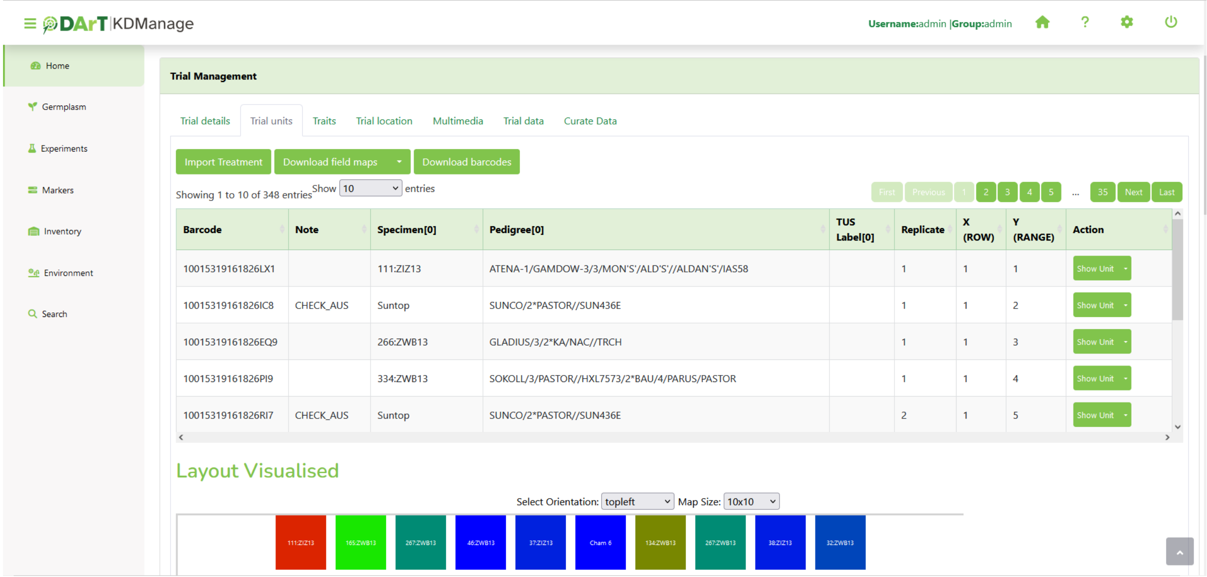
Trial number:	1
Trial Dates	2014-05-01 00:00:00 - No date entered
Season:	Winter
Design type name:	Digger
Project:	No project
Trial Acronym:	none
Trial Note:	

Max X:	
Max Y:	
Entry Id:	

Fig. 34: Update Trial Window

5.6.2 Trial Units Tab

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



Showing 1 to 10 of 348 entries Show 10 entries

Barcode	Note	Specimen[0]	Pedigree[0]	TUS Label[0]	Replicate	X (ROW)	Y (RANGE)	Action
10015319161826LX1		111:ZIZ13	ATENA-1/GAMDOW-3/3/MON'S'/ALD'S'//ALDAN'S'/IAS58		1	1	1	Show Unit
10015319161826IC8	CHECK_AUS	Suntop	SUNCO/2*PASTOR//SUN436E		1	1	2	Show Unit
10015319161826EQ9		266:ZWB13	GLADIUS/3/2*KA/NAC//TRCH		1	1	3	Show Unit
10015319161826PI9		334:ZWB13	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR		1	1	4	Show Unit
10015319161826RI7	CHECK_AUS	Suntop	SUNCO/2*PASTOR//SUN436E		2	1	5	Show Unit

Select Orientation: topleft Map Size: 10x10

Fig. 35: Trial Units Tab

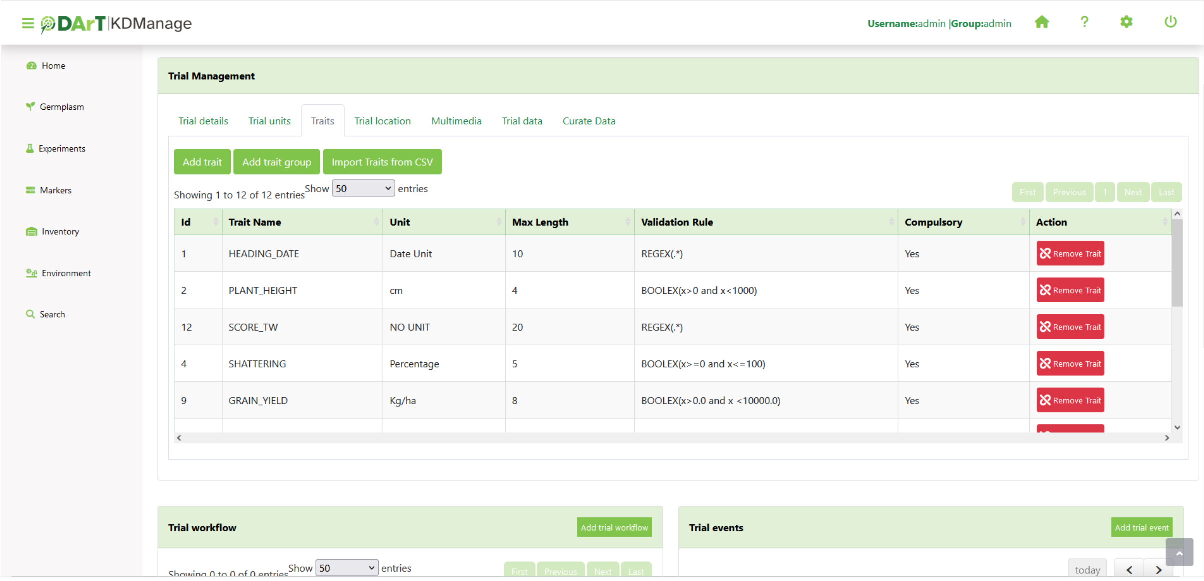
Newly created trials can have trial unit layouts added via CSV or KDCompute methods (see *Adding Trial Unit Layouts*).

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

5.6.3 Traits Tab

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



Showing 1 to 12 of 12 entries Show 50 entries

Id	Trait Name	Unit	Max Length	Validation Rule	Compulsory	Action
1	HEADING_DATE	Date Unit	10	REGEX(.*)	Yes	Remove Trait
2	PLANT_HEIGHT	cm	4	BOOLEX(x>0 and x<1000)	Yes	Remove Trait
12	SCORE_TW	NO UNIT	20	REGEX(.*)	Yes	Remove Trait
4	SHATTERING	Percentage	5	BOOLEX(x>=0 and x<=100)	Yes	Remove Trait
9	GRAIN_YIELD	Kg/ha	8	BOOLEX(x>0.0 and x <10000.0)	Yes	Remove Trait

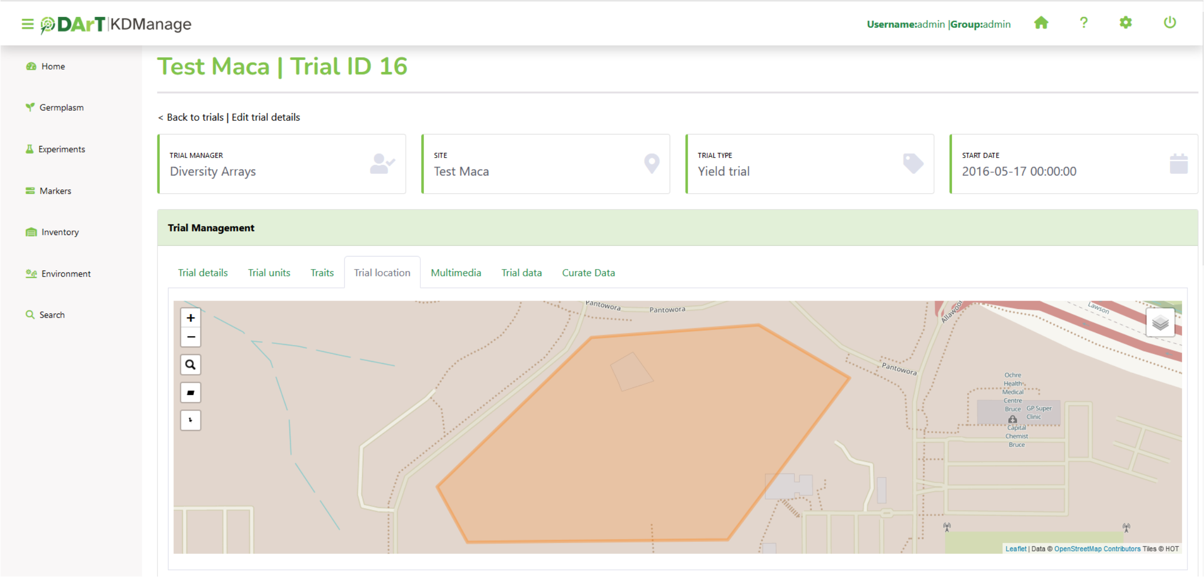
Showing 0 to 0 of 0 entries Show 50 entries

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).



Test Maca | Trial ID 16

TRIAL MANAGER Diversity Arrays

SITE Test Maca

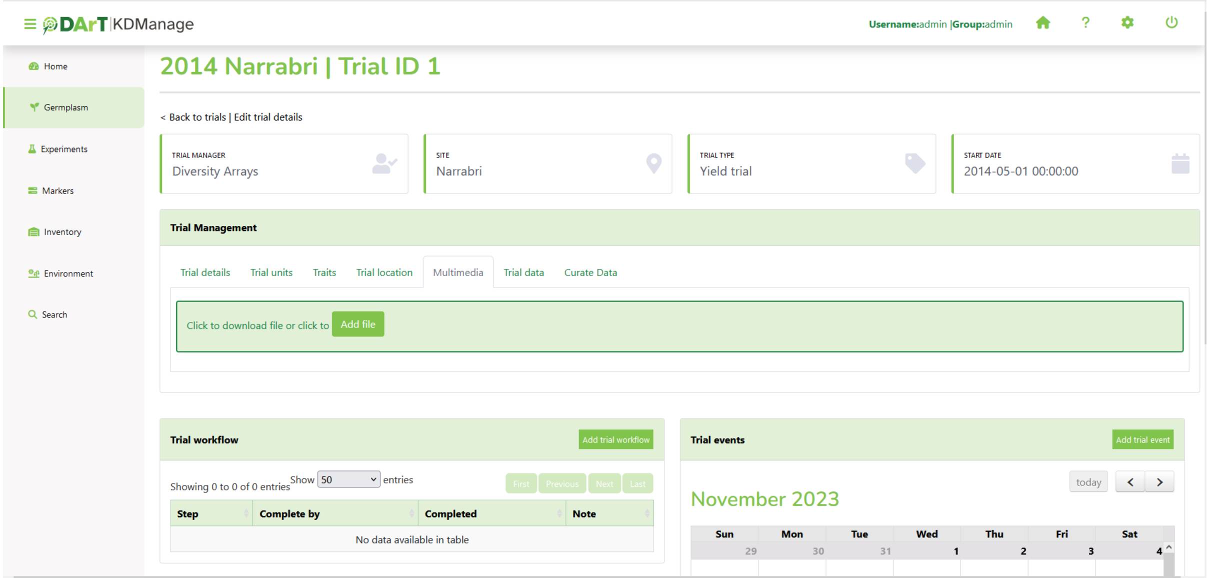
TRIAL TYPE Yield trial

START DATE 2016-05-17 00:00:00

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*).



2014 Narrabri | Trial ID 1

TRIAL MANAGER Diversity Arrays

SITE Narrabri

TRIAL TYPE Yield trial

START DATE 2014-05-01 00:00:00

Click to download file or click to Add file

Showing 0 to 0 of 0 entries

Step	Complete by	Completed	Note
No data available in table			

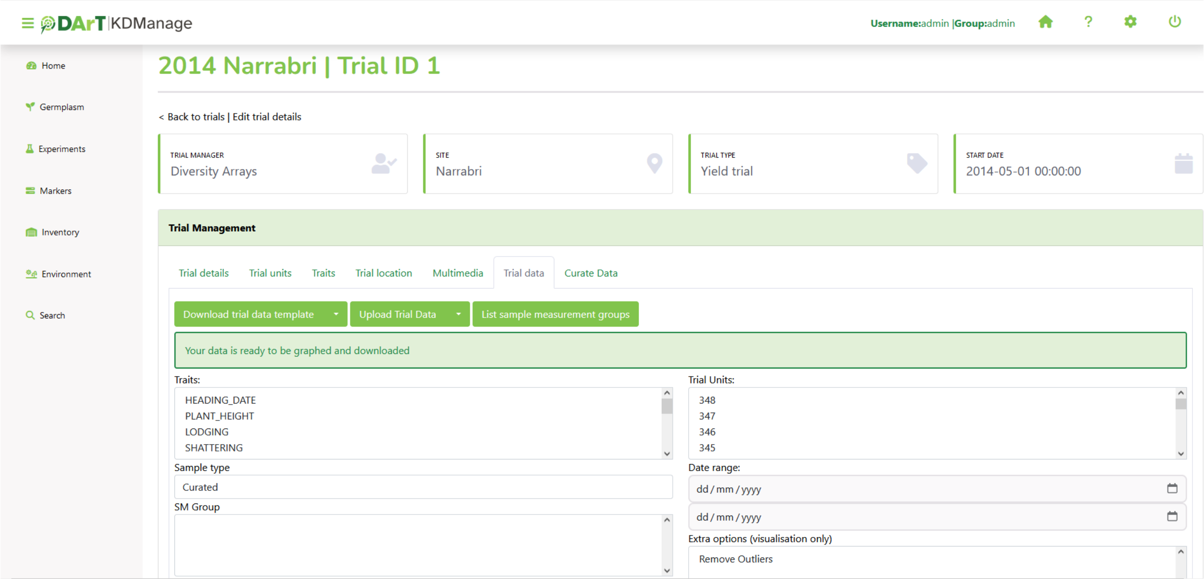
November 2023

Sun	Mon	Tue	Wed	Thu	Fri	Sat
29	30	31	1	2	3	4

Fig. 38: Multimedia Tab

5.6.6 Trial Data Tab

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



2014 Narrabri | Trial ID 1

TRIAL MANAGER Diversity Arrays

SITE Narrabri

TRIAL TYPE Yield trial

START DATE 2014-05-01 00:00:00

Trial Management

Your data is ready to be graphed and downloaded

Traits: HEADING_DATE, PLANT_HEIGHT, LODGING, SHATTERING

Trial Units: 348, 347, 346, 345

Sample type: Curated

Date range: dd / mm / yyyy – dd / mm / yyyy

SM Group:

Extra options (visualisation only): Remove Outliers

Fig. 39: Trait Data Tab

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

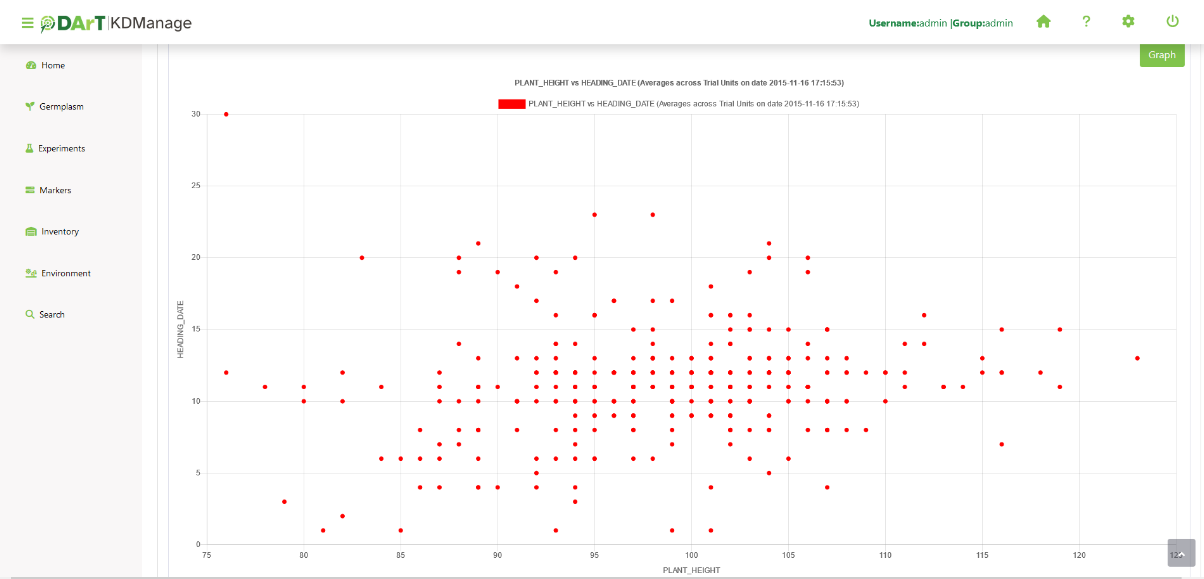
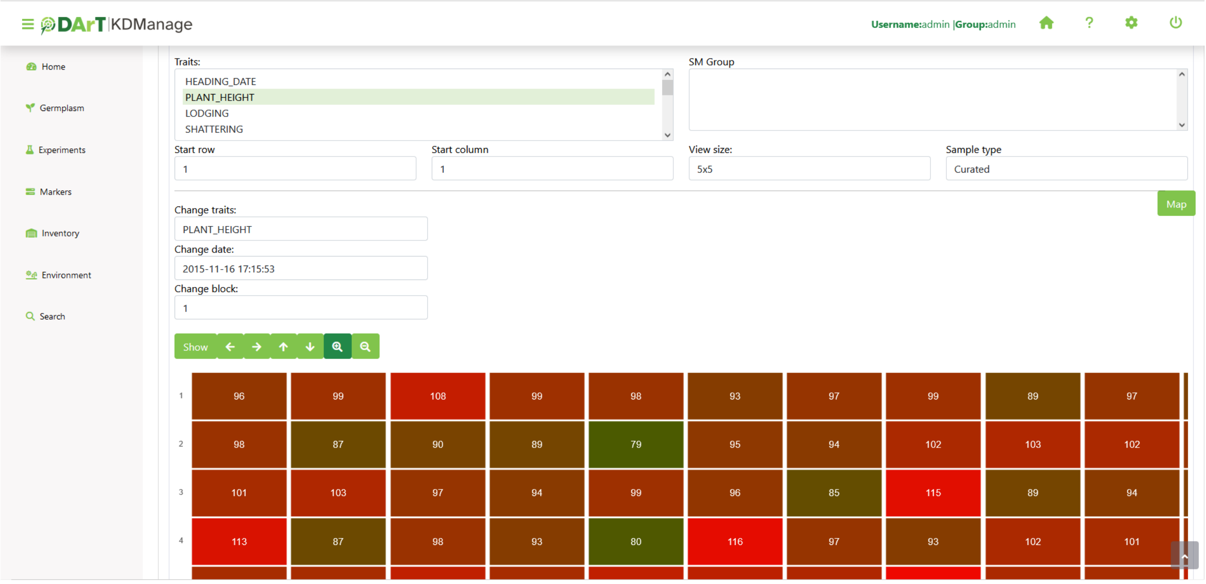


Fig. 40: Trial Data Graph

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



Traits:
HEADING_DATE
PLANT_HEIGHT
LODGING
SHATTERING

SM Group

Start row: 1
Start column: 1
View size: 5x5
Sample type: Curated

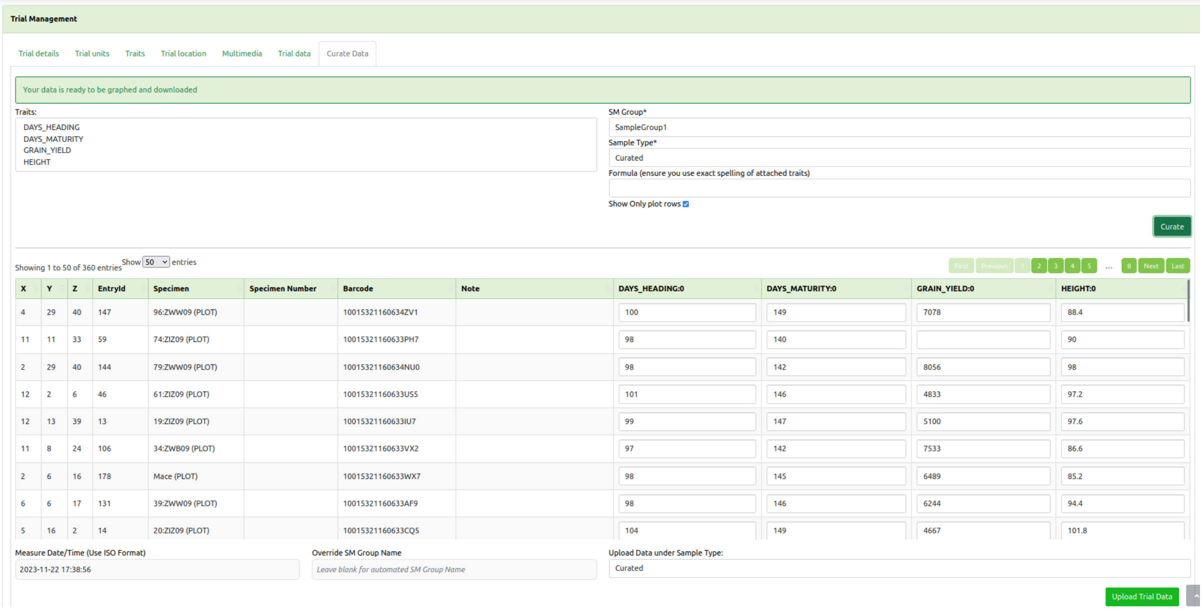
Change traits: PLANT_HEIGHT
Change date: 2015-11-16 17:15:53
Change block: 1

1	96	99	108	99	98	93	97	99	89	97
2	98	87	90	89	79	95	94	102	103	102
3	101	103	97	94	99	96	85	115	89	94
4	113	87	98	93	80	116	97	93	102	101

Fig. 41: Trial Data Map

5.6.7 Curate Data Tab

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



Your data is ready to be graphed and downloaded

Traits:
DAYS_HEADING
DAYS_MATURITY
GRAIN_YIELD
HEIGHT

SM Group*: SampleGroup1
Sample Type*: Curated
Formula (ensure you use exact spelling of attached traits)
Show Only plot rows ☑

Showing 1 to 50 of 360 entries Show 50 entries

X	Y	Z	EntryId	Specimen	Specimen Number	Barcode	Note	DAYS_HEADING:0	DAYS_MATURITY:0	GRAIN_YIELD:0	HEIGHT:0
4	29	40	147	96:ZWW09 (PLOT)		10015321160634ZV1		100	149	7078	88.4
11	11	33	59	74:ZIZ09 (PLOT)		10015321160633PH7		98	140		90
2	29	40	144	79:ZWW09 (PLOT)		10015321160634NU0		98	142	8056	98
12	2	6	46	61:ZIZ09 (PLOT)		10015321160633US5		101	146	4833	97.2
12	13	39	13	19:ZIZ09 (PLOT)		10015321160633IU7		99	147	5100	97.6
11	8	24	106	34:ZWB09 (PLOT)		10015321160633VX2		97	142	7533	86.6
2	6	16	178	Mace (PLOT)		10015321160633WX7		98	145	6489	85.2
6	6	17	131	39:ZWW09 (PLOT)		10015321160633AF9		98	146	6244	94.4
5	16	2	14	20:ZIZ09 (PLOT)		10015321160633CQ5		104	149	4667	101.8

Measure Date/Time (Use ISO Format): 2023-11-22 17:38:56
Override SM Group Name: *Leave blank for automated SM Group Name*
Upload Data under Sample Type: Curated

Fig. 42: Curate Data Tab

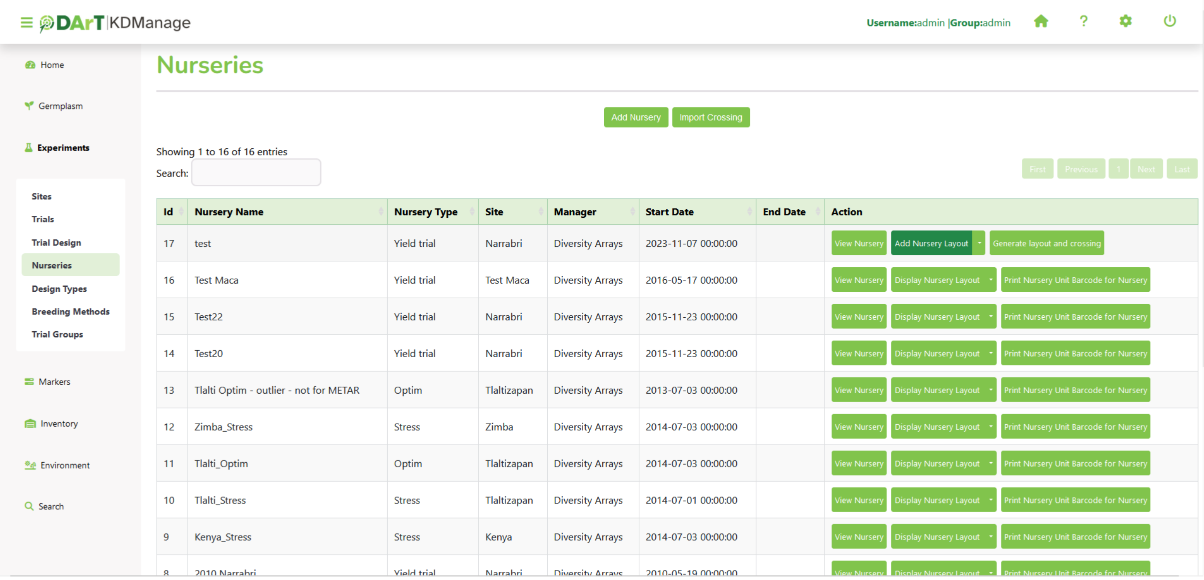
Existing trial data can be curated and imported as a separate instance in the **Curate Data Tab**.

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

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:



Showing 1 to 16 of 16 entries

Search:

Id	Nursery Name	Nursery Type	Site	Manager	Start Date	End Date	Action
17	test	Yield trial	Narrabri	Diversity Arrays	2023-11-07 00:00:00		View Nursery, Add Nursery Layout, Generate layout and crossing
16	Test Maca	Yield trial	Test Maca	Diversity Arrays	2016-05-17 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
15	Test22	Yield trial	Narrabri	Diversity Arrays	2015-11-23 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
14	Test20	Yield trial	Narrabri	Diversity Arrays	2015-11-23 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
13	Tlalti Optim - outlier - not for METAR	Optim	Tlaltizapan	Diversity Arrays	2013-07-03 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
12	Zimba_Stress	Stress	Zimba	Diversity Arrays	2014-07-03 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
11	Tlalti_Optim	Optim	Tlaltizapan	Diversity Arrays	2014-07-03 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
10	Tlalti_Stress	Stress	Tlaltizapan	Diversity Arrays	2014-07-01 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
9	Kenya_Stress	Stress	Kenya	Diversity Arrays	2014-07-03 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery
8	2010 Narrabri	Yield trial	Narrabri	Diversity Arrays	2010-05-19 00:00:00		View Nursery, Display Nursery Layout, Print Nursery Unit Barcode for Nursery

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.
Nursery Name	The user provided name of the nursery.
Nursery Type	The selected nursery type (user defined specific trial *types* 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

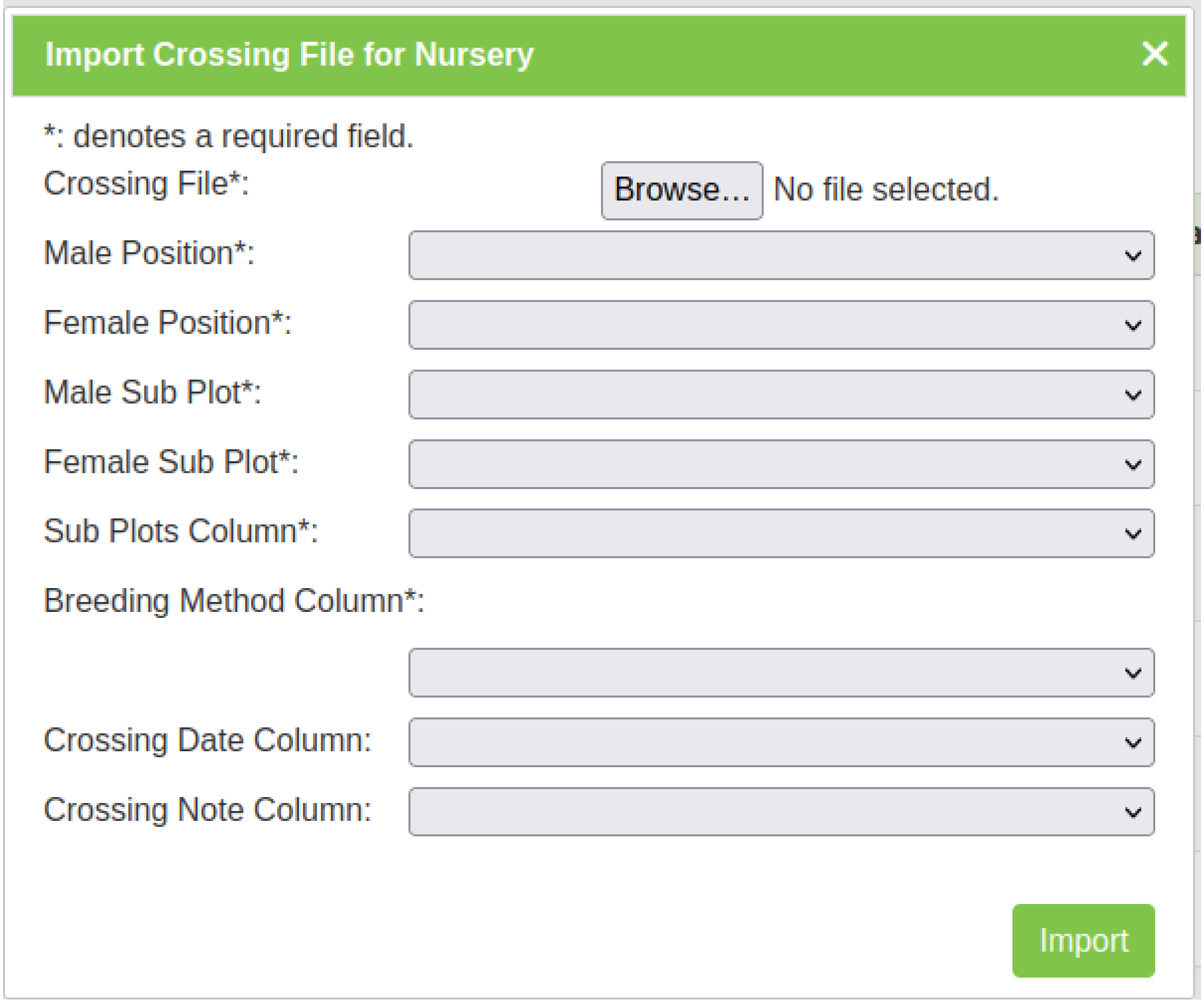
Action	Description	Parent Button
Generate Layout and Crossing	Automatically generate layout and crossing, if required, from two specimen lists. See *Generating Layouts and Crossings*.	
Add Nursery Layout	Import a nursery layout for the nursery. See *Displaying Trial Unit Layouts*.	
Display Nursery Layout	Display the nursery layout for the nursery. See *Displaying Trial Unit Layouts*.	
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 *Harvest Crossing*.	Display Nursery Layout
Show Nursery Info	Display general information about the nursery including permissions.	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:



Import Crossing File for Nursery

*: denotes a required field.

Crossing File*: No file selected.

Male Position*:

Female Position*:

Male Sub Plot*:

Female Sub Plot*:

Sub Plots Column*:

Breeding Method Column*:

Crossing Date Column:

Crossing Note Column:

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.

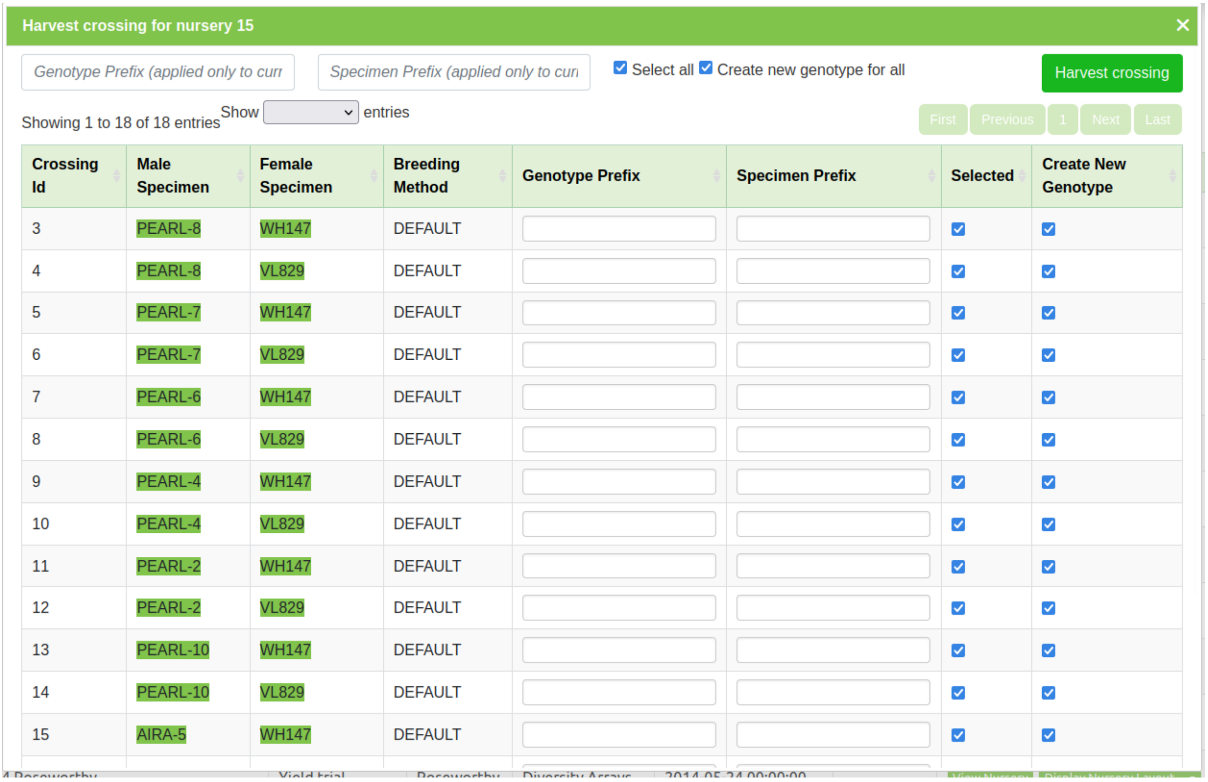
Table 17: Import Crossing Fields

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 the **Display Nursery Layout 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.



Harvest crossing for nursery 15

Genotype Prefix (applied only to curr | Specimen Prefix (applied only to curr | ☑ Select all ☑ Create new genotype for all

Showing 1 to 18 of 18 entries Show entries

Crossing Id	Male Specimen	Female Specimen	Breeding Method	Genotype Prefix	Specimen Prefix	Selected	Create New Genotype
3	PEARL-8	WH147	DEFAULT			☑	☑
4	PEARL-8	VL829	DEFAULT			☑	☑
5	PEARL-7	WH147	DEFAULT			☑	☑
6	PEARL-7	VL829	DEFAULT			☑	☑
7	PEARL-6	WH147	DEFAULT			☑	☑
8	PEARL-6	VL829	DEFAULT			☑	☑
9	PEARL-4	WH147	DEFAULT			☑	☑
10	PEARL-4	VL829	DEFAULT			☑	☑
11	PEARL-2	WH147	DEFAULT			☑	☑
12	PEARL-2	VL829	DEFAULT			☑	☑
13	PEARL-10	WH147	DEFAULT			☑	☑
14	PEARL-10	VL829	DEFAULT			☑	☑
15	AIRA-5	WH147	DEFAULT			☑	☑

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.

CHAPTER

SIX

MARKER MENU

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

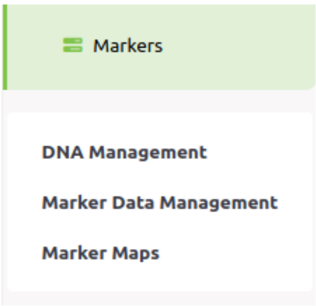


Fig. 1: Marker Menu

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)

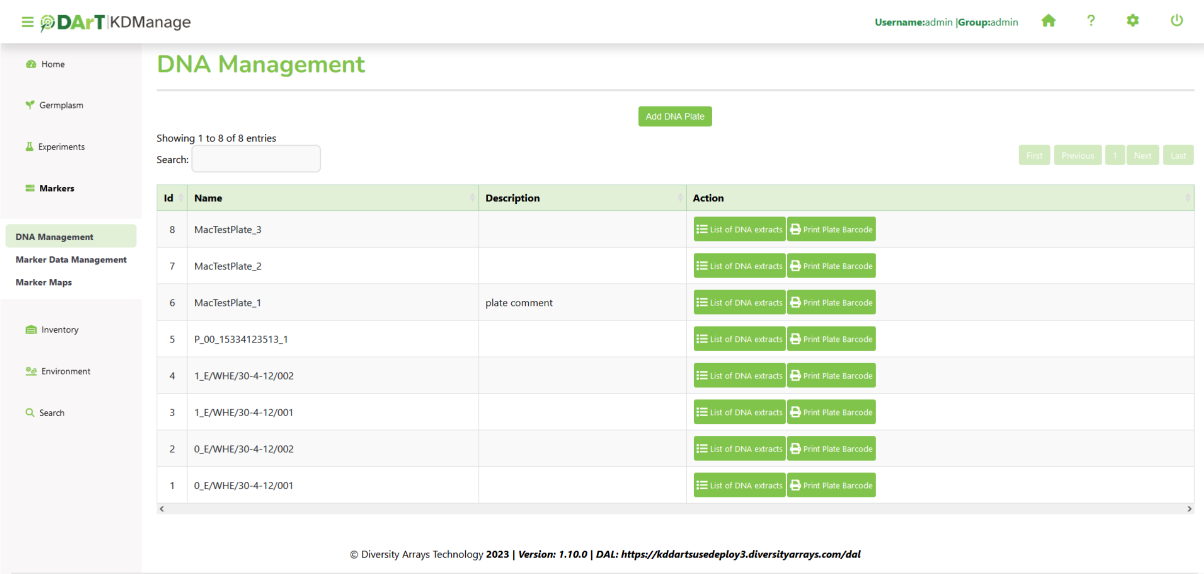
Table 4: Genotyping Marker Process - KDManage Collect Order via BrAPI

Step	Activity	Action
1.	Retrieve **Authentication Token** and **Order ID** from vendors.	*This step may vary depending on choice of vendor.*
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.



Showing 1 to 8 of 8 entries

Id	Name	Description	Action
8	MacTestPlate_3		List of DNA extracts Print Plate Barcode
7	MacTestPlate_2		List of DNA extracts Print Plate Barcode
6	MacTestPlate_1	plate comment	List of DNA extracts Print Plate Barcode
5	P_00_15334123513_1		List of DNA extracts Print Plate Barcode
4	1_E/WHE/30-4-12/002		List of DNA extracts Print Plate Barcode
3	1_E/WHE/30-4-12/001		List of DNA extracts Print Plate Barcode
2	0_E/WHE/30-4-12/002		List of DNA extracts Print Plate Barcode
1	0_E/WHE/30-4-12/001		List of DNA extracts Print Plate Barcode

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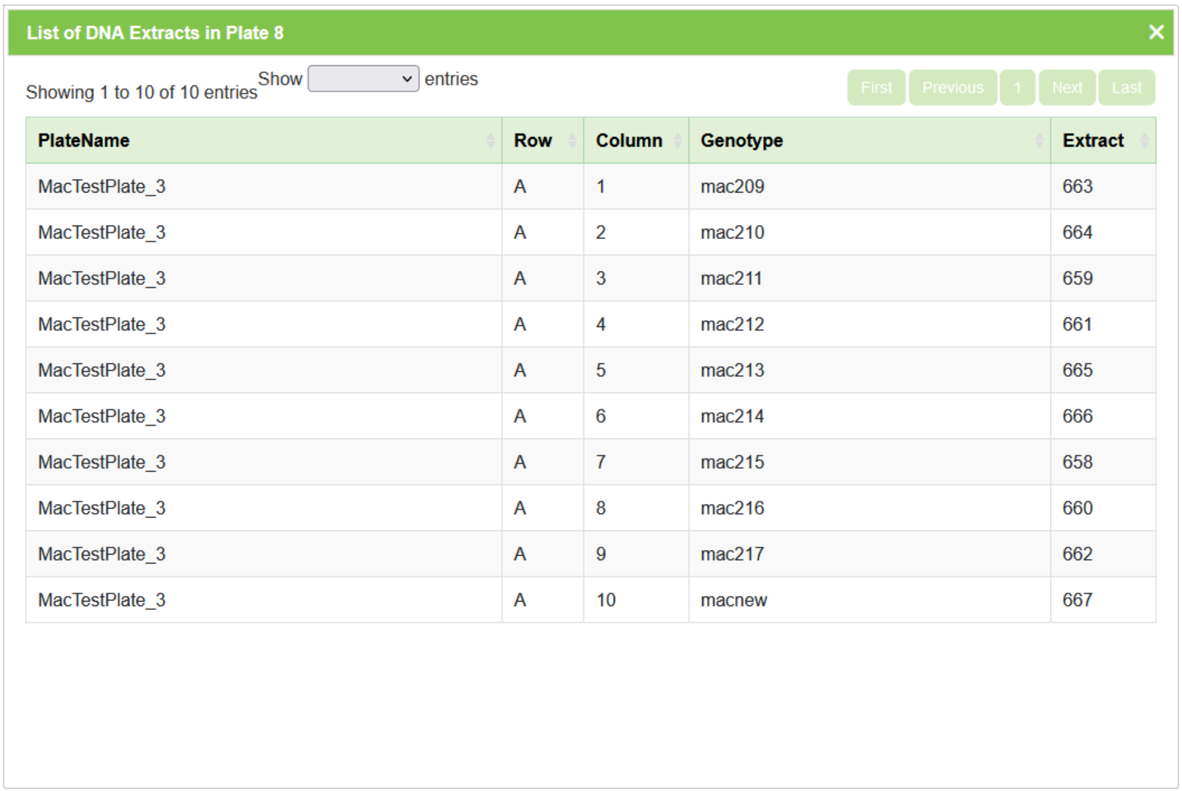
Fig. 2: Data Management Page

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



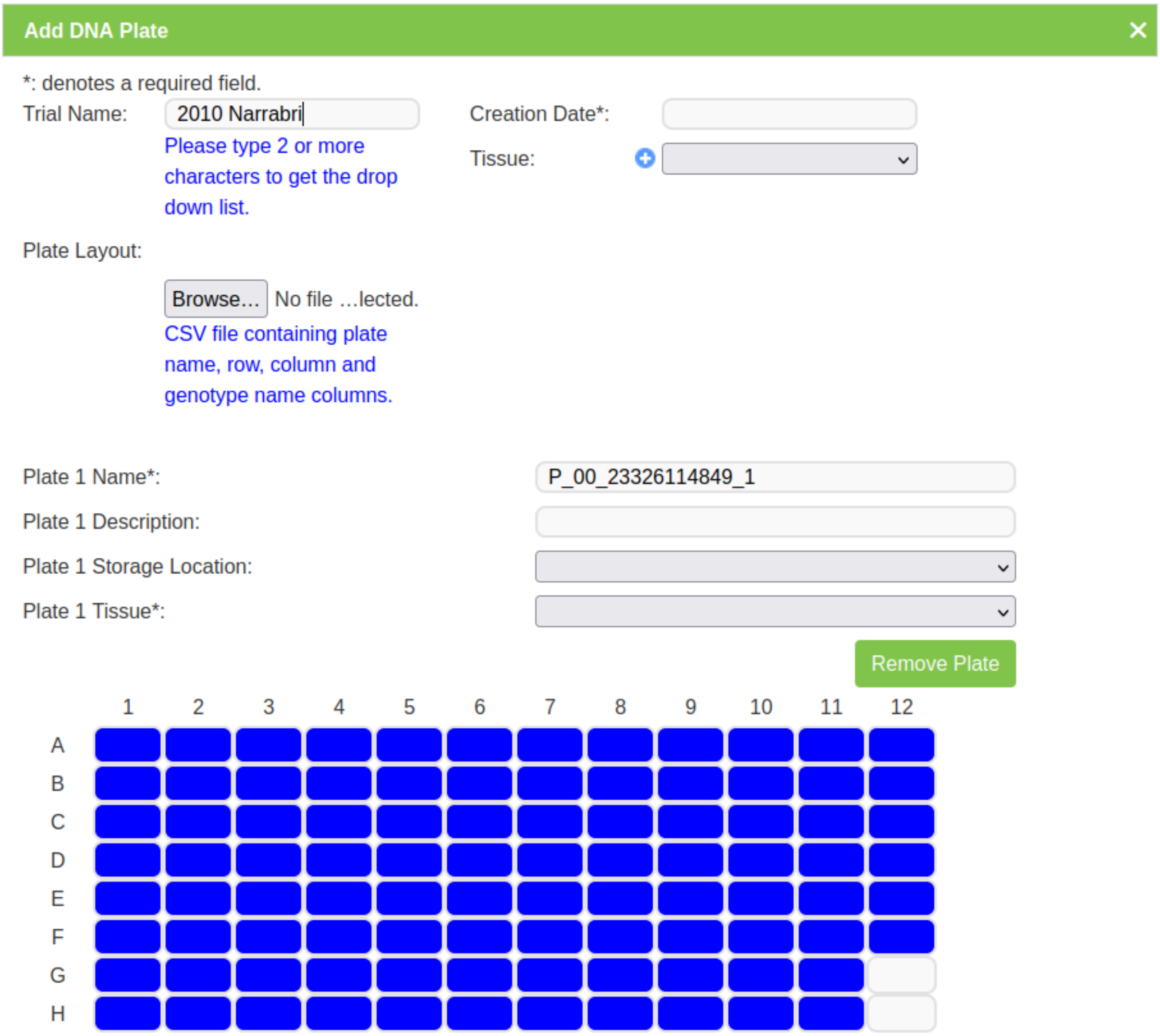
Showing 1 to 10 of 10 entries

PlateName	Row	Column	Genotype	Extract
MacTestPlate_3	A	1	mac209	663
MacTestPlate_3	A	2	mac210	664
MacTestPlate_3	A	3	mac211	659
MacTestPlate_3	A	4	mac212	661
MacTestPlate_3	A	5	mac213	665
MacTestPlate_3	A	6	mac214	666
MacTestPlate_3	A	7	mac215	658
MacTestPlate_3	A	8	mac216	660
MacTestPlate_3	A	9	mac217	662
MacTestPlate_3	A	10	macnew	667

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: 2010 Narrabri

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

Creation Date*:

Tissue:

Plate Layout: Browse… No file …lected.

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

Plate 1 Name*: P_00_23326114849_1

Plate 1 Description:

Plate 1 Storage Location:

Plate 1 Tissue*:

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

Individual plates may be edited or removed as required. The image and table below contain more information:

Table 6: Add DNA Plate Fields - Individual Plates

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.

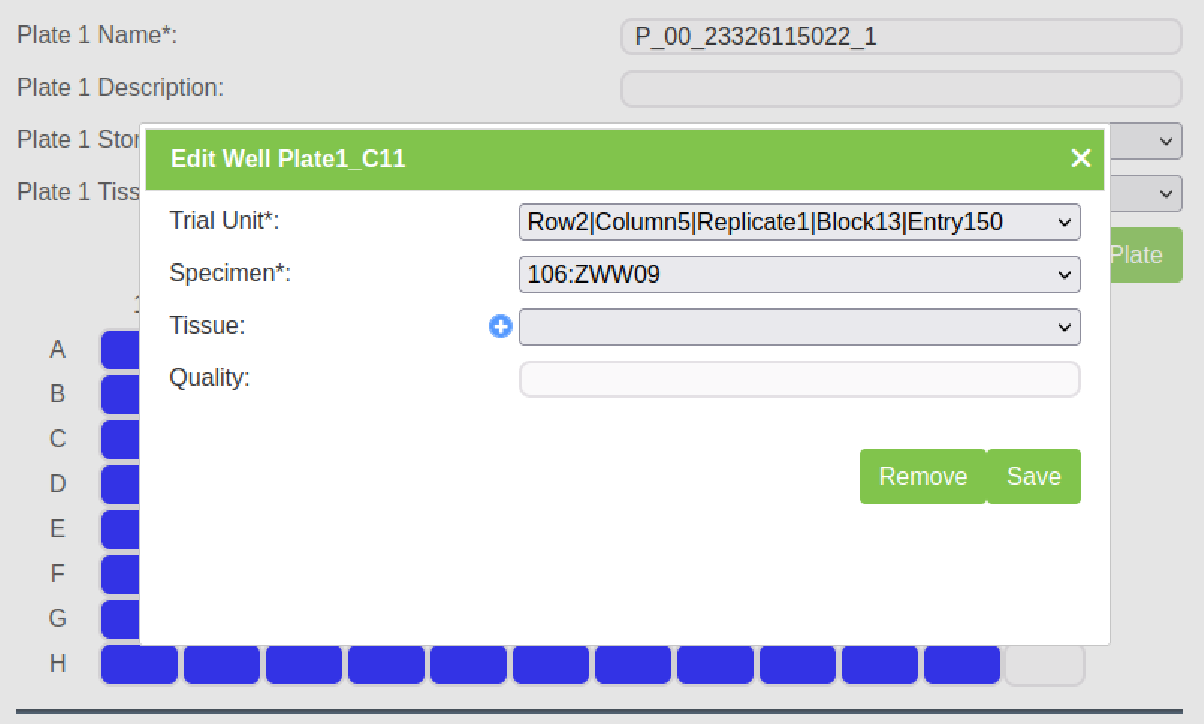


Plate 1 Name*: P_00_23326115022_1

Plate 1 Description:

Plate 1 Stor

Plate 1 Tiss

Edit Well Plate1_C11

Trial Unit*: Row2|Column5|Replicate1|Block13|Entry150

Specimen*: 106:ZWW09

Tissue:

Quality:

Fig. 5: 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.

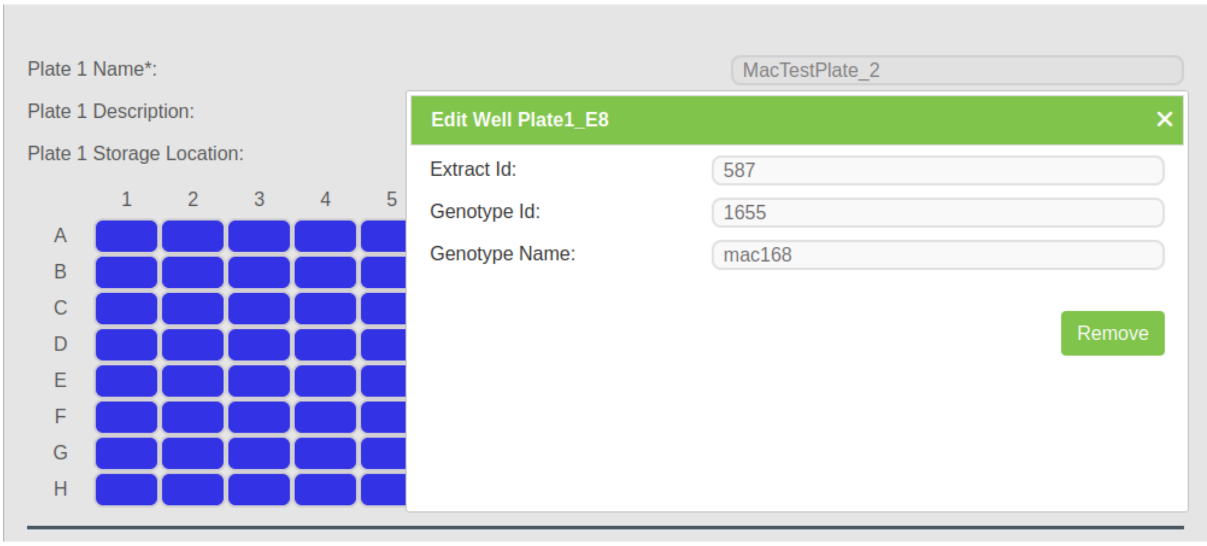


Plate 1 Name*: MacTestPlate_2

Plate 1 Description:

Plate 1 Storage Location:

Edit Well Plate1_E8

Extract Id: 587

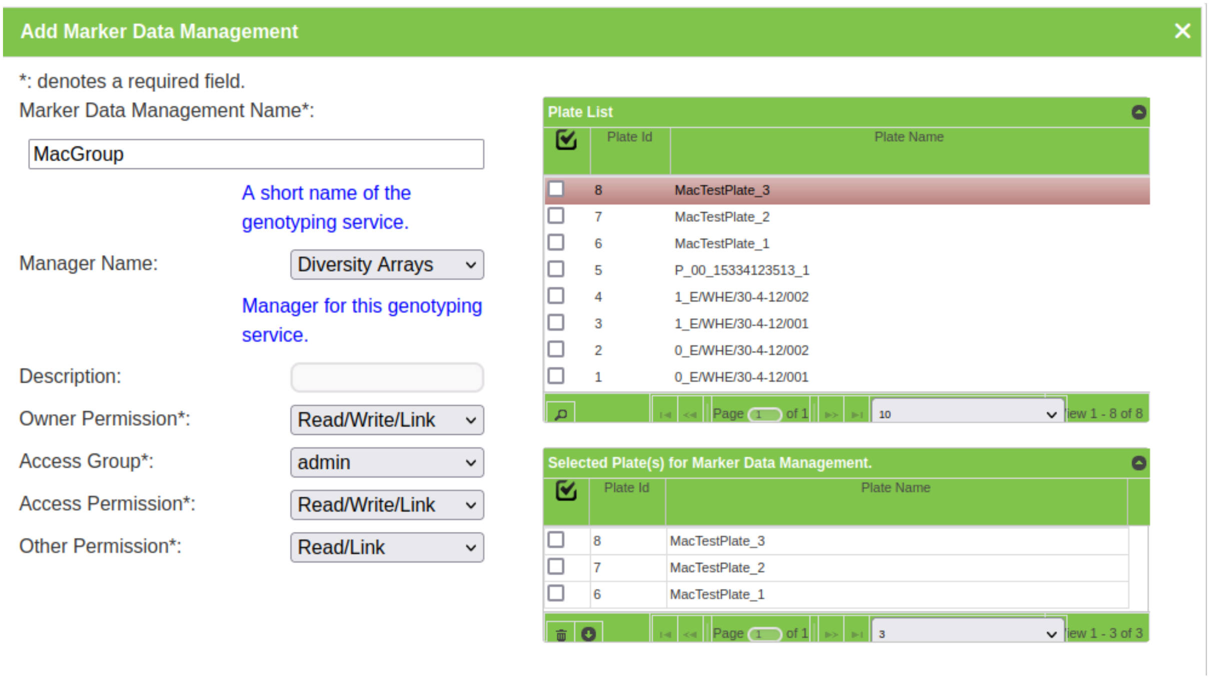
Genotype Id: 1655

Genotype Name: mac168

Fig. 6: 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**:



Add Marker Data Management

*: denotes a required field.

Marker Data Management Name*: MacGroup

A short name of the genotyping service.

Manager Name: Diversity Arrays

Manager for this genotyping service.

Description:

Owner Permission*: Read/Write/Link

Access Group*: admin

Access Permission*: Read/Write/Link

Other Permission*: Read/Link

Plate List

☑	Plate Id	Plate Name
☐	8	MacTestPlate_3
☐	7	MacTestPlate_2
☐	6	MacTestPlate_1
☐	5	P_00_15334123513_1
☐	4	1_E/WHE/30-4-12/002
☐	3	1_E/WHE/30-4-12/001
☐	2	0_E/WHE/30-4-12/002
☐	1	0_E/WHE/30-4-12/001

Page 1 of 1 10 iew 1 - 8 of 8

Selected Plate(s) for Marker Data Management.

☑	Plate Id	Plate Name
☐	8	MacTestPlate_3
☐	7	MacTestPlate_2
☐	6	MacTestPlate_1

Page 1 of 1 3 iew 1 - 3 of 3

Fig. 7: 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 *Access Settings and Permissions* topic.

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

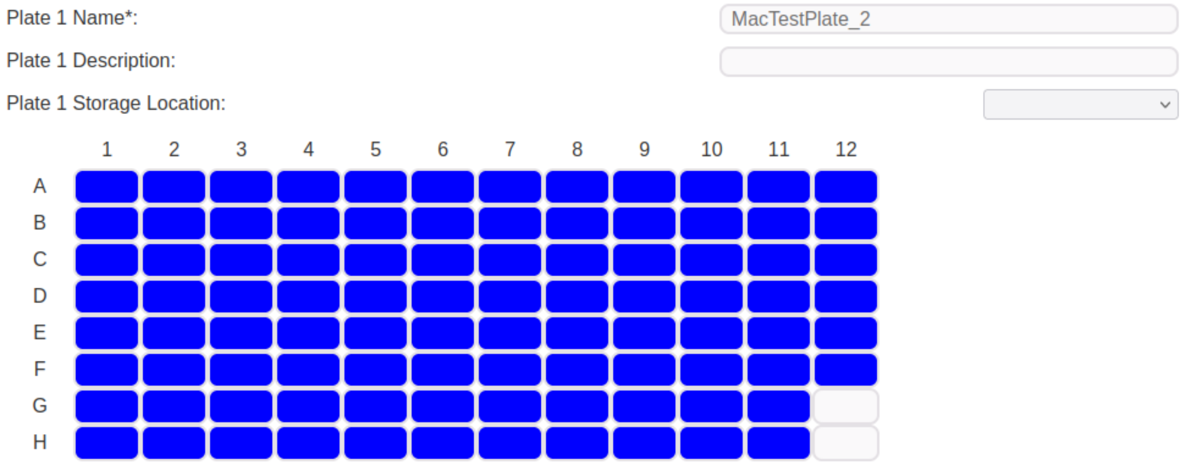


Plate 1 Name*: MacTestPlate_2

Plate 1 Description:

Plate 1 Storage Location:

Fig. 8: Plate Added to the Add Marker Data Management Window

Table 7: Add Marker Data Management Window - Plate Fields

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.

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.

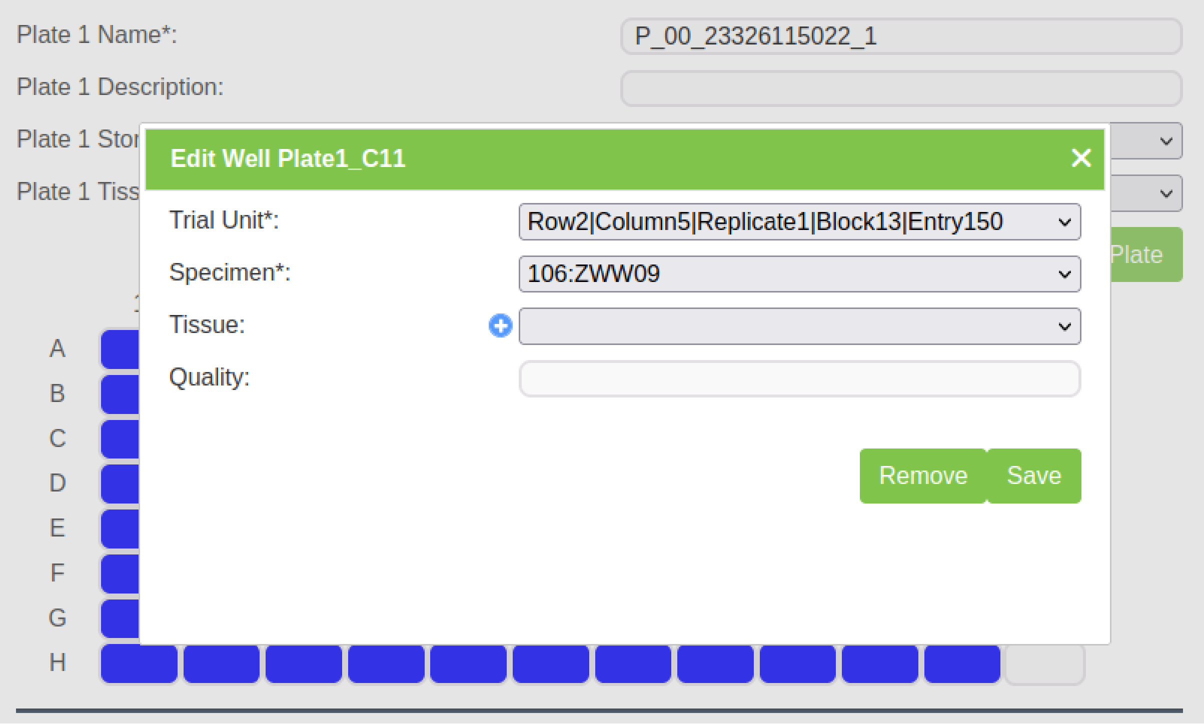


Plate 1 Name*: P_00_23326115022_1

Plate 1 Description:

Edit Well Plate1_C11

Trial Unit*: Row2|Column5|Replicate1|Block13|Entry150

Specimen*: 106:ZWW09

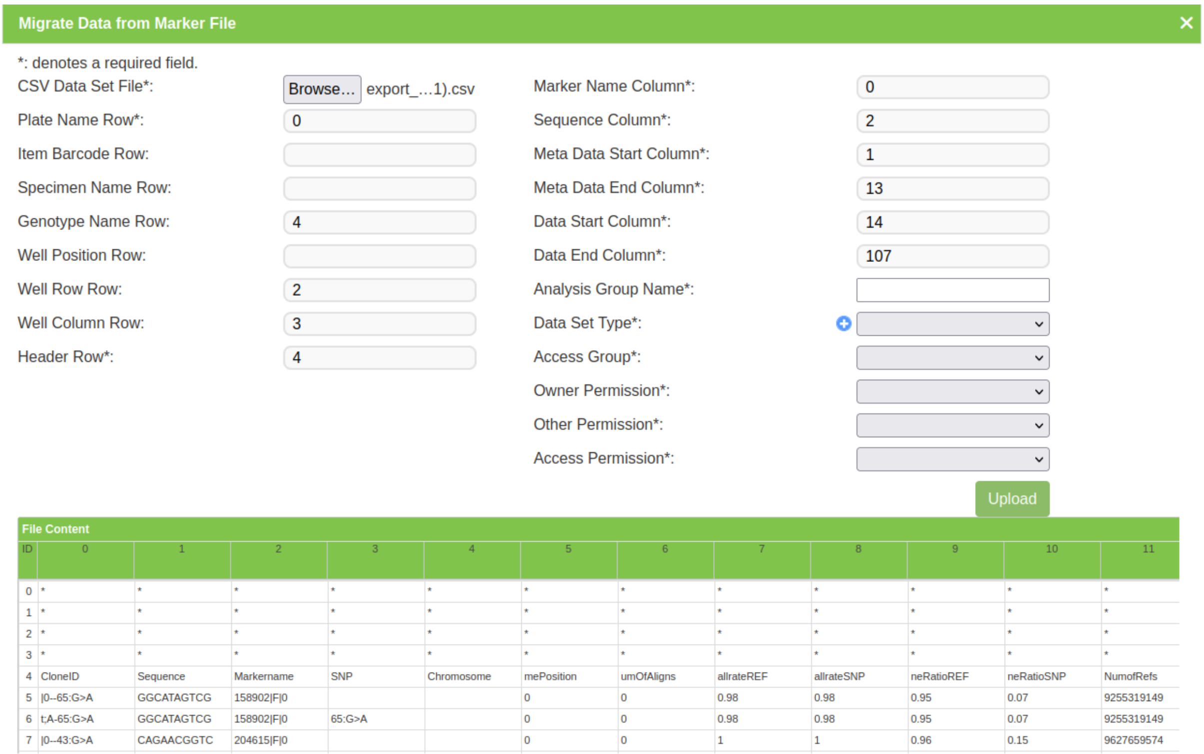
Tissue:

Quality:

Fig. 9: 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:



*: denotes a required field.

CSV Data Set File*:	export_...1).csv	Marker Name Column*:	0
Plate Name Row*:	0	Sequence Column*:	2
Item Barcode Row:		Meta Data Start Column*:	1
Specimen Name Row:		Meta Data End Column*:	13
Genotype Name Row:	4	Data Start Column*:	14
Well Position Row:		Data End Column*:	107
Well Row Row:	2	Analysis Group Name*:	
Well Column Row:	3	Data Set Type*:	
Header Row*:	4	Access Group*:	
		Owner Permission*:	
		Other Permission*:	
		Access Permission*:	

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	|0--65:G>A	GGCATAGTCG	158902|F|0			0	0	0.98	0.98	0.95	0.07	9255319149
6	t;A-65:G>A	GGCATAGTCG	158902|F|0	65:G>A		0	0	0.98	0.98	0.95	0.07	9255319149
7	|0--43:G>A	CAGAACGGTC	204615|F|0			0	0	1	1	0.96	0.15	9627659574

Fig. 10: 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

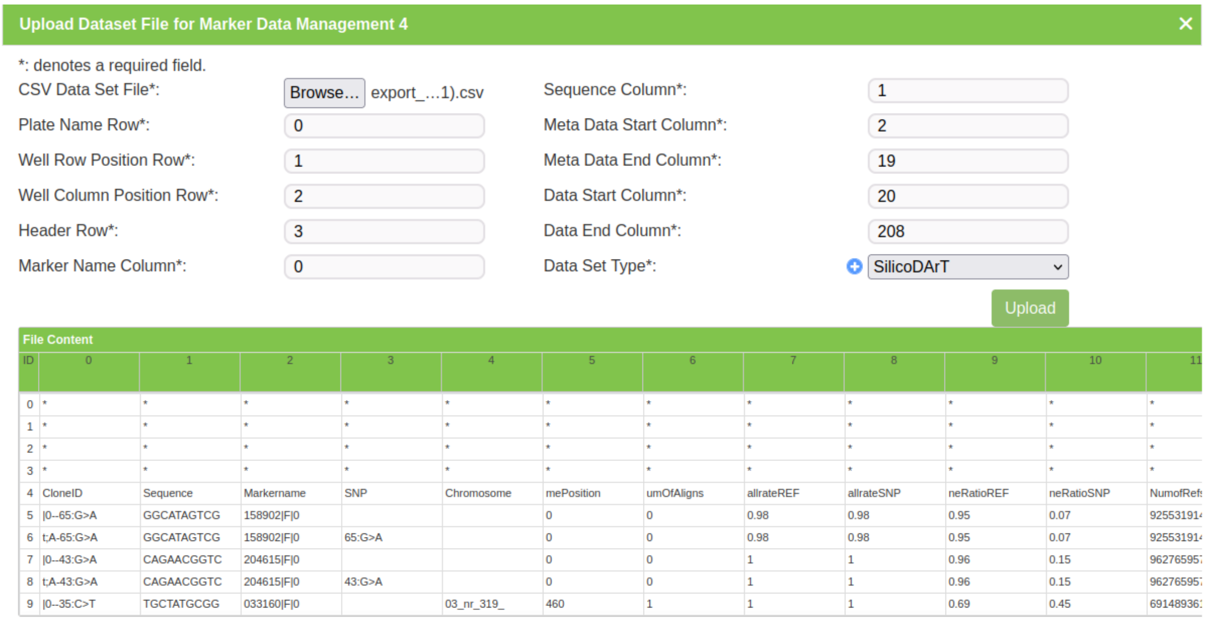
Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

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 *Access Settings and Permissions* 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 4

*: denotes a required field.

CSV Data Set File*:	export_...1).csv	Sequence Column*:	1
Plate Name Row*:	0	Meta Data Start Column*:	2
Well Row Position Row*:	1	Meta Data End Column*:	19
Well Column Position Row*:	2	Data Start Column*:	20
Header Row*:	3	Data End Column*:	208
Marker Name Column*:	0	Data Set Type*:	SilicoDArT

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	NumofRef
5	|0--65:G>A	GGCATAGTCG	158902|F|0			0	0	0.98	0.98	0.95	0.07	92553191
6	t;A-65:G>A	GGCATAGTCG	158902|F|0	65:G>A		0	0	0.98	0.98	0.95	0.07	92553191
7	|0--43:G>A	CAGAACGGTC	204615|F|0			0	0	1	1	0.96	0.15	96276595
8	t;A-43:G>A	CAGAACGGTC	204615|F|0	43:G>A		0	0	1	1	0.96	0.15	96276595
9	|0--35:C>T	TGCTATGCGG	033160|F|0		03_nr_319_	460	1	1	1	0.69	0.45	69148936

Fig. 11: Edit Well Plate Window

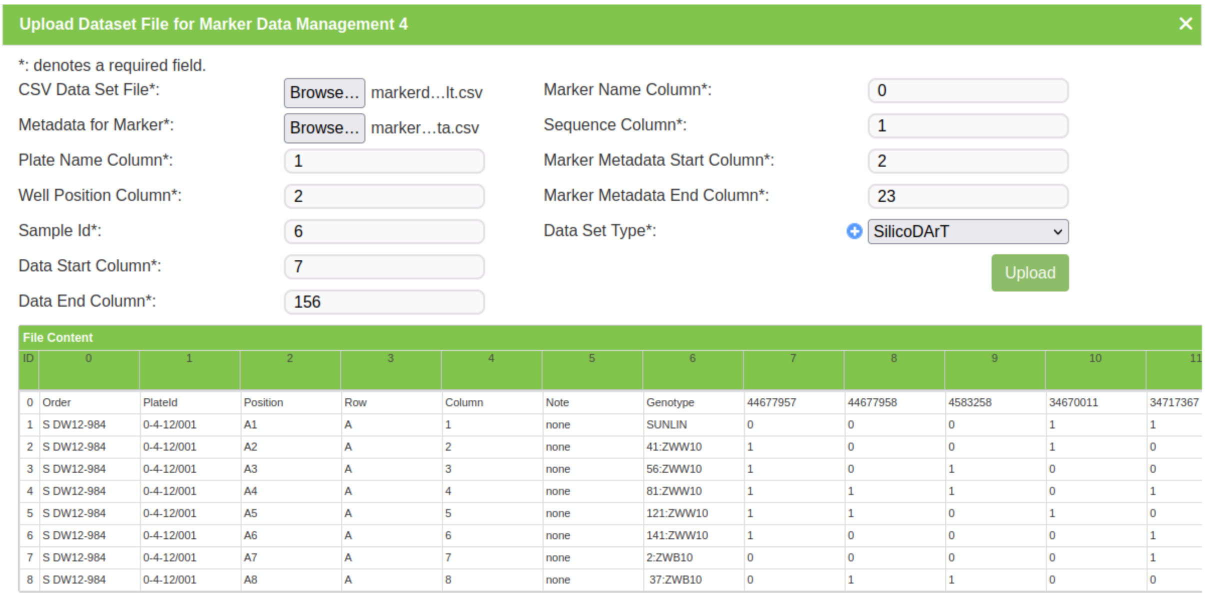
Note: For referencing the CSV file contents, column and row numbering commences with zero.

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 4

*: denotes a required field.

CSV Data Set File*:	Browse… markerd…lt.csv	Marker Name Column*:	0
Metadata for Marker*:	Browse… marker…ta.csv	Sequence Column*:	1
Plate Name Column*:	1	Marker Metadata Start Column*:	2
Well Position Column*:	2	Marker Metadata End Column*:	23
Sample Id*:	6	Data Set Type*:	SilicoDArT
Data Start Column*:	7		
Data End Column*:	156		

File Content

ID	0	1	2	3	4	5	6	7	8	9	10	11
0	Order	PlateId	Position	Row	Column	Note	Genotype	44677957	44677958	4583258	34670011	34717367
1	S DW12-984	0-4-12/001	A1	A	1	none	SUNLIN	0	0	0	1	1
2	S DW12-984	0-4-12/001	A2	A	2	none	41:ZWW10	1	0	0	1	0
3	S DW12-984	0-4-12/001	A3	A	3	none	56:ZWW10	1	0	1	0	0
4	S DW12-984	0-4-12/001	A4	A	4	none	81:ZWW10	1	1	1	0	1
5	S DW12-984	0-4-12/001	A5	A	5	none	121:ZWW10	1	1	0	1	0
6	S DW12-984	0-4-12/001	A6	A	6	none	141:ZWW10	1	0	0	0	1
7	S DW12-984	0-4-12/001	A7	A	7	none	2:ZWB10	0	0	0	0	1
8	S DW12-984	0-4-12/001	A8	A	8	none	37:ZWB10	0	1	1	0	0

Fig. 12: 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.

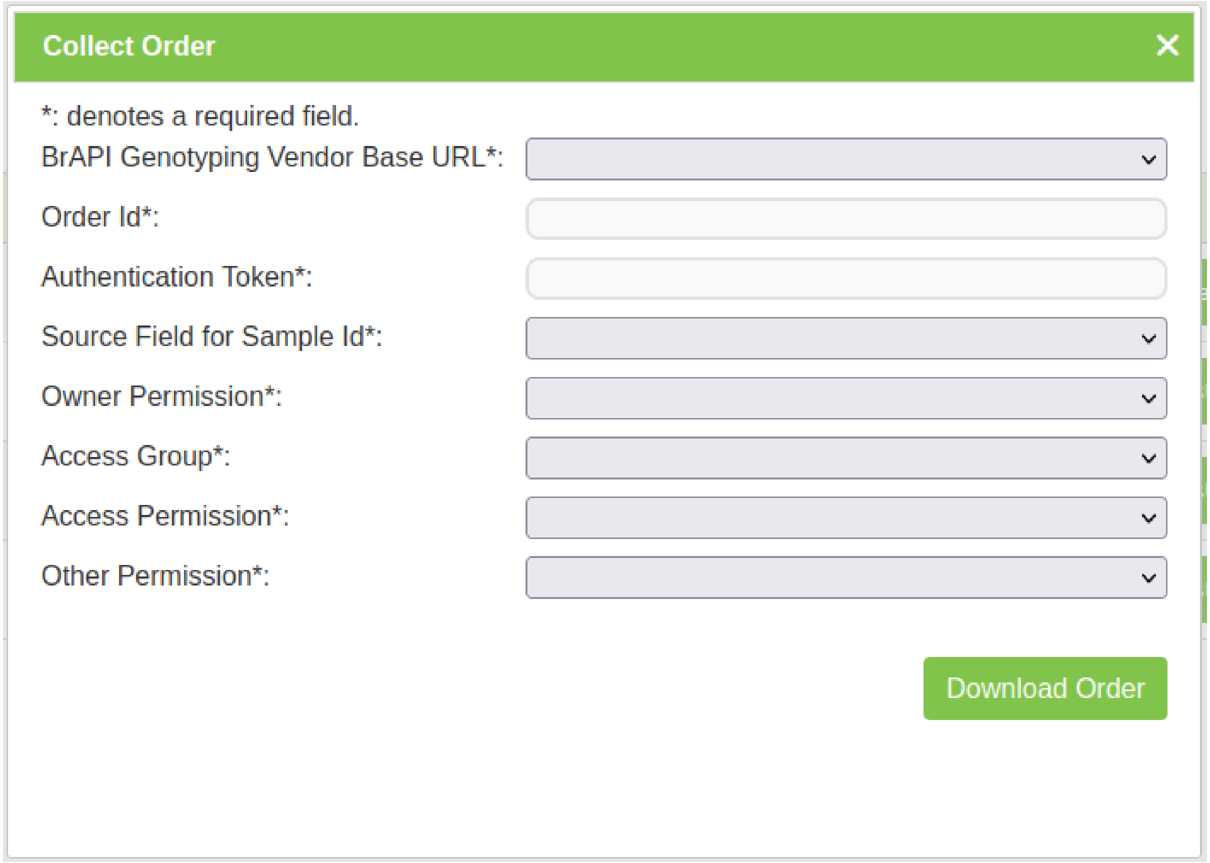
Tip: After selecting a file to upload, the file contents will be displayed underneath the form. This can be used to refer to the correct columns as required.

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. 13: Collect Order Window

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

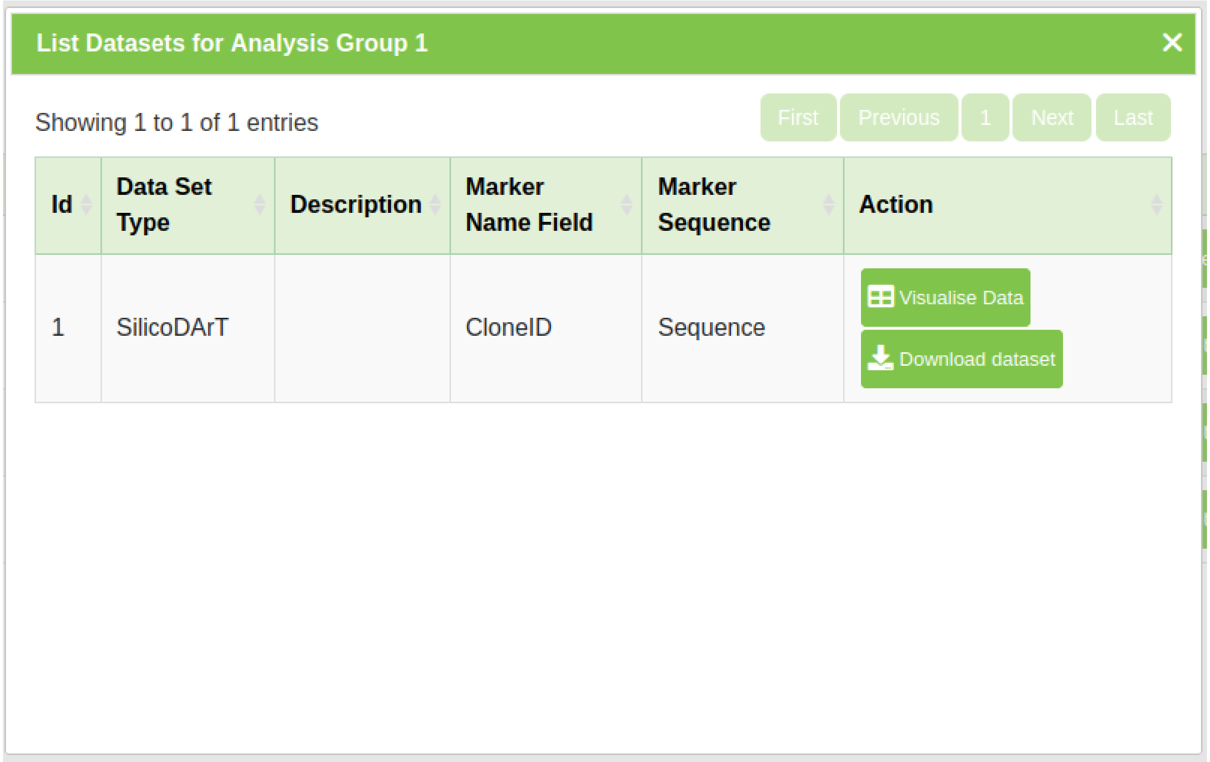
Field	Mandatory?	Description
BrAPI Genotyping Vendor Base URL	Mandatory	Select the vendor BrAPI URL.
Order ID	Mandatory	Full Order ID of completed order for import.
Authentication Token	Mandatory	Authentication token from genotyping vendor.
Source Field for Sample ID	Mandatory	KDDart entity that will be created or linked to sample ID.
Access Fields	Mandatory	Access and permissions. See the *Access Settings and Permissions* 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 **List Datasets** in the **Actions Column** for the required group in the **Marker Data Management Page**.



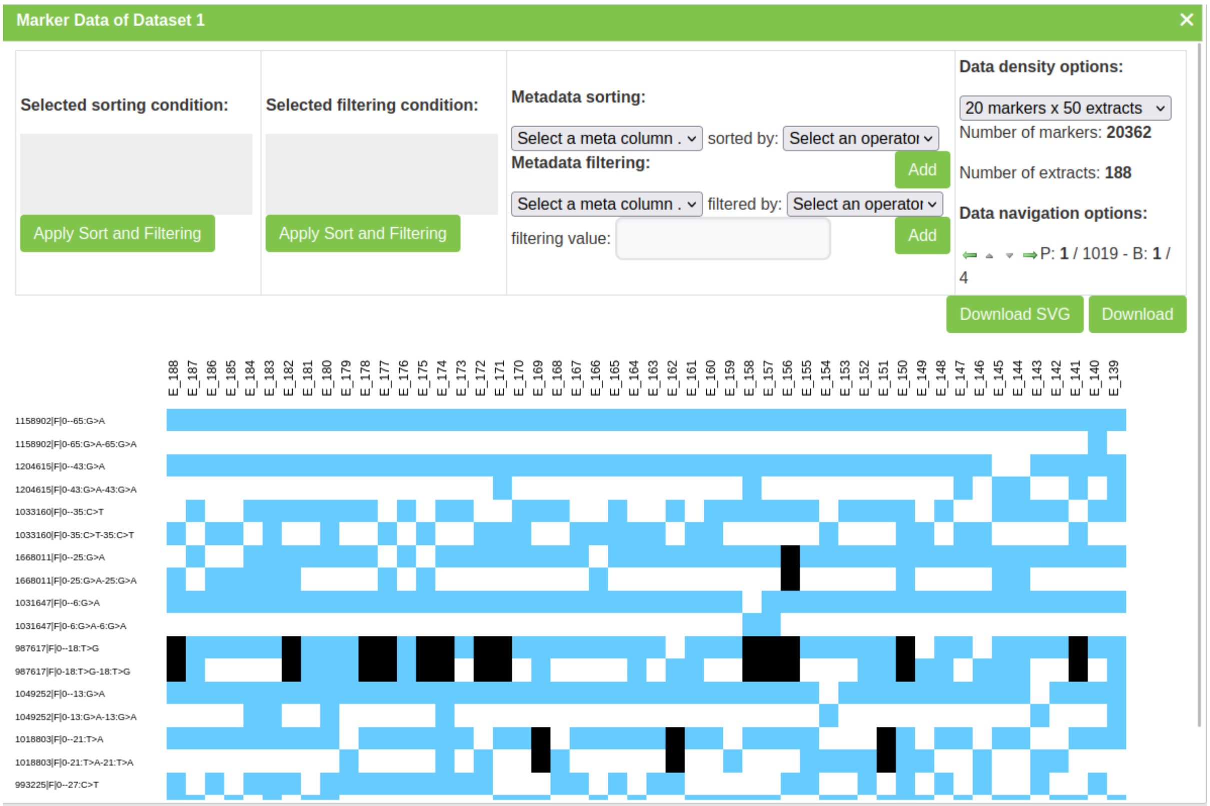
Showing 1 to 1 of 1 entries

Id	Data Set Type	Description	Marker Name Field	Marker Sequence	Action
1	SilicoDArT		CloneID	Sequence	Visualise Data Download dataset

Fig. 14: List Datasets Window

6.3.9 Visualising a Dataset with a Heatmap

To visualise a dataset with a heatmap, select Visualise Data **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:



20 markers x 50 extracts

Number of markers: **20362**

Number of extracts: **188**

⇦ ▲ ▼ ⇨ P: **1** / 1019 - B: **1** / 4

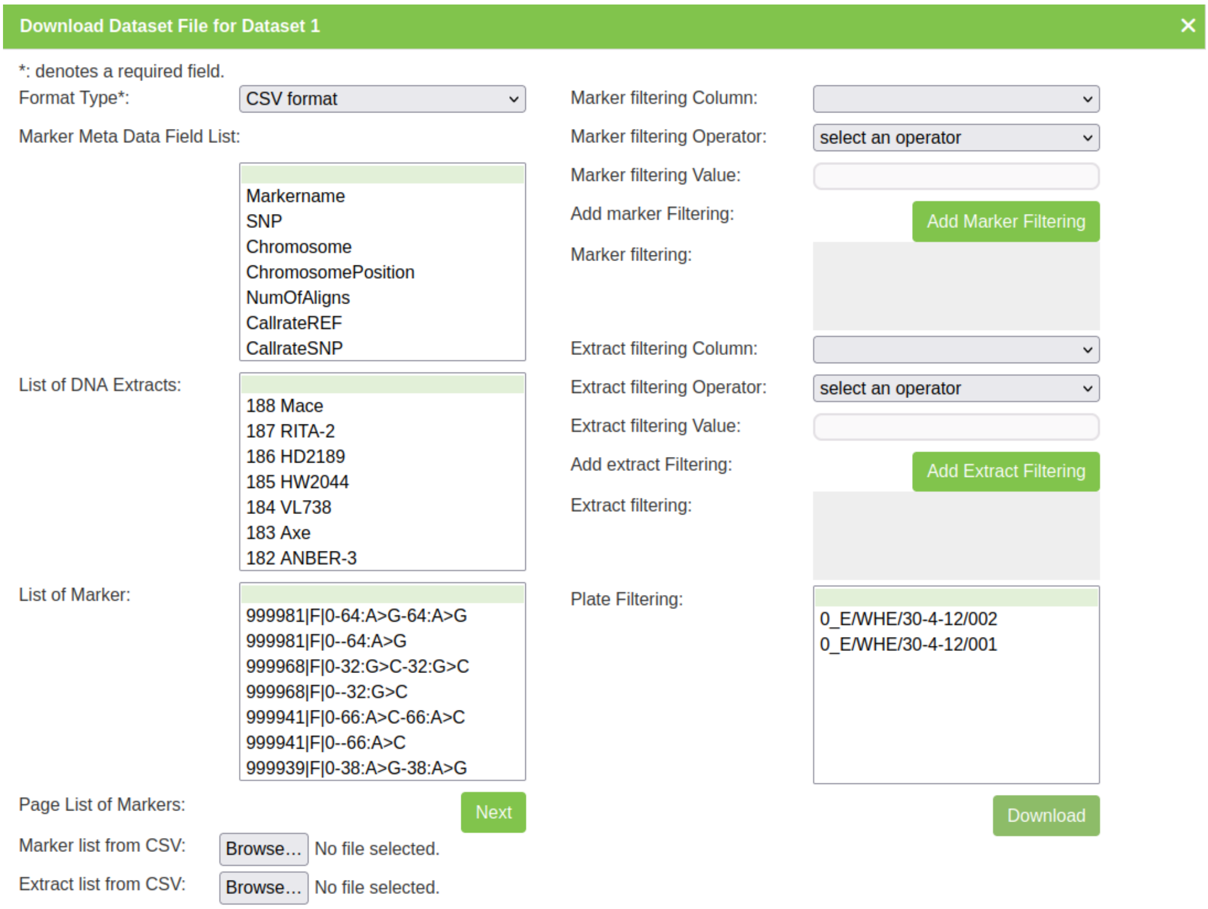
Fig. 15: Marker Data Window

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:



Download Dataset File for Dataset 1

*: denotes a required field.

Format Type*: CSV format

Marker Meta Data Field List:
Markername
SNP
Chromosome
ChromosomePosition
NumOfAligns
CallrateREF
CallrateSNP

List of DNA Extracts:
188 Mace
187 RITA-2
186 HD2189
185 HW2044
184 VL738
183 Axe
182 ANBER-3

List of Marker:
999981|F|0-64:A>G-64:A>G
999981|F|0--64:A>G
999968|F|0-32:G>C-32:G>C
999968|F|0--32:G>C
999941|F|0-66:A>C-66:A>C
999941|F|0--66:A>C
999939|F|0-38:A>G-38:A>G

Page List of Markers:

Marker list from CSV: No file selected.

Extract list from CSV: No file selected.

Marker filtering Column:

Marker filtering Operator: select an operator

Marker filtering Value:

Add marker Filtering:

Marker filtering:

Extract filtering Column:

Extract filtering Operator: select an operator

Extract filtering Value:

Add extract Filtering:

Extract filtering:

Plate Filtering:
0_E/WHE/30-4-12/002
0_E/WHE/30-4-12/001

Fig. 16: Download Dataset Window

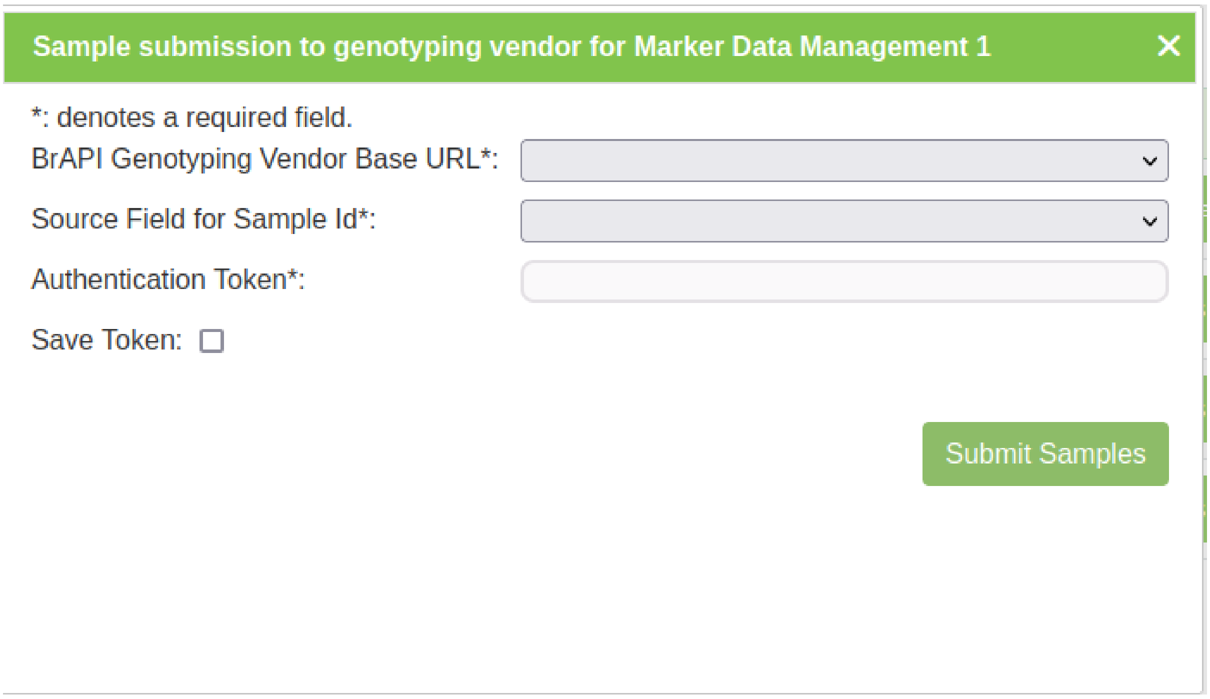
Table 10: Download Dataset Fields

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 Metadata 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 bee 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 it's fields:



Sample submission to genotyping vendor for Marker Data Management 1 ✕

*: denotes a required field.

BrAPI Genotyping Vendor Base URL*:

Source Field for Sample Id*:

Authentication Token*:

Save Token: ☐

Fig. 17: Download Dataset Window

Table 11: Sample Submission to Genotyping Vendor Fields

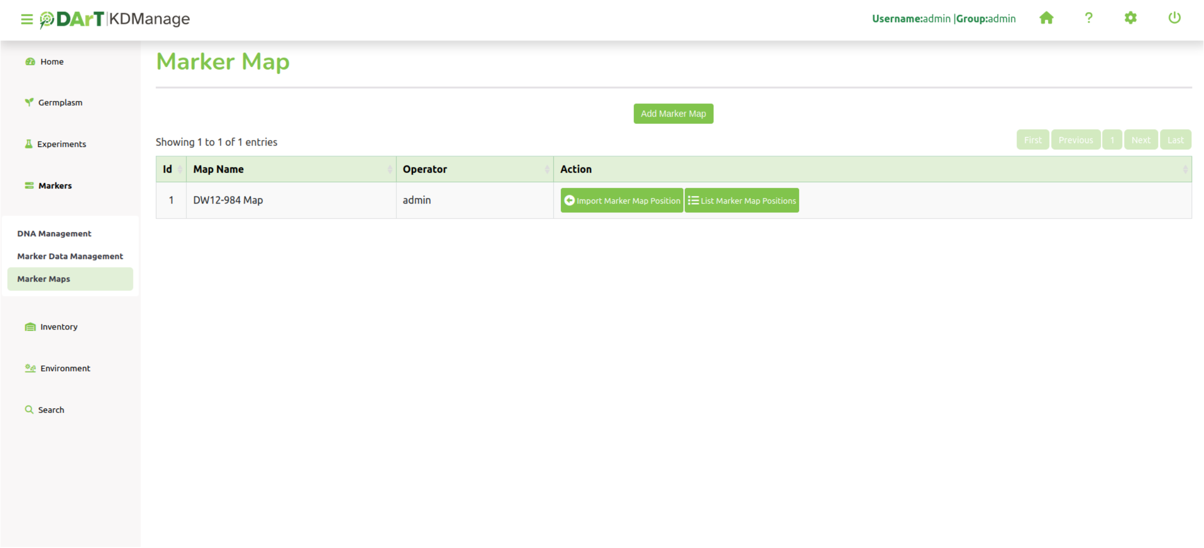
Field	Description
BrAPI Genotyping Vendor Base URL	The URL for genotyping vendors. These must be configured by a system administrator.
Source Field for Sample ID	How samples will be identified.
Authentication Token	Authentication token from vendor.

6.3.12 Downloading Genotyping Results from a Vendor

If KDManage has bee 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.



Showing 1 to 1 of 1 entries

Id	Map Name	Operator	Action
1	DW12-984 Map	admin	Import Marker Map Position List Marker Map Positions

Fig. 18: 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:

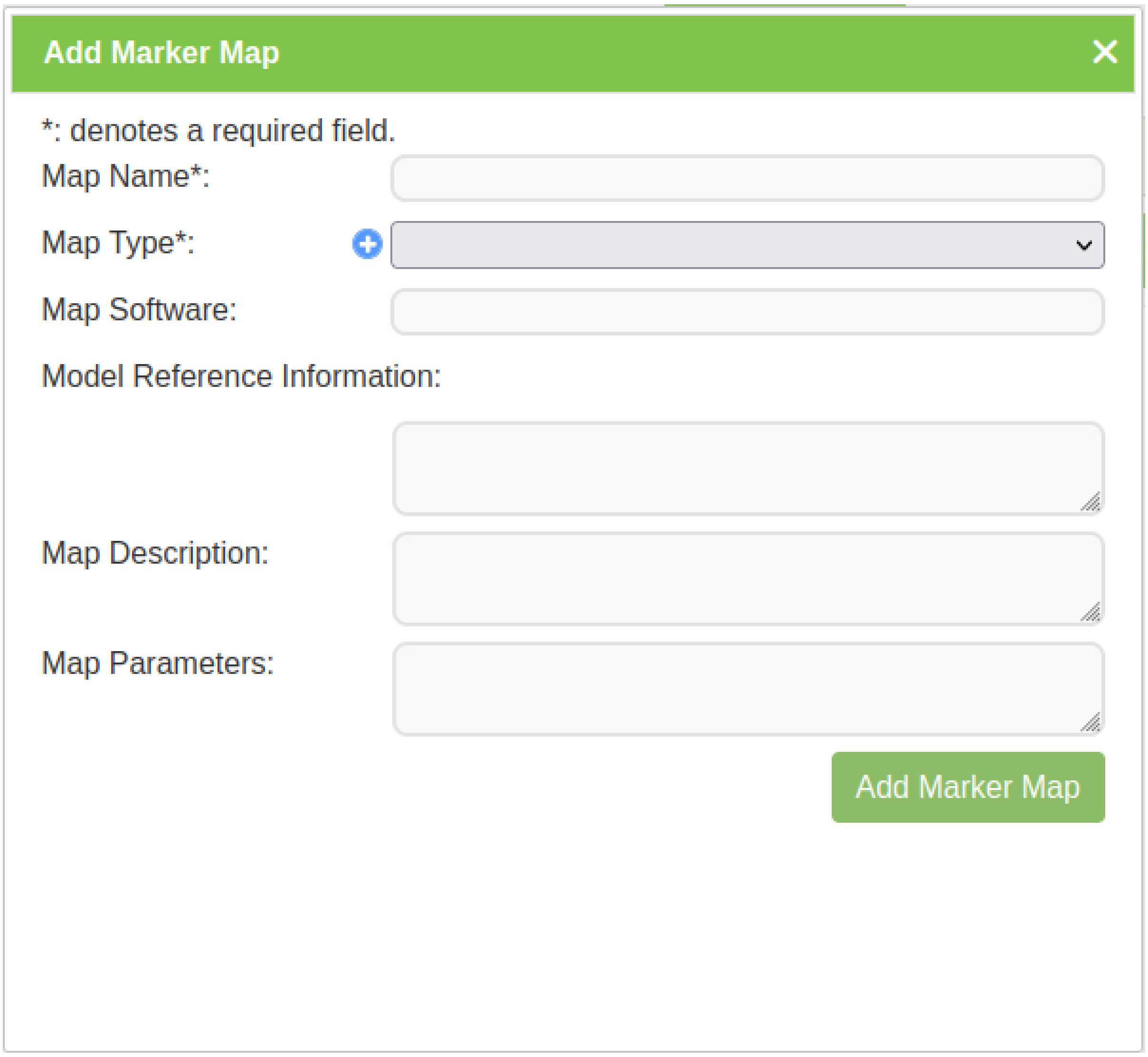


Fig. 19: Add Marker Map Window

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 Position **Import Marker Map**. This will open the **Import Marker Map Position Window** which is pictured below, along with a table that details related fields:

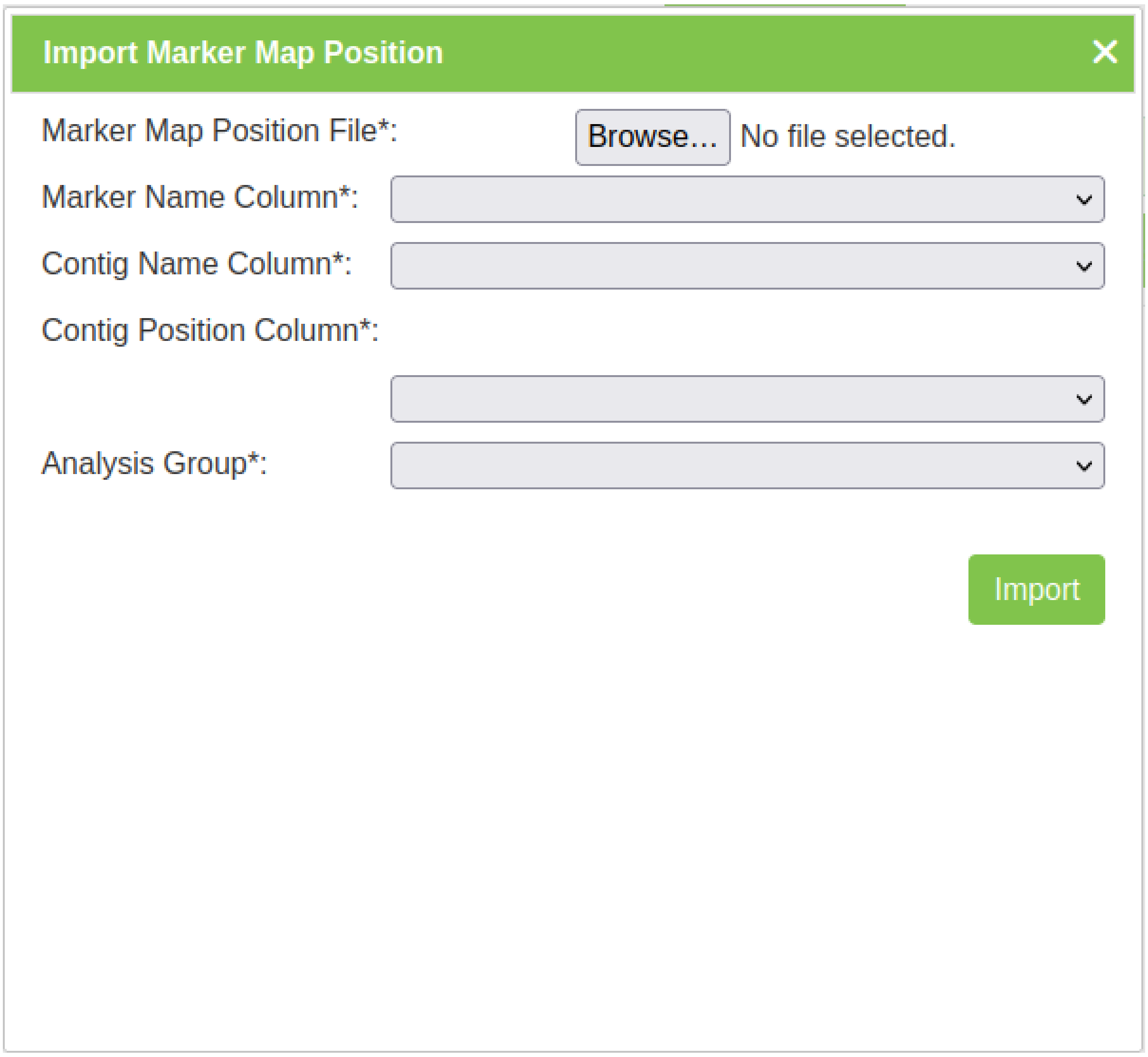


Fig. 20: Import Marker Map Position Window

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.

CHAPTER

SEVEN

INVENTORY MENU

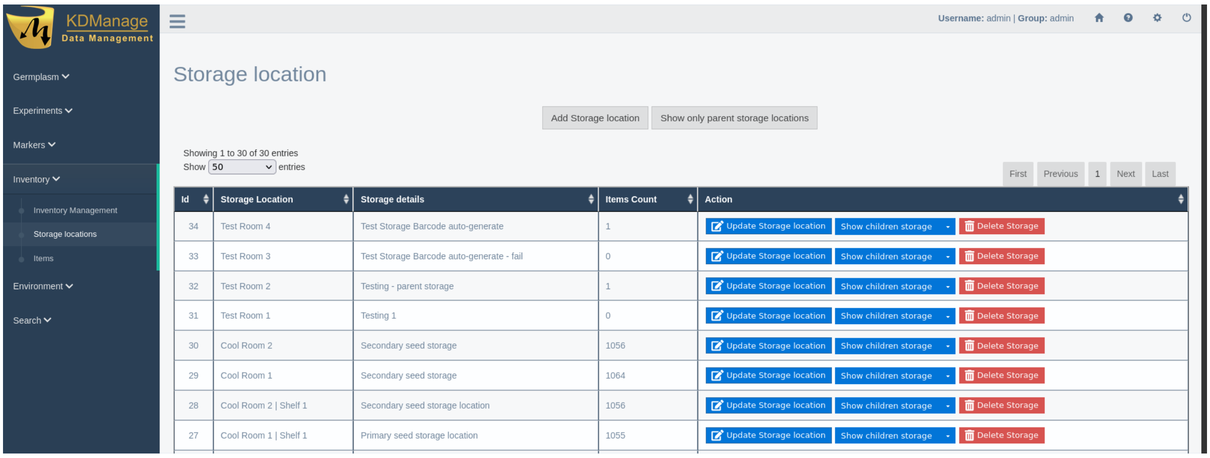
The KDManage **Inventory menu** provides tools that you can use to manage inventory items and locations, including performing stocktakes or adding/removing items. The tools available in the **Inventory** are listed below:

- *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:



Storage location

Showing 1 to 30 of 30 entries
Show 50 entries

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

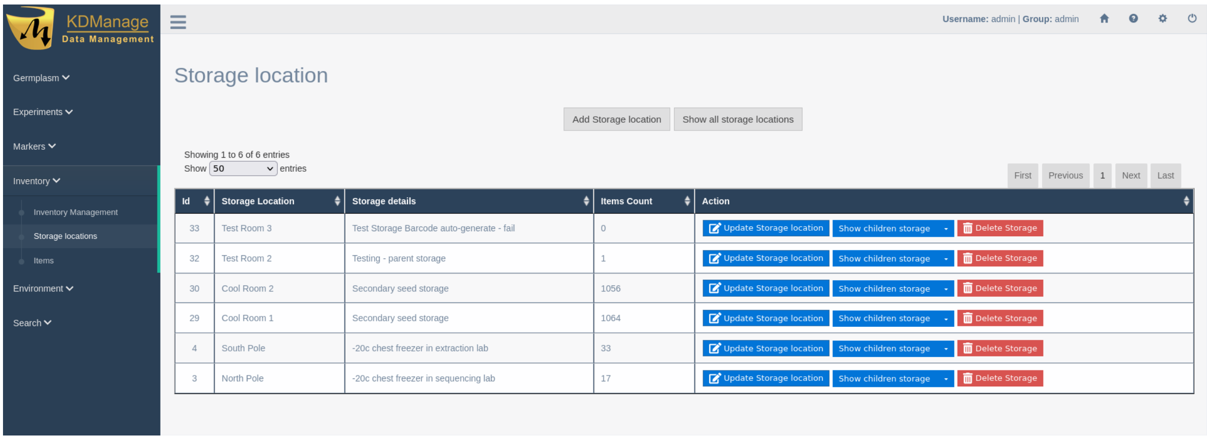
Fig. 1: Storage Locations

Table 1: Storage Location Fields

Field	**Mandatory**	**Description**
Storage Barcode		A barcode to identify the storage location.
Storage Location	Mandatory	A name to identify the storage location.
Storage Parent ID		The ID of the parent of the storage location (e.g. *North Pole Building 1* can be the parent of *North Pole Building 1 | Room A*).
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.



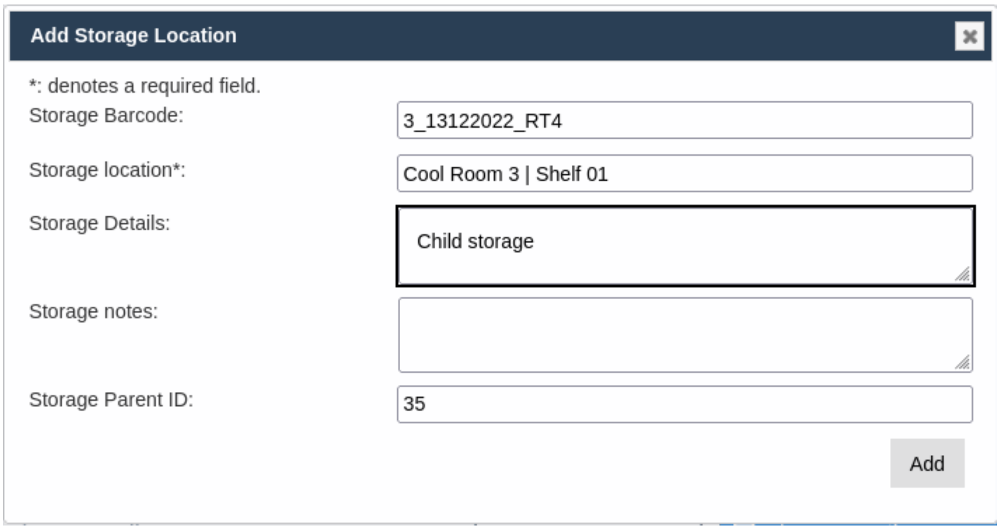
Showing 1 to 6 of 6 entries
Show 50 entries

Id	Storage Location	Storage details	Items Count	Action
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
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
4	South Pole	-20c chest freezer in extraction lab	33	Update Storage location Show children storage Delete Storage
3	North Pole	-20c chest freezer in sequencing lab	17	Update Storage location Show children storage Delete Storage

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:



Add Storage Location

*: denotes a required field.

Storage Barcode: 3_13122022_RT4

Storage location*: Cool Room 3 | Shelf 01

Storage Details: Child storage

Storage notes:

Storage Parent ID: 35

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** • 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 **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 ▾ **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.

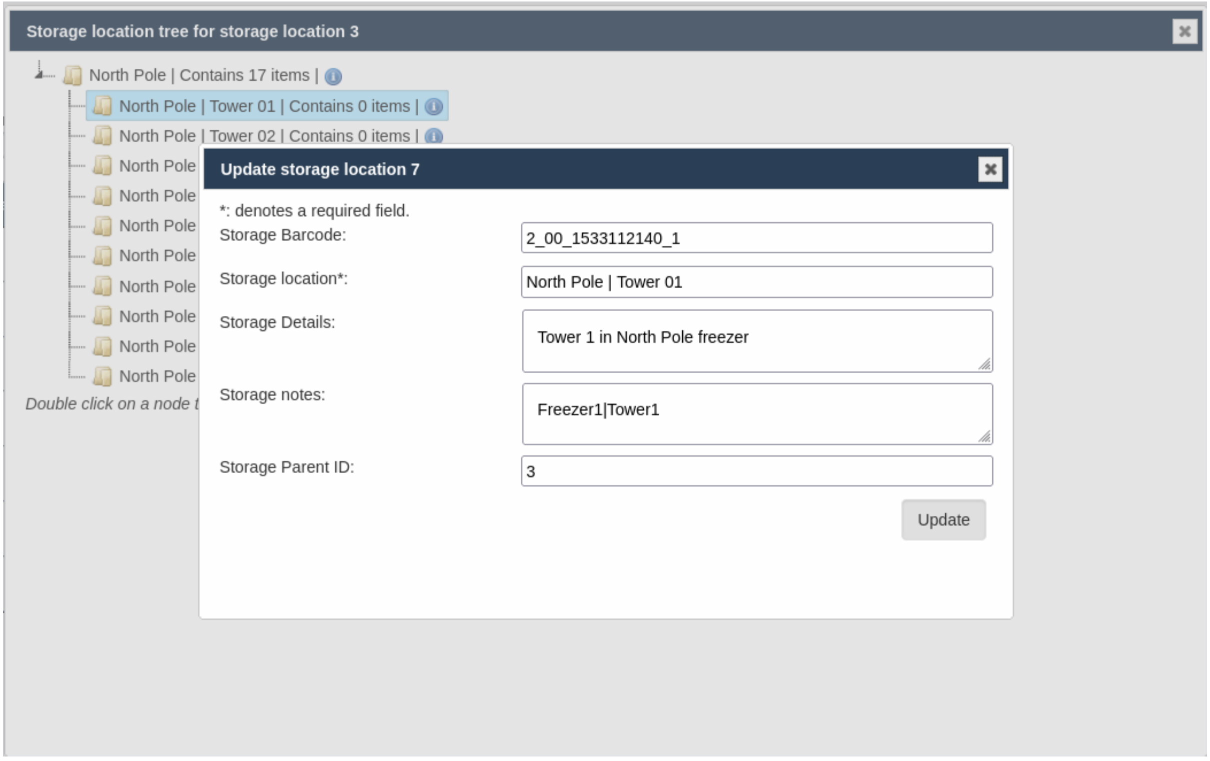
Storage location tree for storage location 3

- North Pole | Contains 17 items | ⓘ
  - North Pole | Tower 01 | Contains 0 items | ⓘ
  - North Pole | Tower 02 | Contains 0 items | ⓘ
  - North Pole | Tower 03 | Contains 0 items | ⓘ
  - North Pole | Tower 04 | Contains 0 items | ⓘ
  - North Pole | Tower 05 | Contains 0 items | ⓘ
  - North Pole | Tower 06 | Contains 0 items | ⓘ
  - North Pole | Tower 07 | Contains 0 items | ⓘ
  - North Pole | Tower 08 | Contains 0 items | ⓘ
  - North Pole | Tower 09 | Contains 0 items | ⓘ
  - North Pole | Tower 10 | Contains 0 items | ⓘ

Double click on a node to expand it

Fig. 4: Storage Tree

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



Storage location tree for storage location 3

- North Pole | Contains 17 items | ⓘ
  - North Pole | Tower 01 | Contains 0 items | ⓘ
  - North Pole | Tower 02 | Contains 0 items | ⓘ
  - North Pole
  - North Pole
  - North Pole
  - North Pole
  - North Pole
  - North Pole
  - North Pole
  - North Pole

Double click on a node t

Update storage location 7

*: denotes a required field.

Storage Barcode: 2_00_1533112140_1

Storage location*: North Pole | Tower 01

Storage Details: Tower 1 in North Pole freezer

Storage notes: Freezer1|Tower1

Storage Parent ID: 3

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	Mandatory	Description
Trial Unit Specimen ID		The ID of the trial unit specimen that the item was harvested from.
Specimen ID	Mandatory	The 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	Mandatory	The 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 *Units* topic).
Date Added	Mandatory, but no user's action required	The date and time that the item was added to the database. This field only displays in Item-related functions of **Inventory Management** page.
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	Mandatory, but no user's action required	The 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.

7.2.1 Adding a New Item

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

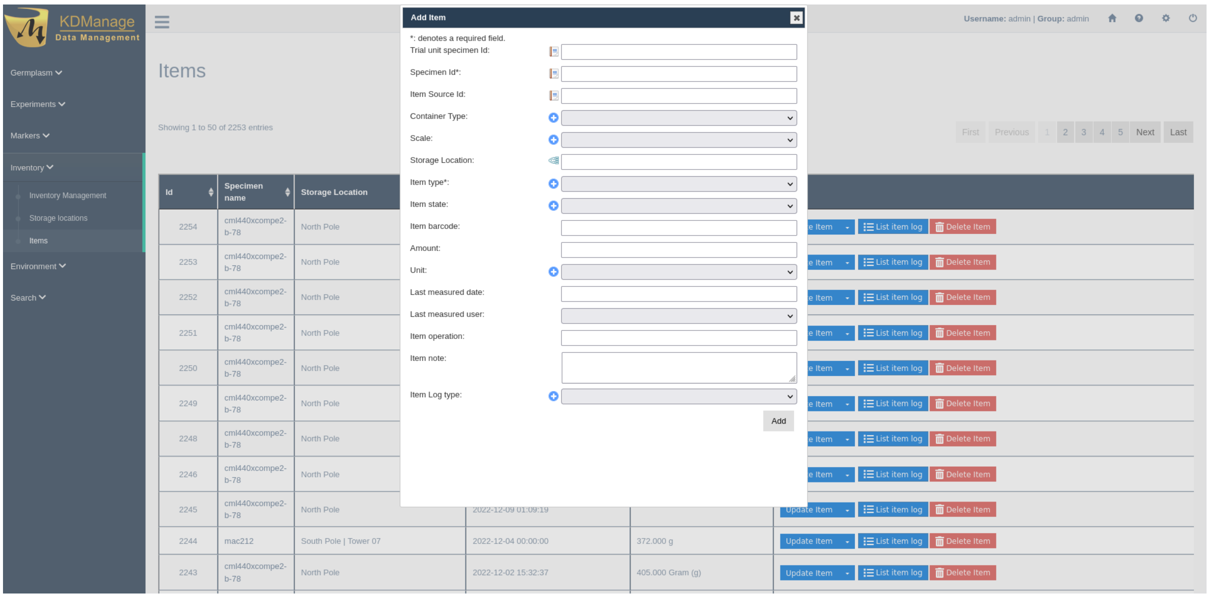


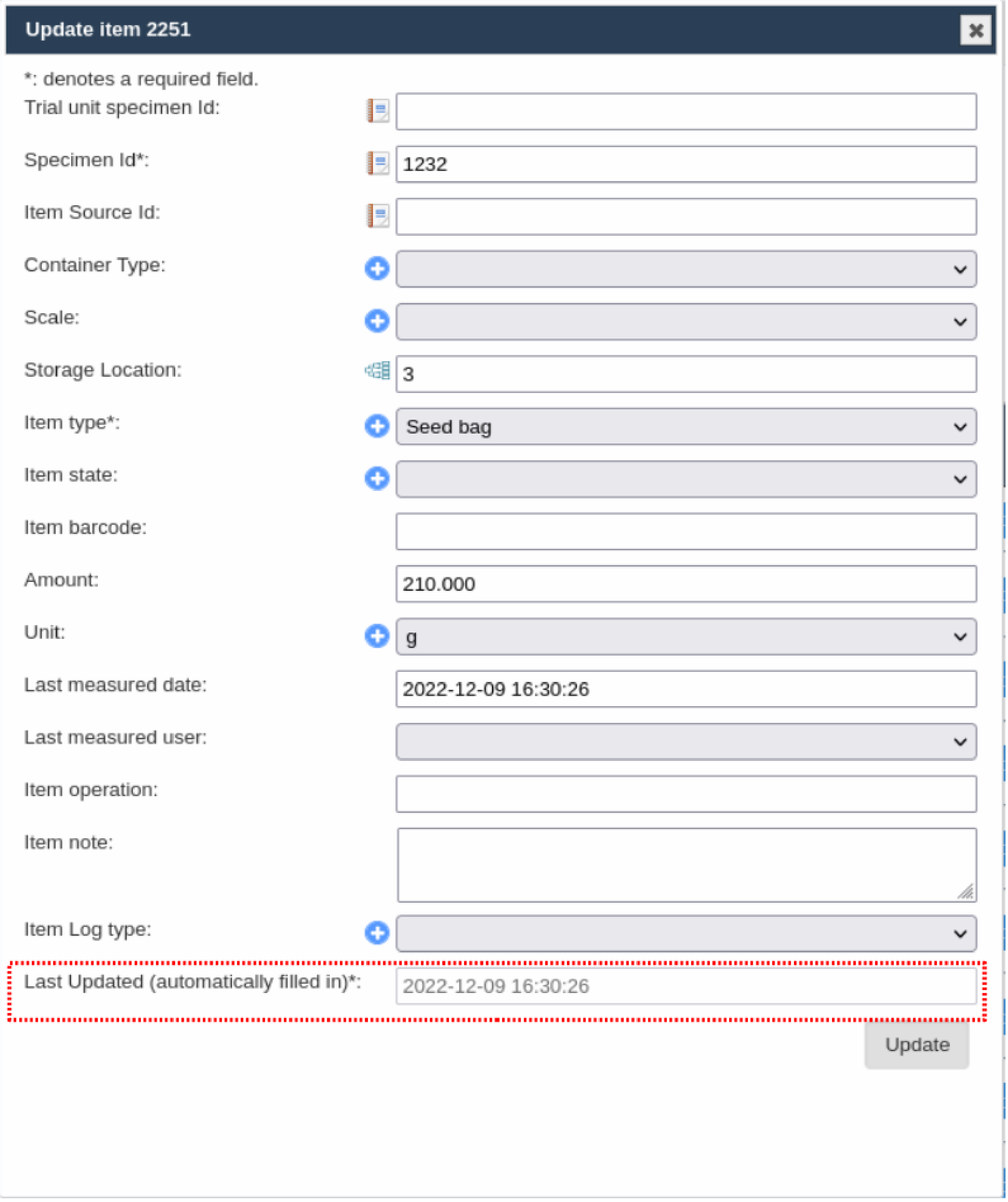
Fig. 6: Adding a New Item

Table 4: Adding a New Item

Step	Action
1.	From the **Items page** in the **Inventory**, select the **Add Item button**. This will display the **Add Item window**.
2.	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: • The *Specimen ID* and *Item Type* fields are mandatory. Whilst *Trial Unit Specimen ID* is not a mandatory field, if used, the *Specimen ID* must match the *Specimen ID* of the *Trial Unit Specimen*. 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 *Storage Location* has the **Storage Tree button** so that an existing storage location can be chosen for the item. • If required, add an *Item Log Type* to add an “Addition” **Item log** for a newly created item.
3.	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 ▾ **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:	
Specimen Id*:	1232
Item Source Id:	
Container Type:	
Scale:	
Storage Location:	3
Item type*:	Seed bag
Item state:	
Item barcode:	
Amount:	210.000
Unit:	g
Last measured date:	2022-12-09 16:30:26
Last measured user:	
Item operation:	
Item note:	
Item Log type:	
Last Updated (automatically filled in)*:	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:

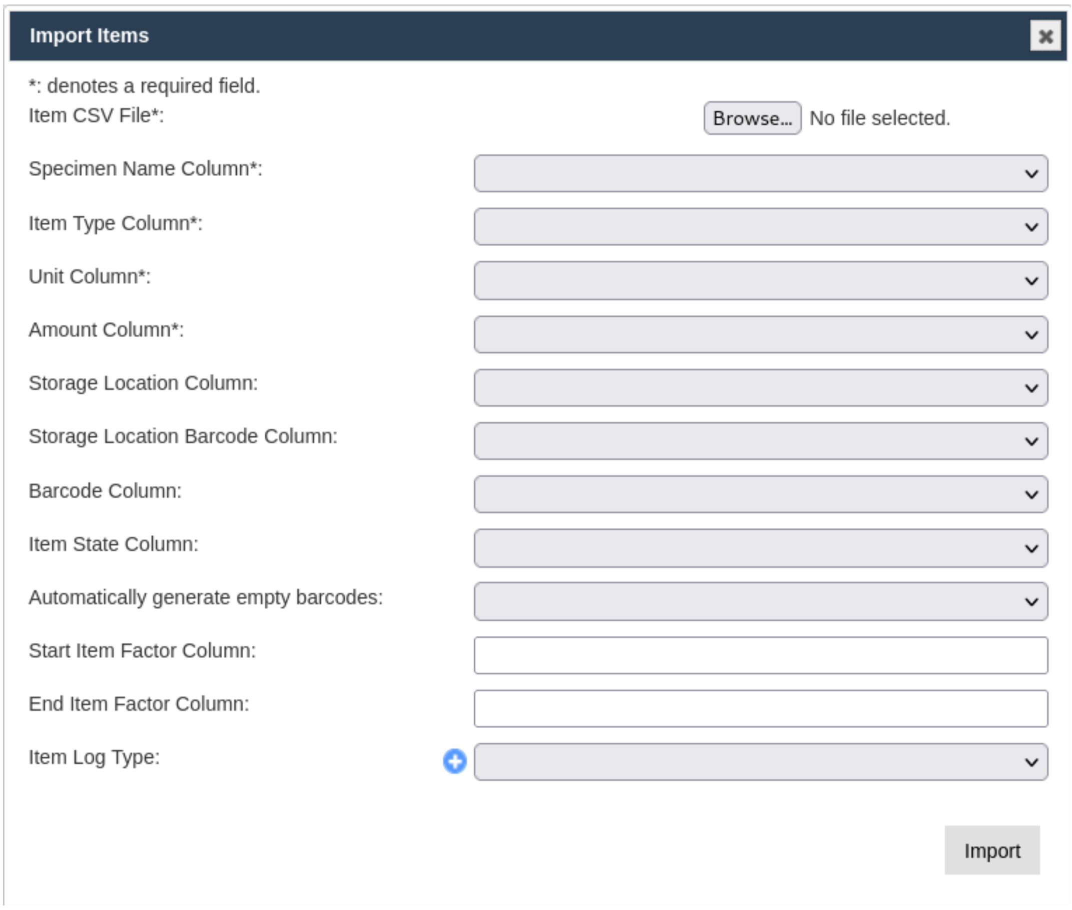


Fig. 9: Importing Items

Table 5: Import CSV

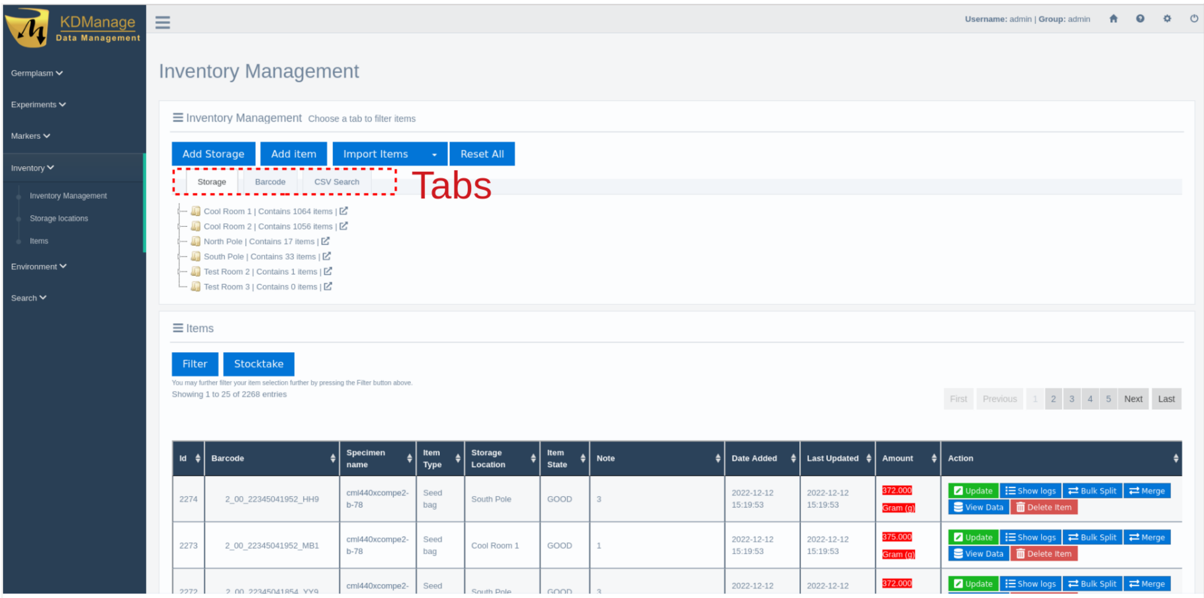
Step	Action
1.	From the **Items tool** in the **Inventory menu**, select the **Import Items button** to display the **Import Items window** (as seen in the image above).
2.	Select the **Choose File button** to open a window to select a file from your local machine. The columns will be automatically mapped to fields if the uploaded CSV has the headings specified in the *Item CSV Preparation* 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 panel** is the **Items panel** which contains the items listed according to selections in the **Storage tab** or **Barcode tab**.



Cool Room 1 | Contains 1064 items |
Cool Room 2 | Contains 1056 items |
North Pole | Contains 17 items |
South Pole | Contains 33 items |
Test Room 2 | Contains 1 items |
Test Room 3 | Contains 0 items |

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

Showing 1 to 25 of 2268 entries

Id	Barcode	Specimen name	Item Type	Storage Location	Item State	Note	Date Added	Last Updated	Amount	Action
2274	2_00_22345041952_HH9	cml440xcompe2-b-78	Seed bag	South Pole	GOOD	3	2022-12-12 15:19:53	2022-12-12 15:19:53	372.000 Gram (g)	Update Show logs Bulk Split Merge View Data Delete Item
2273	2_00_22345041952_MB1	cml440xcompe2-b-78	Seed bag	Cool Room 1	GOOD	1	2022-12-12 15:19:53	2022-12-12 15:19:53	375.000 Gram (g)	Update Show logs Bulk Split Merge View Data Delete Item
2272	2_00_22345041854_YY9	cml440xcompe2-	Seed	South Pole	GOOD	3	2022-12-12	2022-12-12	372.000	Update Show logs Bulk Split Merge

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.

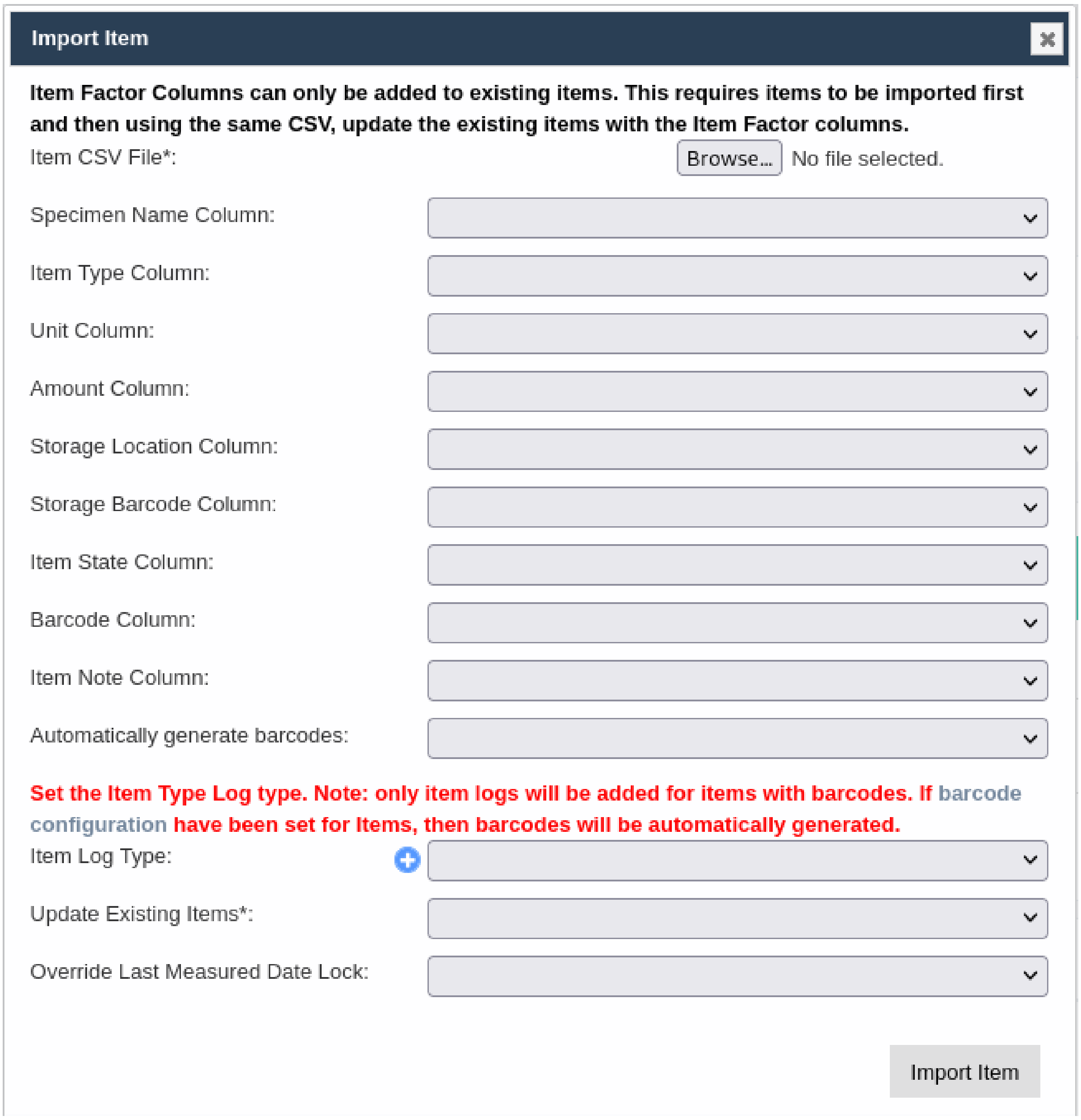
Item CSV Preparation for Inventory Management

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*).



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*: Browse... 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:

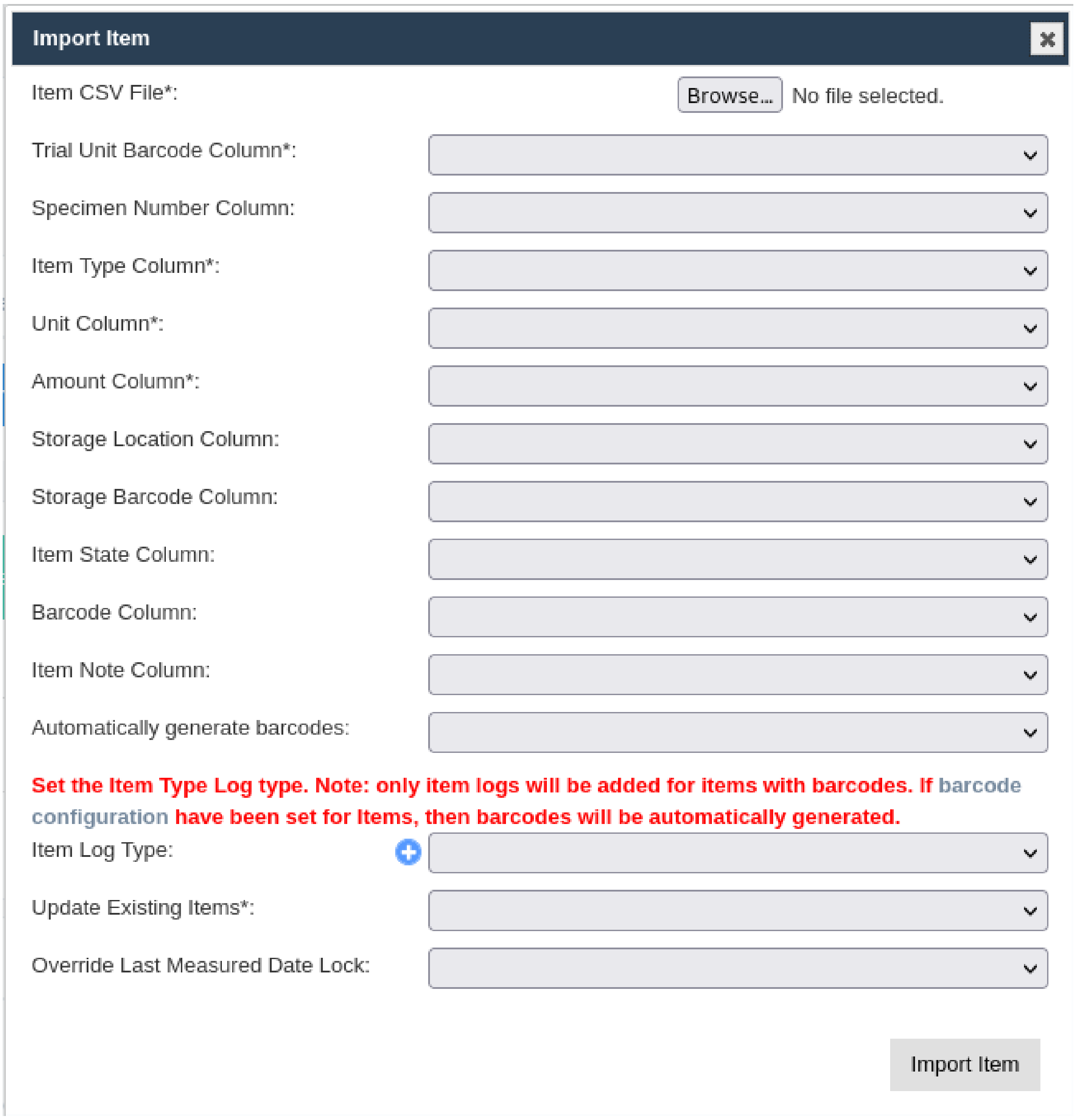
Set the Item Type Log type. Note: only item logs will be added for items with barcodes. If barcode configuration have been set for Items, then barcodes will be automatically generated.

Item Log Type:

Update Existing Items*:

Override Last Measured Date Lock:

Fig. 11: Item Import with Specimen Names



Item CSV File*: 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:

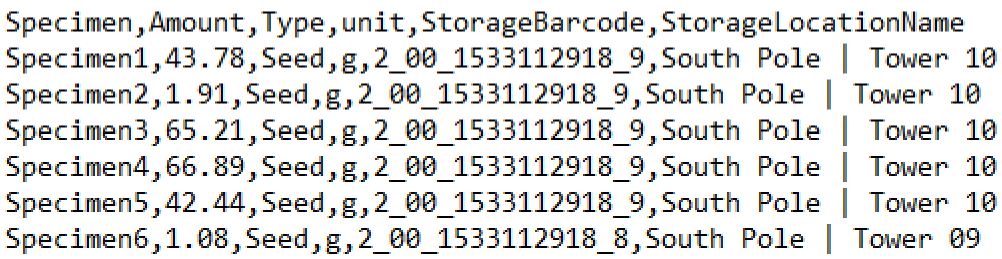
Fig. 12: Item Import with Trial Unit Barcodes

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.



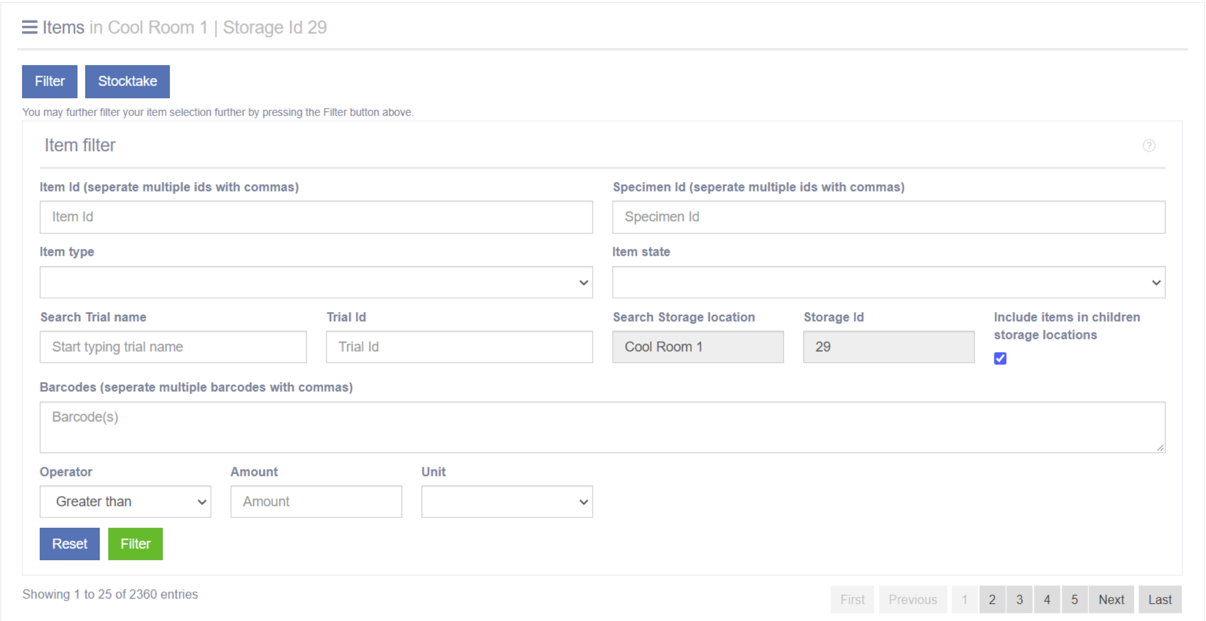
```
Specimen,Amount,Type,unit,StorageBarcode,StorageLocationName
Specimen1,43.78,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen2,1.91,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen3,65.21,Seed,g,2_00_1533112918_9,South Pole | Tower 10
Specimen4,66.89,Seed,g,2_00_1533112918_9,South Pole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

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

Item filter

Item Id (seperate multiple ids with commas): Item Id
Specimen Id (seperate multiple ids with commas): Specimen Id
Item type:
Item state:
Search Trial name: Start typing trial name
Trial Id: Trial Id
Search Storage location: Cool Room 1
Storage Id: 29
Include items in children storage locations ☑
Barcodes (seperate multiple barcodes with commas): Barcode(s)
Operator: Greater than
Amount: Amount
Unit:

Showing 1 to 25 of 2360 entries

Fig. 14: Filtering Inventory Items

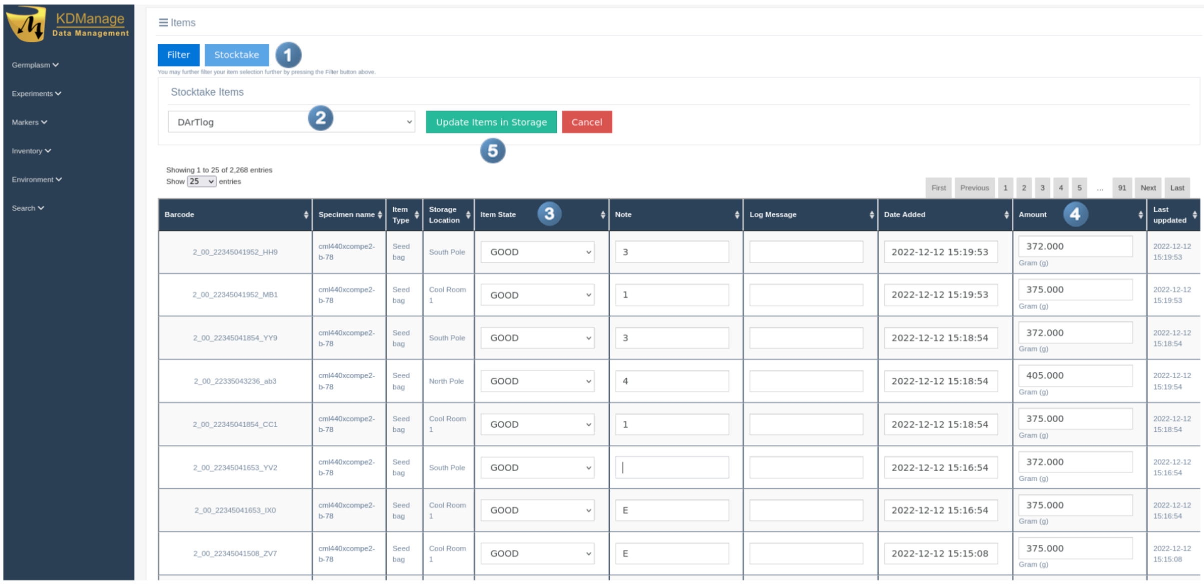
Table 6: Filtering Inventory Items

Step	Action
1.	Select the **Filter** button Filter 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 Filter 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 **Stocktate 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.



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

Stocktake Items

DArTlog

Showing 1 to 25 of 2,268 entries

Show 25 entries

Barcode	Specimen name	Item Type	Storage Location	Item State	Note	Log Message	Date Added	Amount	Last uppdated
2_00_22345041952_HH9	cml440xcompe2-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	cml440xcompe2-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_22345041854_YY9	cml440xcompe2-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	cml440xcompe2-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_22345041854_CC1	cml440xcompe2-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_22345041653_YV2	cml440xcompe2-b-78	Seed bag	South Pole	GOOD			2022-12-12 15:16:54	372.000 Gram (g)	2022-12-12 15:16:54
2_00_22345041653_IX0	cml440xcompe2-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_22345041508_ZV7	cml440xcompe2-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

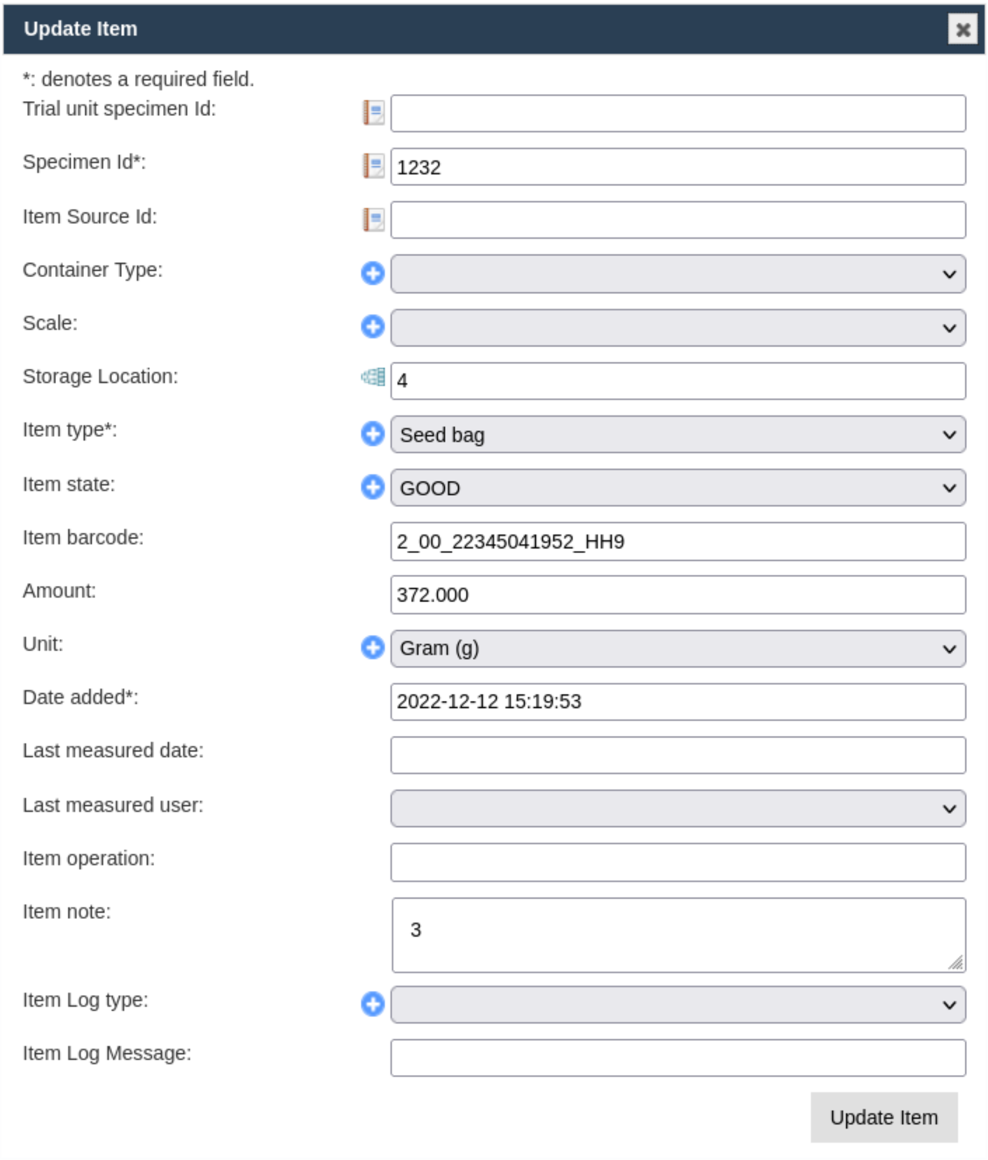
Fig. 15: Conducting a Stocktake

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 *item state* from the **Item State column** at ③.
4.	If required, edit the *amount* 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.



*: denotes a required field.

Trial unit specimen Id:

Specimen Id*: 1232

Item Source Id:

Container Type:

Scale:

Storage Location: 4

Item type*: Seed bag

Item state: GOOD

Item barcode: 2_00_22345041952_HH9

Amount: 372.000

Unit: Gram (g)

Date added*: 2022-12-12 15:19:53

Last measured date:

Last measured user:

Item operation:

Item note: 3

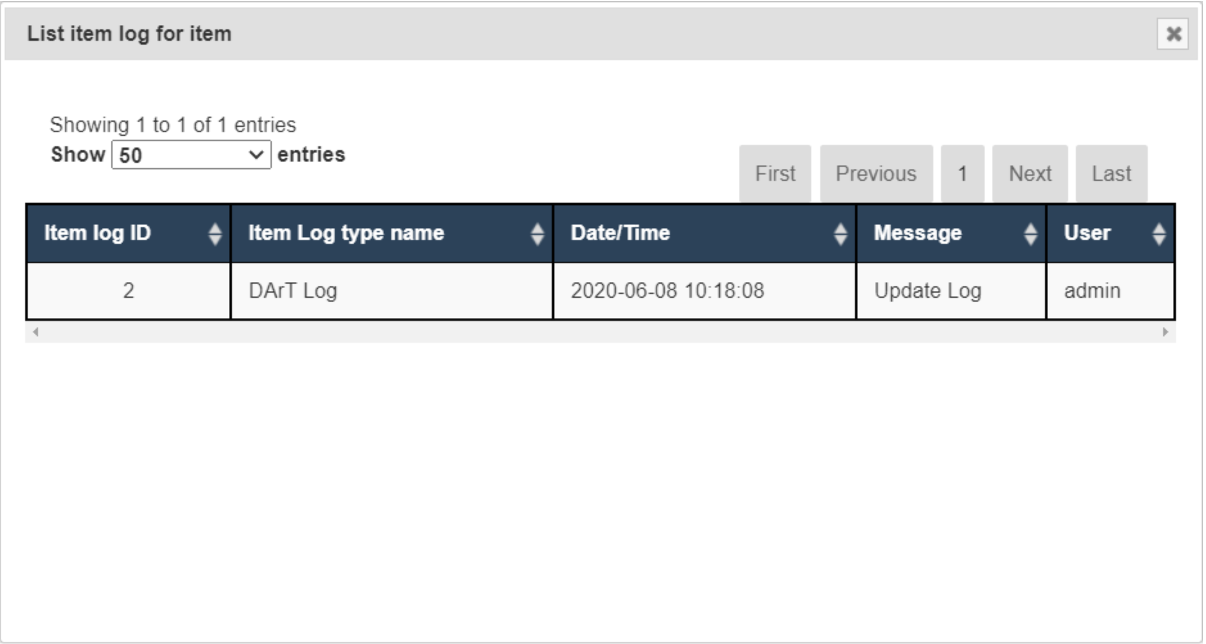
Item Log type:

Item Log Message:

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**.


List item log for item

Showing 1 to 1 of 1 entries

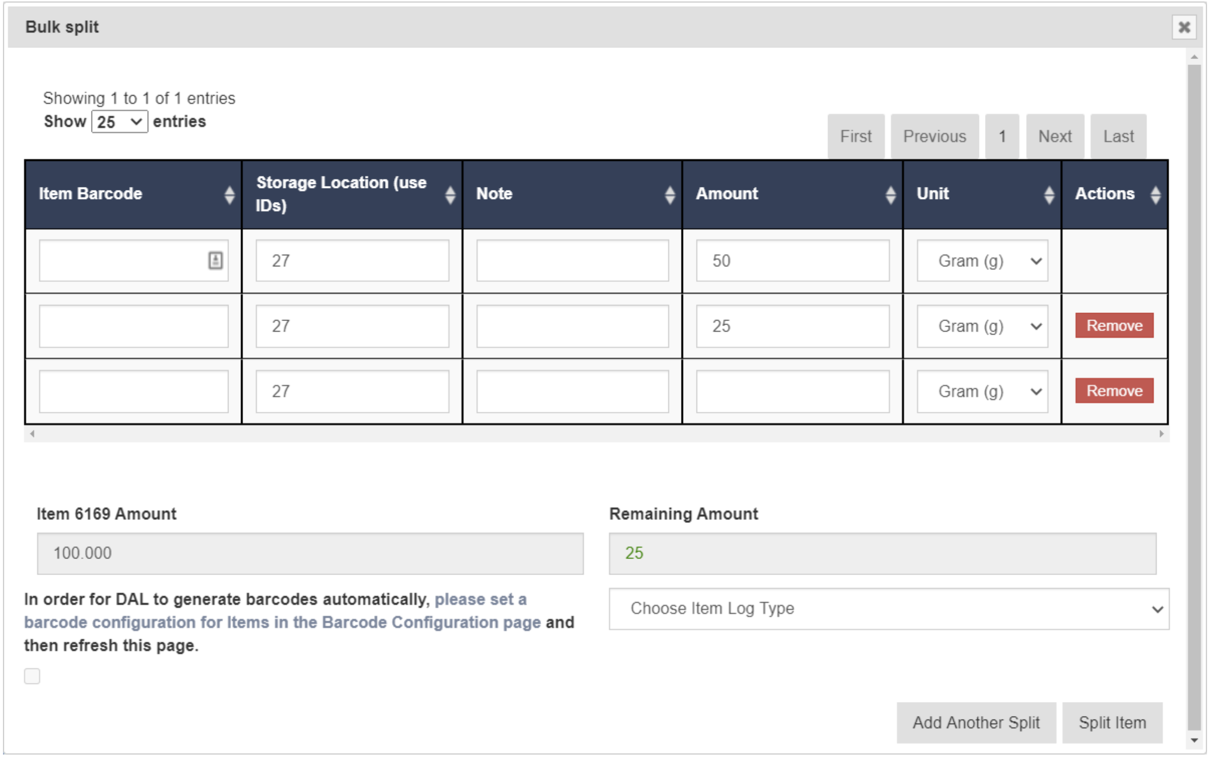
Show 50 entries

Item log ID	Item Log type name	Date/Time	Message	User
2	DArT Log	2020-06-08 10:18:08	Update Log	admin

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.


Bulk split

Showing 1 to 1 of 1 entries

Show 25 entries

Item Barcode	Storage Location (use IDs)	Note	Amount	Unit	Actions
	27		50	Gram (g)	
	27		25	Gram (g)	Remove
	27			Gram (g)	Remove

Item 6169 Amount: 100.000

Remaining Amount: 25

In order for DAL to generate barcodes automatically, please set a barcode configuration for Items in the Barcode Configuration page and then refresh this page.

☐

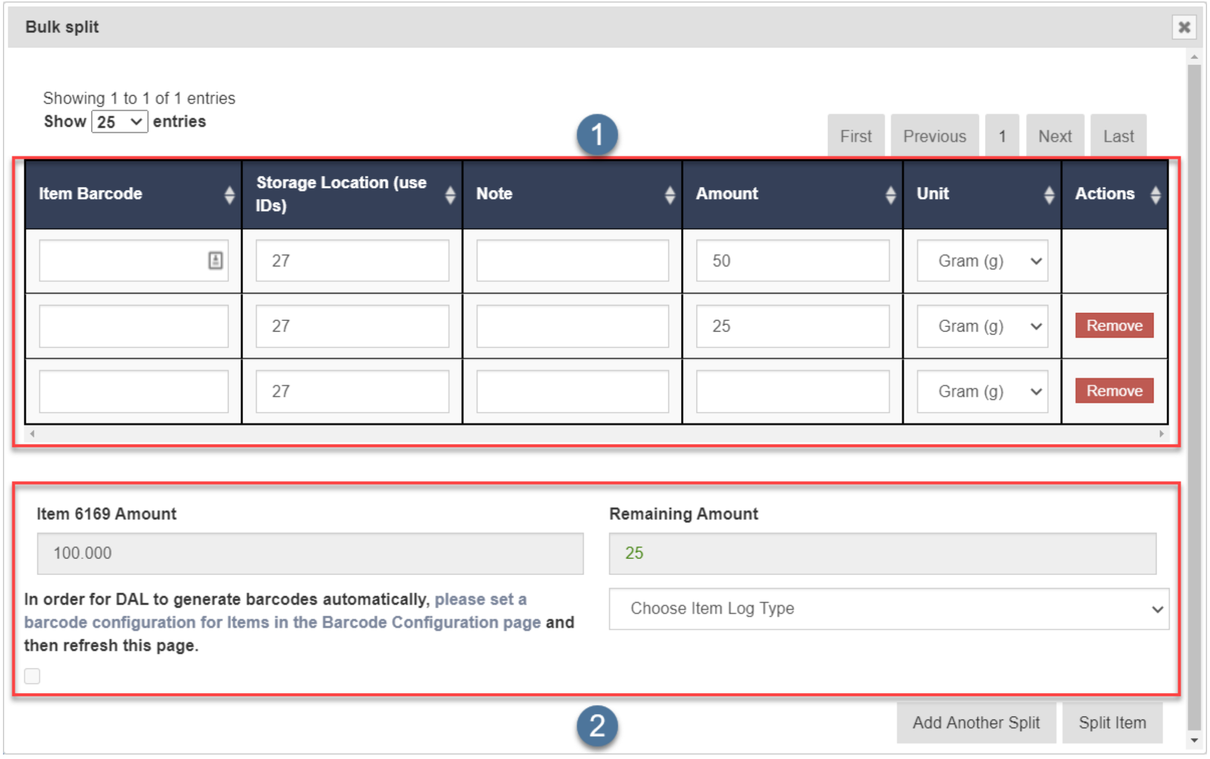
Choose Item Log Type

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 **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.



Showing 1 to 1 of 1 entries
Show 25 entries

Item Barcode	Storage Location (use IDs)	Note	Amount	Unit	Actions
	27		50	Gram (g)	
	27		25	Gram (g)	Remove
	27			Gram (g)	Remove

Item 6169 Amount: 100.000

Remaining Amount: 25

In order for DAL to generate barcodes automatically, please set a barcode configuration for Items in the Barcode Configuration page and then refresh this page.

☐

Choose Item Log Type

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

Table 9: Newly Split Items

Field	Mandatory	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	Mandatory	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.

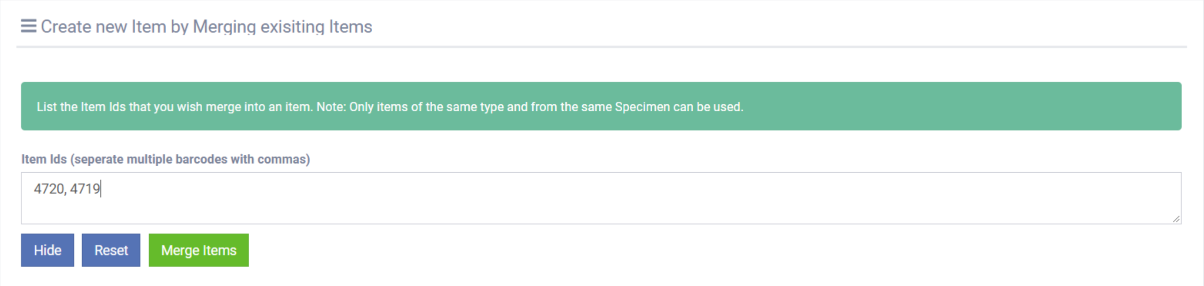
Table 10: Existing Item

Field	Mandatory	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 Checkbox		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:



Create new Item by Merging exisiting Items

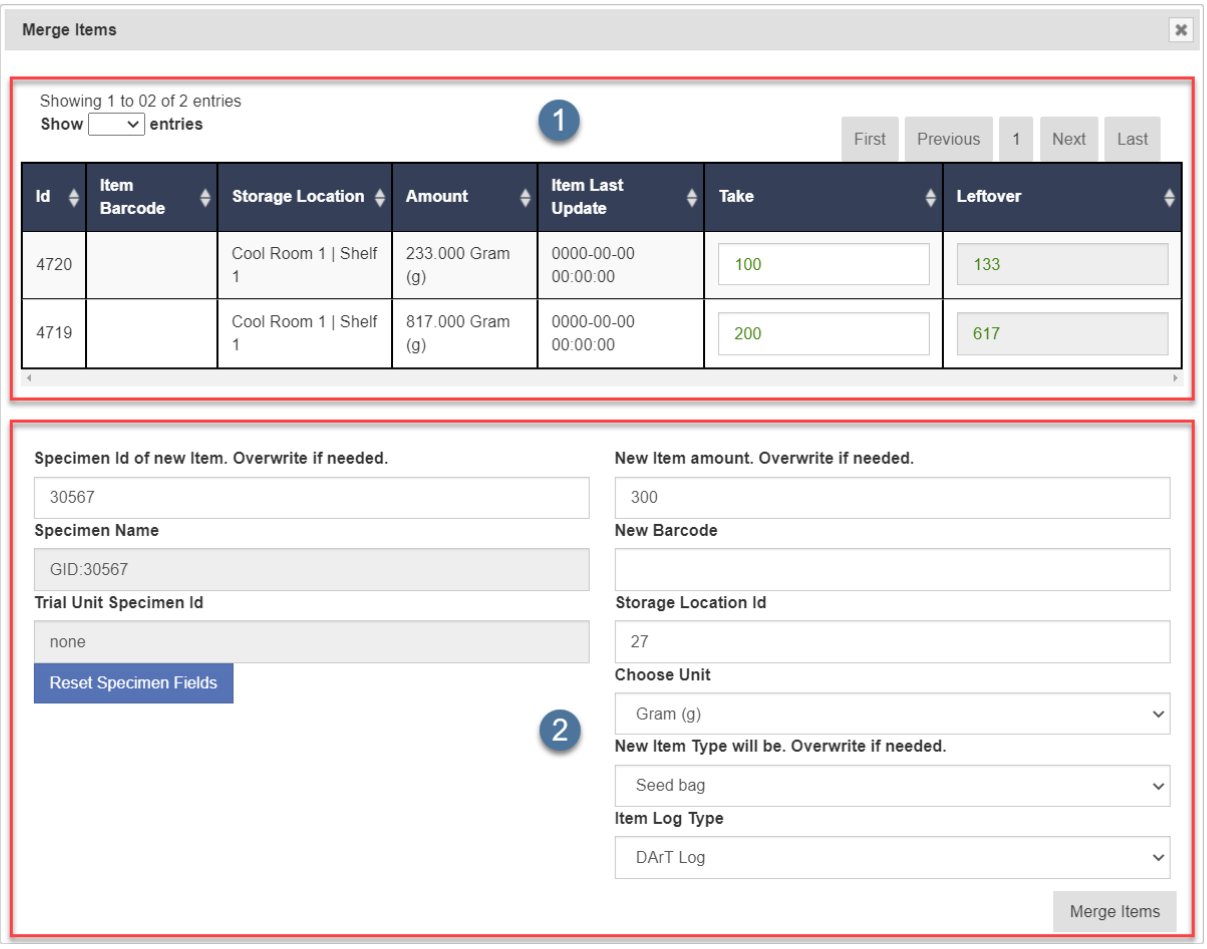
List the Item Ids that you wish merge into an item. Note: Only items of the same type and from the same Specimen can be used.

Item Ids (seperate multiple barcodes with commas): 4720, 4719

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 ⇄ Merge **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. Altenatively, user can select ⇄ Merge for each item that is included in the merge.
3.	After all items have been chosen, select the **Merge Items** button Merge Items to display the **Merge Items window**, as seen in the image below.



Showing 1 to 02 of 2 entries

Show ☐ entries

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	100	133
4719		Cool Room 1 | Shelf 1	817.000 Gram (g)	0000-00-00 00:00:00	200	617

Specimen Id of new Item. Overwrite if needed.: 30567

Specimen Name: GID:30567

Trial Unit Specimen Id: none

New Item amount. Overwrite if needed.: 300

New Barcode:

Storage Location Id: 27

Choose Unit: Gram (g)

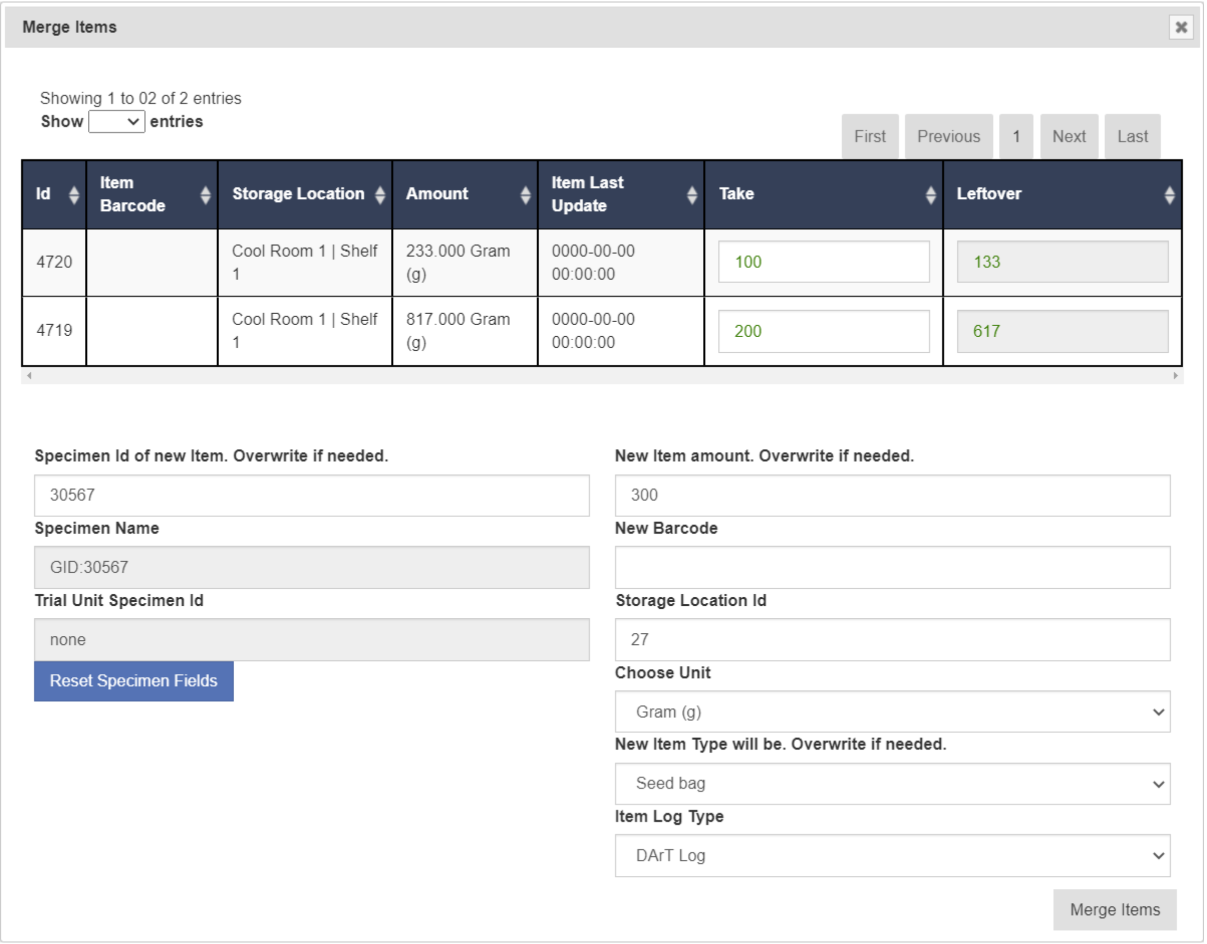
New Item Type will be. Overwrite if needed.: Seed bag

Item Log Type: DArT Log

Fig. 21: Merge Items Window

Table 12: Merging Items (2/2)

Step	Action
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**.



Showing 1 to 02 of 2 entries

Show entries

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	100	133
4719		Cool Room 1 | Shelf 1	817.000 Gram (g)	0000-00-00 00:00:00	200	617

Specimen Id of new Item. Overwrite if needed.: 30567

Specimen Name: GID:30567

Trial Unit Specimen Id: none

New Item amount. Overwrite if needed.: 300

New Barcode:

Storage Location Id: 27

Choose Unit: Gram (g)

New Item Type will be. Overwrite if needed.: Seed bag

Item Log Type: DArT Log

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.

CHAPTER

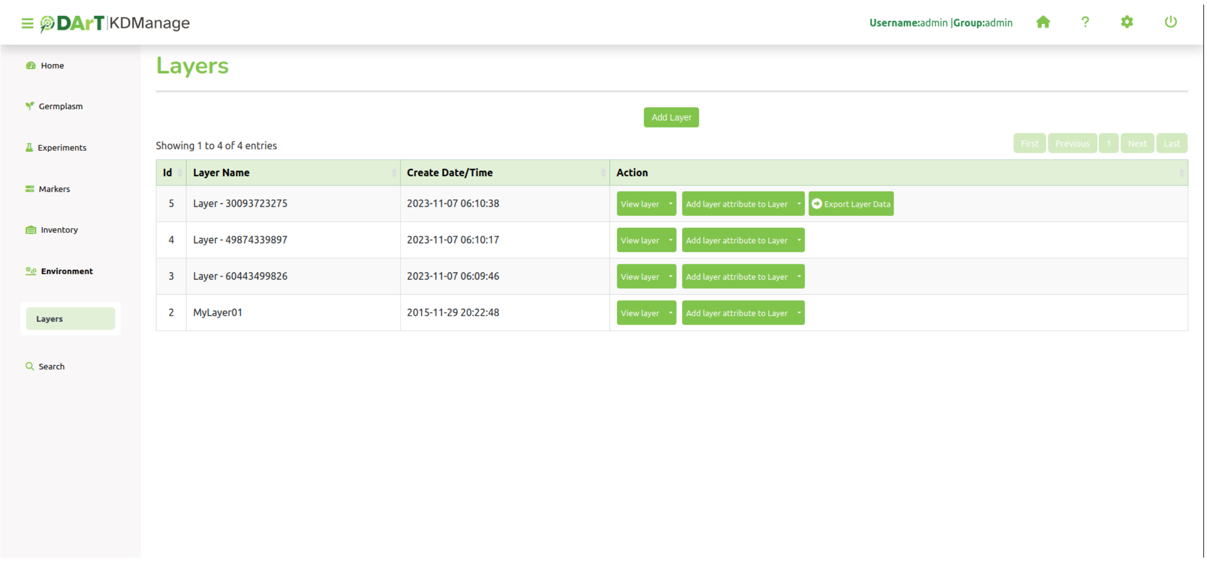
EIGHT

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:



Username:admin |Group:admin

Showing 1 to 4 of 4 entries

Id	Layer Name	Create Date/Time	Action
5	Layer - 30093723275	2023-11-07 06:10:38	View layer Add layer attribute to Layer Export Layer Data
4	Layer - 49874339897	2023-11-07 06:10:17	View layer Add layer attribute to Layer
3	Layer - 60443499826	2023-11-07 06:09:46	View layer Add layer attribute to Layer
2	MyLayer01	2015-11-29 20:22:48	View layer Add layer attribute to Layer

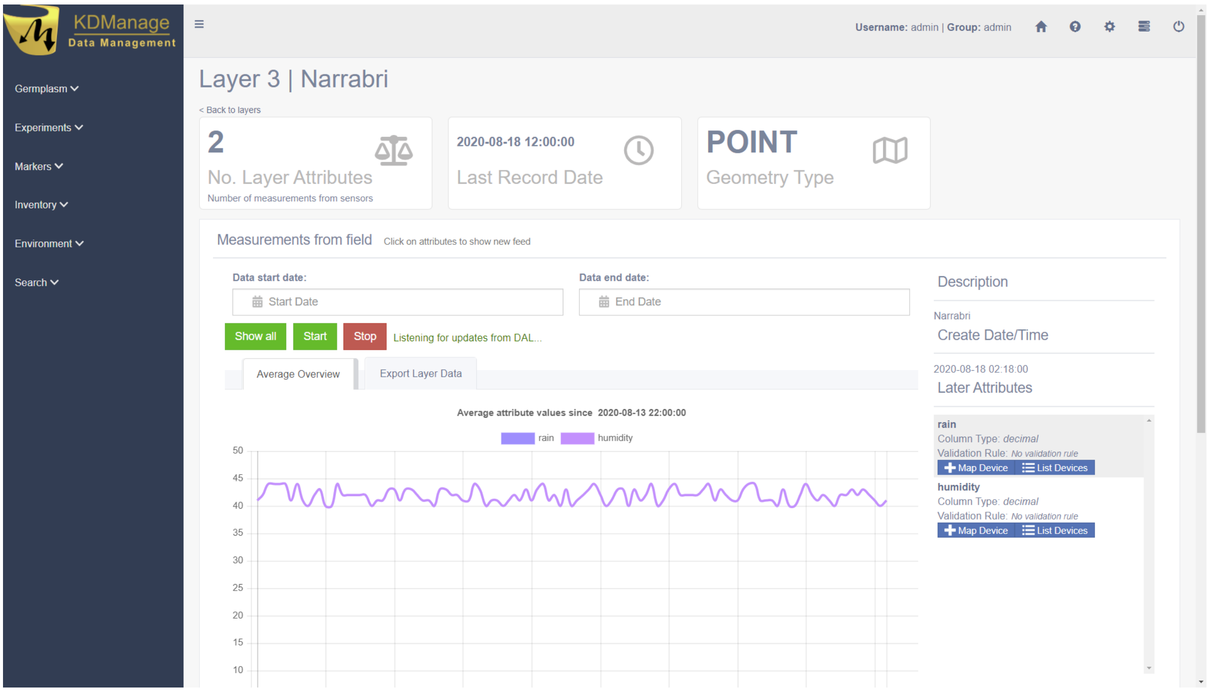
Fig. 1: Layers Page

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’:



Layer 3 | Narrabri

2
No. Layer Attributes
Number of measurements from sensors

2020-08-18 12:00:00
Last Record Date

POINT
Geometry Type

Measurements from field Click on attributes to show new feed

Data start date: Start Date

Data end date: End Date

Listening for updates from DAL...

Average attribute values since 2020-08-13 22:00:00

Description
Narrabri

Create Date/Time
2020-08-18 02:18:00

Later Attributes

rain
Column Type: decimal
Validation Rule: No validation rule

humidity
Column Type: decimal
Validation Rule: No validation rule

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:

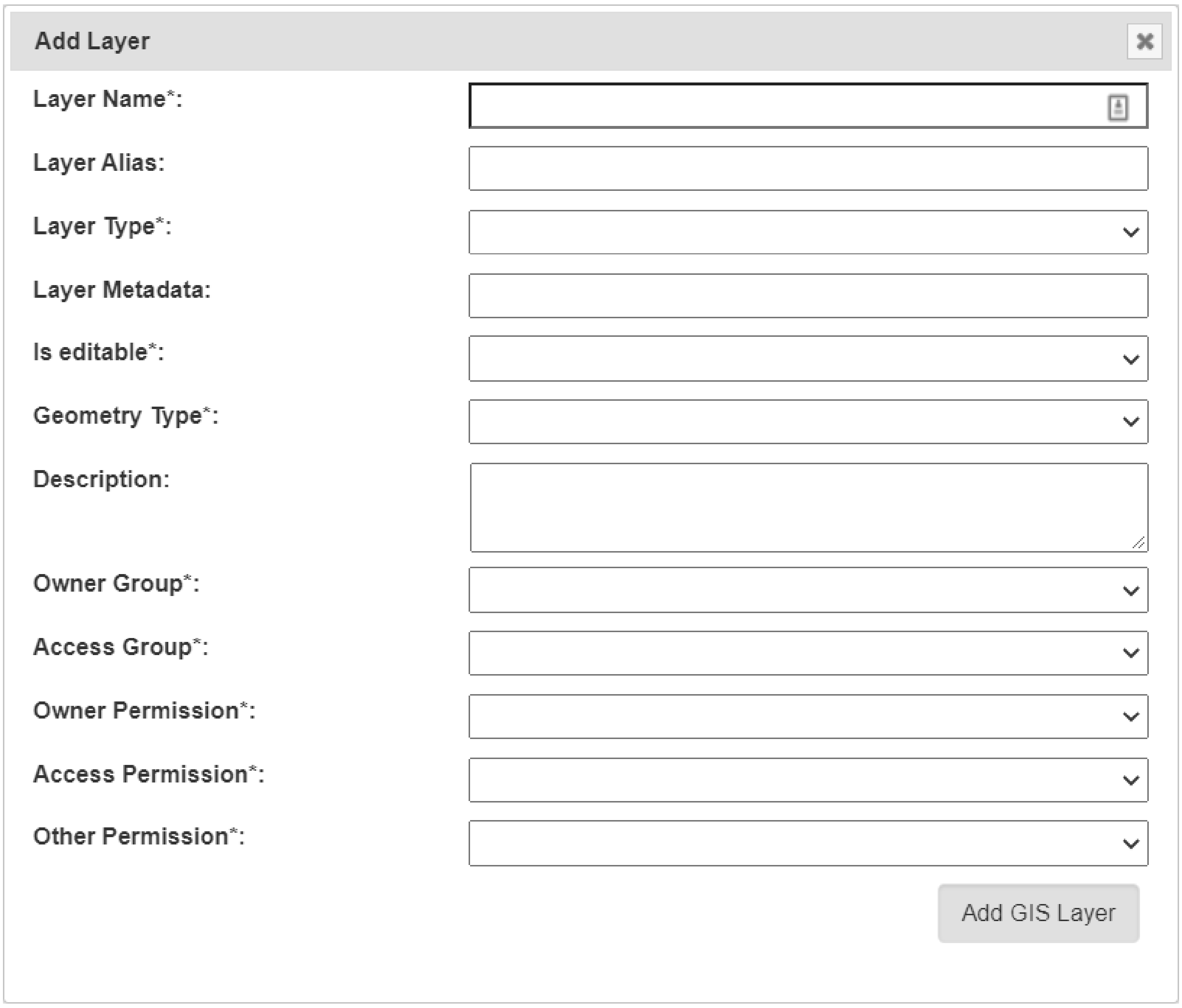


Fig. 3: Add Layer Window

The fields for the **Add Trial 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	*Access Settings and Permissions*

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.

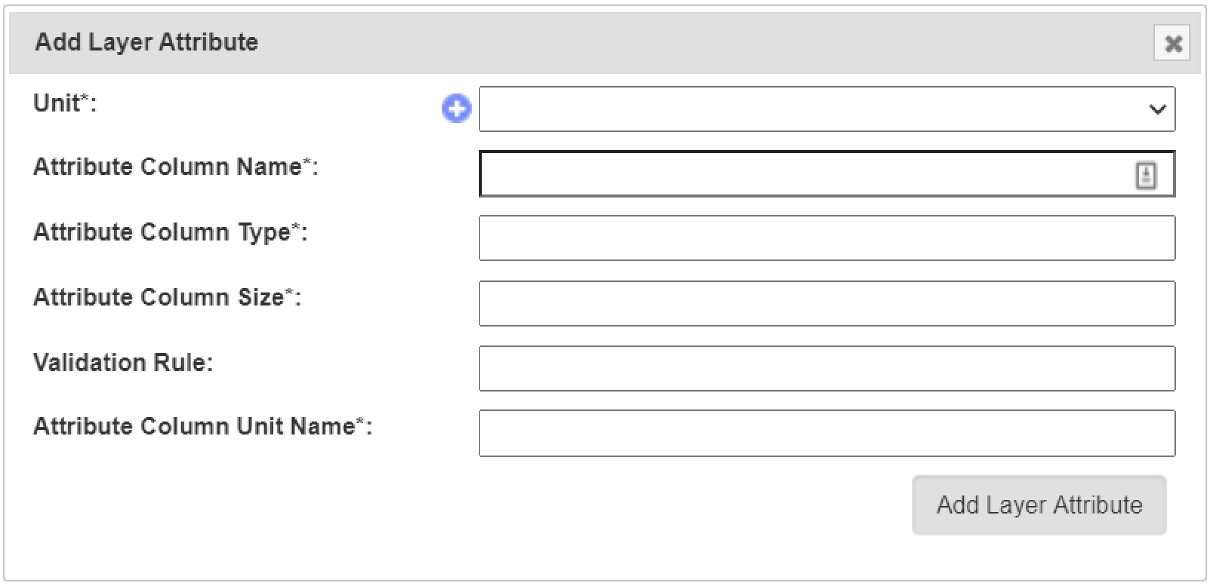


Fig. 4: Add Layer Attribute Window

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 *Units* 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.

Add Unit

Layer data file*: Choose File No file chosen

Geometry Column*:

Time Stamp Column*:

RAIN (attrib_5) Column*:

HUMIDITY (attrib_6) Column*:

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 (*RAIN* and *HUMIDITY* 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.

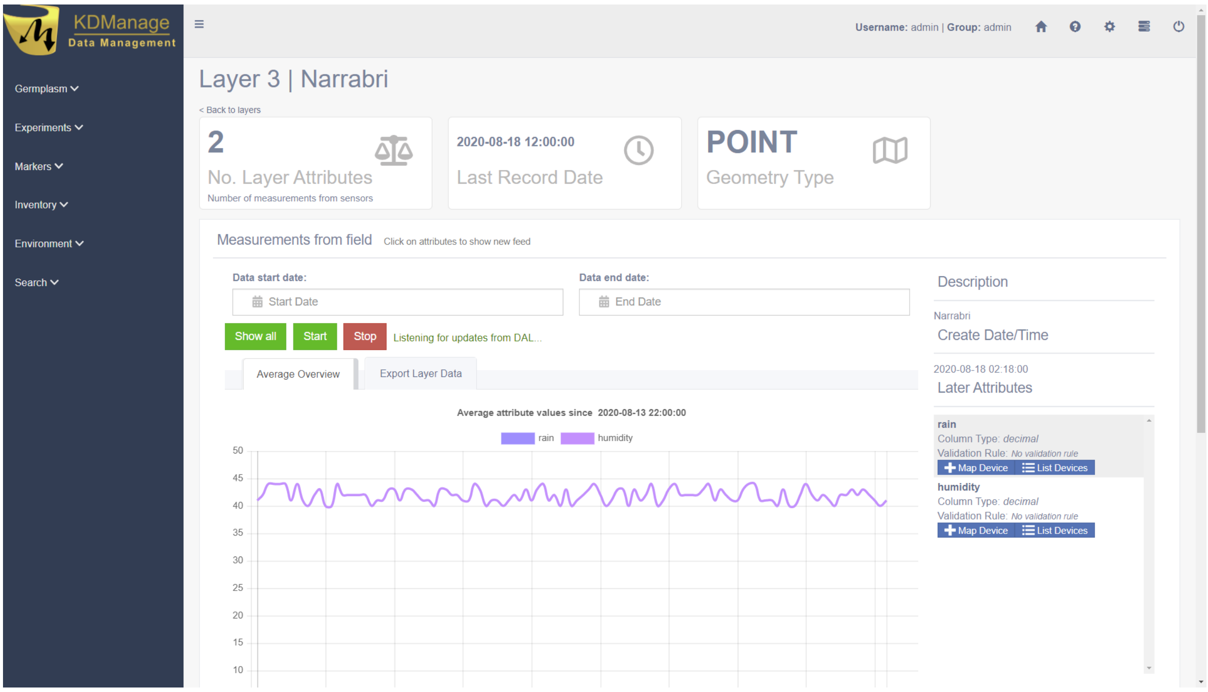


Fig. 6: Layer Example

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


rain

Column Type: *decimal*

Validation Rule: *No validation rule*

Fig. 7: Mapping a Device

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

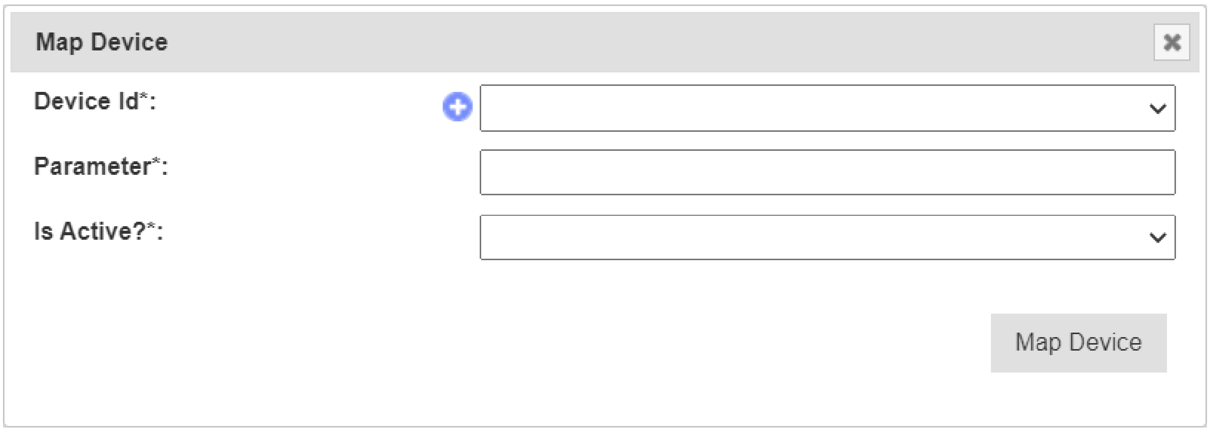


Fig. 8: Map Device Window

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.

CHAPTER

NINE

SEARCH MENU

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

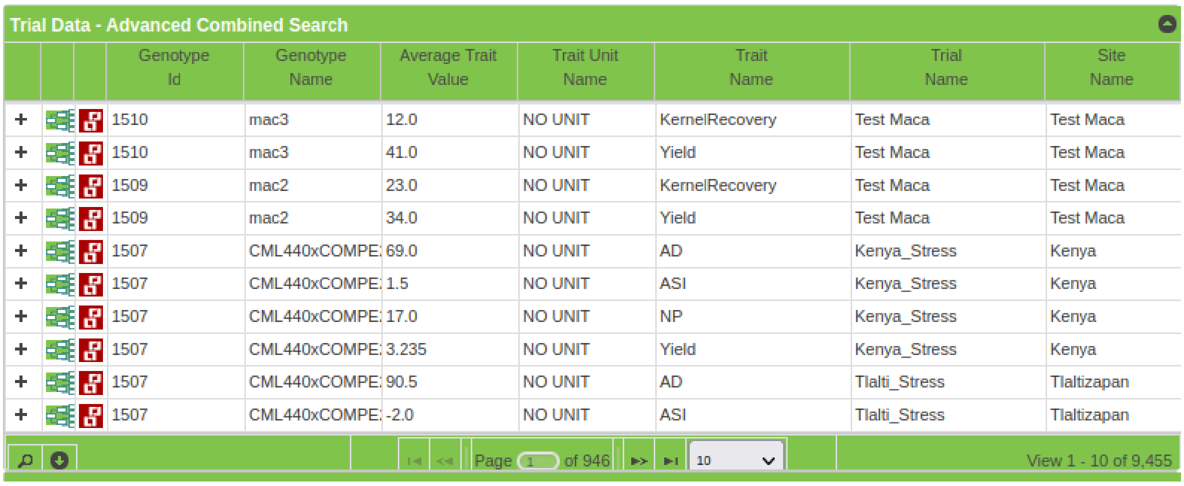
- Trial data (all four data sets combined);
- Inventory data;
- Ancestor data;
- Genotype trait data; and
- Genotype specimen data.

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:

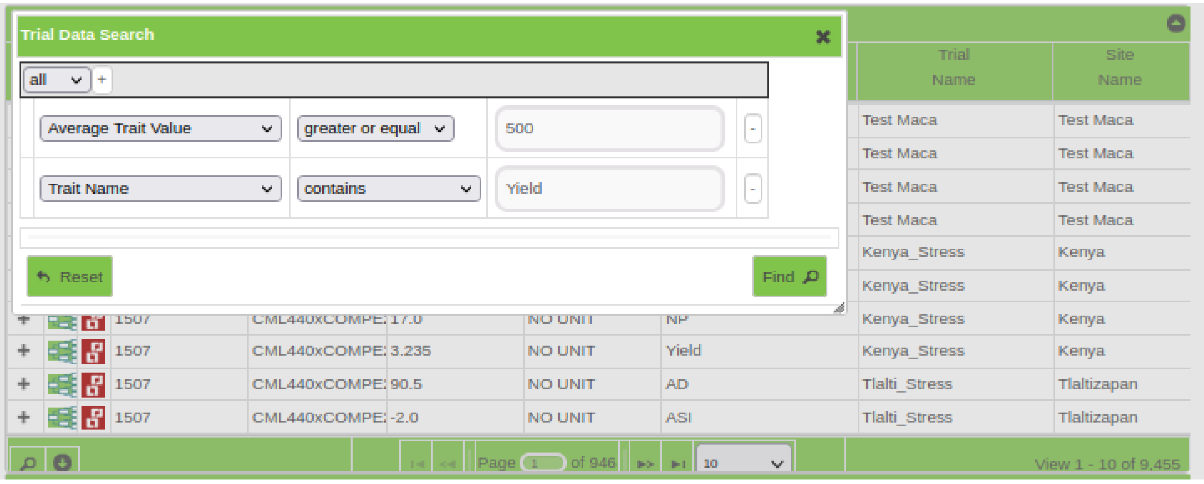


	Genotype Id	Genotype Name	Average Trait Value	Trait Unit Name	Trait Name	Trial Name	Site Name
+	1510	mac3	12.0	NO UNIT	KernelRecovery	Test Maca	Test Maca
+	1510	mac3	41.0	NO UNIT	Yield	Test Maca	Test Maca
+	1509	mac2	23.0	NO UNIT	KernelRecovery	Test Maca	Test Maca
+	1509	mac2	34.0	NO UNIT	Yield	Test Maca	Test Maca
+	1507	CML440xCOMPE	69.0	NO UNIT	AD	Kenya_Stress	Kenya
+	1507	CML440xCOMPE	1.5	NO UNIT	ASI	Kenya_Stress	Kenya
+	1507	CML440xCOMPE	17.0	NO UNIT	NP	Kenya_Stress	Kenya
+	1507	CML440xCOMPE	3.235	NO UNIT	Yield	Kenya_Stress	Kenya
+	1507	CML440xCOMPE	90.5	NO UNIT	AD	Tlalti_Stress	Tlaltizapan
+	1507	CML440xCOMPE	-2.0	NO UNIT	ASI	Tlalti_Stress	Tlaltizapan

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.



Average Trait Value | greater or equal | 500

Trait Name | contains | Yield

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**.

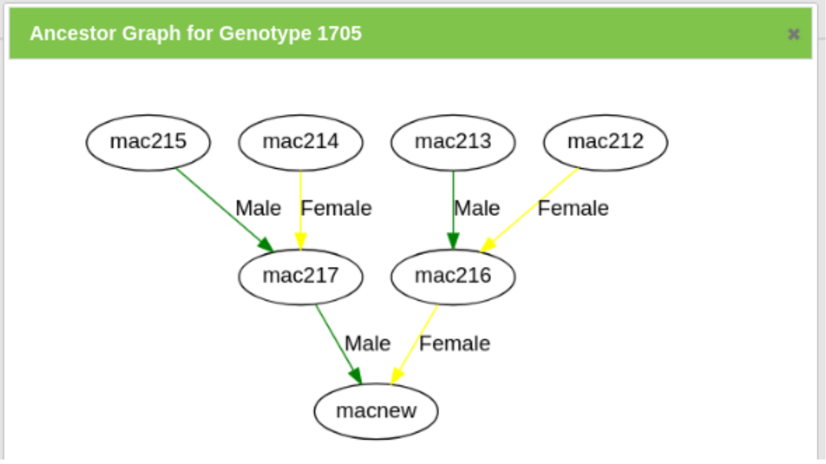
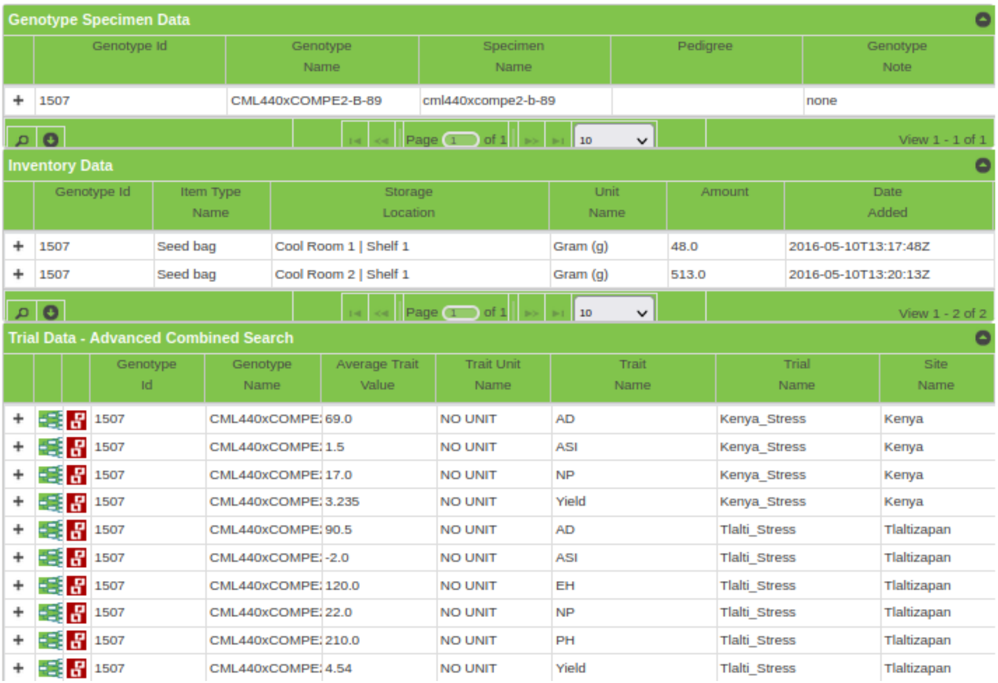


Fig. 3: Pedigree Tree

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:



Genotype Specimen Data

	Genotype Id	Genotype Name	Specimen Name	Pedigree	Genotype Note
+	1507	CML440xCOMPE2-B-89	cml440xcompe2-b-89		none

Page 1 of 1 10 View 1 - 1 of 1

Inventory Data

	Genotype Id	Item Type Name	Storage Location	Unit Name	Amount	Date Added
+	1507	Seed bag	Cool Room 1 | Shelf 1	Gram (g)	48.0	2016-05-10T13:17:48Z
+	1507	Seed bag	Cool Room 2 | Shelf 1	Gram (g)	513.0	2016-05-10T13:20:13Z

Page 1 of 1 10 View 1 - 2 of 2

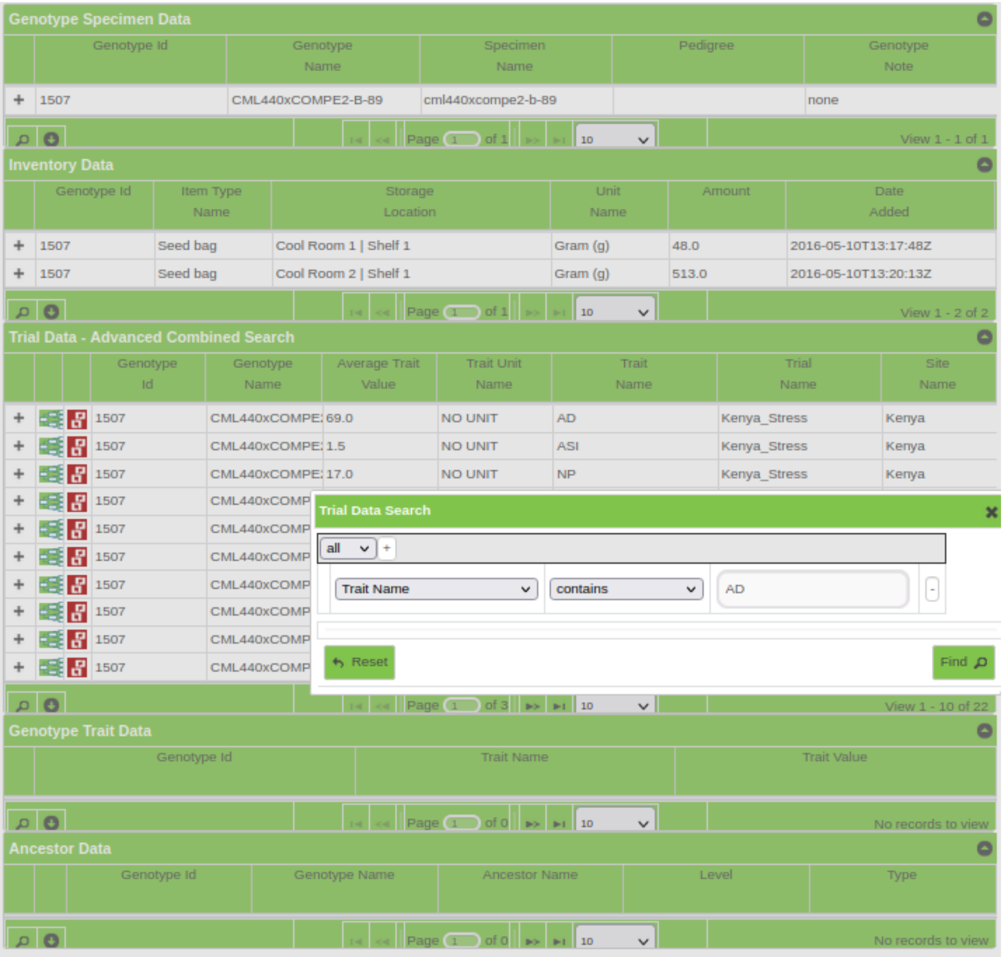
Trial Data - Advanced Combined Search

			Genotype Id	Genotype Name	Average Trait Value	Trait Unit Name	Trait Name	Trial Name	Site Name
+			1507	CML440xCOMPE	69.0	NO UNIT	AD	Kenya_Stress	Kenya
+			1507	CML440xCOMPE	1.5	NO UNIT	ASI	Kenya_Stress	Kenya
+			1507	CML440xCOMPE	17.0	NO UNIT	NP	Kenya_Stress	Kenya
+			1507	CML440xCOMPE	3.235	NO UNIT	Yield	Kenya_Stress	Kenya
+			1507	CML440xCOMPE	90.5	NO UNIT	AD	Tlalti_Stress	Tlaltizapan
+			1507	CML440xCOMPE	-2.0	NO UNIT	ASI	Tlalti_Stress	Tlaltizapan
+			1507	CML440xCOMPE	120.0	NO UNIT	EH	Tlalti_Stress	Tlaltizapan
+			1507	CML440xCOMPE	22.0	NO UNIT	NP	Tlalti_Stress	Tlaltizapan
+			1507	CML440xCOMPE	210.0	NO UNIT	PH	Tlalti_Stress	Tlaltizapan
+			1507	CML440xCOMPE	4.54	NO UNIT	Yield	Tlalti_Stress	Tlaltizapan

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.	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**.  Fig. 5: CSV Search Options
3.	The results table has the same functionality as a standard search. The image below demonstrates CSV search results for *GenotypeID*.

Genotype Specimen Data

	Genotype Id	Genotype Name	Specimen Name	Pedigree	Genotype Note
+	1507	CML440xCOMPE2-B-89	cml440xcompe2-b-89		none

Page 1 of 1 10 View 1 - 1 of 1

Inventory Data

	Genotype Id	Item Type Name	Storage Location	Unit Name	Amount	Date Added
+	1507	Seed bag	Cool Room 1 | Shelf 1	Gram (g)	48.0	2016-05-10T13:17:48Z
+	1507	Seed bag	Cool Room 2 | Shelf 1	Gram (g)	513.0	2016-05-10T13:20:13Z

Page 1 of 1 10 View 1 - 2 of 2

Trial Data - Advanced Combined Search

	Genotype Id	Genotype Name	Average Trait Value	Trait Unit Name	Trait Name	Trial Name	Site Name
+	1507	CML440xCOMPE:	69.0	NO UNIT	AD	Kenya_Stress	Kenya
+	1507	CML440xCOMPE:	1.5	NO UNIT	ASI	Kenya_Stress	Kenya
+	1507	CML440xCOMPE:	17.0	NO UNIT	NP	Kenya_Stress	Kenya
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					
+	1507	CML440xCOMP					

Page 1 of 3 10 View 1 - 10 of 22

Trial Data Search

all +

Trait Name contains AD -

Reset Find

Genotype Trait Data

	Genotype Id	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

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.

CHAPTER

TEN

KDMANAGE QUICK START GUIDE

This guide gives new user a general overivew on using KDManage for managing phenotypic data import.

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. *Creating a Trial*
2. *Uploading Material/Genotype list*
3. *Uploading Layout*
4. *Adding Traits*
5. *Importing to KDSmart*
6. *Uploading Trial Data*
7. *Accessing Trial Data*

It's important for all users to be familar with each step indvidually. However, Trial Super Import is a migration tool that can package all these steps into a single action. This can be easier and save time.

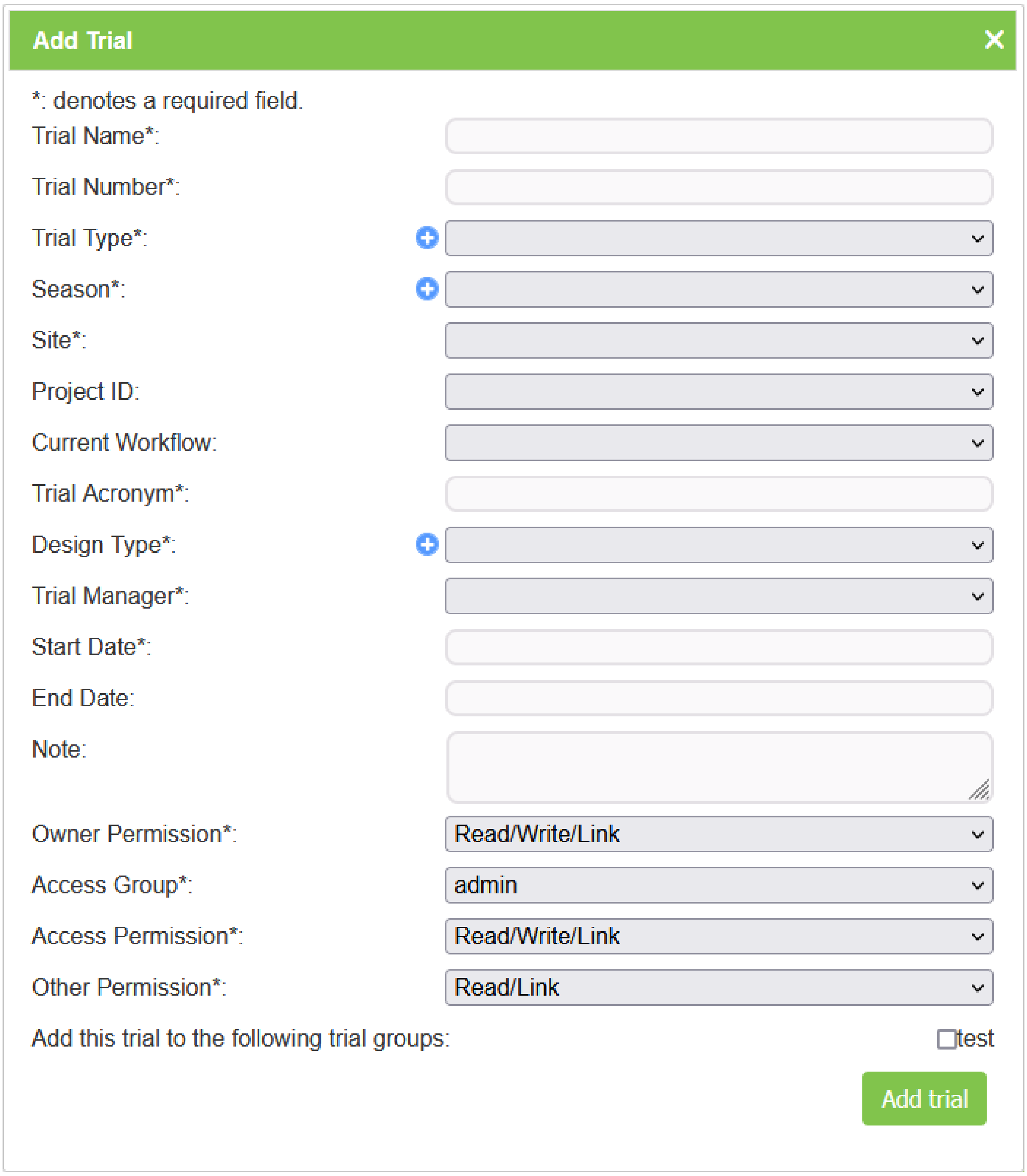
1. *Using Trial Super Import*

10.1 Creating a Trial

Trials should be created with as much information possible. Alternatively, users can use *Trial Super Import* to automatically add much of the data needed to import trial and genotype data from a single CSV.

More details can be found at *Adding Trials* and *Trial Super Import*

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*:

Trial Number*:

Trial Type*:

Season*:

Site*:

Project ID:

Current Workflow:

Trial Acronym*:

Design Type*:

Trial Manager*:

Start Date*:

End Date:

Note:

Owner Permission*: Read/Write/Link

Access Group*: admin

Access Permission*: Read/Write/Link

Other Permission*: Read/Link

Add this trial to the following trial groups: ☐ test

Fig. 1: Add Trial Window

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. Check with your manager that a Site has been created.

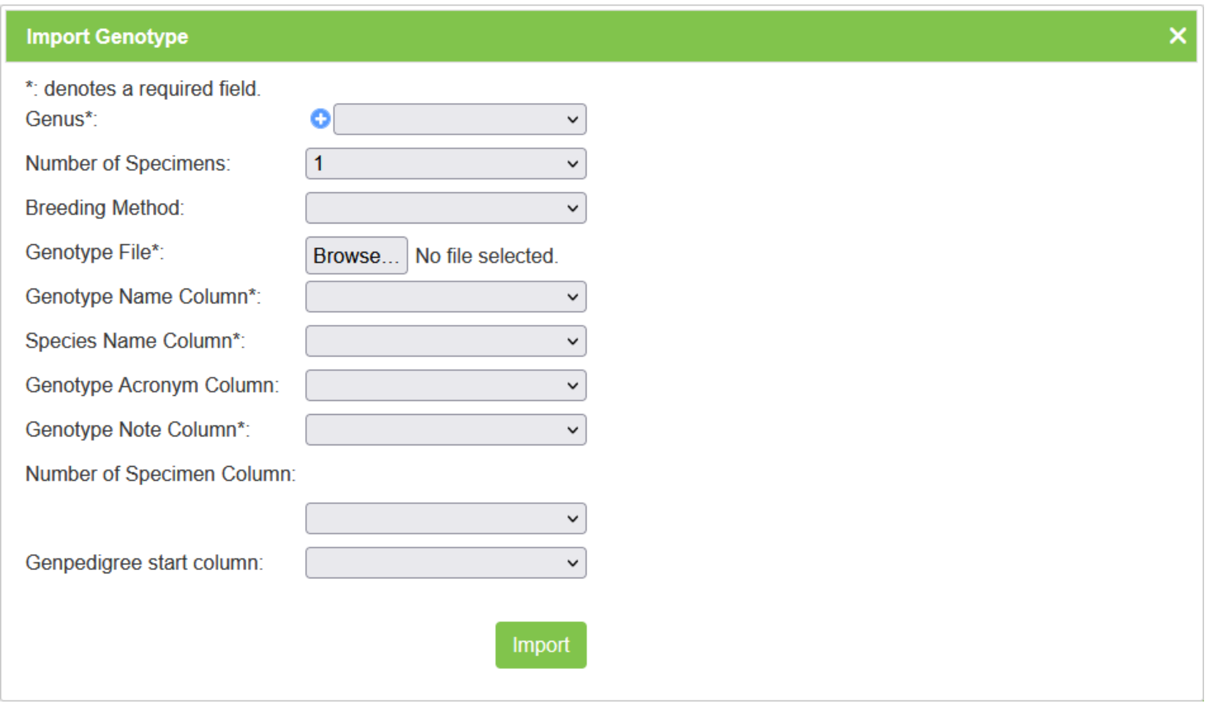
10.2 Uploading Material/Genotype list

In order to ensure Genotype and Material Ids can be properly managed and linked, users should ensure that the materials they wish to run their trials on are uploaded in the system.

More details can be found at *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.

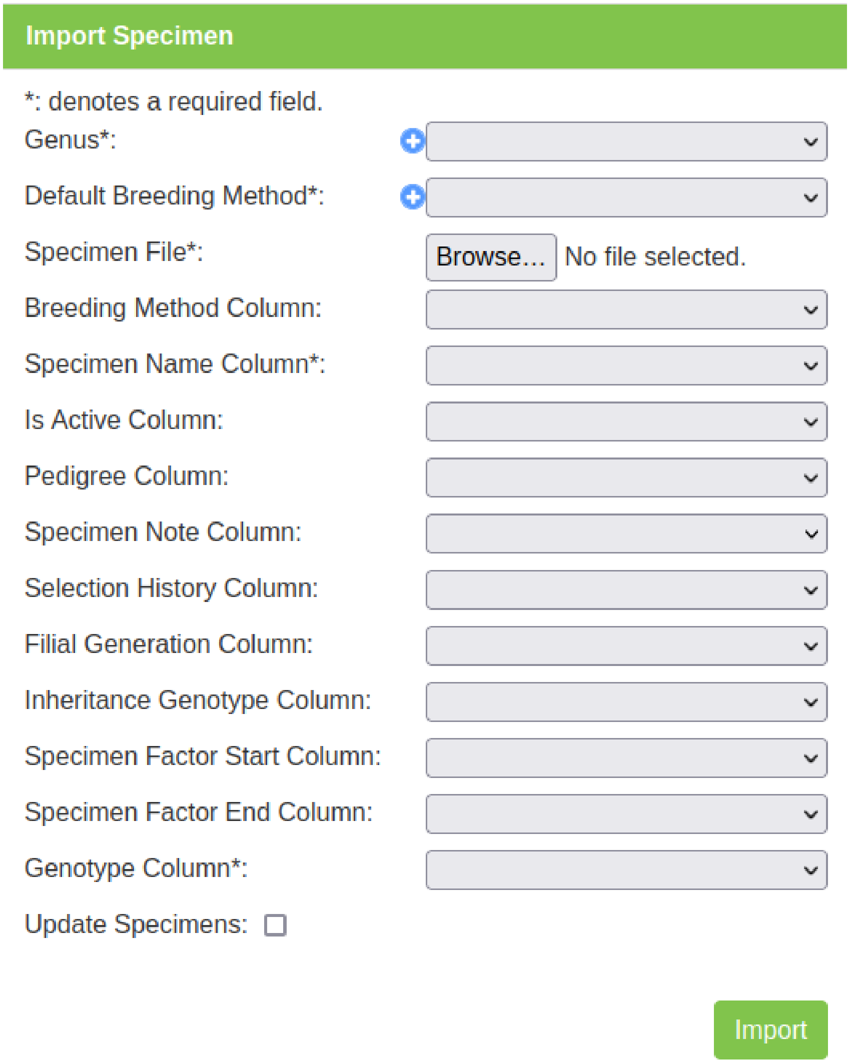

Import Genotype

*: denotes a required field.
Genus*:
Number of Specimens: 1
Breeding Method:
Genotype File*: No file selected.
Genotype Name Column*:
Species Name Column*:
Genotype Acronym Column:
Genotype Note Column*:
Number of Specimen Column:
Genpedigree start column:

Fig. 2: Import Genotypes Window

Note: When importing a list of genotypes without the need for secondary specimens, users can simply tick "Add Specimens" to automatically add Specimens with the same name as the Genotype.

Specimens are the physical representation of Genotypes and can similarly imported using the *Specimen* page.



Import Specimen

*: denotes a required field.

Genus*:

Default Breeding Method*:

Specimen File*: Browse… No file selected.

Breeding Method Column:

Specimen Name Column*:

Is Active Column:

Pedigree Column:

Specimen Note Column:

Selection History Column:

Filial Generation Column:

Inheritance Genotype Column:

Specimen Factor Start Column:

Specimen Factor End Column:

Genotype Column*:

Update Specimens: ☐

Import

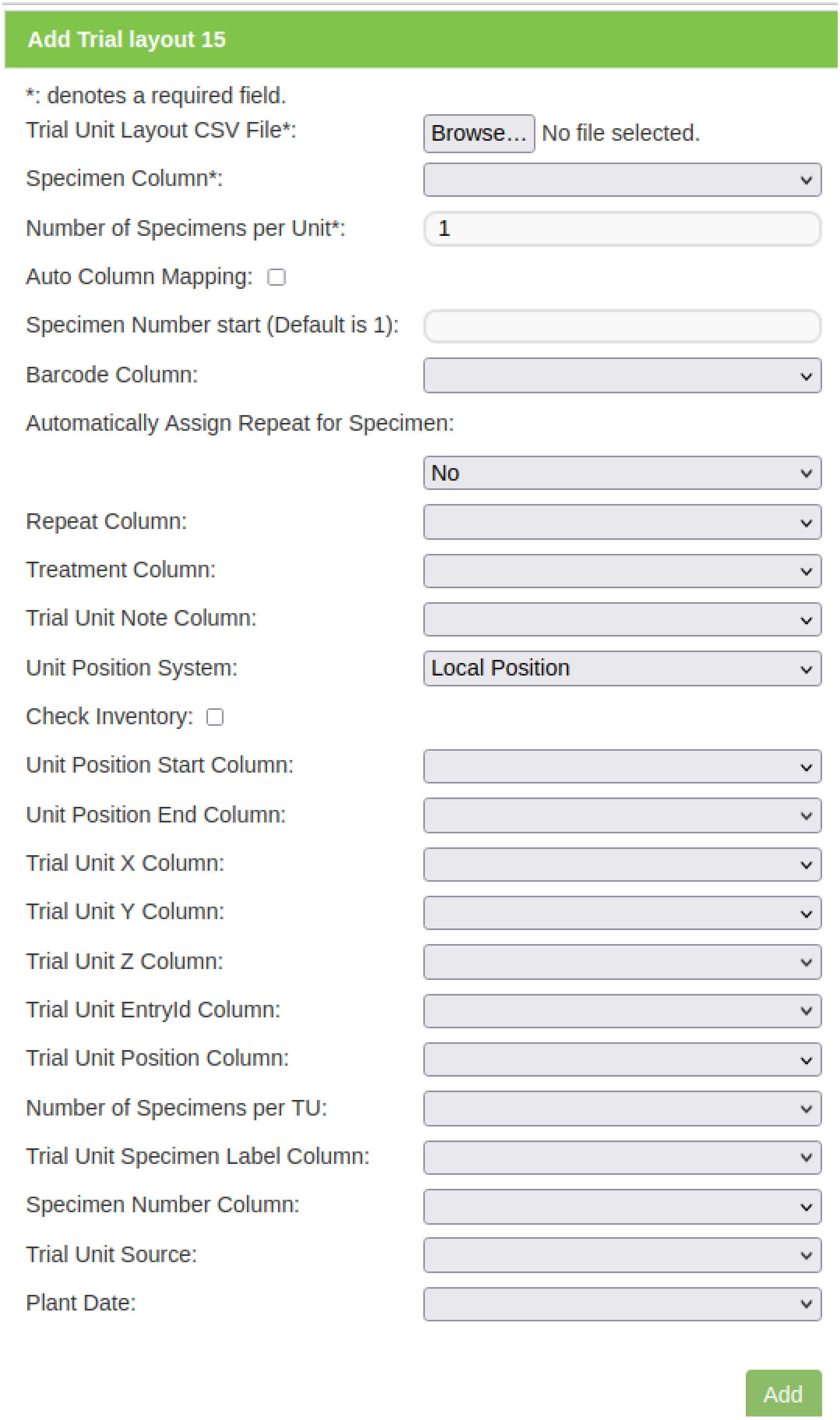
Fig. 3: Import Specimen Window

Note: The Genotypes and Specimens are the what will keep Phenotypic and Genotypic data connected so it is important the names are accurately defined across the entire system.

10.3 Uploading Layout

After Genotypes and Trials are created, users can then upload their trial layouts to the database for later use. This can be done using the *Adding Trial Unit Layouts*. Users can also use *Trial Super Import* tool.

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 15

*: denotes a required field.

Trial Unit Layout CSV File*: Browse… No file selected.

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

Check Inventory: ☐

Unit Position Start Column:

Unit Position End Column:

Trial Unit X Column:

Trial Unit Y Column:

Trial Unit Z Column:

Trial Unit EntryId Column:

Trial Unit Position Column:

Number of Specimens per TU:

Trial Unit Specimen Label Column:

Specimen Number Column:

Trial Unit Source:

Plant Date:

Fig. 4: Adding Trial Unit Layouts Window

Note: It's highly recommended that a layout that includes database wide unique barcodes.

More details can be found at *Adding Trials* and *Adding Trial Unit Layouts*

10.4 Adding Traits

Once a trial is created with materials and genotypes added in a layout, users can define the traits needed to be measured.

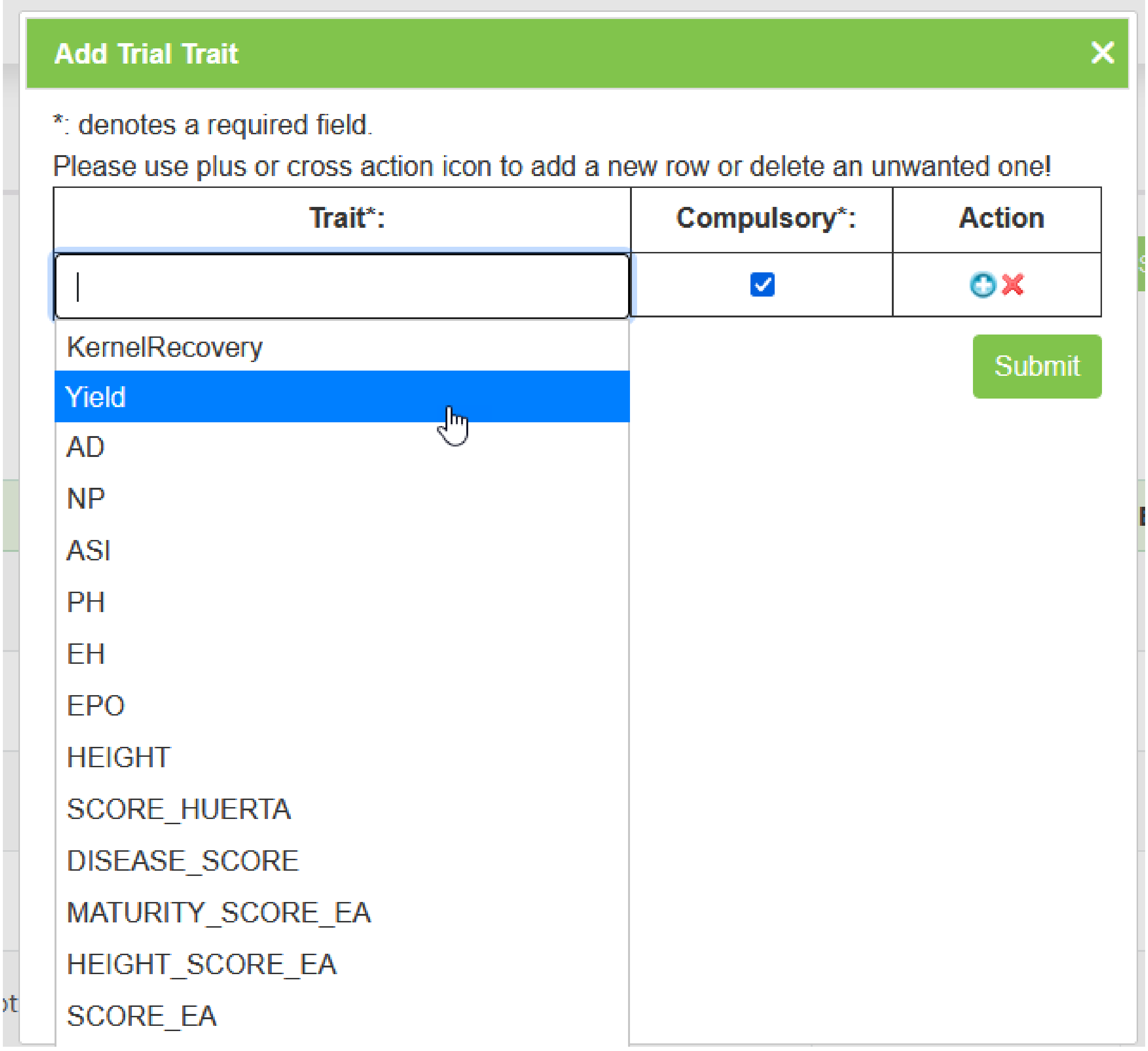
Note: Traits should only be added and defined by administrator level users. Please check with your administrator on what Traits can be added.

More details can be found at *Traits* and *Add Traits to a Trial*

Selecting **Add a Trait to Trial** (under **Edit Trial 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
	☑	⊕ ✖

Fig. 5: 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 the **Edit Trial dropdown**) from the **Action Column**.

10.5 Importing to KDSmart

With Trial layouts, Genotypes/Materials and Traits set up on the database, all of this setup can be than transferred to KDSmart and scored.

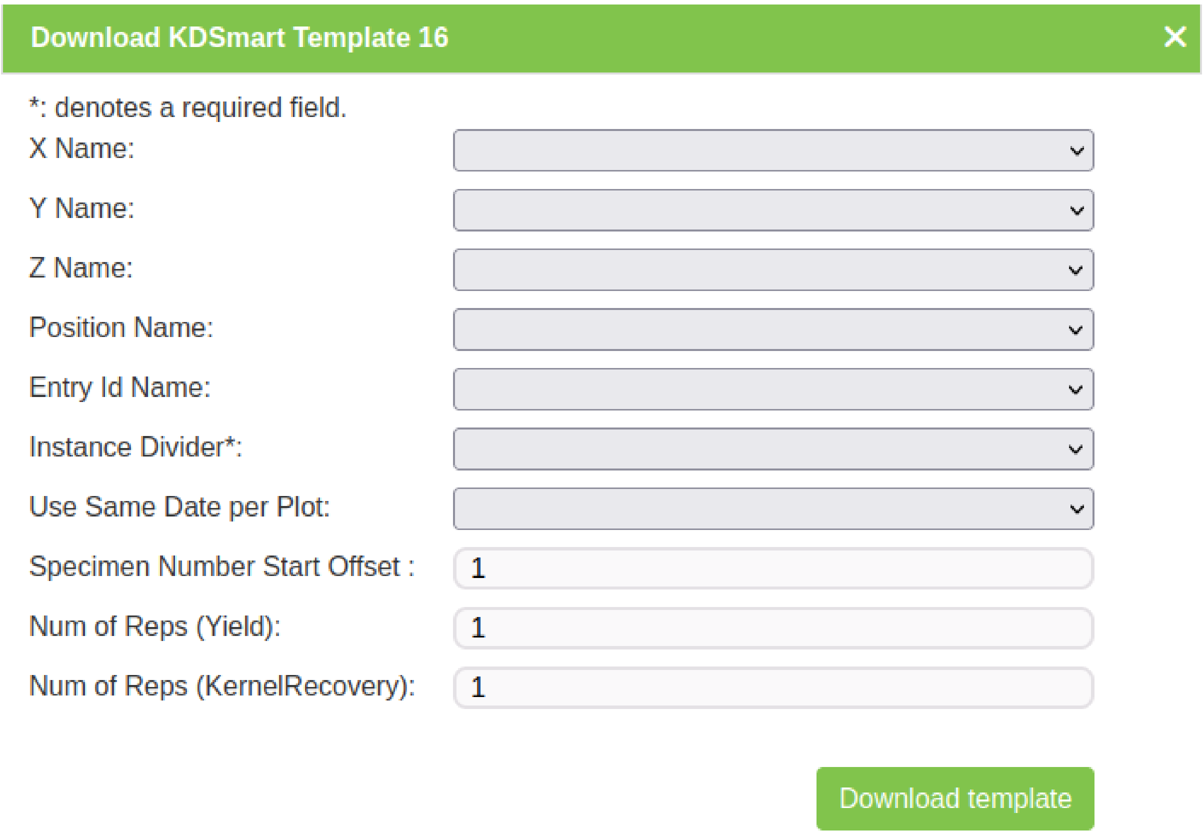
Once this data is scored, we can then export this in CSV format, transfer to a computer and then uploaded through KDManage to the database.

More details on downloading the KDSmart can be found at *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.

Users will be given the option to offset the specimen number. This should normally set to 0 unless legacy trials have specimen number 0.


Download KDSmart Template 16

*: 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 :	1
Num of Reps (Yield):	1
Num of Reps (KernelRecovery):	1

Fig. 6: Exporting a KDSmart CSV Format Template

After this file is generated, this file can then be imported into KDSmart.

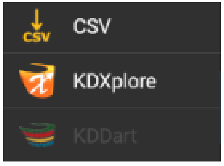
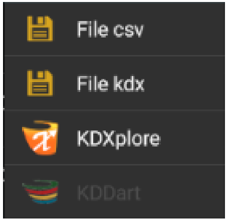
More details can be found at https://www.kddart.org/help/kdsmart/html/data-import-export-backup.html#csv-import

Comma Separated Value (CSV) files are a common file format that many users collect data with prior to using KDDart. Some users also use CSV files if they use KDSmart as a standalone application. More information about formatting CSV files can be found on the *CSV Formats* page at http://www.kddart.org/help/kdsmart/html/kdsmart-app-b.html

After selecting a file to import, each column in the CSV must be assigned an attribute type. This determines how the data in the column will be interpreted. Columns can be selected as **Don't Import** as well as whether the data is related to the trial, a plot, or a trait name to be scored.

TO successfully import a CSV trial, the file must contain at least a Plot ID **OR** both Plot Column and Plot Row **OR** all three columns.

Table 1: CSV Import (SAF)

Step	Action
1.	Open the **Trial Screen**, **Trait Screen**, or **Tag Screen** on KDSmart and select the ↓ **Import Button** or the *Import As* option in the ⋮ **Menu Options**.
2.	The **Import Options** will open. If you are importing traits or tags, there will be the following options: -  Importing from the **Trials Screen** will result in an additional option to import KDX files: - 
3.	Choose the **File CSV Button**. This will open the SAF as pictured below:
4.	Select the CSV file you want to import and then select the **Open Button**.
5.	Ensure that all headings are present and the *Import As* options are correct such as plot attributes and traits for plots.
6.	Select the **Import Button** to finalise the trial import.

Note: All types of CSV files (trials, traits, and tags) can be imported into KDSmart.

After this is done, please follow instructions at for full functionality of KDSmart https://www.kddart.org/help/kdtutorials/html/KDSTutorial.html

When scoring is complete, we can now export the data in a format that can be imported into the database through KDManage.

More details can be found at https://www.kddart.org/help/kdsmart/html/data-import-export-backup.html#exporting-sharing-data

The video available at https://www.youtube.com/embed/WJsHN0tApWo provides a guide and instructions to exporting data:

Note: The video provides an example of exporting trials but the same process can also be used for traits and tags.

Table 2: Exporting Data

Step	Action
1.	Depending on what sort of data you would like to export, navigate to the **Trial Screen**, **Trait Screen**, or **Tag Screen**. Choose a trial to export.

continues on next page

Table 2 – continued from previous page

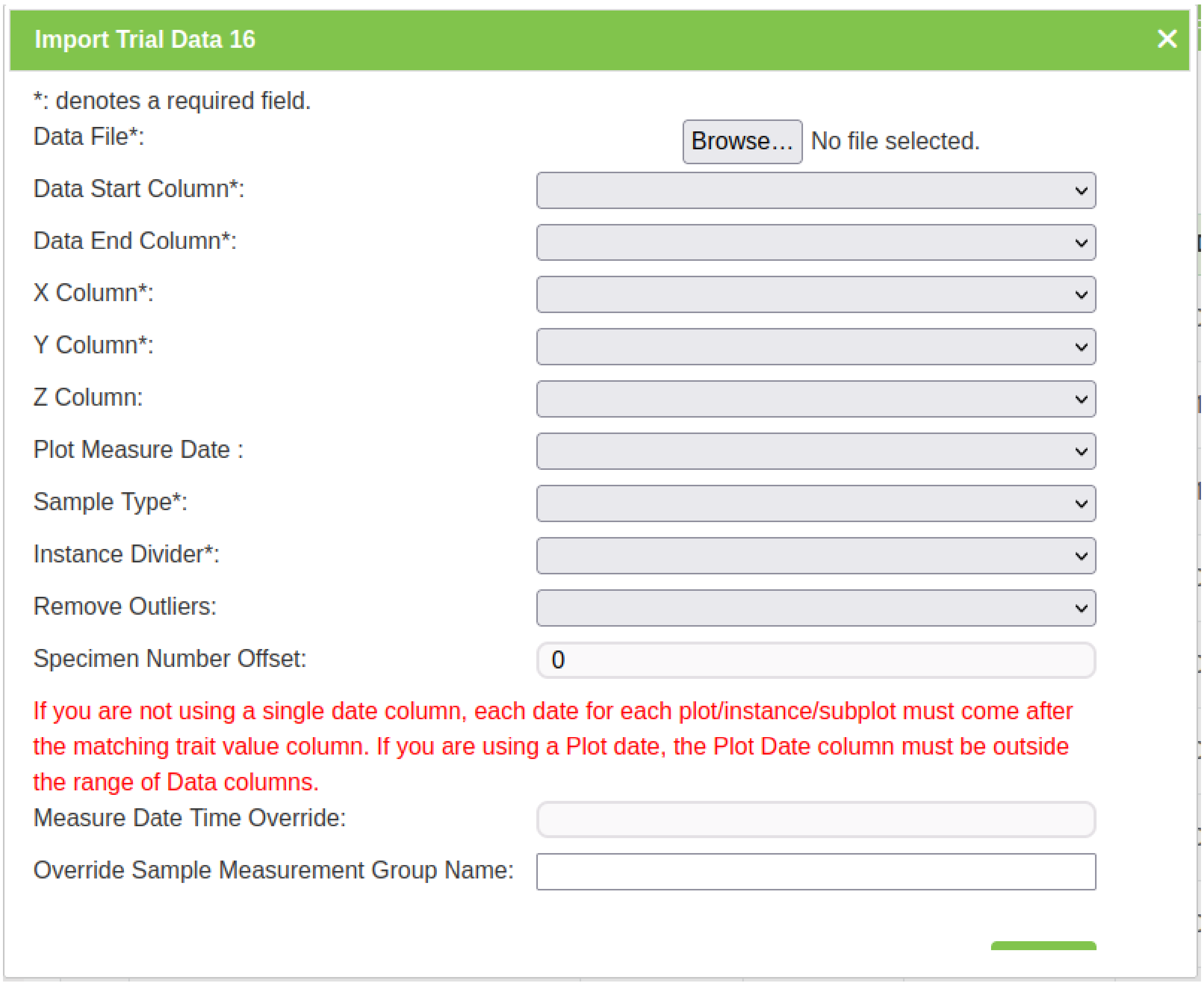
Step	Action
2.	Select the **Export To Button**. You will be presented with the **Export To Options**.
3.	Select the **Tablet Button** to export a data file directly to the device that you are using. The **Choose Export Option Window** will appear with the options that are listed above these instructions.
4.	Choose an export option. The Storage Access Framework (SAF) File Chooser will open.
5.	Select a file location on your device to save the exported file to.
6.	Select the **Select Button** to finalise the export. There will be a notification on your device when the exported file has saved to that location.

10.6 Uploading Trial Data

When the export data file from KDSmart is ready for import on a computer, users can use KDManage to import it into the database.

More details can be found at *Trial Data CSV Format* and *Importing CSV Data - KDSmart Format*

hen 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 16

*: denotes a required field.

Data File*:

No file selected.

Data Start Column*:

Data End Column*:

X Column*:

Y Column*:

Z Column:

Plot Measure Date :

Sample Type*:

Instance Divider*:

Remove Outliers:

Specimen Number Offset: 0

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.

Measure Date Time Override:

Override Sample Measurement Group Name:

Fig. 7: Import Trial Data Window - KDSmart Format

Note: It's highly recommended that all data should be uploaded with barcodes.

10.7 Accessing Trial Data

Once data is uploaded, data can be access and viewed on trial page.

More details can be found at *Trial View Page* and *Downloading Trial Data*

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

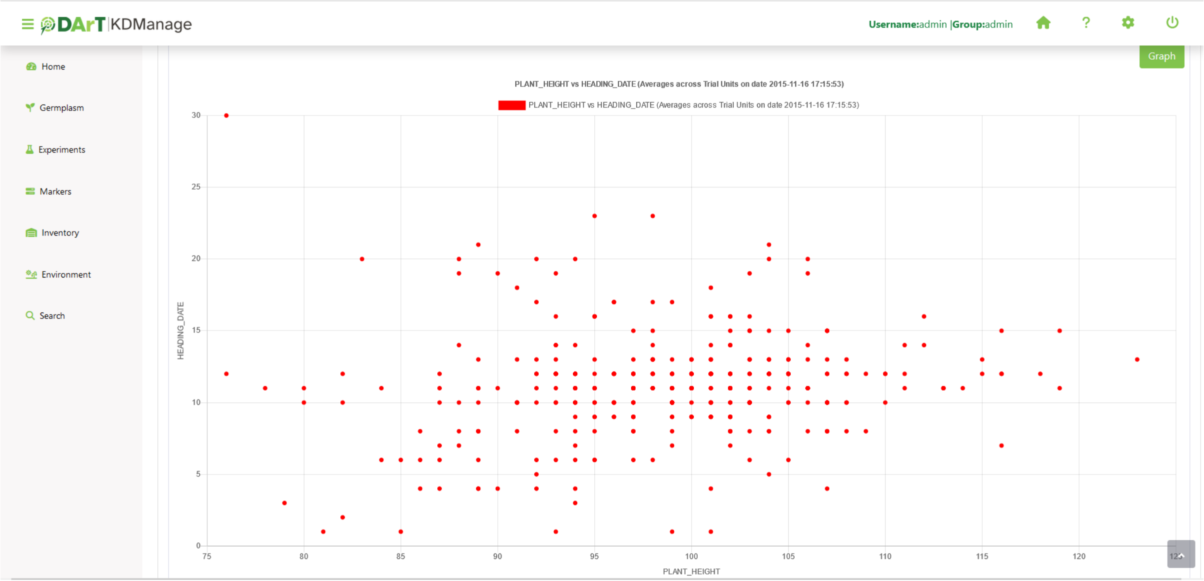
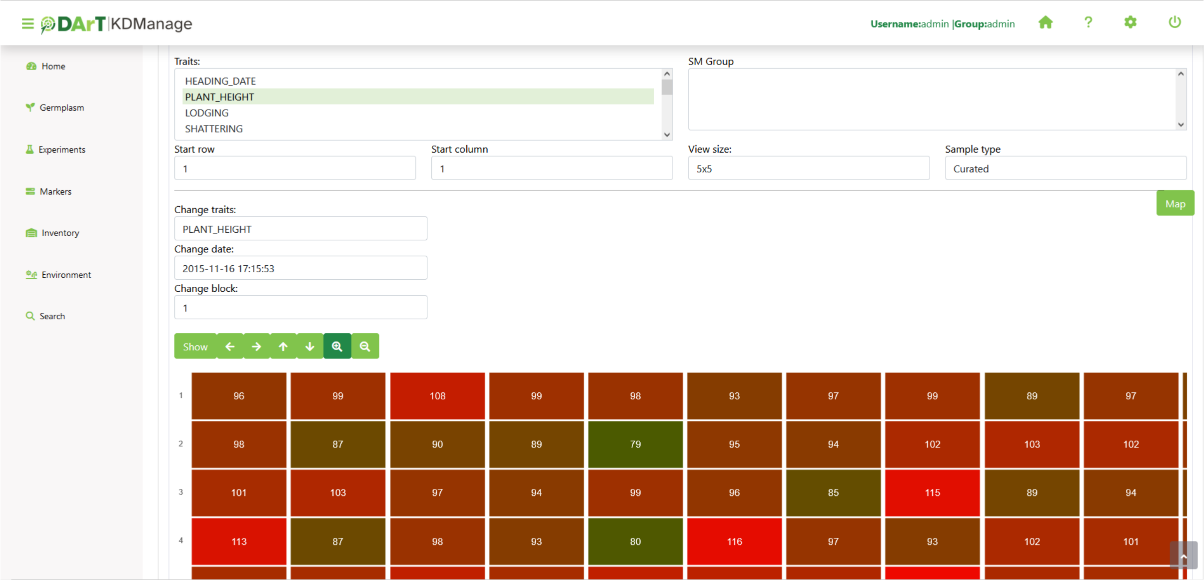


Fig. 8: Trial Data Graph

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



Traits:
HEADING_DATE
PLANT_HEIGHT
LODGING
SHATTERING

SM Group

Start row: 1

Start column: 1

View size: 5x5

Sample type: Curated

Change traits: PLANT_HEIGHT

Change date: 2015-11-16 17:15:53

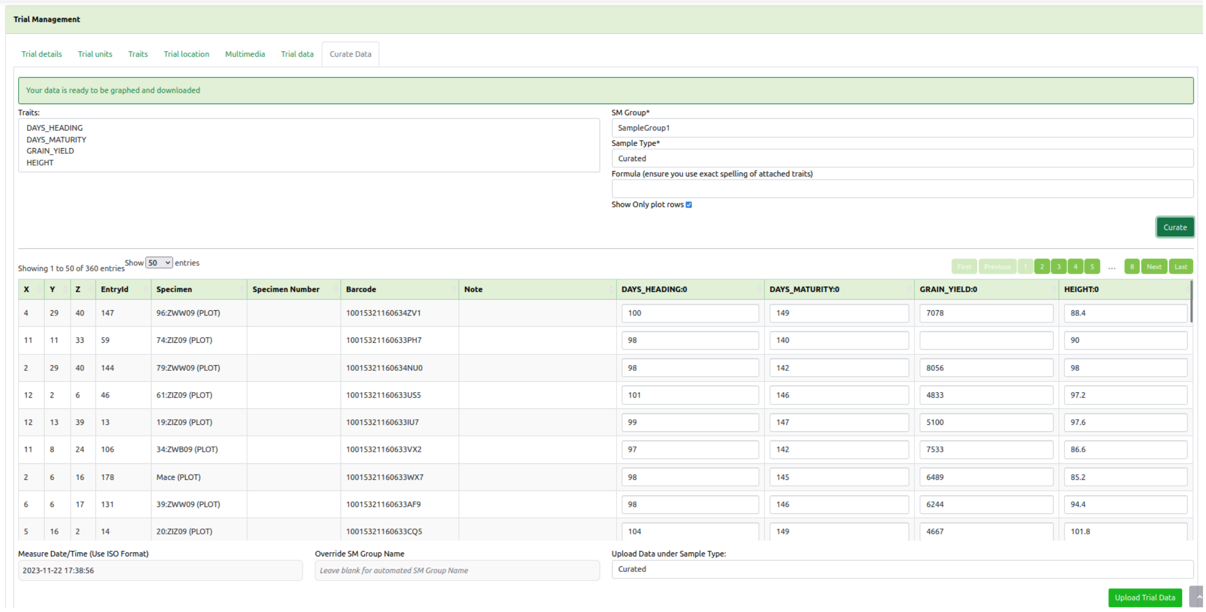
Change block: 1

1	96	99	108	99	98	93	97	99	89	97
2	98	87	90	89	79	95	94	102	103	102
3	101	103	97	94	99	96	85	115	89	94
4	113	87	98	93	80	116	97	93	102	101

Fig. 9: Trial Data Map

10.7.1 Curate Data Tab

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



Your data is ready to be graphed and downloaded

Traits:
DAYS_HEADING
DAYS_MATURITY
GRAIN_YIELD
HEIGHT

SM Group*: SampleGroup1
Sample Type*: Curated
Formula (ensure you use exact spelling of attached traits):
Show Only plot rows ☑

Showing 1 to 50 of 360 entries Show 50 entries

X	Y	Z	EntryId	Specimen	Specimen Number	Barcode	Note	DAYS_HEADING:0	DAYS_MATURITY:0	GRAIN_YIELD:0	HEIGHT:0
4	29	40	147	96:ZWW09 (PLOT)		10015321160634ZV1		100	149	7078	88.4
11	11	33	59	74:ZIZ09 (PLOT)		10015321160633PH7		98	140		90
2	29	40	144	79:ZWW09 (PLOT)		10015321160634NU0		98	142	8056	98
12	2	6	46	61:ZIZ09 (PLOT)		10015321160633US5		101	146	4833	97.2
12	13	39	13	19:ZIZ09 (PLOT)		10015321160633IU7		99	147	5100	97.6
11	8	24	106	34:ZWB09 (PLOT)		10015321160633VX2		97	142	7533	86.6
2	6	16	178	Mace (PLOT)		10015321160633WX7		98	145	6489	85.2
6	6	17	131	39:ZWW09 (PLOT)		10015321160633AF9		98	146	6244	94.4
5	16	2	14	20:ZIZ09 (PLOT)		10015321160633CQ5		104	149	4667	101.8

Measure Date/Time (Use ISO Format): 2023-11-22 17:38:56
Override SM Group Name: *Leave blank for automated SM Group Name*
Upload Data under Sample Type: Curated

Fig. 10: 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.

10.8 Using Trial Super Import

Trial Super Import allows to the above steps to be streamlined and done in a single CSV upload, including any collected data from KDSmart if included.

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.

Phenotypic data can also be included and the columns containing measurements should follow the same format as seen in KDManage and KDSmart format data import CSV files.

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

More details can be found at *Trial Super Import*.