

GeneLink User Guide

version 4.0

GeneLink

May, 2004

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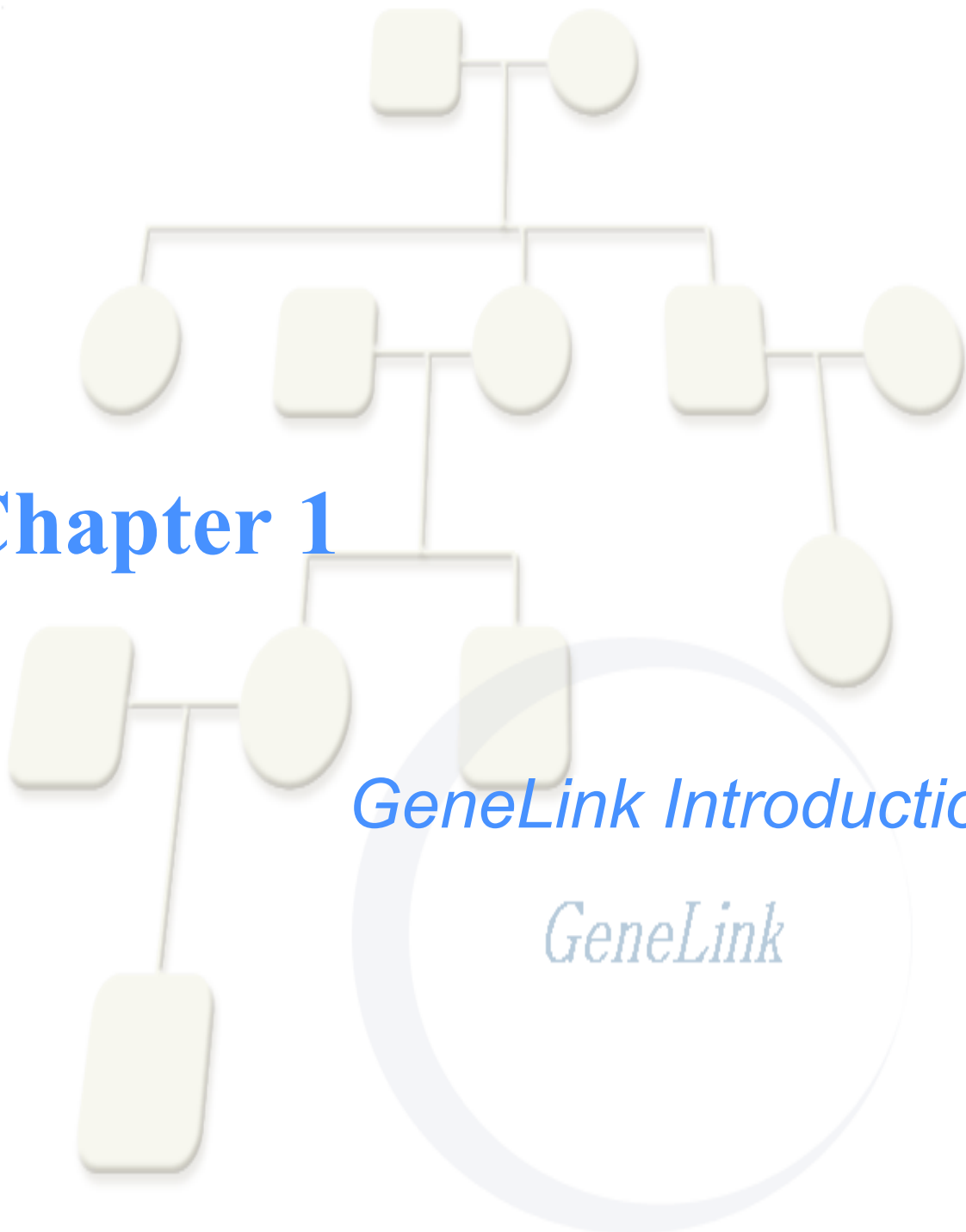
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Chapter 1



GeneLink Introduction

GeneLink

Overview

The GeneLink application stores and manages genotyping data for researchers performing linkage and/or association studies to identify gene(s) involved in disease etiology. For complex hereditary diseases, high-throughput genotyping is frequently performed on large collections of DNA samples using hundreds of microsatellite or SNP markers. Large amounts of data are generated during these studies, posing significant data management challenges.

To collect a sufficiently powerful dataset, collaborative efforts are often required. The web-based interface of this application facilitates collaborative efforts since data can be accessed via the internet. All data are password protected. Access privileges are assigned to each user granting collaborators the ability to view and/or manipulate all or a subset of data.

GeneLink provides many functions that make it a powerful tool. For instance, GeneLink carries out quality control checks on data imported into the database by checking for differences between genotype data analyzed independently by two researchers. Furthermore, GeneLink merges genotypic data with pedigree, phenotypic, and genetic or physical map information. When data are ready for export, GeneLink can properly format and export data to be analyzed in the GAS, LINKAGE, and RelCheck computer software packages. Furthermore, allele translation is performed when data are exported for LINKAGE and RelCheck. Detailed reports are generated for download and/or printing, showing details and success of import and export functions, status of projects, and statistical information about markers and DNA samples tested.

Sections in This Chapter

- Conventions Used in this Guide, page 1-3
- Functionality Devices, page 1-4
- Definitions of GeneLink Terms, page 1-5
- Definitions of GeneLink Database Tables, page 1-6
- Abbreviations, page 1-7
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Conventions Used in this Guide

The GeneLink User Guide contains conventions that assist the readers with their use of the application. The following table identifies the conventions and their use in this particular guide.

Table 1: GeneLink User Guide Conventions

Convention	Definition	Example
Small Caps	Specific names of menu items, screens, text fields, keys, and buttons.	Select the SELECT PROJECT button.
Bulleted Lists	Provides a list of information to the reader. These lists are not providing instruction for a particular action.	The following links are contained in the Administration Menu: <ul style="list-style-type: none"> • Add User • Add Group • Change Group Name
Numbered Lists	Step-by-step procedure to be followed to perform a specific action.	To change your password, perform the following actions: <ol style="list-style-type: none"> 1. Select CHANGE PASSWORD. 2. Enter your USERNAME. 3. Enter your CURRENT PASSWORD.

Functionality Devices

This section describes the functionality devices as used in the GeneLink application. These devices may or may not be valid for use in other applications.

Table 2: Functionality Devices



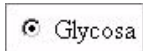

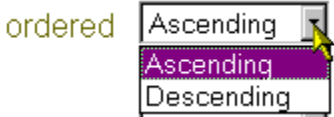



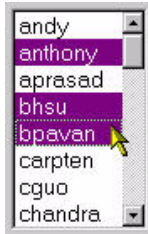
Device	Description	Example
Button	Used to select an option or to perform a command.	
Link	Used as a reference to another document or page.	
Radio Button	Indicates a mutually exclusive option.	
Check Box	A box used to turn an option on or off. When a check mark is displayed, the option is turned on.	
Drop-down List (Combo Box)	A menu of commands or options.	
Text Box	A field used to enter text.	
GeneLink Logo	When selected, will return the user to the GeneLink home page. To access project information, the user will have to reselect a project.	
Shift Select	When holding the SHIFT key down, the mouse can be used to select a range of options. The user can click the first item in a list, then the last item to select the entire range.	

Table 2: Functionality Devices

Device	Description	Example
Control Select (Windows) Apple Select (Mac)	When holding the CTRL/APPLE key down, the mouse can be used to select specific options.	

Definitions of GeneLink Terms

The following table defines the terms used in discussions of the GeneLink application.

Table 3: Definitions

Term	Definition
Activity	Defines the level of access a user has to the database and the GeneLink application.
Delimiter	A delimiter is a character that identifies the beginning or the end of a string (a contiguous sequence of characters) where the delimiting character is not part of the string. The delimiter is often a tab. Delimiters can also be used to separate data items in a database when importing the data from the database to another application.
Differences	Genotype scoring discrepancies between two independent users (scorers). If a panel is double scored: each user imports his or her table into the database and the application will identify differences between reported genotypes.
Duplicates	Defined as two records within the temporary or final genotypes table with the same FamInd ID and marker. An individual may be genotyped more than once during a scan for quality control purposes. The database will check to confirm that scores for allele 1 and 2 are the same. The database checks for duplicates within each table imported into the database. Furthermore, prior to finalizing and exporting the data, the application conducts an additional check for duplicates. Record may have a R (replaced DNA sample) flag are not included in duplicates check.
Export	A download of data from the database to the user's local computer.

Table 3: Definitions

Term	Definition
Family	Contains the family data and is assigned to a project. A project may have unlimited families associated with it. Each family belongs to a group, which defines its user access.
Group	Administrator defined collection of users. A group is provided access to the application at the family (site) level.
Import	An upload of data from the user's local computer to the database.
Panel	A group of microsatellite or SNP markers whose PCR products are capable of being electrophoresed simultaneously by taking advantage of different fluorescent dye labels and varying amplicon sizes.
Project	A data set containing pedigree, phenotype and genotype, and marker information for a specific disease.
User	An individual who uses the GeneLink application.

Definitions of GeneLink Database Tables

The following table defines the database tables used in the GeneLink application:

Table 4: GeneLink Database Tables

Table Name	Definition
Allele Translations	Responsible for translating each allele for each marker. When exporting from the genotypes table in "LINKAGE" or "RelCheck" format, genotype labels are systematically recoded (1, 2, 3...) to provide properly formatted data for analysis by these programs. The allele translation table provides a key or legend linking the new "translated" score to the original genotype score. Future exports will use identical "allele translation codes." New alleles identified after the first export will be added to the end of the allele translation, to ensure consistent recoding of alleles across exports.
Families	Each record reflects a single family included in a genetic study. The families table also stores pertinent clinical information about the family, such as number of affecteds, or number of affecteds with DNA.
Genotypes	"Final genotypes" table: Table in which final genotype data are stored. NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

Table 4: GeneLink Database Tables

Table Name	Definition
Liability Class	Stores information regarding specific liability classes to be incorporated in LINKAGE exports. Liability classes can be defined using a combination of age, sex, and affection status.
Maps	Provides the following information for markers used in a given project: location of the marker within the genome, relative order of markers along a chromosome, and the intermarker distance of adjacent markers within a chromosome. The maps database table also determines the relative order in which data are exported by chromosome. NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)
Markers	Provides information regarding microsatellite or SNP markers used in a given linkage project. Provides the panel in which the marker was run, as well as the allele size range (ASR) of the marker, dye color and genotype for a CEPH control individual (1347-02). NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)
Pedigrees	Provides pedigree and phenotype information for each individual within a family. Two qualitative traits can be stored as Status Narrow, Status Broad.
DNA	Stores information regarding all available DNA samples in the laboratory.
Primers	Provides additional information for each specific marker, including UniSTS ID, GenBank accession number, forward primer sequence, reverse primer sequence, primer ordering information, and inventory information.
Trait Translation	Contains details for phenotypes stored in Trait Score table.
Trait Score	Stores individual values for an unlimited number of phenotypes (either qualitative or quantitative).

Abbreviations

The following table defines the abbreviations used in discussions of the GeneLink application.

Table 5: Abbreviations

Abbreviation	Definition
NHGRI	National Human Genome Research Institute (http://www.nhgri.nih.gov/)

Table 5: Abbreviations

Abbreviation	Definition
NIH	National Institutes of Health (http://www.nih.gov/)

Contact Us

To contact us regarding GeneLink, please send an e-mail or letter to:

E-mail: GeneLink@nhgri.nih.gov

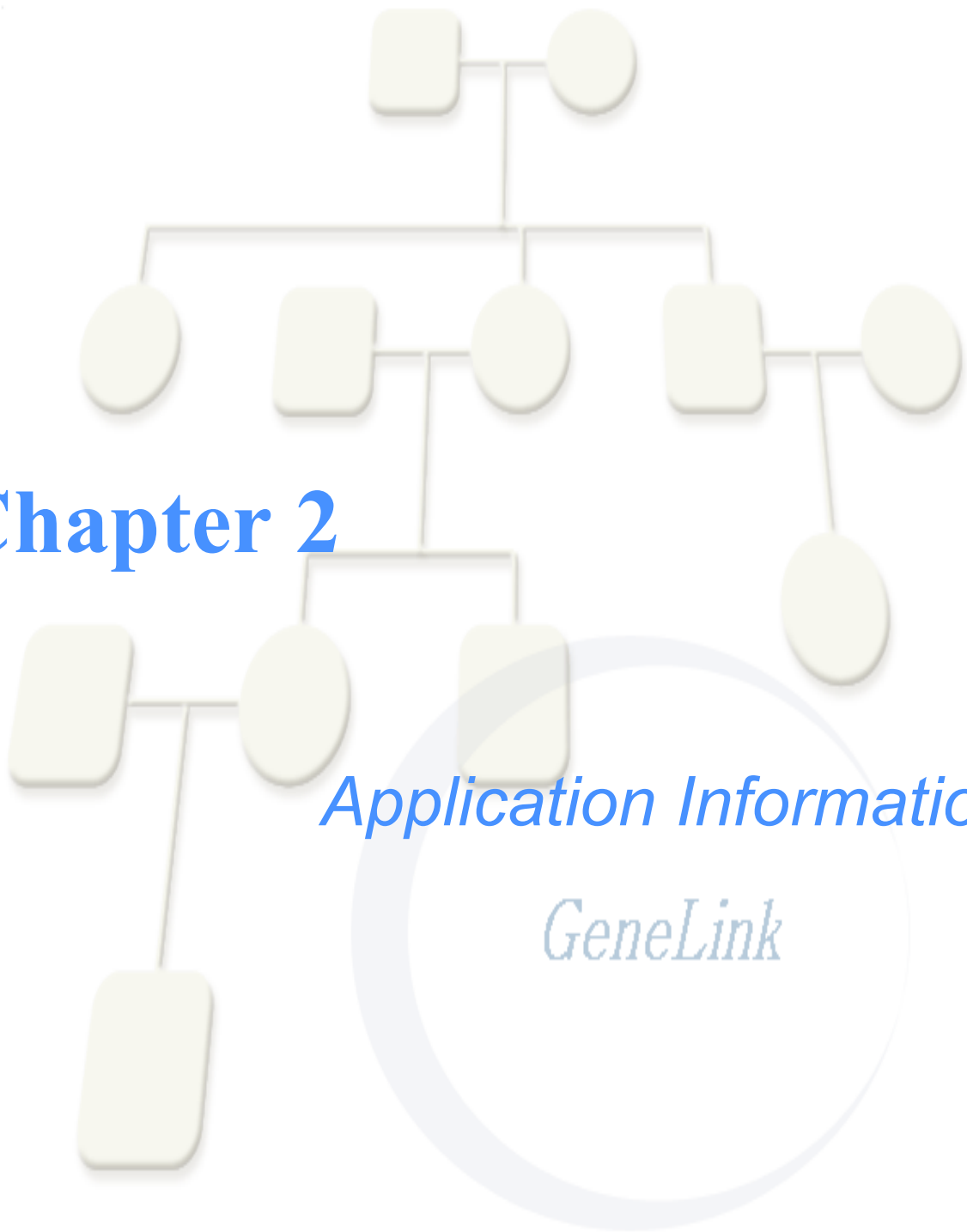
Mailing Address: National Human Genome Research Institute
National Institutes of Health
Bioinformatics and Scientific Programming Core
Attn: GeneLink Administrator
50 South Drive, Building 50, Room 5228B
Bethesda, MD 20892

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Chapter 2



Overview

In order to use GeneLink properly, the application needs to be set up prior to its initial use. Setting up the application means that users and projects need to be created, users need to be assigned to groups, groups need to be assigned privileges, and finally groups need to be associated with families (by site). The Root Administrator and users with Administrative privileges have the ability to add users and manage groups via the Administration Menu. The Root Administrator is the only user permitted to create new projects, add new activities, and reset passwords. These administrative tasks must be completed prior to importing genotypes into GeneLink's database.

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 - Primers Table, page 2-52*
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Login to GeneLink

To use the GeneLink application, a user must have a unique username and password (initial user created by root). The username and password are created by ADD USER link from the Administration Menu. The username and password are case sensitive and each is limited to 8 characters.

To Login

1. Enter the URL for GeneLink in your Web browser ().
2. The **LOGIN** screen displays. Enter your **USERNAME** and **PASSWORD**.



The screenshot shows a web browser window titled "Please Login". Inside the window, there are two text input fields. The first is labeled "Username:" and contains the text "jmurphy". The second is labeled "Password:" and contains masked characters (asterisks). Below these fields is a button labeled "Login". A mouse cursor is pointing at the "Login" button.

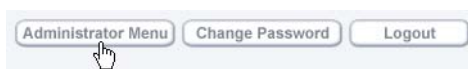
3. Select **LOGIN**. You are now logged into the GeneLink application.

Projects

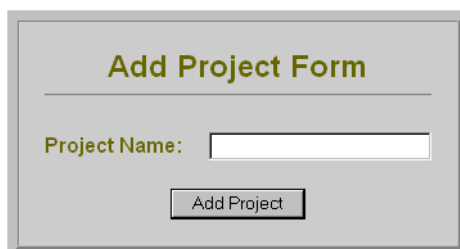
A Project is typically defined as a data set containing pedigree, phenotypic, genotypic, and marker data for a disease-specific genetic study. Projects are added to GeneLink by the Root Administrator only. Once a project has been created, authorized users, can import or insert families, which house the family specific data.

To Add a Project (Root Administrator Only)

1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link on the upper right-hand corner of the **GENELINK** main page.



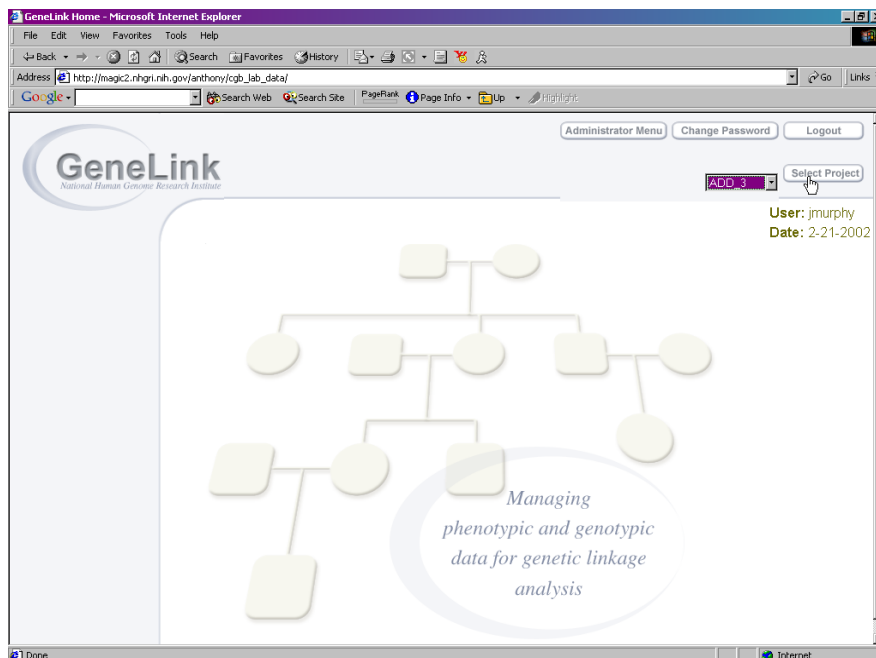
3. Select **CREATE NEW PROJECT** from the **ROOT ONLY OPTIONS** section of the **ADMINISTRATION MENU**. The **ADD PROJECT FORM** displays:

A form titled "Add Project Form" with a "Project Name:" label and a text input field. Below the input field is an "Add Project" button.

4. Enter the name of the project in **PROJECT NAME** text box.
5. Select **ADD PROJECT**.
6. The **ADMINISTRATION MENU** displays with a confirmation message advising that the project has been added.

To Select a Project

1. The GeneLink home page displays:



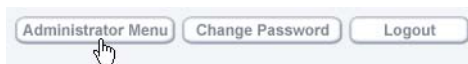
2. Select a project from the drop-down list.
3. Click **SELECT PROJECT**.

Users

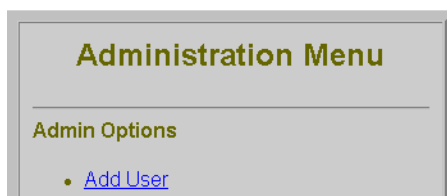
Users are added to GeneLink by the Root Administrator or any user with Administrative privileges. Users access to the application is based upon the assignment of privileges to a group (to which a user might belong). Users are associated to groups, and groups are granted access to GeneLink by associating groups with specific Activities (privileges). Finally, in order for access to be collection site specific, families (sites) are associated with groups.

To Add a User

1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link on the upper right-hand corner of the **GENELINK** main page.



3. Select **ADD USER** from the **ADMIN OPTIONS** on the **ADMINISTRATION MENU**.



4. The **ADD USER FORM** displays. Enter the **FULL NAME**, **E-MAIL** address, **USERNAME**, **PASSWORD**, and the **PASSWORD** again for the user.

***NOTE: USERNAME AND PASSWORD ARE CASE SENSITIVE AND LIMITED TO 8 CHARACTERS**

5. Select **ADD USER**.

- The **ADMINISTRATION MENU** displays and confirms that the user has been added.

To Change a User's Password

- Login to **GENELINK**, see page 2-4 for directions.
- Select the **CHANGE PASSWORD** link on the upper right-hand corner of the **GENELINK** main page:

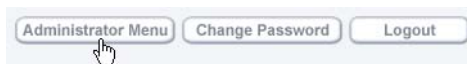


- The **CHANGE YOUR PASSWORD** dialog displays:

- Enter the **USERNAME**.
- Enter the **CURRENT PASSWORD**.
- Enter the **NEW PASSWORD**.
- Verify the **NEW PASSWORD**.
- Select **CHANGE PASSWORD**.
- A confirmation message displays.
- Use the back arrow on your browser to return to the GeneLink home page.

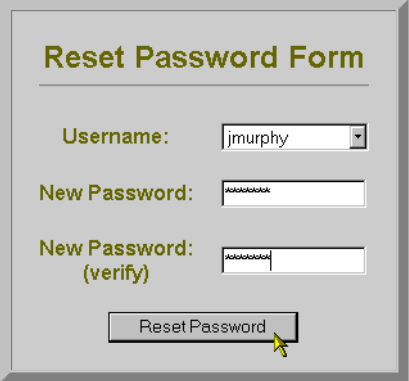
To Reset Passwords (Root Administrators only)

- Login to **GENELINK**, see page 2-4 for directions.
- Select the **ADMINISTRATOR MENU** link on the upper right-hand corner of the **GENELINK** main page.



- Select **RESET PASSWORDS** in the **ROOT ONLY OPTIONS** section of the **ADMINISTRATION MENU**.

4. The **RESET PASSWORD FORM** displays:



The screenshot shows a web form titled "Reset Password Form" with a grey background. It contains three input fields: a dropdown menu for "Username" with "jmurphy" selected, a text box for "New Password" with masked characters, and another text box for "New Password (verify)" also with masked characters. A "Reset Password" button is located at the bottom, with a mouse cursor pointing to it.

5. Select the **USERNAME** from the drop-down list.
6. Enter the **NEW PASSWORD**.
7. Verify the **NEW PASSWORD**.
8. Select **RESET PASSWORD**. The **ADMINISTRATION MENU** displays a confirmation message.

Managing Groups

A group is a collection of users who should have equal access to the same family sites. Privileges granting access to the data is defined on a group-by-group basis. The MANAGE GROUPS link in the administrator menu enables the Root Administrator or a user with Administrator privileges to add users to a group, remove users from a group, assign privileges to a group, and associate families (sites) with groups. Normally, all groups could begin with site-specific view privileges and then additional activities can be added.

To Add a Group

1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link on the upper right-hand corner of the **GENELINK** main page.



3. From the **ADMINISTRATION MENU**, select **ADD GROUP**. The **ADD GROUP FORM** displays:

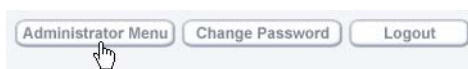
4. Enter a **GROUP NAME** and select a **PROJECT NAME** from the drop-down list.

***NOTE: THE GROUP NAME MUST BE UNIQUE TO THE GENELINK APPLICATION.**

5. Select **ADD GROUP**.
6. A confirmation message displays at the top of the **ADMINISTRATION MENU**.

To Add a User to a Group

1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link on the upper right-hand corner of the **GENELINK** main page.



- From the **ADMINISTRATION MENU**, select **MANAGE GROUPS**. The **MANAGE GROUP FORM** displays.

- Select the appropriate **GROUP** from the drop-down list.
- Select **CHANGE GROUP MEMBERS** from the **ACTION** drop-down list.
- Select **MANAGE GROUP**. The **"GROUP NAME" GROUP** dialog displays:

- Select the users you wish to add to the group from the **AVAILABLE USERS** list and add them to the **USERS ASSIGNED TO "GROUP NAME"** list by highlighting the users and selecting the right arrow **->**. See the tips on selecting multiple items in the Functionality Devices section, page 1-4.
- To return to the **ADMINISTRATION MENU**, select **ADMINISTRATOR MENU** on the upper right-hand corner of the window.

To Remove a User from a Group

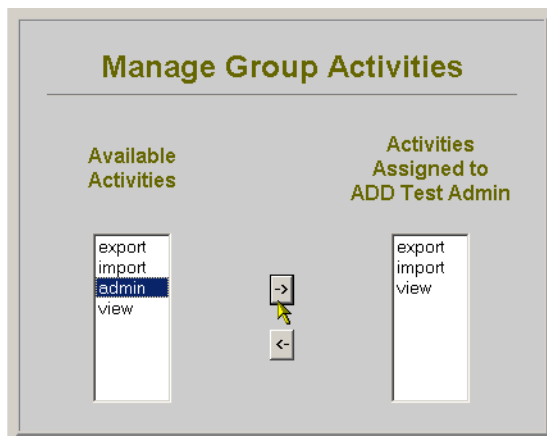
- Follow directions 1-6 from To Add a User to a Group, page 2-10.
- Select the users you wish to remove from the group from the **USERS ASSIGNED TO "GROUP NAME"** list by highlighting the appropriate user(s) and selecting the left arrow **<-**. See the tips on selecting multiple items in the Functionality Devices section, page 1-4.
- To return to the **ADMINISTRATION MENU**, select **ADMINISTRATOR MENU** on the upper right-hand corner of the window.

To Assign Privileges (Activities) to a Group

1. From the **ADMINISTRATION MENU**, select **MANAGE GROUPS**.
2. Select the appropriate group from the **GROUP** drop-down list.
3. Select **CHANGE GROUP ACTIVITIES** from the **ACTION** list:



4. Select **MANAGE GROUP**. The **MANAGE GROUP ACTIVITIES** dialog displays:



5. Select **EXPORT**, **IMPORT**, **ADMIN**, **MODIFY** or **VIEW** from the **AVAILABLE ACTIVITIES** list and move the privilege to the **ACTIVITIES ASSIGNED TO "GROUP NAME"** list by using your right arrow **->**. See the table below for the definitions of the privileges. See the tips on selecting multiple items in the Functionality Devices section, page 1-4.

Table 1: Group Activity (Privileges)

Activity	Definition
Admin (Administrator)	Provides the user with the ability to view the data (see View privilege) as well as to access the Administration Menu and perform all included actions. The Admin and Browse Database Tables options are available to users with this privilege. The user can access only the site(s) with which his/her group is associated. The Admin privilege does not provide access to the Root Only Options displayed in the Administration Menu.
Export	Provides privilege to Export data in files formatted for downstream analysis. The user can access only the site(s) with which his/her group is associated.

Table 1: Group Activity (Privileges)

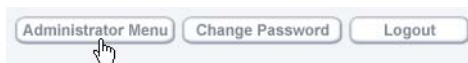
Activity	Definition
Import	Access to the Import options only. The import activity refers only to the process of importing genotypes into the final genotypes table via the temporary genotypes table. A user must have modify privileges in order to import, insert or modify the other tables. The user can access only the site(s) with which his/her group is associated.
Modify	Provides user modify Database Tables. A user must have modify privileges in order to import, insert or modify the database tables. The user can access only the site(s) with which his/her group is associated.
View	Provides user access to the View and Browse Database Tables options. The user can access only the site(s) with which his/her group is associated.

- To return to the **ADMINISTRATION MENU**, select **ADMINISTRATOR MENU** on the upper right-hand corner of the window.

To Add an Activity (Root Administrators Only)

***NOTE: THIS STEP IS ONLY NEEDED IF YOU WANT AN ADDITIONAL LAYER OF SECURITY. THE SOURCE CODE WILL NEED ALTERATIONS TO ACCOMMODATE ANY ADDED ACTIVITIES.**

- Login to **GENELINK**, see page 2-4 for directions.
- Select the **ADMINISTRATOR MENU** link located in the upper right-hand corner of the **GENELINK** main page.



- Select **ADD AN ACTIVITY** from the Root Only Options section of the **ADMINISTRATION MENU**.
- The **ADD ACTIVITY FORM** displays:

- Enter the **NEW ACTIVITY NAME**.
- Select **ADD ACTIVITY**.

Importing Tables

GeneLink requires that the Families, Maps, Markers, and Pedigrees tables be populated prior to importing genotype data. Populating these tables prior to importing genotypes allows GeneLink to employ all of its quality control measures, as well as properly prepare the genotype data for export. Data can be imported or inserted into each table. In contrast to the IMPORT option, which allows multiple records to be imported from a text file, the INSERT option adds a single record at a time to the database table. Note, as specified above in table 1: a user must have modify privileges in order to import or insert data into most GeneLink tables. The import activity refers only to the process of importing genotypes into the final genotypes table via the genotype import process (see chapter 3).

To IMPORT (INSERT) into the Families Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **FAMILIES** link:



5. Select the **IMPORT** (or INSERT) link:



6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

Date: 3-28-2002

[Search] [Modify] [Delete] [Insert] [Import] [Export]

Import Data

NOTE: The data file for the **FAMILIES** table must follow this format. It needs to be a delimited text file, and can not be an Excel Workbook.

Exclude: Site: FamID: OriginalFamID: OtherID: Race: MMTrans: Bilineal: Loops: Twins: OtherCancers: Phase: Criteria: Comments: In

Data File:

Skip Header Row

Delimiter:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE FAMILIES TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-46.**

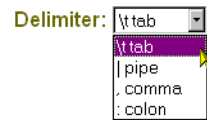
Table 2: Families Table

Field Name	Valid Characters(length)	Can field be null?
Exclude	varchar(10)	Y
Site	varchar(25)	N
FamID	number	N
OriginalFamID	number	Y
OtherID	varchar(20)	Y
Race	varchar(5)	Y
MMTrans	varchar(5)	Y
Bilineal	varchar(5)	Y
Loops	varchar(5)	Y
Twins	varchar(5)	Y

Table 2: Families Table

Field Name	Valid Characters(length)	Can field be null?
OtherPhenotypes	varchar(100)	Y
Phase	varchar(100)	Y
Criteria	varchar(100)	Y
Comments	varchar(255)	Y

7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

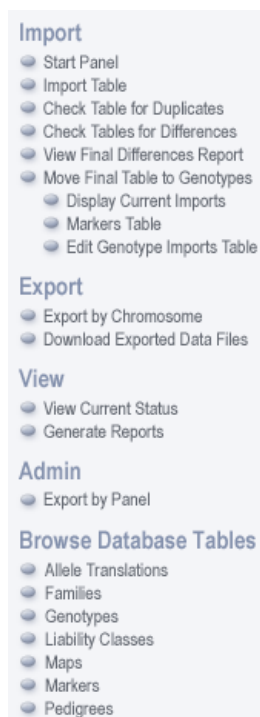
To IMPORT (INSERT) directly into the Genotypes Table

NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

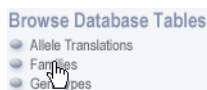
The primary way that data is imported into the final genotypes table is using the import process. This process is described in detail in chapter 3. Alternatively genotypes can be imported directly into the final genotypes table in 2 ways. First is similar to imports described for other tables (Standard import). Second is what we refer to as the “Multiple Genotypes Import Loader” which allows genotypes to be imported from LINKAGE formatted files. Both methods are described below:

Standard Import:

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **GENOTYPES** link under **BROWSE DATABASE TABLES**:



5. Select the **IMPORT** (or INSERT) link:



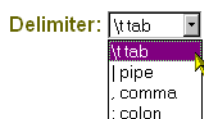
6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE GENOTYPES TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-46.**

Table 3: Genotypes Table

Field Name	Valid Characters(length)	Can field be null?
FamIndID	number	N
MarkerName	varchar(10)	N
Allele1	number	Y
Allele2	number	Y
Grid	varchar(20)	Y
Lane	number	Y
Flag	varchar(20)	Y

7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

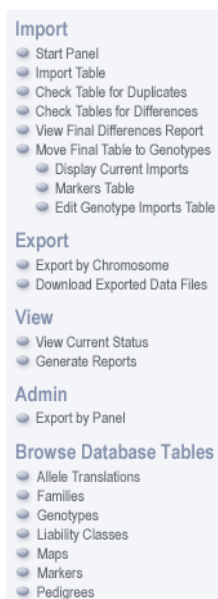
Multiple Genotype Import Loader:

1. Repeat steps 1-5
2. Select Multiple Genotype Import Loader
3. Select Click here for directions and format your upload. This link provides detailed information regarding importing from a LINKAGE file, including sample formats for Input file.

To IMPORT (INSERT) into the Liability Classes Table

Liability class information can be stored in GeneLink in two ways. First each individual's liability class can be specifically stored in the pedigrees table. These liability classes are defined by the user and could be based on any number of variables. Liability classes defined based on an individual's age, gender and affection status (either status broad or status narrow) can be stored in the liability classes table. Most often Liability classes can be inserted directly into the Liability class tables. To import:

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **LIABILITY CLASSES** link:



5. Select the **IMPORT** (or INSERT) link:



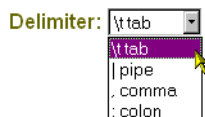
6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE LIABILITY CLASSES TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-47.**

Table 4: Liability Classes Table

Field Name	Valid Characters(length)	Can field be null?
Disease	varchar(30)	Y
LiabilityClass	number	N
AgeFrom	number	Y
AgeTo	number	Y
Sex	varchar(5)	Y
Affected	varchar(10)	Y

7. Select a delimiter from the **DELIMITER** drop-down list:

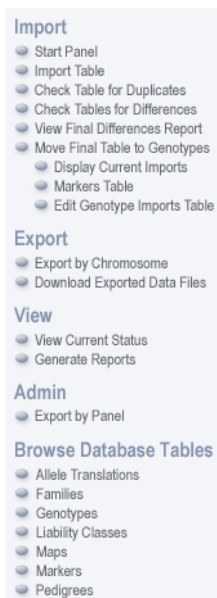


8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

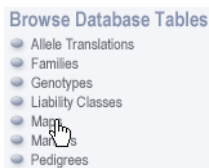
To IMPORT (INSERT) into the Maps Table

NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **MAPS** link:



5. Select the **IMPORT** (or INSERT) link:



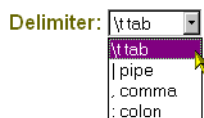
6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE MAPS TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-48.**

Table 5: Maps Table

Field Name	Valid Characters(length)	Can field be null?
Chromosome	number	N
Location	number(6,3)	N
DistanceFromAbove	varchar(10)	Y
MarkerName	varchar(10)	N
Heterozygosity	number(4,2)	Y

7. Select a delimiter from the **DELIMITER** drop-down list (for information regarding Delimiters, see the Definitions of GeneLink Terms, page 1-5):

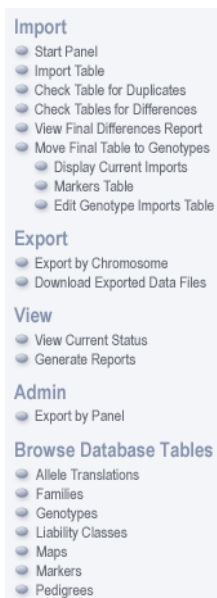


8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the Markers Table

NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **MARKERS** link:



5. Select the **IMPORT** (or INSERT) link:



6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

[\[Search\]](#) [\[Modify\]](#) [\[Delete\]](#) [\[Insert\]](#) [\[Import\]](#) [\[Export\]](#)

Import Data

NOTE: The data file for the **MARKERS** table must follow this format. It needs to be a delimited text file, and can not be an Excel Workbook.

MarkerName|Panel|PreviousPanel|AlleleSizeRange|CEPH_134702
|Chromosome|Dye|Pool|PkHt|Comments|n

Data File:

Skip Header Row
 Skip Column One

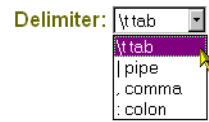
Delimiter:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE MARKERS TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-49.**

Table 6: Markers Table

Field Name	Valid Characters(length)	Can field be null?
MarkerName	varchar(10)	N
Panel	varchar(10)	Y
PreviousPanel	varchar(10)	Y
AlleleSizeRange	varchar(15)	Y
CEPH_134702	varchar(15)	Y
Chromosome	number	Y
Dye	varchar(10)	Y
Pool	number(4,1)	Y
PkHt	number	Y
Comments	varchar(255)	Y

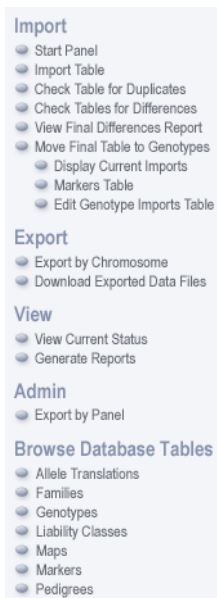
7. Select a delimiter from the **DELIMITER** drop-down list:



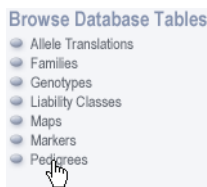
8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the Pedigrees Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **PEDIGREES** link:



5. Select the **IMPORT** (or INSERT) link:



6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

[Search]
[Modify]
[Delete]
[Insert]
[Import]
[Export]

Import Data

NOTE: The data file for the **PEDIGREES** table must follow this format. It needs to be a delimited text file, and can not be an Excel Workbook.

PedID\FamIndID\FamID\IndID\FatherID\MotherID\Sex\DNA\Age\Diagnosis>StatusBroad>StatusNarrow\LiabilityClass\In

Data File:

Skip Header Row

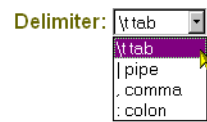
Delimiter:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE PEDIGREES TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-50.**

Table 7: Pedigrees Table

Field Name	Valid Characters(length)	Can field be null?
PedID	number	N
FamIndID	number	N
FamID	number	N
IndID	number	N
FatherID	number	N
MotherID	number	N
Sex	char(1)	N
DNA	number	N
Age	varchar(10)	N
Diagnosis	varchar(10)	Y
StatusBroad	varchar(10)	N
StatusNarrow	varchar(10)	Y
LiabilityClass	number	Y
Exclude	varchar(10)	Y

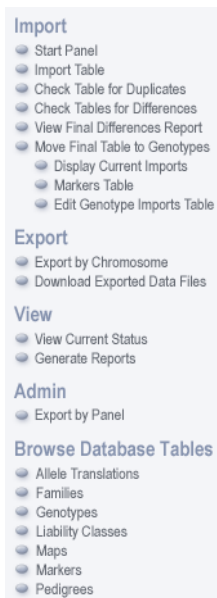
7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the DNA Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **DNA** link:
5. Select the **IMPORT** (or INSERT) link:



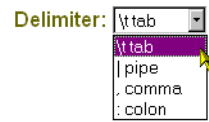
6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE DNA TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-51.**

Table 8: DNA Table

Field Name	Valid Characters(length)	Can field be null?
FamID	number	N
IndID	number	N
FamIndID	number	N
DNA_Source	varchar(25)	N
Date_Recorded	datetime	N
Tube_Label	varchar(100)	N
DNA	Y/A/P/N	N
Prep	char(5)	N
DNA_Conc	numeric(5,2)	N
Init_DNA_Vol	numeric(5,2)	N
Total_DNA_Amt	numeric(5,2)	N
Comment	varchar(255)	Y
First_Vol_DNA	numeric(5,2)	Y
Second_Vol_DNA	numeric(5,2)	Y
Third_Vol_DNA	numeric(5,2)	Y
DNA_remaining	numeric(5,2)	Y
Freezer	varchar(25)	Y
Rack	varchar(10)	Y
Box	varchar(10)	Y
Location	varchar(10)	Y

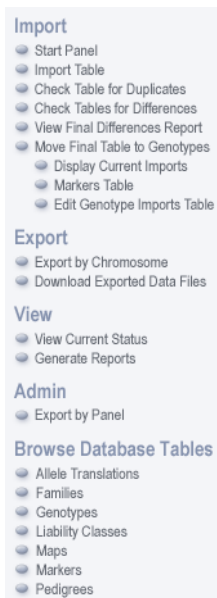
7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the Primers Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **PRIMERS** link:
5. Select the **IMPORT** (or INSERT) link:



6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE PRIMERS TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-52.**

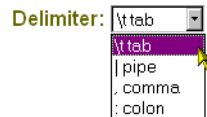
Table 9: Primers Table

Field Name	Valid Characters(length)	Can field be null?
MarkerName	varchar(25)	N
Alt_Name	varchar(25)	Y
UniSTS_ID	int	Y
GeneBank_Acc	varchar(25)	Y
Fwd_Primer_Seq	varchar(50)	Y
Rev_Primer_Seq	varchar(50)	Y
AlleleSizeRange	varchar(15)	N
Chr	int	N
Phys_Start_Pos	int	Y
Phys_Stop_Pos	int	Y
Build	varchar(25)	Y
deCode_Pos	numeric(6,2)	Y
Genethon_Pos	numeric(6,2)	Y
Marshfield_Pos	numeric(6,2)	Y
Order_Number_1	varchar(25)	N
Order_Scale_1	varchar(25)	N
Order_Date_1	varchar(25)	N
Order_Number_2	varchar(25)	Y
Order_Scale_2	varchar(25)	Y
Order_Date_2	varchar(25)	Y
Order_Number_3	varchar(25)	Y
Order_Scale_3	varchar(25)	Y
Order_Date_3	varchar(25)	Y

Table 9: Primers Table

Field Name	Valid Characters(length)	Can field be null?
Comments	varchar(255)	Y
Amount_Remain	varchar(25)	Y

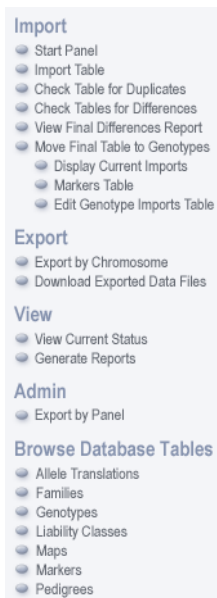
7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the Trait Translation Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **TRAIT TRANSLATION** link:

5. Select the **IMPORT** (or INSERT) link:



6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE TRAIT TRANSLATION TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-50.**

Table 10: Trait Translation Table

Field Name	Valid Characters(length)	Can field be null?
Trait_ID	number	N
Phenotype	varchar(100)	N
Comment	varchar(255)	Y

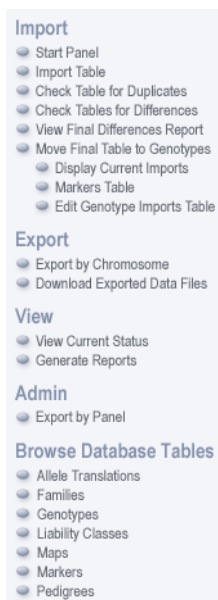
7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

To IMPORT (INSERT) into the Trait Score Table

1. Login to **GENELINK**.
2. Select your project from the drop-down list and click **SELECT PROJECT**.
3. Dependent upon your assigned privileges, the various menu options display on the left side of the screen. You will need the **BROWSE DATABASE TABLES** menu in order to perform the remaining steps.



4. Select the **TRAIT SCORE** link:

5. Select the **IMPORT** link:



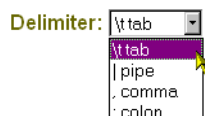
6. The **IMPORT DATA** screen displays. Enter the file name in the **DATA FILE** text box, or click **BROWSE** to search for the file you wish to import:

***NOTE: THE FILE NEEDS TO BE IN THE FORMAT AND ORDER SPECIFIED ON THIS SCREEN (ALSO SHOWN BELOW). SEE THE COMPLETE TRAIT SCORE TABLE STRUCTURE (INCLUDING HIDDEN FIELDS), PAGE 2-50.I**

Table 11: Trait Score Table

Field Name	Valid Characters(length)	Can field be null?
FamIndID	number	N
TT_ID	number	N
Score	varchar	N

7. Select a delimiter from the **DELIMITER** drop-down list:



8. Select the **IMPORT DATA** button.
9. A confirmation message displays advising that the data was successfully imported.

IMPORT INTO THE TRAIT SCORE TABLE IS DIFFERENT THAN OTHER TABLE IMPORTS. PLEASE BE SURE TO READ DETAILED IMPORT INSTRUCTIONS.


Associating Groups with Families

To Associate Groups with Families

This option allows GeneLink to provide a user access to all or only a subset of data. Site information is stored in the families table. Associating a group with families (via their site) facilitates multi-center collaborations as access to the data can be limited by site.

1. From the **ADMINISTRATION MENU**, select **MANAGE GROUPS**. The **MANAGE GROUP FORM** displays.
2. Select the appropriate group from the **GROUP** drop-down list.
3. Select **ASSOCIATE GROUP WITH FAMILIES** from the **ACTION** list:

4. Select **MANAGE GROUP**. The **ASSOCIATE GROUP WITH FAMILIES** dialog displays:

5. Highlight the appropriate families that you wish to associate with the group from the **AVAILABLE FAMILIES** (List represents all sites referenced in the families table) list and move them to the **FAMILIES ASSIGNED TO "GROUP NAME"** list by using the right arrow .
6. To return to the **ADMINISTRATION MENU**, select **ADMINISTRATOR MENU** on the upper right-hand corner of the window.

Reports

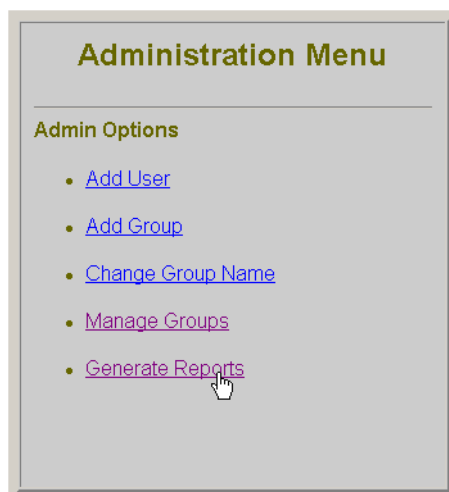
Managing access to the GeneLink database is simplified by the GENERATE REPORTS option. The Generate Reports option in the Administration Menu enables the administrator to run a report on either a specified user or a specified project. The User Report provides a list of the projects and families which the user can access. The View Project Report lists the groups and users associated with a project. Any user with access to the Administration Menu can run reports.

To View the User Report

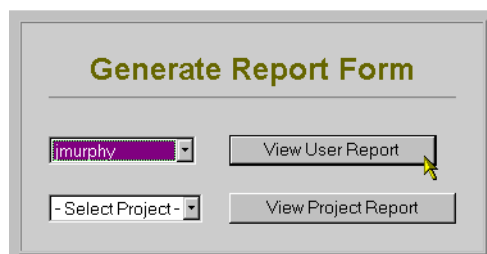
1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link located in the upper right-hand corner of the **GENELINK** main page.



3. The **ADMINISTRATION MENU** displays. Select **GENERATE REPORTS**:



4. The **GENERATE REPORT FORM** displays. Select the appropriate user from the **SELECT USER** drop-down list.



5. Select **VIEW USER REPORT**.

6. The **USER REPORT** displays:

GeneLink
National Human Genome Research Institute

Administrator Menu Change Password Logout

— none — Select Project

User: root
Date: 3-7-2002

User Report

Julie Murphy

Username:	jmurphy
E-mail:	jmurphy@mail.nih.gov
ADD_Test Project	
Permissions:	export, import, admin, view
Family Sites:	ADD1, ADD2, ADD3
ADD_3 Project	
Permissions:	export
Family Sites:	(ALL)

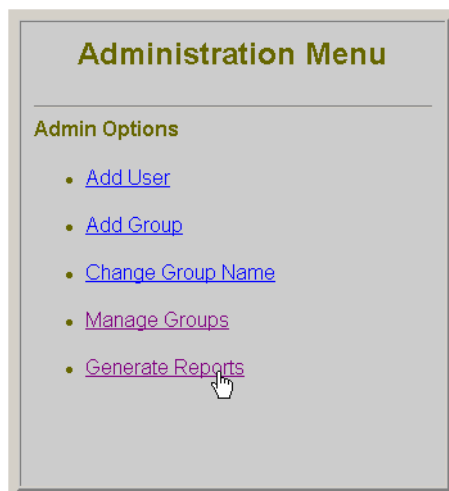
7. To print the **USER REPORT**, select the print icon on your web browser.

To View the Project Report

1. Login to **GENELINK**, see page 2-4 for directions.
2. Select the **ADMINISTRATOR MENU** link located in the upper right-hand corner of the **GENELINK** main page.



- The **ADMINISTRATION MENU** displays. Select **GENERATE REPORTS**.



- The **GENERATE REPORT FORM** displays. Select the appropriate project from the **SELECT PROJECT** drop-down list.
- Select **VIEW PROJECT REPORT**. The "**PROJECT NAME**" **PROJECT REPORT** displays. The report is divided into two tables: one for the Group assigned to the project, and the other identifies the users assigned to the project.

The screenshot shows the GeneLink web application interface. The page title is "HPC_GWS Project Report". The report is divided into two tables. The first table, titled "HPC_GWS Groups", lists various groups and their permissions and assigned family sites.

Group Name	Group Permissions	Family Sites Assigned
AAHPC_admin	admin	AAHPC, Control
AAHPC_export	export	AAHPC, Control
AAHPC_import	import	AAHPC, Control
AAHPC_view	view	AAHPC, Control
Finland_admin	admin	Control, Finland
Finland_export	export	Control, Finland
Finland_import	import	Control, Finland
Finland_view	view	Control, Finland

- To print the "**PROJECT NAME**" **PROJECT REPORT**, select the print icon on your web browser.

The screenshot shows a web browser window titled 'GeneLink Home - Microsoft Internet Explorer'. The address bar contains the URL: http://magic2.nhgri.nih.gov/anthony/cgb_lab_data/admin.cgi?report_form=1. The main content area displays a report titled 'HPC_GWS Users' with a sub-header 'Sweden_view view Control, Sweden'. The report is presented as a table with three columns: 'Full Name', 'Username', and 'Groups'.

Full Name	Username	Groups
Agnes Baffoe-Bonnie	abonnie	AAHPC_export AAHPC_view Finland_export Finland_view
Derek Gildea	dgildea	AAHPC_admin AAHPC_export AAHPC_import AAHPC_view Finland_admin Finland_import Finland_view Hopkins_admin Hopkins_import Hopkins_view Michigan_admin Michigan_import Michigan_view Sweden_admin Sweden_import Sweden_view
Diana Freas-Lutz	dlutz	AAHPC_import AAHPC_view Finland_import Finland_view Hopkins_import Hopkins_view Michigan_import Michigan_view

GeneLink Database Tables

Definitions of the GeneLink Database Tables

The following table defines the purpose of the database tables used in the GeneLink application:

Table 12: GeneLink Database Tables

Table Name	Definition
Allele Translations	Responsible for translating each allele for each marker. When exporting from the genotypes table in “LINKAGE” or “RelCheck” format, genotype labels are systematically recoded (1, 2, 3...) to provide properly formatted data for analysis by these programs. The allele translation table provides a key or legend linking the new “translated” score to the original genotype score. Future exports will use identical “allele translation codes.” New alleles identified after the first export will be added to the end of the allele translation, to ensure consistent recoding of alleles across exports.
Families	Each record reflects a single family included in a genetic study. The families table also stores pertinent clinical information about the family, such as number of affecteds, or number of affecteds with DNA.
Genotypes	“Final genotypes” table: Table in which final genotype data are stored. NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)
Liability Class	Stores information regarding specific liability classes to be incorporated in LINKAGE exports. Liability classes can be defined using a combination of age, sex, and affection status.
Maps	Provides the following information for markers used in a given project: location of the marker within the genome, relative order of markers along a chromosome, and the intermarker distance of adjacent markers within a chromosome. The maps database table also determines the relative order in which data are exported by chromosome. NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)
Markers	Provides information regarding microsatellite or SNP markers used in a given linkage project. Provides the panel in which the marker was run, as well as the allele size range (ASR) of the marker, dye color and genotype for a CEPH control individual (1347-02). NOTE: all marker names are capitalized on import (d9s1232 would become D9S1232)

Table 12: GeneLink Database Tables

Table Name	Definition
Pedigrees	Provides pedigree and phenotype information for each individual within a family. Two qualitative traits can be stored as Status Narrow, Status Broad.
DNA	Stores information regarding all available DNA samples in the laboratory.
Primers	Provides additional information for each specific marker, including UniSTS ID, GenBank accession number, forward primer sequence, reverse primer sequence, primer ordering information, and inventory information.
Trait Translation	Contains details for phenotypes stored in Trait Score table.
Trait Score	Stores individual values for an unlimited number of phenotypes (either qualitative or quantitative).

Structure of the GeneLink Database Tables

The structure of the GeneLink database tables are defined below. The tables identify the database name, the field name, the field constraints, and whether or not the field allows null values. Primary Keys are denoted by an asterisk (*). **Fields that are italicized and gray are database fields that are not presented to the user for entry.** Bold and underlined cells are used for “duplicate” record definition.

Table 13: Allele Translations Table

Field Name	Valid Characters(length)	Can field be null?
<i>TranslationID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>MarkerName</u>	varchar(10)	N
<u>Allele</u>	number	N
<u>Translation</u>	number	N
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 14: Families Table

Field Name	Valid Characters(length)	Can field be null?
<i>FamilyID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
Exclude	varchar(10)	Y
Site	varchar(25)	N
<u>FamID</u>	number	N
OriginalFamID	number	Y
OtherID	varchar(20)	Y
Race	varchar(5)	Y
MMTrans	varchar(5)	Y
Bilineal	varchar(5)	Y
Loops	varchar(5)	Y
Twins	varchar(5)	Y
OtherPhenotypes	varchar(100)	Y
Phase	varchar(100)	Y
Criteria	varchar(100)	Y
Comments	varchar(255)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 15: Genotypes Table

Field Name	Valid Characters(length)	Can field be null?
<i>GenotypeID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>FamIndID</u>	varchar(10)	N
<u>MarkerName</u>	varchar(10)	N
Allele1	number	Y
Allele2	number	Y
Grid	varchar(20)	Y
Lane	number	Y
Flag	varchar(20)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 16: Liability Classes Table

Field Name	Valid Characters(length)	Can field be null?
<i>Liability*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
Disease	varchar(30)	Y
<u>LiabilityClass</u>	number	N
AgeFrom	number	Y
AgeTo	number	Y
Sex	varchar(5)	Y
Affected	varchar(10)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 17: Maps Table

Field Name	Valid Characters(length)	Can field be null?
<i>MapID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>Chromosome</u>	number	N
<u>Location</u>	number(6,3)	N
DistanceFromAbove	varchar(10)	Y
MarkerName	varchar(10)	N
Heterozygosity	number(4,2)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 18: Markers Table

Field Name	Valid Characters(length)	Can field be null?
<i>MarkerID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>MarkerName</u>	varchar(10)	N
Panel	varchar(10)	Y
PreviousPanel	varchar(10)	Y
AlleleSizeRange	varchar(15)	Y
CEPH_134702	varchar(15)	Y
Chromosome	number	Y
Dye	varchar(10)	Y
Pool	number(4,1)	Y
PkHt	number	Y
Comments	varchar(255)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 19: Pedigrees Table

Field Name	Valid Characters(length)	Can field be null?
<i>PedigreeID*</i>	<i>number(18,0)</i>	<i>identity</i>
<i>ProjectID</i>	<i>number</i>	<i>N</i>
PedID	number	N
<u>FamIndID</u>	number	N
FamID	number	N
IndID	number	N
FatherID	number	N
MotherID	number	N
Sex	char(1)	N
DNA	number	N
Age	varchar(10)	N
Diagnosis	varchar(10)	Y
StatusBroad	varchar(10)	N
StatusNarrow	varchar(10)	Y
LiabilityClass	number	Y
Exclude	varchar(10)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 20: DNA Table

Field Name	Valid Characters(length)	Can field be null?
<i>ProjectID</i>	<i>number</i>	<i>N</i>
FamID	number	N
IndID	number	N
<u>FamIndID</u>	number	N
DNA_Source	varchar(25)	N
Date_Recorded	datetime	N
Tube_Label	varchar(100)	N
DNA	Y/A/P	N
<u>Prep</u>	char(5)	N
DNA_Conc	numeric(5,2)	N
Init_DNA_Vol	numeric(5,2)	N
Total_DNA_Amt	numeric(5,2)	N
Comment	varchar(255)	Y
First_Vol_DNA	numeric(5,2)	Y
Second_Vol_DNA	numeric(5,2)	Y
Third_Vol_DNA	numeric(5,2)	Y
DNA_remaining	numeric(5,2)	Y
Freezer	varchar(25)	Y
Rack	varchar(10)	Y
Box	varchar(10)	Y
Location	varchar(10)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 21: Primers Table

Field Name	Valid Characters(length)	Can field be null?
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>MarkerName</u>	varchar(25)	N
Alt_Name	varchar(25)	Y
UniSTS_ID	int	Y
GeneBank_Acc	varchar(25)	Y
Fwd_Primer_Seq	varchar(50)	Y
Rev_Primer_Seq	varchar(50)	Y
AlleleSizeRange	varchar(15)	N
Chr	int	N
Phys_Start_Pos	int	Y
Phys_Stop_Pos	int	Y
Build	varchar(25)	Y
deCode_Pos	numeric(6,2)	Y
Genethon_Pos	numeric(6,2)	Y
Marshfield_Pos	numeric(6,2)	Y
Order_Number_1	varchar(25)	N
Order_Scale_1	varchar(25)	N
Order_Date_1	varchar(25)	N
Order_Number_2	varchar(25)	Y

Table 21: Primers Table

Field Name	Valid Characters(length)	Can field be null?
Order_Scale_2	varchar(25)	Y
Order_Date_2	varchar(25)	Y
Order_Number_3	varchar(25)	Y
Order_Scale_3	varchar(25)	Y
Order_Date_3	varchar(25)	Y
Comments	varchar(255)	Y
Amount_Remain	varchar(25)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 22: Trait Translation Table

Field Name	Valid Characters(length)	Can field be null?
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>Trait ID</u>	number	N
<u>Phenotype</u>	varchar(100)	N
Comment	varchar(255)	Y
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Table 23: Trait Score Table

Field Name	Valid Characters(length)	Can field be null?
<i>ProjectID</i>	<i>number</i>	<i>N</i>
<u>FamIndID</u>	number	N
<u>Phenotype</u>	number	N
Score	varchar	N
<i>ModDate</i>	<i>datetime</i>	<i>N</i>
<i>ModBy</i>	<i>varchar(8)</i>	<i>N</i>
<i>InsertDate</i>	<i>datetime</i>	<i>N</i>

Chapter 3

Using GeneLink

Overview

This chapter highlights the general use of GeneLink, explaining how to import data and carry out quality control checks on user-analyzed data. Instructions are provided to view, format, and export data that will be analyzed using “GAS”, “LINKAGE”, and “RelCheck” computer software packages. In addition, this chapter discusses how to view status reports of your project.

Sections in This Chapter

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 - *To Change a Password, page 3-4*
- **Families, page 3-5**
 - *To Associate Groups with Families, page 3-5*
- **Selecting a Project, page 3-6**
 - *To Select a Project, page 3-6*
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 - *GeneLink Statuses, in Order of Progression, page 3-8*
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 - *To Import a Table, page 3-10*
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 - *To View the Families Table, page 3-34*
 - *To View the Genotypes Table, page 3-34*
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 - *To View the Pedigrees Table, page 3-37*
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 - *To View the Primers Table, page 3-39*
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 - *To View the Trait Score Table, page 3-40*

Login to GeneLink

To use the GeneLink application, a user must have a unique username and password. The user name and password are created when adding users from the Administration Menu. The user name and password are case sensitive.

To Login

1. Enter the URL for GeneLink in your Web browser.
2. The **LOGIN** screen displays. Enter your **USERNAME** and **PASSWORD**.



The image shows a login form titled "Please Login". It contains two input fields: "User Name:" with the text "jmurphy" and "Password:" with masked characters. Below the fields is a "Login" button with a mouse cursor pointing to it.

3. Select **LOGIN**. You are now logged into the GeneLink application.

To Change a Password

1. Login to **GENELINK**, see directions on page 3-4.
2. Select the **CHANGE PASSWORD** link on the upper right-hand corner of the **GENELINK** main page:



3. The **CHANGE YOUR PASSWORD** form displays:



The image shows a form titled "Change Your Password". It contains four input fields: "Username:" with the text "jmurphy", "Password:" with masked characters, "New Password:" with masked characters, and "New Password: (Verify)" with masked characters. Below the fields is a "Change Password" button with a mouse cursor pointing to it.

4. Enter the **USERNAME**.
5. Enter the **PASSWORD**.

6. Enter the **NEW PASSWORD**.
7. Verify the **NEW PASSWORD**.
8. Select **CHANGE PASSWORD**. A confirmation message displays:

Password Changed

Your password has been changed, and you may now access the Lab Data Management database with your new password.

Families

GeneLink users are granted access to specific families associated with a site. This section shows how to assign access to families.


To Associate Groups with Families

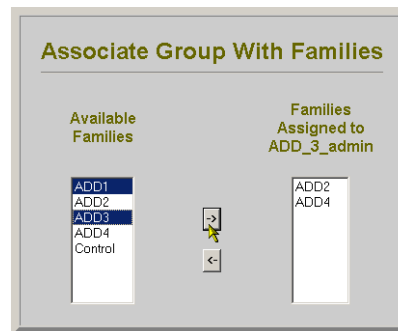
1. From the **ADMINISTRATION MENU**, select **MANAGE GROUPS**. The **MANAGE GROUP FORM** displays.
2. Select the appropriate group from the **GROUP** drop-down list.
3. Select **ASSOCIATE GROUP WITH FAMILIES** from the **ACTION** list:



The screenshot shows a web form titled "Manage Group Form". It contains two columns: "Group" and "Action". Under "Group", there is a dropdown menu with "AAHPC_admin" selected. Under "Action", there is a dropdown menu with "Associate Group With Families" selected. Below these is a "Manage Group" button with a mouse cursor pointing to it.

4. Select **MANAGE GROUP**.

- Highlight the appropriate families that you wish to associate with the group from the **AVAILABLE FAMILIES** list and move them to the **FAMILIES ASSIGNED TO “GROUP NAME”** **GROUP** list by using the right arrow :



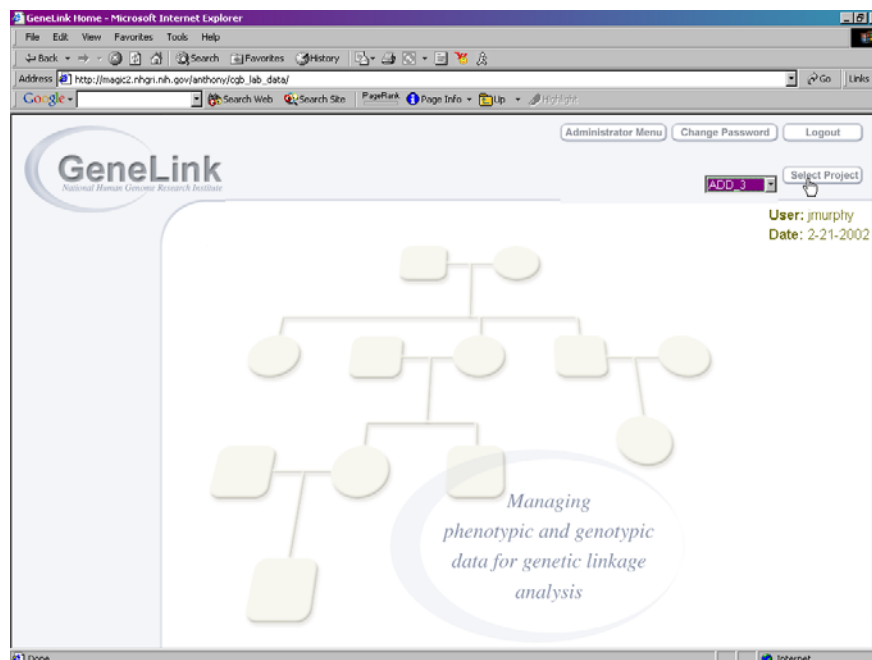
- To return to the **ADMINISTRATION MENU**, select the **ADMINISTRATOR MENU** button on the upper right-hand corner of the window.

Selecting a Project

A project is a data set containing pedigree, phenotype and genotype, and marker information for a specific linkage analysis study. This section shows how to select projects to which you have access privileges.

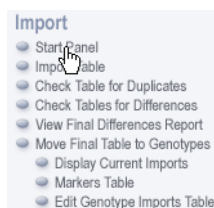
To Select a Project

- Login to **GENELINK**, see directions on page 3-4.
- The GeneLink home page displays:



3. Select a project from the drop-down list.
4. Click **SELECT PROJECT**.

Import Privilege Menu



You need the Import privilege(activity) to access this menu. The import privilege menu refers only to the process of importing genotypes into the final genotypes table via the genotype imports table. A user must have modify privileges in order to directly import, insert or modify the other tables. The user can access only the site(s) with which his/her group is associated.

Genotypes can be imported into GeneLink in three ways. First, a user may perform a “single table import” into the genotype import table. GeneLink’s import process will prompt the user to check imported table of genotypes for duplicated records. Second, as presented in detail below, two users can import double scored genotypes into the genotype imports table. Again GeneLink will prompt each user to check imported file for duplicates. Furthermore, GeneLink will also prompt users to cross-check tables for differences. Once differences have been resolved, the genotypes can be transferred (finalized) into the “final” genotypes table. The final way to import genotypes into GeneLink is to import directly into the “final” genotypes table. This import will bypass some of GeneLinks more elaborate quality control checks.

The following table identifies the changing status of the data during the progression from temporary to final data:

Table 1: GeneLink Statuses, in Order of Progression

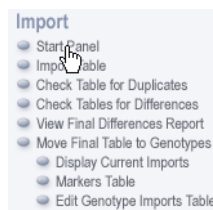
Status	Definition
Not Started	Lab work not yet started for this marker.
In Lab	Lab work in progress for this marker.
Genotypes Imported	One genotype data table is imported and is awaiting second table from another user independently analyzing data for comparison and quality checks.
Single Table Imported	One genotype table is imported and no comparison checks will be performed.
Waiting for Comparison	Two corresponding genotype tables analyzed and imported by different users are ready to be compared and quality checked for differences.
Compared and Ready	Two corresponding genotype data tables have been compared and are ready to be finalized and moved to the “final genotypes table.”

Table 1: GeneLink Statuses, in Order of Progression

Status	Definition
Ready to Finalize	When quality checks have been bypassed (using a single table import), the genotype table is ready to be moved to the “final genotypes table.”
Ready to Export	Genotypes are ready to be exported for further analysis.

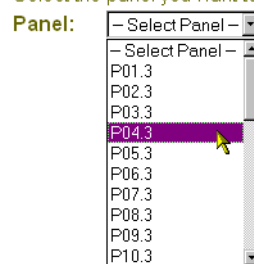
To Start a Panel (Not started -> In Lab)

1. Login to **GENELINK**.
2. Select a project from the drop-down list.
3. Click **SELECT PROJECT**. The privileges to which you have access will display on the left side of the screen.
4. Select **START PANEL** from the **IMPORT** menu:



5. Select the panel you want to start from the drop-down list (List is generated from panel field in Markers table) :

Select the panel you want to start.

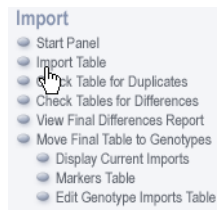


6. Select **START PANEL**. A confirmation message displays:

Panel P10.3 now has a status of "In Lab"

To Import a Table

1. Select **IMPORT TABLE** from the **IMPORT** menu:

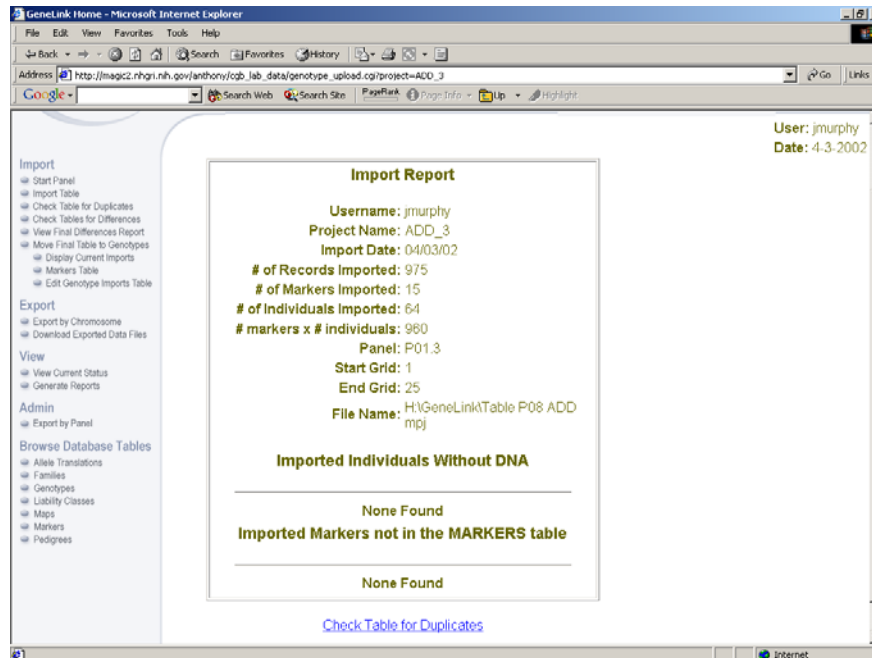


2. The **IMPORT TABLE** screen displays:

The screenshot shows the 'Import Table' screen in GeneLink. The header row is defined as: FamIndID\tMarkerName\tAllele1\tAllele2\tGrid\tLane\n. The 'Panel' dropdown is set to '- Select Panel -'. The 'Grids' are set to 1 - 25. The 'Table' text box is empty, with a 'Browse...' button next to it. The 'Skip Header Row' checkbox is checked. The 'Upload Table' button is visible. A warning box states: This is a single table import. No one else will be importing this panel for these grids, so it will not need to be compared to another import by a different user.

3. Select a **PANEL** from the drop-down list.
4. Enter the grid range in the **GRIDS** text boxes.
5. Enter the path/filename for the table in the **TABLE** text box, or click the **BROWSE** button search for the table.
6. To skip the header row upon import, select the **SKIP HEADER ROW** check box.
7. If this is a single table import and therefore will not be compared with a table imported by another user, select the **SINGLE TABLE IMPORT** check box.
8. Select **UPLOAD TABLE**.

9. The **IMPORT REPORT** displays:

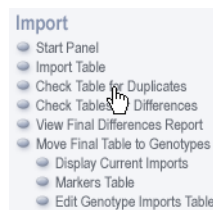


10. To print the report, select the print icon on your web browser.

11. To go to the next step in the import process, duplicate checking, select either the **CHECK TABLE FOR DUPLICATES** link on the bottom of the report, or **CHECK TABLE FOR DUPLICATES** from the **IMPORT** menu.

To Check Table for Duplicates

1. Select **CHECK TABLE FOR DUPLICATES** from the **IMPORT** menu:



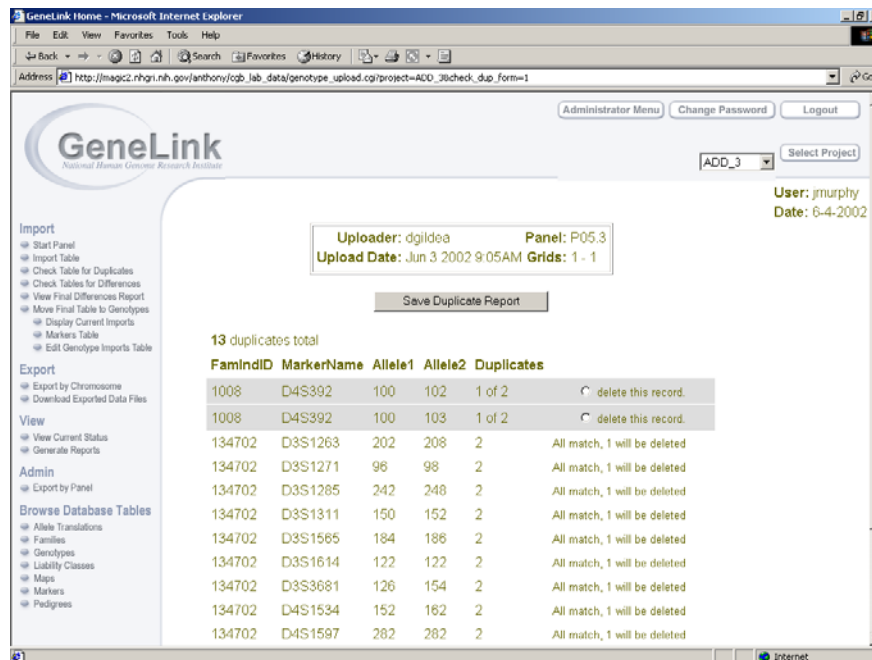
2. The check duplicate screen displays. Select the table upload from the **UPLOAD** drop-down list and click **CHECK FOR DUPLICATES**:

The following uploads still contain duplicate records.

Upload: P01.3 (1 - 25) by jmurphy on 04/01/2002

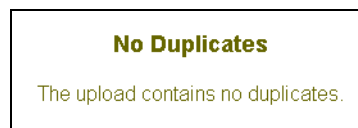


- If duplicates exist in the imported table, they will be displayed for your review:



If the duplicates are not identical, radio buttons will display next to each record, and the user will need to select the record for deletion.

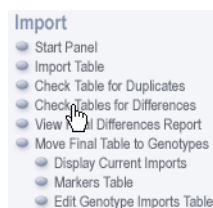
- To save the duplicate report, select **SAVE DUPLICATE REPORT**.
- To cancel the upload without editing the duplicates, select **CANCEL UPLOAD**.
- To continue with the upload and, in turn, remove the duplicates, select **CONTINUE WITH UPLOAD**. If you select this option, the duplicates are removed and a confirmation message displays:



To Check Tables for Differences

Same panel scored by 2 different users.

- Select **CHECK TABLES FOR DIFFERENCES** from the **IMPORT** menu:



- If no tables are ready for comparison, a message stating such will display.

3. Select the tables to compare from the **TABLES** drop-down list and select **COMPARE UPLOADS**.

Select Tables to Compare

Tables

4. If no differences exist, a message stating such will display.
5. If differences exist, the **IMPORT COMPARISON** displays:

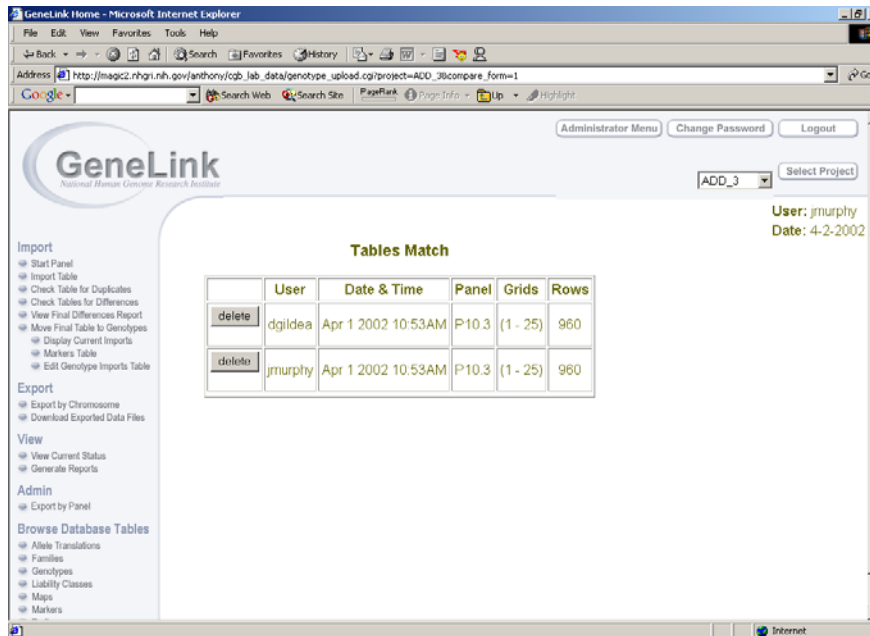
	User	Date & Time	Panel	Grids	Rows
<input type="button" value="delete"/>	dgildea	Apr 1 2002 10:53AM	P10.3	(1 - 25)	960
<input type="button" value="delete"/>	jmurphy	Apr 1 2002 10:53AM	P10.3	(1 - 25)	960

Total Differences: 6 Total Displayed: 6

Name	FamIndID	MarkerName	Allele1	Allele2	Grid	Lane	Comments
dgildea	1003	D6S262	186	186	ADD	31	<input type="button" value="Update Row"/>
jmurphy	1003	D6S262	0	0	ADD	31	<input type="button" value="Update Row"/>
dgildea	1004	D5S424	0	0	ADD	26	<input type="button" value="Update Row"/>
jmurphy	1004	D5S424	218	222	ADD	26	<input type="button" value="Update Row"/>
dgildea	1004	D6S262	0	0	ADD	25	<input type="button" value="Update Row"/>
jmurphy	1004	D6S262	187	189	ADD	26	<input type="button" value="Update Row"/>
dgildea	1006	D5S419	0	0	ADD	13	<input type="button" value="Update Row"/>
jmurphy	1006	D5S419	276	200	ADD	13	<input type="button" value="Update Row"/>
dgildea	1006	D6S281	0	0	ADD	13	<input type="button" value="Update Row"/>
jmurphy	1006	D6S281	140	144	ADD	13	<input type="button" value="Update Row"/>
dgildea	1007	D6S262	186	186	ADD	7	<input type="button" value="Update Row"/>
jmurphy	1007	D6S262	0	0	ADD	7	<input type="button" value="Update Row"/>

6. The differences are grouped in pairs. The users can now decide to make any changes as needed in the **ALLELE** text boxes as needed. **COMMENTS** can also be added.
7. When the adjustments are complete, select **UPDATE ROW**. That **GENOTYPE** is removed from the **DIFFERENCES** list.

8. When all **GENOTYPES** have been updated, **GENELINK** will advise that the tables match:



9. If needed, a **DELETE** button is made available to delete an invalid table.
10. Additionally, if differences among two tables exist, an e-mail will be sent to the two users who imported the tables advising that the tables have been compared and genotypes must be reviewed. An e-mail is also sent to both users when the tables match:

From: genelink@nhgri.nih.gov [SMTP:genelink@nhgri.nih.gov]
To: dgildea@nhgri.nih.gov, Murphy, Juliane (NHGRI)
Cc:
Subject: Tables are ready to be compared
Sent: 4/1/2002 10:54 AM

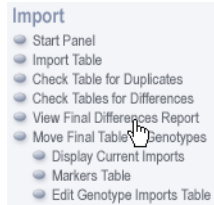
The following conflicts were found between these tables after each import was checked for duplicates.

Project	Username	Panel	Start	End	Date
ADD_3	dgildea	P10.3	1	25	04/01/2002
ADD_3	jmurphy	P10.3	1	25	04/01/2002

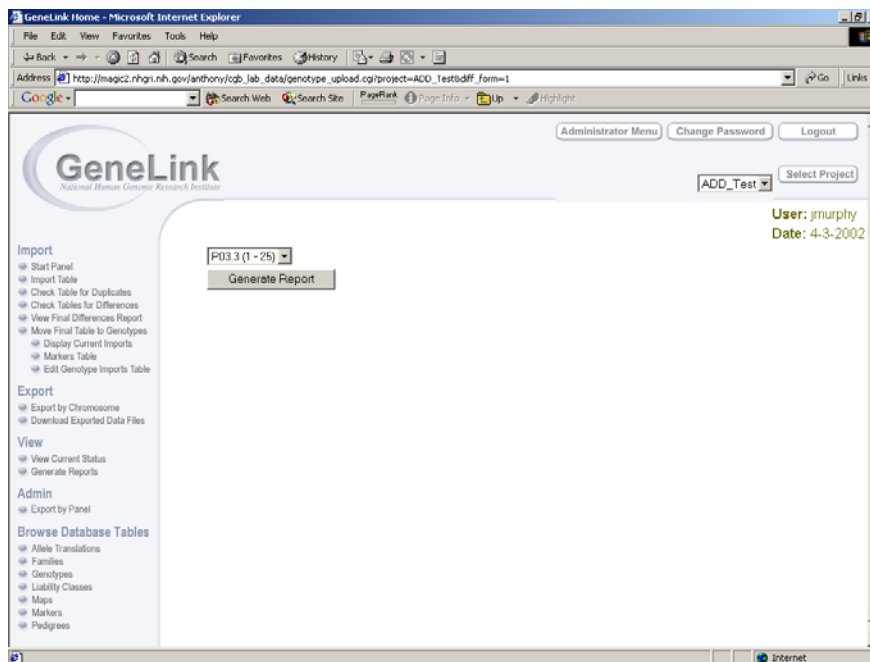
IndID	Marker	Grid	Lane	dgildea	jmurphy
1003	D6S262	ADD	31	186	186
1004	D5S424	ADD	25	0	218
1004	D6S262	ADD	25	0	187
1006	D5S419	ADD	13	0	276
1006	D6S281	ADD	13	0	140
1007	D6S262	ADD	7	186	186

To View the Final Differences Report

1. After differences are resolved, a final differences report is generated, showing changes, which have been made to the data. To view a Final Differences Report Select **VIEW FINAL DIFFERENCES REPORT** from the **IMPORT** menu:



2. Select an import from the drop-down list:



3. Select **GENERATE REPORT**.
4. The **DIFFERENCES REPORT** displays:

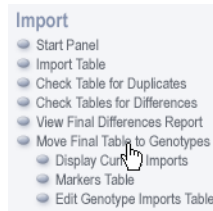
Differences Report

Panel: P03.3

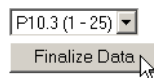
FamIndID	MarkerName	Grid	jmurphy	old	final	Comments
1010	D3S1267	ADD	116 128	0 0	116 128	
1026	D3S3726	ADD	99 103	0 0	99 103	
2043	D3S1289	ADD	212 220	0 0	212 220	

To Move Final Table to Genotypes (Finalize Table)

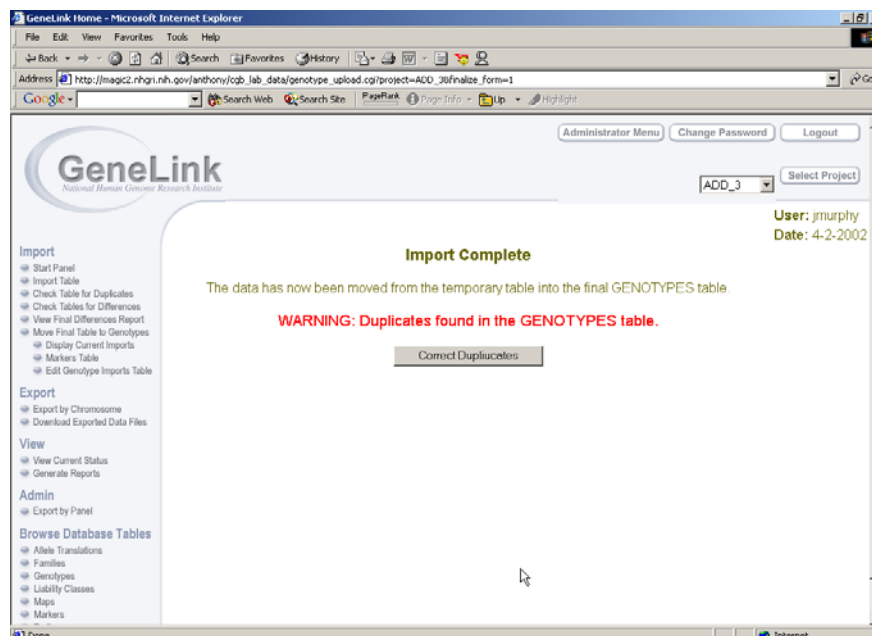
1. To finalize your table(s), select **MOVE FINAL TABLE TO GENOTYPES** from the **IMPORT** menu:



2. The tables ready to be finalized display. Select the table from the drop-down list and click **FINALIZE DATA**:



3. If **GENELINK** is unable to finalize the data, a notification will display and **GENELINK** will allow you to correct the problem. Please note that in the example below, the data already exists in the final table. The data was reuploaded and **GENELINK** forces you to conduct a duplicate check to ensure that only one copy of the genotype data is stored in the database: **Duplicate records have the same FamIndID and Marker.** A “R flag” could be used to mark a “replaced” DNA sample. Before eliminating the original genotypes (marked with a “R flag”) one could compare new genotypes to the old as they are not seen as duplicate records. Records with an “R flag” are excluded from the duplicates check.

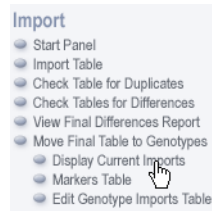


4. If no problems exist, or once the problems are resolved, the data will be finalized. If you attempt to select the table again from the **MOVE FINAL TABLE TO GENOTYPES** option, the table will no longer be available for selection:

No tables to finalize at this time.

To Display Current Imports

1. To display imported tables that have not yet been finalized, select **DISPLAY CURRENT IMPORTS** from the **IMPORT** menu:

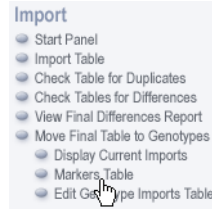


2. A table identifies the imported data that has not been finalized, by **PANEL**, **START GRID** number, **END GRID** number, **USER**, **DATE**, and **STATUS** for the data (for a list of Statuses, see the GeneLink Statuses Table, page 3-8):

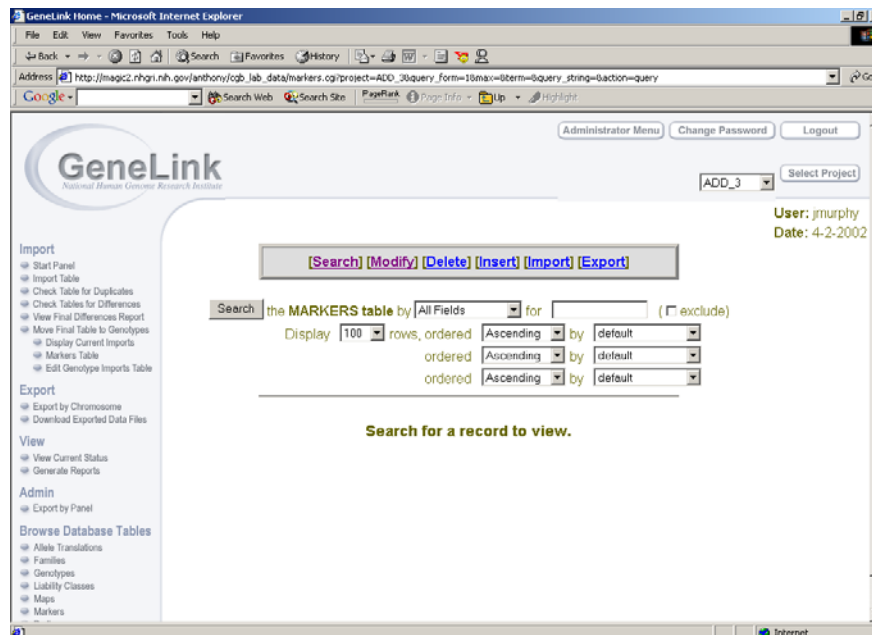
	Panel	Start Grid	End Grid	User	Date	Status
<input type="button" value="delete"/>	P01.3	1	1	dgildea	02/20/2002	Genotypes Imported
<input type="button" value="delete"/>	P22.3	1	1	old	03/19/2002	Genotypes Imported

To View the Markers Table

1. Select **MARKERS TABLE** from the **IMPORT** menu:

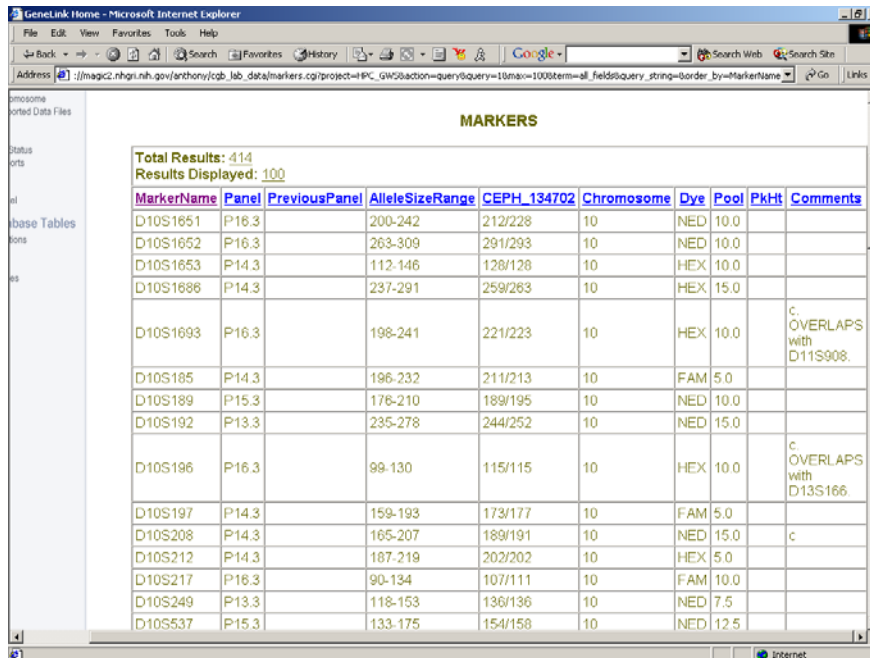


- Depending upon your privileges, the **SEARCH**, **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, and **EXPORT** options will be available for selection. **SEARCH** is selected by default:



- To **SEARCH**, select a field from the drop-down list.
- Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
- Select the number of display rows from the drop-down list.
- Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
- Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **MARKERNAME**, **ASCENDING** by **DYE**, and **ASCENDING** by **PANEL**, the results will display in ascending order according to the following fields, in order of priority: **MARKERNAME**, **DYE**, and **PANEL**.
- Select the **SEARCH** button.

9. The results display in table format:



GeneLink Home - Microsoft Internet Explorer

Address: http://magic2.nhgri.nih.gov/anthony/cb_data/markers.cgi?project=IPC_gw&action=query&query=10&max=100&term=all_fields&query_string=border_by=MarkerName

MARKERS

Total Results: 414
Results Displayed: 100

MarkerName	Panel	PreviousPanel	AlleleSizeRange	CEPH_134702	Chromosome	Dye	Pool	PkHt	Comments
D10S1651	P16.3		200-242	212/228	10	NED	10.0		
D10S1652	P16.3		263-309	291/293	10	NED	10.0		
D10S1653	P14.3		112-146	128/128	10	HEX	10.0		
D10S1686	P14.3		237-291	259/263	10	HEX	15.0		
D10S1693	P16.3		198-241	221/223	10	HEX	10.0		c OVERLAPS with D11S908.
D10S185	P14.3		196-232	211/213	10	FAM	5.0		
D10S189	P15.3		176-210	189/195	10	NED	10.0		
D10S192	P13.3		235-278	244/252	10	NED	15.0		
D10S196	P16.3		99-130	115/115	10	HEX	10.0		c OVERLAPS with D13S166.
D10S197	P14.3		159-193	173/177	10	FAM	5.0		
D10S208	P14.3		165-207	189/191	10	NED	15.0		c
D10S212	P14.3		187-219	202/202	10	HEX	5.0		
D10S217	P16.3		90-134	107/111	10	FAM	10.0		
D10S249	P13.3		118-153	136/136	10	NED	7.5		
D10S537	P15.3		133-175	154/158	10	NED	12.5		

10. The query is located on the top of the screen for editing, if necessary.

11. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **MARKERNAME**, but now you want the data to display in ascending order by **DYE**, select the column header **DYE** to sort the data. Select the column header again to sort in descending order.

12. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:

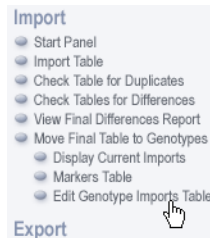


13. Follow steps 3-11 to continue with the selected action.

To Edit the Genotype Imports Table

***NOTE: THESE STEPS ARE USEFUL IF THE USER WOULD LIKE TO MAKE CHANGES AT ANY TIME AFTER COMPARISON, BUT PRIOR TO FINALIZING THE TABLE.**

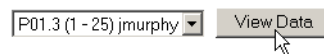
1. Select **EDIT GENOTYPE IMPORTS TABLE** from the **IMPORTS** menu:



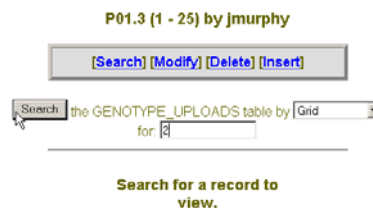
2. If there are no uploads to edit, the following message will display:

There are no Uploads to View/Edit at this time

3. If there are uploads available for editing, select the upload from the drop-down list and click **VIEW DATA**:



4. The following screen displays. Please note that the actions listed are dependent upon your group's privileges:



5. To search for a record to view, select an item from the drop-down list and enter your search information in the **FOR** text box.
6. Select **SEARCH**.
7. To **MODIFY**, **DELETE**, or **INSERT** a record, select the appropriate action. Select an item from the drop-down list and enter the search information in the **FOR** text box. Select **SEARCH**.
8. To **MODIFY** or **DELETE** a record, the table will display with a **MODIFY** button or **DELETE** button before each record. Select the **MODIFY** or **DELETE** button for the record you wish to perform such action:

	GenotypeUploadID	FamIndID	MarkerName	Allele1	Allele2	Grid	Lane	Flag	Comment
<input type="button" value="modify"/>		1008	D4S392	100	102	ADD	1		
<input type="button" value="delete"/>		1008	D4S392	100	102	ADD	1		

9. If records are available, they will be displayed in a tabular format:

FamIndID	MarkerName	Allele1	Allele2	Grid	Lane	Flag	Comment
1008	D4S392	100	102	ADD	1		
1008	D3S1311	140	158	ADD	1		
1008	D3S1585	188	198	ADD	1		
1008	D4S406	260	264	ADD	1		
1008	D3S1271	98	100	ADD	1		
1008	D3S3881	158	158	ADD	1		
1008	D4S405	291	297	ADD	1		
1008	D3S1614	116	124	ADD	1		
1008	D4S1534	152	160	ADD	1		
1008	D3S1263	194	200	ADD	1		
1008	D3S1285	240	240	ADD	1		
1008	D4S1597	282	288	ADD	1		
2054	D4S392	102	106	ADD	2		
2054	D3S1311	140	140	ADD	2		
2054	D3S1585	182	190	ADD	2		
2054	D4S406	252	262	ADD	2		
2054	D3S1271	97	98	ADD	2		
2054	D3S3881	158	158	ADD	2		
2054	D4S405	295	303	ADD	2		
2054	D3S1614	116	124	ADD	2		

10. To sort the data, click on the column header once for ascending order, twice for descending order.

11. To insert a record, select the **INSERT** button. The **INSERT A RECORD SCREEN** displays:

P01.3 (1 - 25) by jmurphy

[Search]
[Modify]
[Delete]
[Insert]

FamIndID: MarkerName:

Allele1: Allele2:

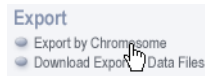
Grid: Lane:

Flag: Comment:

12. Enter the record data in the text boxes and select **INSERT RECORD**. To clear the information without inserting, select the **RESET** button.

13. All actions display a confirmation message.

Export Privilege Menu



The Export Privilege Menu allows you to retrieve data from GeneLink for further analysis. Exported data can be formatted for analysis in GAS, LINKAGE, or RelCheck computer software programs. Allele translations are performed at this stage as needed. Pedigree and phenotype data are also incorporated into these exports.

Data can be exported in three ways: First using the **EXPORT BY CHROMOSOME** menu link, a user with export privileges can export site-specific data by chromosome. Second, family specific data can be exported by chromosome using the “Export these families” button which appears with the families table (post search). Data for a given chromosome can only be exported once every individual with DNA equal to Y in the pedigrees table (for a given site) has a genotype for every marker on a chromosome specified in the markers table. Additionally, map location, which provides the order of the markers for export, must be in the Maps table. GeneLink does allow for three exceptions to this rule. First different markers may be typed for different sites by using the **DROPPED MARKERS** function. Second, an individual can be excluded from exports if the exclude field in the pedigrees table is Y. Finally a family can be excluded from exports if the exclude field in the families table is Y

Finally a user with admin privileges can also export files by Panel. This is done using the **EXPORT BY PANEL** link under the Admin menu. For more details: , page 3-31.

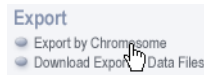
The export genotype data screen, from the **EXPORT BY CHROMOSOME** menu link prompts users to specify which chromosome to export, which trait(s) to export, how to define liability classes if necessary, what file format is desired and which families to include in the export.

NOTE: Liability class information can be stored or determined in GeneLink in two ways. First each individual’s liability class can be specifically stored in the pedigrees table (*LiabilityClass* field). These liability classes (stored in the pedigrees table) are determined outside of GeneLink by the user and could be based on any number of variables. Alternatively, Liability class definitions, which are based on age, gender and affection status can be stored in the liability classes table. Using the Liability_Classes table means that each individual’s liability class is dynamically determined (based on their age, gender and affection status specified in the pedigrees table) at the time of each export. NOTE: Only a single qualitative trait (either *StatusBroad* or *Status Narrow*) can be exported when Liability classes are defined using the “Liability_classes table”. Furthermore in the Liability_Classes table the “affection” field refers to either *StatusBroad* or *Status Narrow* depending on which field was selected for export.

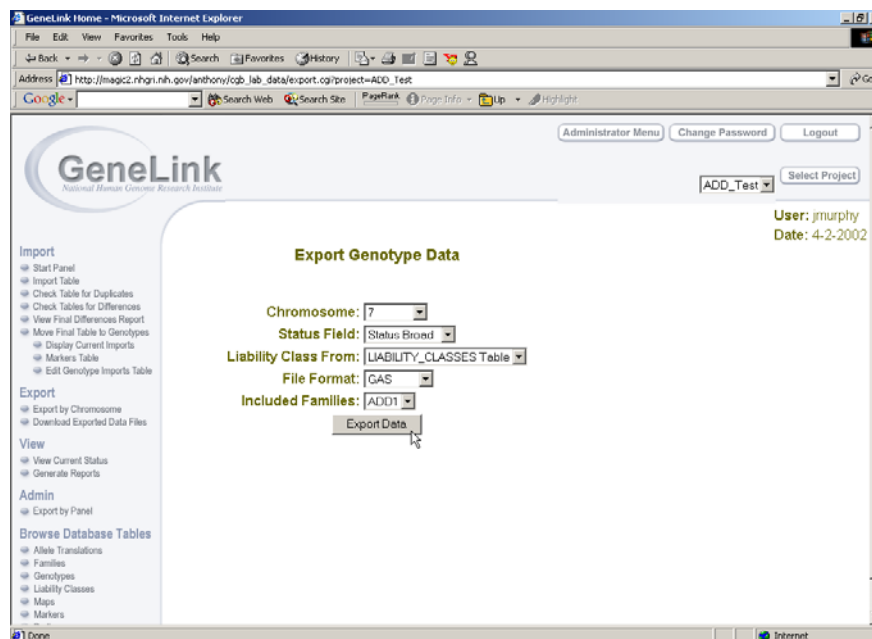
NOTE: ALL DATA FLAGGED WITH A T OR R (T OR R PRESENT IN THE FLAG FIELD) ARE NOT INCLUDED IN CHROMOSOME OR PANEL SPECIFIC GAS AND LINKAGE EXPORTS. RELCHECK FILES DO INCLUDE T (TEMPORARILY DROPPED) GENOTYPES, WHICH MAY HAVE BEEN REMOVED TO ELIMINATE INCONSISTENCIES BUT SHOULD BE INCLUDED WHEN TRYING TO EVALUATE PUTATIVE RELATIONSHIPS.

To Export by Chromosome

1. Select **EXPORT BY CHROMOSOME** from the **EXPORT** menu. (Or Search Families table and select “Export these families”.)



2. The **EXPORT BY CHROMOSOME** screen displays:



3. Select a **CHROMOSOME** from the drop-down list.
4. Select a **PHENOTYPE** (Status Field) by highlighting the Phenotype name and hitting the right arrow. The order in which phenotypes are exported is determined by the order in which they were selected (right-hand list).

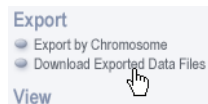
Two qualitative definitions of affection status can be stored (**STATUS BROAD** and **STATUS NARROW**) in the pedigrees table. Additional qualitative or quantitative traits can be stored in the Trait score table.

5. Select from where the **LIABILITY CLASS** is derived from the drop-down list.
6. Select the **FILE FORMAT** from the drop-down list. **GAS**, **LINKAGE**, **RELCHECK**.
7. Select the **INCLUDED FAMILIES** from the drop-down list.
8. Select **EXPORT DATA**.

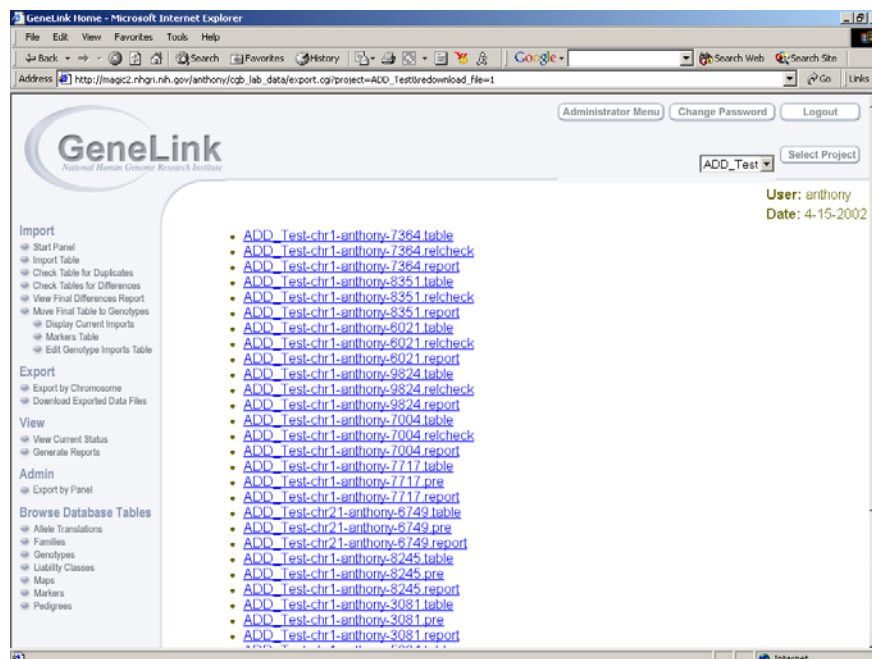
9. A export report displays when the export is successful. If there is an error with the export, an error report will display. Export reports can be downloaded at any time.
10. Exports are given file names, which incorporate project name, chromosome exported, user who exported data, and a 4 digit random number. This naming convention was designed to facilitate file management.

To Download Exported Data Files

1. Select **DOWNLOAD EXPORTED DATA FILES** from the **EXPORT** menu:



2. A list of exported data files displays:



- Select a data file hyperlink. The example below depicts what would happen when a “.report” data file was selected and displays the Export Report:

EXPORT REPORT

GENERATED BY: anthony
 PROJECT: ADD_Test
 CHROMOSOME: 1
 STATUS FIELD: broad
 LIABILITY CLASS: liability_class

LIABILITY CLASS TABLE

Disease	Class	AgeFrom	AgeTo	Sex	Affected
add	1	0	100	m	120
add	2	0	10	f	12
add	3	11	20	f	12
add	4	21	30	f	12
add	5	31	40	f	12
add	6	41	50	f	12
add	7	51	60	f	12
add	8	61	70	f	12
add	9	71	80	f	12
add	10	81	90	f	12
add	11	91	100	f	12
add	12	0	100	f	0

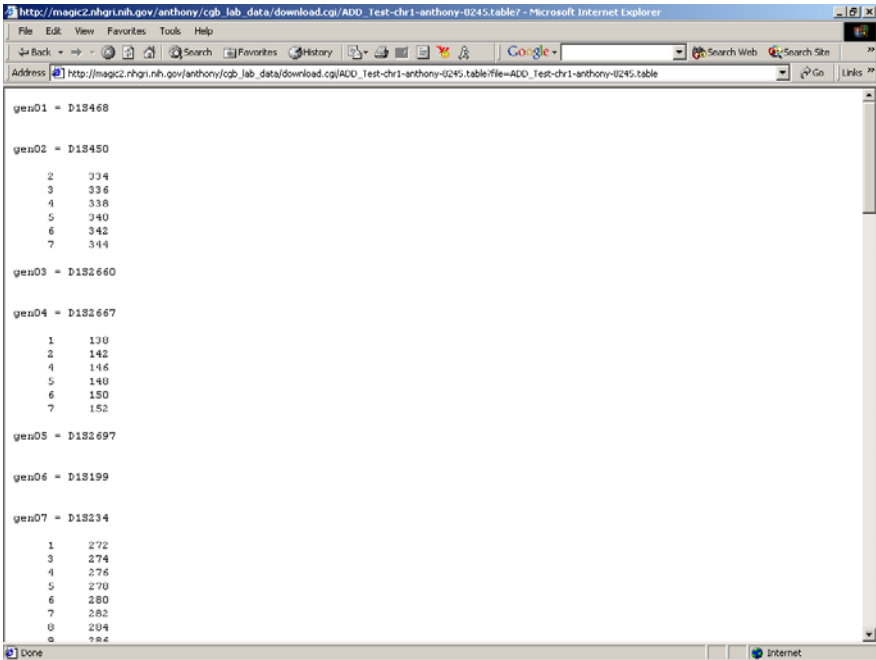
FILE FORMAT: linkage
 INCLUDED FAMILIES: all
 DISTANCES: 10.5 5 3.0 14.4 7.4 0.6 11.7 7.0 11.1 9.2 11.5 7.5 20.4 12.3 5 5.4 14.4 7.4 4.2 0.6 0.1 9.0 0.0 11.5 10.5

TOTAL INDIVIDUALS IN EXPORTED FAMILIES: 64
 TOTAL INDIVIDUALS EXPORTED: 64
 INDIVIDUALS EXCLUDED:
 MARKERS: D18468, D18450, D182660, D182667, D182697, D18199, D18234, D18255, D182713, D182890, D18230, D182841, D182842
 FAMILIES: 1

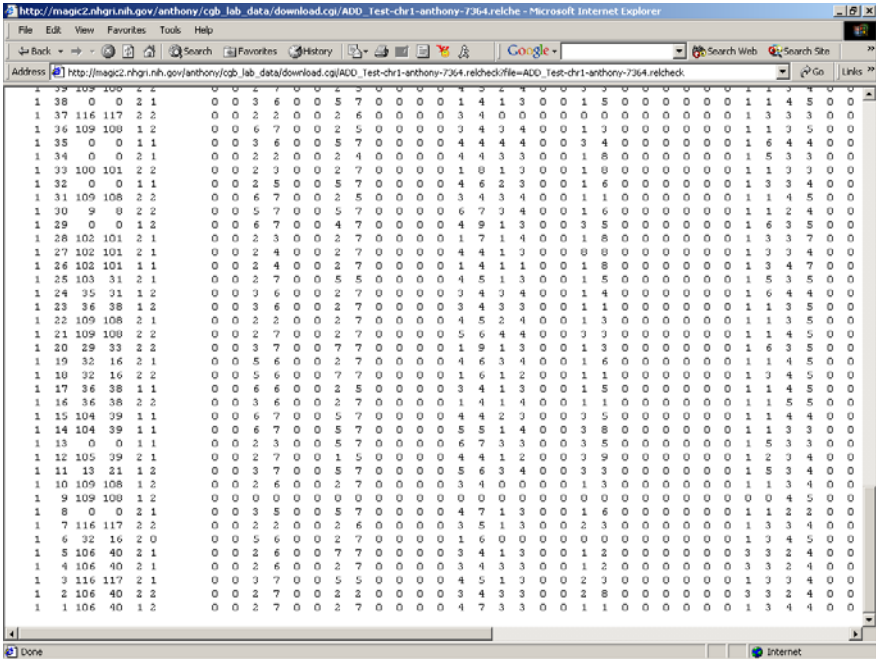
- If a “.pre” data file was selected, the following screen will display:

	gen01	gen02	gen03	gen04	gen05	gen06	gen07	gen08	gen09	gen10	gen11	gen12	gen13	gen14	gen15	gen16
1	123	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0
1	122	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0
1	121	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	120	122	123	2	2	2	0	0	0	0	0	0	0	0	0	0
1	119	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	118	122	123	2	2	2	0	0	0	0	0	0	0	0	0	0
1	117	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0
1	116	121	120	1	2	1	0	0	0	0	0	0	0	0	0	0
1	115	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	114	121	120	2	2	2	0	0	0	0	0	0	0	0	0	0
1	113	119	119	1	2	1	0	0	0	0	0	0	0	0	0	0
1	112	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0
1	111	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0
1	110	115	114	1	2	1	0	0	0	0	0	0	0	0	0	0
1	109	115	114	1	2	1	0	0	0	0	0	0	0	0	0	0
1	108	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0
1	107	113	112	1	2	1	0	0	0	0	0	0	0	0	0	0
1	106	110	111	1	2	1	0	0	0	0	0	0	0	0	0	0
1	105	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	104	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	103	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	102	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	101	107	34	2	2	2	0	0	0	0	0	0	0	0	0	0
1	100	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
1	40	0	0	2	1	9	0	0	2	7	0	0	0	0	0	0
1	39	109	108	2	2	0	0	0	2	7	0	0	0	0	0	0
1	38	0	0	2	1	8	0	0	3	6	0	0	0	0	0	0
1	37	116	117	2	2	10	0	0	2	2	0	0	0	0	0	0
1	36	109	108	1	2	1	0	0	6	7	0	0	0	0	0	0
1	35	0	0	1	1	1	0	0	3	6	0	0	0	0	0	0
1	34	0	0	2	1	10	0	0	2	2	0	0	0	0	0	0
1	33	100	101	2	2	6	0	0	2	3	0	0	0	0	0	0
1	32	0	0	1	1	1	0	0	2	5	0	0	0	0	0	0
1	31	109	108	2	2	9	0	0	6	7	0	0	0	0	0	0
1	30	9	8	2	2	4	0	0	5	7	0	0	0	0	0	0
1	29	0	0	1	2	1	0	0	6	7	0	0	0	0	0	0
1	28	102	101	2	1	5	0	0	2	3	0	0	0	0	0	0
1	27	102	101	2	1	5	0	0	2	3	0	0	0	0	0	0

5. If a “.table” data file was selected, the following screen will display:



6. If a “.relcheck” data file was selected, the following screen will display.:



7. You can save any of the data files through the browser **SAVE** function.

View Privilege Menu



The View Privilege Menu allows a user to **BROWSE DATABASE TABLES**. It also contains functions that allow the user to **VIEW CURRENT STATUS** and **GENERATE REPORTS**.

VIEW CURRENT STATUS shows the current state of the genotype data entry process for all markers used in your genome scan. The status is particularly important as it determines when a chromosome is “ready for export”. All markers on a given chromosome must have data in the database before the chromosome can be exported for analyses.

NOTE: STATUS IS TRACKED BY SITE.

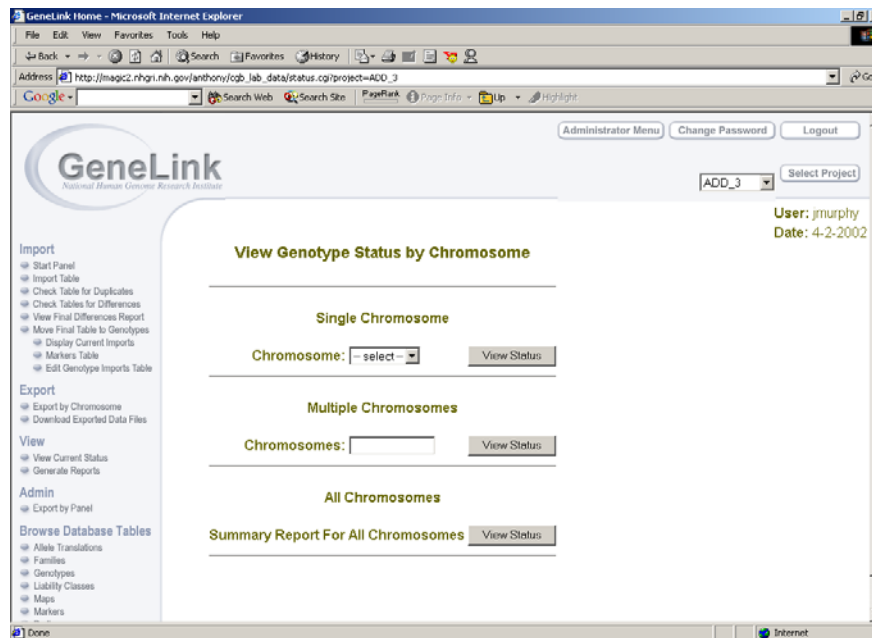
The **GENERATE REPORTS** function allows you to create summaries showing various characteristics of the markers, individuals, or families used in your study. The **GENERATE REPORTS** function also allows users to view or modify genotype data which can be searched for by combinations of 1) family and marker, 2) famInd and marker, 3) site and marker, 4) family and panel and 5) FamIndID and panel.

To View the Current Status

1. Select **VIEW CURRENT STATUS** from the **VIEW** menu:



2. The **VIEW GENOTYPE STATUS BY CHROMOSOME** screen displays:

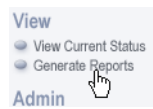


- To view a **SINGLE CHROMOSOME**, select a number from the **CHROMOSOME** drop-down list (available chromosomes come from the maps table) and click **VIEW STATUS**.
- To view **MULTIPLE CHROMOSOMES**, enter the numbers in the **CHROMOSOMES** text box, separated by commas.
- To view a **SUMMARY REPORT FOR ALL CHROMOSOMES**, select **VIEW STATUS**.
- The status report for the chromosome(s) selected displays. Note that the status is defined by site:

Chromosome	Marker Name	Panel	Location	Distance Cm	ADD1	ADD2	ADD3	ADD4	Control
1	D1S468	P02.3	1.000		Ready to Export	Ready to Export	Ready to Export	Not Started	Not Started
1	D1S2660	P31.3	2.000	5	Ready to Export	Ready to Export	Ready to Export	Not Started	Not Started
1	D1S450	P01.3	2.500	10.5	Ready to Export	Ready to Export	Ready to Export	In Lab	In Lab
1	D1S2667	P01.3	4.000	3.8	Ready to Export	Ready to Export	Ready to Export	In Lab	In Lab
1	D1S2697	P02.3	5.000	14.4	Ready to Export	Ready to Export	Ready to Export	Not Started	Not Started

To Generate Quality Control Reports

1. Select **GENERATE REPORTS** from the **VIEW** menu:



2. To view the **MARKER SUMMARY** report, enter the **MARKERNAME** and click **GENERATE REPORT**.

The asterisk “*” can be used as a wildcard in your search. For example, “9*” would return all Markers that begin with the number 9.

3. To view the **INDIVIDUAL SUMMARY** report, enter the **INDIVIDUALID** and click **GENERATE REPORT**.

The asterisk “*” can be used as a wildcard in your search. For example, “9*” would return all IDs that begin with the number 9.

4. To view the **FAMILY SUMMARY** report, enter the **FAMILYID** and click **GENERATE REPORT**.

The asterisk “*” can be used as a wildcard in your search. For example, “9*” would return all IDs that begin with the number 9.

5. The report displays:

 A screenshot of a web browser displaying the GeneLink Family Summary report. The browser title is 'GeneLink Home - Microsoft Internet Explorer'. The address bar shows 'http://mag2.nhgr.nih.gov/anthony/cqb_lab_data/reports.cgi?project=ADD_Test'. The page header includes 'GeneLink National Human Genome Research Institute', 'Administrator Menu', 'Change Password', 'Logout', and 'Select Project' (ADD_Test). The user is identified as 'User: jmurphy' and the date is 'Date: 4-15-2002'. The main content area is titled 'Family Summary' and includes a 'Download This Report' button. Below the title is a table with the following data:

FamilyID	Site	Individuals we Have DNA for	Affected Individuals	Affected and Have DNA	Average Age of Affected Individuals	Average Age of Affected Individuals With DNA
2	ADD2	23/92	7	6	34.71	40.50

 The left sidebar contains navigation links for Import, Export, View, Admin, and Browse Database Tables.

Admin Privilege Menu

EXPORT BY PANEL

MANAGE DROPPED MARKERS

TABLE HISTORIES

The Admin Privilege Menu allows users who have administrative privileges to export data for markers grouped by panel (**EXPORT BY PANEL**). Exported data can be formatted for analysis in GAS, LINKAGE, or RelCheck computer software programs. This function has been chosen as an administrator-only privilege because it allows for the export of data prior to having the genotyping process complete for a given chromosome.

The admin menu also provides a user access to **MANAGE DROPPED MARKERS** and **TABLE HISTORIES**.

MANAGE DROPPED MARKERS was designed to account for multi-site projects in which markers genotyped per site are not identical. In this scenario a marker could be indicated as “dropped” for one site, which would eliminate GeneLink’s search for data for this marker prior to export.

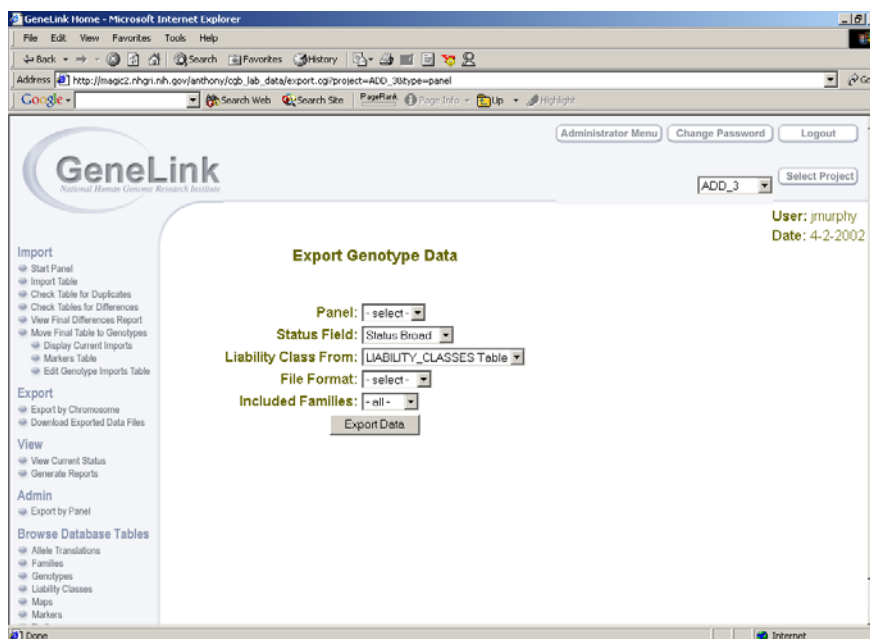
TABLE HISTORIES provides an easy way to view all changes made to the families, genotypes and pedigrees tables. All changes to the data are time stamped, thus allowing a log to be maintained of all changes.

To Export by Panel

1. Select **EXPORT BY PANEL** from the **ADMIN** menu:



- The **EXPORT GENOTYPE DATA** screen displays:



- Select a **PANEL** from the drop-down list.
- Select a **STATUS FIELD** from the drop-down list.

Two definitions of affection status can be stored. For example, **STATUS BROAD** and **STATUS NARROW**. Status Broad is defined by the following categories: 0=unknown, 1=unaffected, and 2=affected. Status Narrow is defined by the following categories: 0=unknown and 2=affected. If you have a genotype marked unaffected Status Broad (1), the genotype will be marked as unknown (0) in Status Narrow.

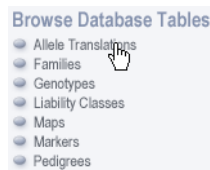
- Select the from where the **LIABILITY CLASS** is derived from the drop-down list.
- Select the **FILE FORMAT** from the drop-down list, **GAS**, **LINKAGE**, **RELCHECK**.
- Select the **INCLUDED FAMILIES** from the drop-down list.
- Select **EXPORT DATA**.
- A confirmation message displays when the export is successful. If there is an error with the export, an error report will display.

Browse Database Tables Menu

The functions found within this menu provide users with the approved privileges to view or manipulate data stored in the following tables: Allele Translations, Families, Genotypes, Liability Classes, Maps, Markers, Pedigrees, DNA, Primers, Trait translation, and Trait score.. See the Definitions of GeneLink Database Tables, page 1-6 for information on what is stored in each table.

To View the Allele Translations Table

1. Select Allele Translations from the Browse Database Tables menu:



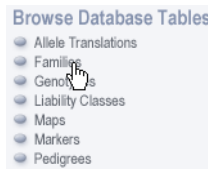
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **MARKERNAME**, **ASCENDING** by **ALLELE**, and **ASCENDING** by **TRANSLATION**, the results will display in ascending order according to the following fields, in order of priority: **MARKERNAME**, **ALLELE**, and **TRANSLATION**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **MARKERNAME**, but now you want the data to display in ascending order by **ALLELE**, select the column header **ALLELE** to sort the data. Select the column header again to sort in descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the Families Table

1. Select Families from the Browse Database Tables menu:



2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **EXCLUDE**, **ASCENDING** by **RACE**, and **ASCENDING** by **LOOPS**, the results will display in ascending order according to the following fields, in order of priority: **EXCLUDE**, **RACE**, and **LOOPS**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **RACE**, but now you want the data to display in ascending order by **LOOPS**, select the column header **LOOPS** to sort the data. Select the column header again to sort in descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the Genotypes Table

1. Select Genotypes from the Browse Database Tables menu:



2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.

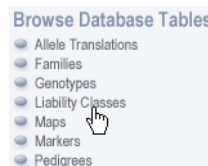
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **MARKERNAME**, **ASCENDING** by **GRID**, and **ASCENDING** by **LANE**, the results will display in ascending order according to the following fields, in order of priority: **MARKERNAME**, **GRID**, and **LANE**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **MARKERNAME**, but now you want the data to display in ascending order by **LANE**, select the column header **LANE** to sort the data. Select the column header again to sort in descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the Liability Classes Table

1. Select Liability Classes from the Browse Database Tables menu:



2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **DISEASE**, **ASCENDING** by **AGEFROM**, and **ASCENDING** by **AGETO**, the results will display in ascending order according to the following fields, in order of priority: **DISEASE**, **AGEFROM**, and **AGETO**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to

display the data in ascending order by **AGEFROM**, but now you want the data to display in ascending order by **DISEASE**, select the column header **DISEASE** to sort the data. Select the column header again to sort in descending order.

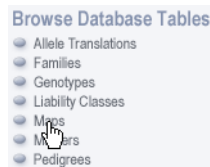
- To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



- Follow steps 3-9 to continue with the selected action.

To View the Maps Table

- Select Maps from the Browse Database Tables menu:



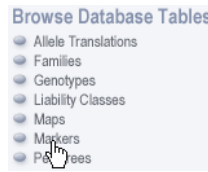
- To **SEARCH**, select a field from the drop-down list.
- Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
- Select the number of display rows from the drop-down list.
- Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
- Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **CHROMOSOME**, **ASCENDING** by **LOCATION**, and **ASCENDING** by **MARKERNAME**, the results will display in ascending order according to the following fields, in order of priority: **CHROMOSOME**, **LOCATION**, and **MARKERNAME**.
- Select the **SEARCH** button. The results display in table format.
- The query is located on the top of the screen for editing, if necessary.
- To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **MARKERNAME**, but now you want the data to display in ascending order by **CHROMOSOME**, select the column header **CHROMOSOME** to sort the data. Select the column header again to sort in descending order.
- To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



- Follow steps 3-9 to continue with the selected action.

To View the Markers Table

1. Select Markers from the Browse Database Tables menu:



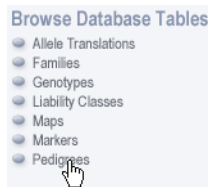
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **MARKERNAME**, **ASCENDING** by **DYE**, and **ASCENDING** by **POOL**, the results will display in ascending order according to the following fields, in order of priority: **MARKERNAME**, **DYE**, and **POOL**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **DYE**, but now you want the data to display in ascending order by **POOL**, select the column header **POOL** to sort the data. Select the column header again to sort in descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the Pedigrees Table

1. Select Pedigrees from the Browse Database Tables menu:



2. To **SEARCH**, select a field from the drop-down list.

3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **PEDID**, **ASCENDING** by **INDID**, and **ASCENDING** by **AGE**, the results will display in ascending order according to the following fields, in order of priority: **PEDID**, **INDID**, and **AGE**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. For example, if your original query stated to display the data in ascending order by **AGE**, but now you want the data to display in ascending order by **PEDID**, select the column header **PEDID** to sort the data. Select the column header again to sort in descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the DNA Table

1. Select DNA from the Browse Database Tables menu:
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **DNA_SOURCE**, **ASCENDING** by **FAMINDID**, and **ASCENDING** by **PREP**, the results will display in ascending order according to the following fields, in order of priority: **DNA_SOURCE**, **FAMINDID**, and **PREP**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order.

10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



11. Follow steps 3-9 to continue with the selected action.

To View the Primers Table

1. Select DNA from the Browse Database Tables menu:
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **CHR**, and **ASCENDING** by **PHYS_START_POSITION**, the results will display in ascending order according to the following fields, in order of priority: **CHR**, and **PHYS_START_POSITION**.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



Follow steps 3-9 to continue with the selected action.

To View the Trait Translation Table

1. Select DNA from the Browse Database Tables menu:
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **PHENOTPYE**, the results will display in ascending order accordingly.

7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



Follow steps 3-9 to continue with the selected action.

To View the Trait Score Table

1. Select DNA from the Browse Database Tables menu:
2. To **SEARCH**, select a field from the drop-down list.
3. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the **EXCLUDE** check box.
4. Select the number of display rows from the drop-down list.
5. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
6. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **TT_ID**, the results will display in ascending order accordingly.
7. Select the **SEARCH** button. The results display in table format.
8. The query is located on the top of the screen for editing, if necessary.
9. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order.
10. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link. For example, **DELETE**:



Follow steps 3-9 to continue with the selected action.