2014

CIAT

CWR Diversity

[CWR QUERIES]

CWR Inventory

Tables, short description

- **Species:** Contain taxonomic information about species and its taxon identification to join with other tables.
- **Concepts:** Has the relation between the gene pool and his associated species.
- **Distribution:** Contain geographic distribution for the species
- **Breeding_data:** Contain information about species breeding
- **Breeding_ref:** Has information about breeding reference used in the inventory
- **Institutions:** This table has information about herbaria and its location

Note: All the joins between the tables must be done using taxon id

Main Fields Explanation

Species	
Taxon_ID	Unique identification for the specie, used in the joins between the tables
Valid_Taxon_ID	When the Taxon ID and the Valid Taxon ID is the same the specie is considered valid otherwise the specie is a synonym.
Main_Crop	This field identify if a specie is a gene pool (when Main_Crop = 1) or is a cwr (when Main_Crop = 0)
Crop_Trust	
Family	Family of the specie
Family_Author	Family author of the specie
Subfamily	Subfamily of the specie
Subfamily_Author	Subfamily author of the specie
Tribe	Tribe of the specie
Tribe_Author	Tribe author of the specie
Subtribe	Subtribe of the specie
Subtribe_Author	Subtribe author of the specie
Genus	Genus of the specie
Genus_Author	Genus author of the specie
Species	Specie
Species_Author	Specie author
Subsp	Subspecie classification, the specie could be has or not a subsp
Subsp_Author	Subspecie author
Var	If the specie has a variety they don't has a Form
Var_Author	Variety author
Form	If the specie has a Form they don't has a Var
Form_Author	Form author
Nothosubsp	Field added to create a new classification order in the specie
Nothosubsp_Author	Nothosubsp Author
Common_Name	Common name of the specie, for example, banana
Scientific_Name	Complete Scientific name without Author names
Is_Hybrid	1 is a hybrid, 0 otherwise

Concepts	
ID	Unique identification for the concept
Crop_ID	Crop identification to join a concept with its species associated
Taxon_ID	Taxon identification to join a concept with the specie specify
Concept_ID	Concept Identification who contain crops and species grouped
Concept_Type	Specify the type of the concept association by specie. Gene Pool, Group Taxa, etc.
Concept_Level	Specify the level of the concept association by specie. Primary, 1B, etc.
CWR_Flag	
General	Comments

Breeding_data	
ID	Unique identification for the Breeding_data
Crop_ID	Crop identification to join a breeding with its associated species
Taxon_ID	Taxon identification to join a breeding with the specie
Pot_Conf	This field has information about the status of the breeding of specie. For example, Confirmed or Potential.
Description	Has information about the type of breeding for the specie
Ref_ID	(Hace referencia a la table de donde se extrae la referencia para el mejoramiento de la especie)

Distribution	
ID	Unique identification for the distribution
Taxon_ID	Taxon identification to join a distribution with the specie
Country	Has the iso country code (3 digits) to join with "countries" table
Type	The specie is Native or Introduced in that country
Detail_ID	Reference to other table who has more geographic information

Utilisation	
ID	Unique identification for the utilization
Taxon_ID	Taxon identification to join a utilization with the specie
Util_Type	Contain information about the type of usage for the specie. For example. Food or Medicine
Util_Use	Contain information about the util usage for the specie

Get the species in a gene pool

1. Select by Crop identificator

SELECT s.*, c*
FROM species s
    JOIN concepts c ON s.Taxon_ID = c.Taxon_ID
 WHERE c.Crop_ID = #Crop_ident.#

2. Select by Crop Name

SELECT s.*, c*
FROM species s
    JOIN concepts c ON s.Taxon_ID = c.Taxon_ID
WHERE c.Crop_ID = (SELECT Taxon_ID FROM species WHERE Scientific_Name = "#Crop Name#")

3. Select by multiple Crop Names

SELECT s.*, c*
FROM species s
       JOIN concepts c ON s.Taxon_ID = c.Taxon_ID
WHERE c.Crop_ID = (SELECT Taxon_ID FROM species WHERE Scientific_Name IN ("#Crop_Name_1",
"#Crop_Name_2", etc))

Get distribution for specie

1. Select by Taxon ID

SELECT s.*, d.*, c.*
FROM species s
     JOIN distribution d ON s.Taxon_ID = d.Taxon_ID
     JOIN countries c ON d.country = c.Code
WHERE s.Taxon_ID = #Taxon_ID#

2. Select by Scientific Name

SELECT s.*, d.*, c.*
FROM species s
     JOIN distribution d ON s.Taxon_ID = d.Taxon_ID
     JOIN countries c ON d.country = c.Code

WHERE s.Scientific_Name = "#Scientific_Name#"

3. Select by multiple Scientific Names

SELECT s.*, d.*, c.*
FROM species s
    JOIN distribution d ON s.Taxon_ID = d.Taxon_ID
    JOIN countries c ON d.country = c.Code
WHERE s.Scientific_Name IN ("#Scientific_Name_1#","#Scientific_Name_2#", etc)

Get breeding information by specie

1. Select by Taxon ID

SELECT s.*, b.*
FROM species s
    JOIN Breeding_data b ON s.Taxon_ID = b.Taxon_ID
WHERE s.Taxon_ID = #Taxon_ID#

2. Select by Scientific Name

SELECT s.*, b.*
FROM species s
    JOIN Breeding_data b ON s.Taxon_ID = b.Taxon_ID
WHERE s.Scientific_Name = "#Scientific_Name#"

3. Select multiple Scientific Names

SELECT s.*, b.*
FROM species s
    JOIN Breeding_data b ON s.Taxon_ID = b.Taxon_ID
WHERE s.Scientific_Name IN ("#Scientific_Name_1#", "#Scientific_Name_2#", etc)

Get Utilization by Specie

1. Select by Taxon ID

SELECT s.*, u.*
FROM species s
        JOIN Utilisation u ON s.Taxon_ID = u.Taxon_ID
WHERE s.Taxon_ID = #Taxon_ID#

2. Select by Scientific Name

SELECT s.*, u.*
FROM species s
        JOIN Utilisation u ON s.Taxon_ID = u.Taxon_ID
WHERE s.Scientific_Name = "#Scientific_Name#"

3. Select multiple Scientific Names

SELECT s.*, u.*
FROM species s
        JOIN Utilisation u ON s.Taxon_ID = u.Taxon_ID
WHERE s.Scientific_Name IN("#Scientific_Name_1#","#Scientific_Name_2#", etc)