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|  | **2014** |
|  | CIAT  CWR Diversity |

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| **[CWR Queries]** |
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# 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

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| --- | --- |
| 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 |

## 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.#

1. 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#”)

1. 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#

1. 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#”

1. 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#

1. 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#”

1. 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.\*, b.\*

FROM species s

JOIN Breeding\_data b ON s.Taxon\_ID = b.Taxon\_ID

WHERE s.Taxon\_ID = #Taxon\_ID#