Xper3 Guide line for Bryology

MADBRYO project

May 23, 2019

Xper3 Mkey provides interactive keys resulting from the description of a given taxa (phyllum, family, genus etc.), using Xper3 software. The web page you are accessing will help you to identify a specimen belonging to the largest taxon analyzed in the key. Using Xper3 key is highly intuitive, but this guide line aims to answer to most of the issues that may arise.

Characters are presented from the most discriminant for the dataset to the less discriminant. The principle is to select one character, which ever you want, then to select 1-n state(s) and to submit your request. Unrelevant taxa will be wripped out, and the other kept. And so on until only one taxon is retained. All the examples / screenshots are based on the East African Aneuraceae knowledge database: http://african-riccardia.identificationkey.org/mkey.html
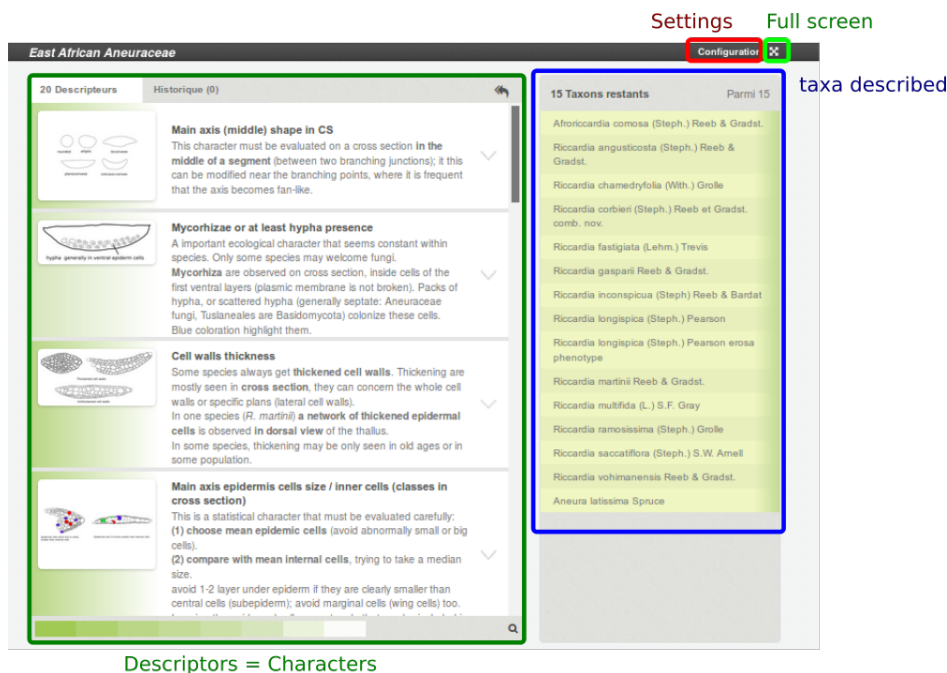
I   Main screen

Figure 1: Xper3 Mkey main screen, from East African Aneuraceae knowledge database. The screen is divided in two main parts : "Descriptors" (or characters) and "Taxa" (or items). The two small areas top right concern settings and full screen display.

I.1 Settings

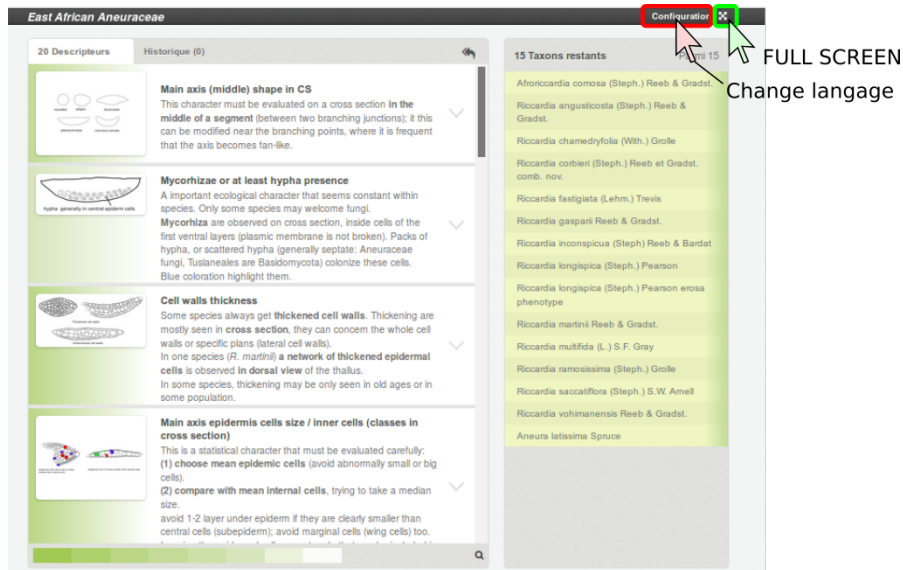Settings may be changed and are available for the session.

Figure 2: Click on **"Configuration"** (in french) or on **"Settings"** (in english) to **change langage** and to access to many other settings. Click on the **cross** to access full screen view. Then click on **"escape"** to exit full screen view.
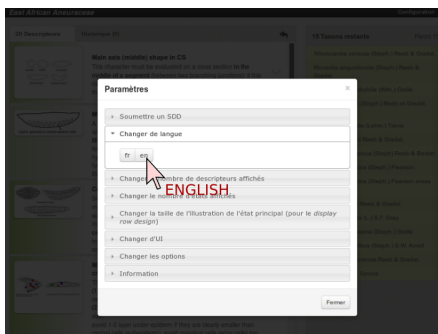

Figure 3: Langage setting.Click on **"en"** for english or on **"fr"** for french.
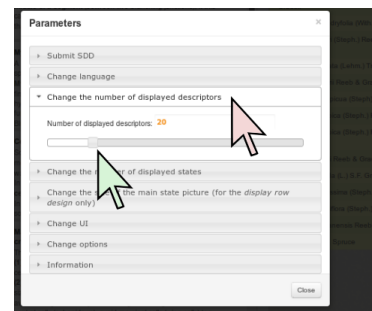

Figure 4: Change the number of displayed descriptors. It will increase (or decrease) the number of available descriptors

I.2 Identification

The number of characters displayed can be modified in "Settings" cf paragraphe 2. One can select any character which seems conspicous or unique to the specimen examined, and decides which state is approriate. Of course, it is recommended to begin by the top characters (more discriminant) if they are available for the specimen.
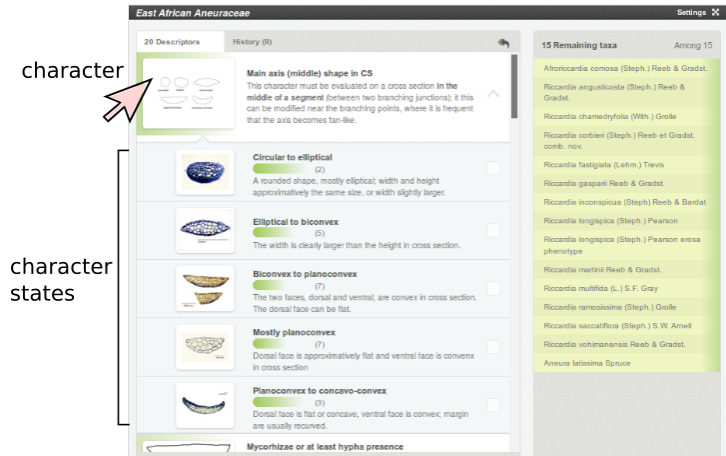
I.2.1 Choose character and character state(s)

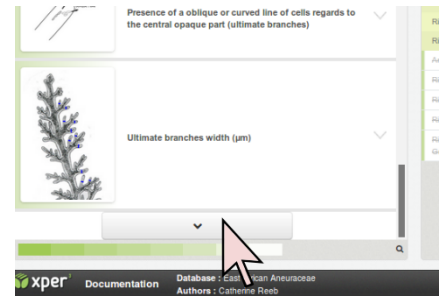Figure 5: Choose a character, then the character states are displayed.

Figure 6: More characters are available at the end of the list. Click on the bottom arrow to get new characters.
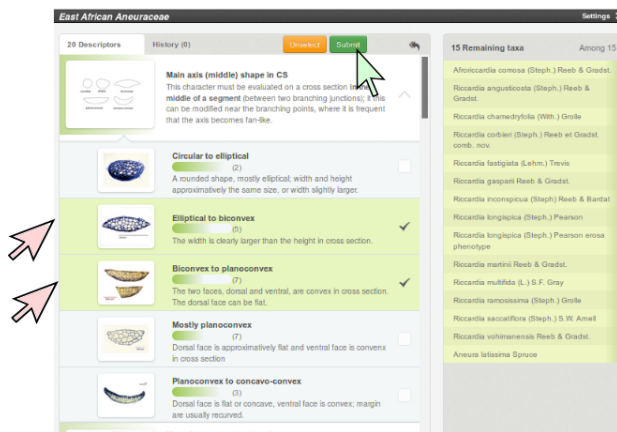

Figure 7: Choose charater state(s) = red pointer. You can choose several states. Then submit yout choice = green pointer.
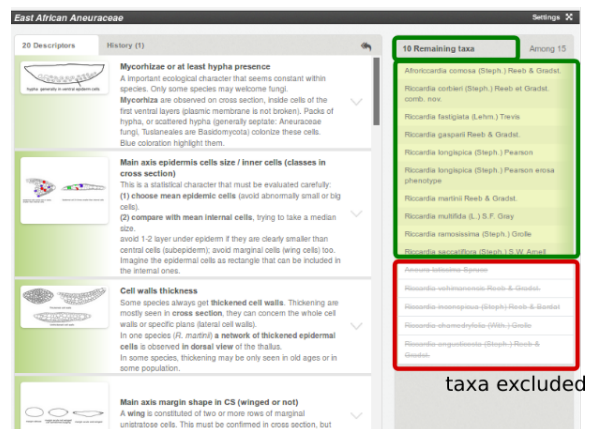

Figure 8: Excluded and remaining candidate taxa are displayed.

I.2.2 Again : choose character and character state(s)

Continue this process until only one taxon remains. Here, we use always the first character, but again you may use the one you want.

Figure 9: Choose character state(s) = red pointer. Submit your choice = green pointer.

Figure 10: Two remaining candidate taxa are displayed.

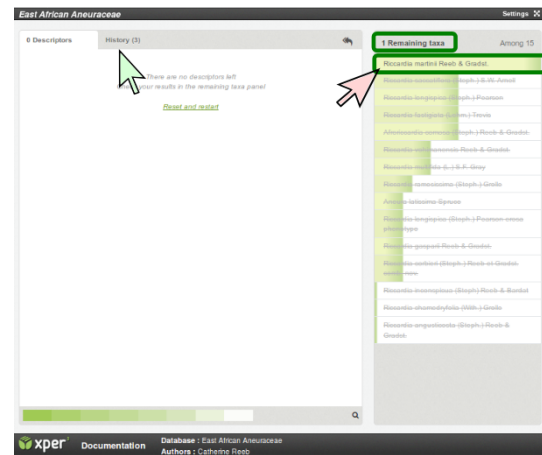Figure 11: Choose character state(s) = red pointer. Submit your choice = green pointer.

Figure 12: Only one taxa matches now your character states choices. Now, you can click on the name of the final taxon = red pointer OR click on the tab "History" = green pointer.

II   Informations about taxa

II.1   Taxon description

If you click on a taxon (red pointer Figure 12) you access to the description of the taxon.

   WARNING 1:   in the actual version of Xper3, the arrows giving access to the following taxon may be confused with the arrows accessing to the following character of the considered taxon. This will be changed in the future.

   WARNING 2:   in the actual version of Xper3 image title and legend do not appear. It is going to be improved very soon.
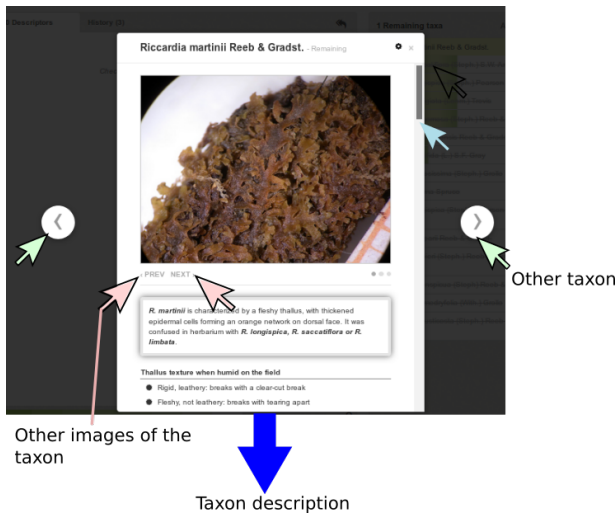
Figure 13: Description of the species (here *R. martinii*); click on these small arrows (red pointer) to access to the following images. Click on the green pointer to access to the following taxa description. Roll down (blue pointer) to get the following of the description.
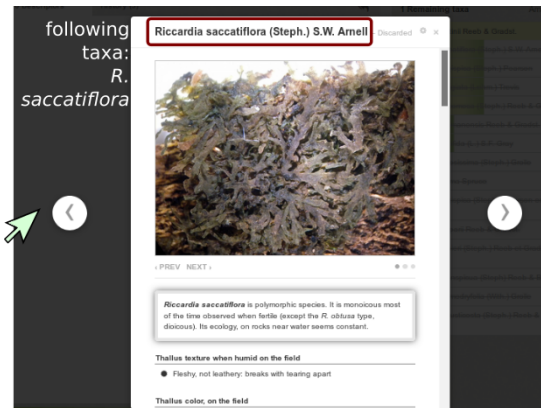

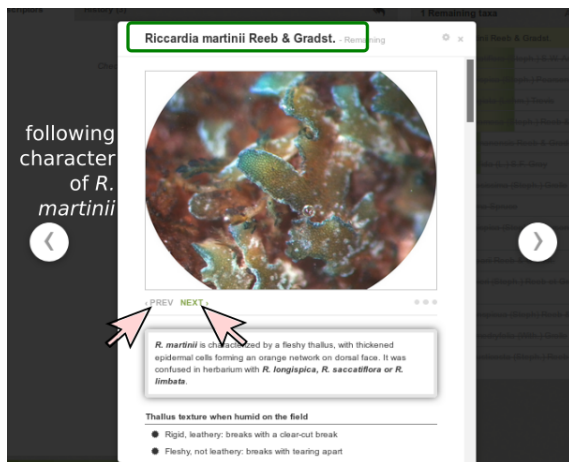Figure 14: Clicking on red pointer displays the following taxon. Here *R. saccatiflora*

Figure 15: Clicking on the small arrows (green pointer) displays the following character of the taxon. here *R. martinii.*

II.2 History and identification modification

Two ways to modify your identification, if the final taxon does not suit to your specimen

- Restart the identification: click on the light green words "reset and restart"

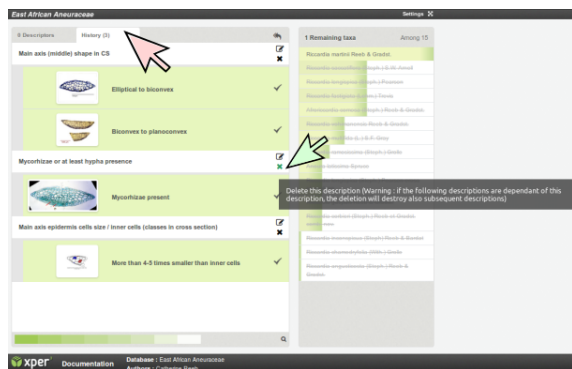- Use History tools, that allows you to go back to the identification path.

Figure 16: Access to the history tab = red pointer. Click on the cross = green pointer deletes the this description; here "Mycorhizae of at least hypha presence".
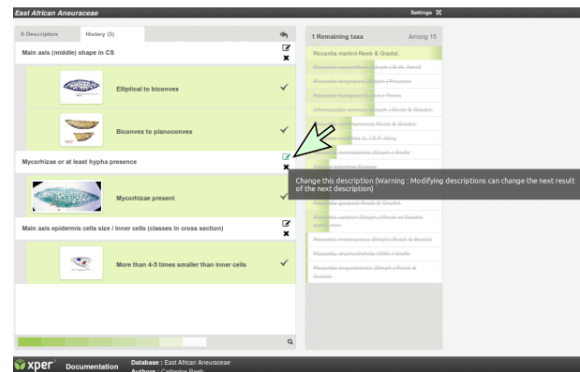

Figure 17: Clicking on the editing symbol = green pointer changes the description.