



Food and Agriculture Organization
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Universidade de Vigo

ISHARKFIN USER MANUAL

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ENGLISH

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iSharkFin is an expert system for the identification of shark fins from their shape. Starting from a standard photograph of the fin, the interactive process conducts the user to select some characteristics of the fin and to measure its shape receiving, as an automatic response, the shark species to which the fin belongs.

1. Installation and language settings

To install **iSharkFin**, download it from the web page and execute the installer. Accept the end user licence agreement and choose where you want the program to be installed. After finishing the installation process, launch the program by executing “iSharkFin.exe”.

At the first start, you will be asked to choose your language.



Image 1: This language dialogue will appear at the first start. Choose the program language you wish to use.

You can change the program language afterwards in the menu “Configuration->language”. In the language dialogue of the configuration menu, you can also select alternative languages for downloading pictures and help files, where they are not available in your preferred language.

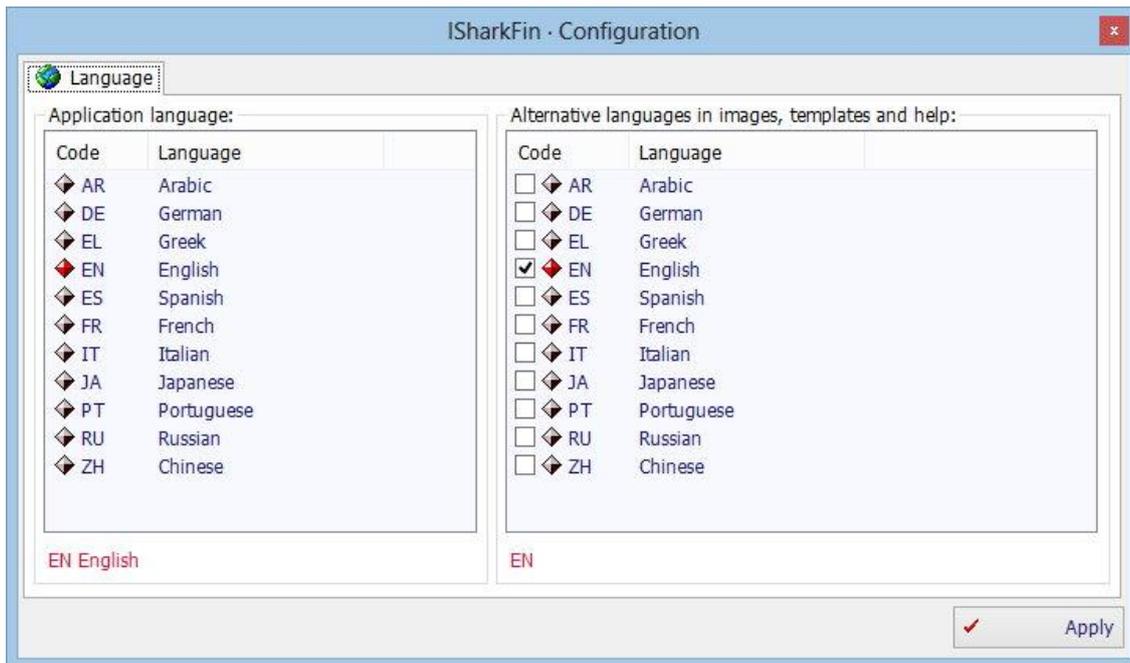


Image 2: You can change the program language afterwards in the menu. Here, you can also specify alternative languages for images, help files, etc.

2. Identifying sharks fins

To identify a shark fin, you need to first take a photograph of the fin and store it on your computer. Follow the “Practical method for taking standard photographs of shark fins” included in the Annex of this manual.

Once you have saved one or more photographs in a dedicated folder, you can proceed in one of two ways:

- 1) For batch identification: prepare the photographs and save the measurements of several fins before using the “**Interactive identification**” or the “**Identification from file**” tools. If you are willing to participate in data collection and help in the development of this software, this is the proper procedure that allows the inclusion of new samples and measurements of fins for which the species is already known.
- 2) For identification of a single fin: the second way to identify a fin is to use the “**Interactive identification**” tool. This tool is immediate and quick. Choose this way when you want to identify just one fin.

2.1 Preparing photographs

For both procedures, “Interactive identification” as well as for the “Identification from file”, you need to prepare the photographs for creating the measurements that will be used by the identification algorithm. Perform the following steps.

Step 1: Load photograph and choose fin type

First, you need to load a photograph and specify the fin type. To create a new isharkfin file use the menu “File->New” or, if you want to continue a project that was saved before, use “File->Open” instead. To load fin photographs, press the button “...” to search and choose the data folder that contains at least one photograph of a shark fin. The file names of the photographs found in your selected folder are then displayed in the list box on the left part of the screen. Now, select the file name for the photograph of the fin you want to identify. Choose the fin type (dorsal or pectoral fin) by clicking on the example pictures.

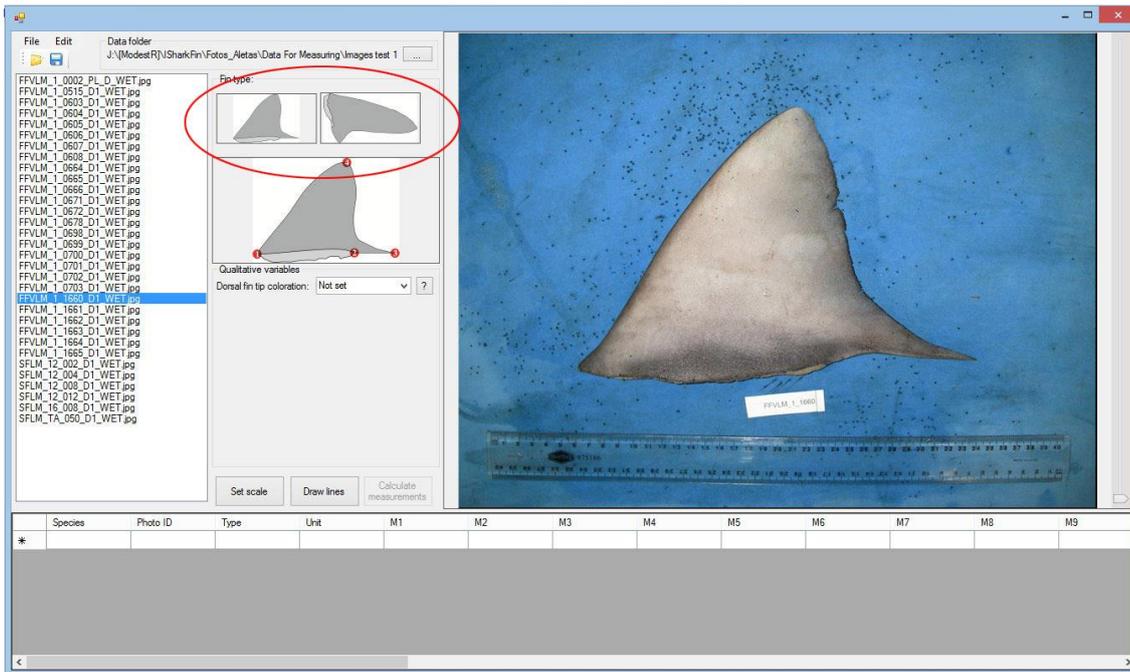


Image 3: Selecting a folder with fin photographs, choosing a photograph in the list and specifying the fin type.

Step 2: Set the four basic points

Set the four basic points on the photograph by clicking four times on the picture at the corresponding four locations. The points can be moved after, but not before, setting all four points. See the help picture for knowing where to put the points, and follow the descriptions below:

POINT 1. DORSAL FIN ORIGIN

In theory, this is the anterior-most point where the dorsal fin joins the dorsal body surface on the shark. Depending on where the fin is cut, you may face different situations:

- **A:** This may correspond to the first part of the fin.



- **B:** If the fin has been cut lower, and it includes some skin from the dorsal surface of the shark body, the "Point 1" will be the most concave portion of the lower anterior portion of the fin.



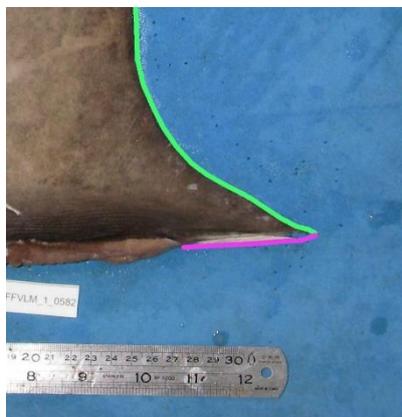
POINT 2. FIN INSERTION

Theoretically, this is the posterior point of attachment of a fin to its base. Considering that the vast majority of fins will be removed from their fin bases (i.e. removed from the animal), this is considered to be the junction between the skin of the inner margin of the free rear tip, the exterior of the animal, and the severed part of the fin.



POINT 3. FREE REAR TIP

This point should be placed at the tip of the free rear tip of the dorsal fin – theoretically, at the junction between the posterior margin and the inner margin of the free rear tip.



POINT 4. DORSAL FIN TIP

In theory, this is the apex of the fin tip, i.e. the “point” of the fin where the anterior margin of the fin (leading edge) meets the posterior margin of the fin (trailing edge). This is **not** the uppermost point of the fin. This is usually the “pointiest” part of the fin, but not always (see examples below). You can look for a change between the “smooth” denticles on the anterior surface of the fin changing to the anterior margin, which is often “feathered”.



Below, you can see several fins of different shape and the position of the point.



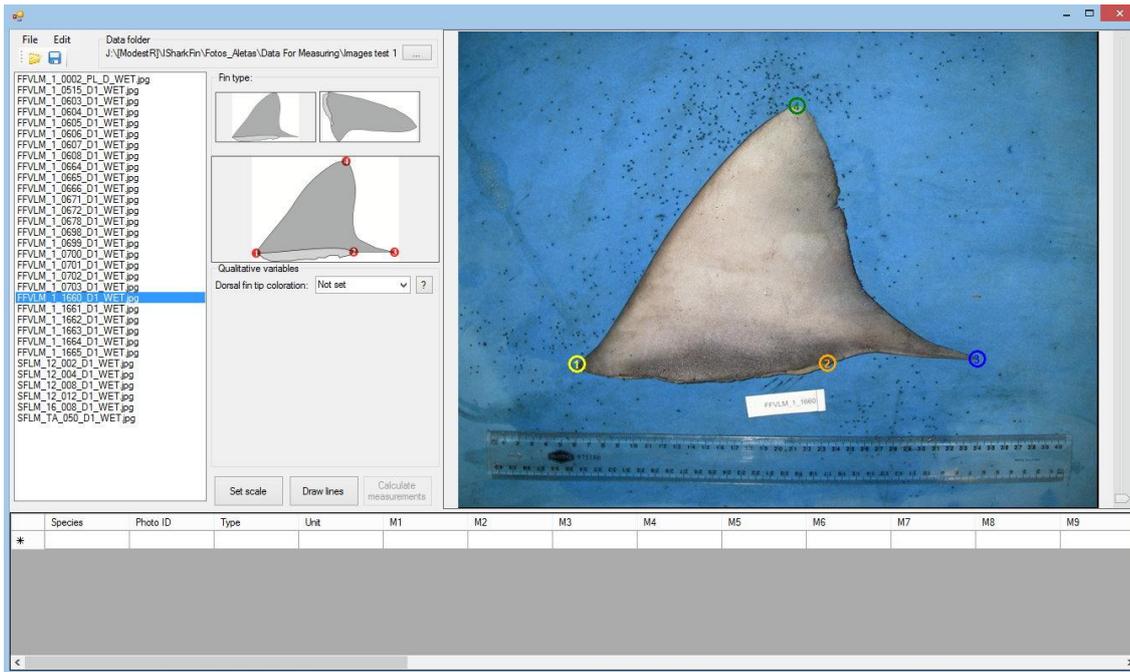


Image 4: Setting of the four basic points.

Note that for taking the four points on pectoral fins, you can follow the analogous method.



Step 3: Define the shape of the fin by setting the remaining points on the auxiliary lines

When the four basic points are set, click the “Draw lines” button. As a result, 20 auxiliary lines will appear with a purple point on each of them, which needs to be positioned exactly on the edge of the fin. Correct the purple points by dragging and dropping them until they are in exactly the right position. Use the zoom scroll bar on the right to place the points more precisely. In order to obtain a reliable identification, the points must be exactly on the edge. In the case of missing skin parts, place the points where you expect the edge should be.

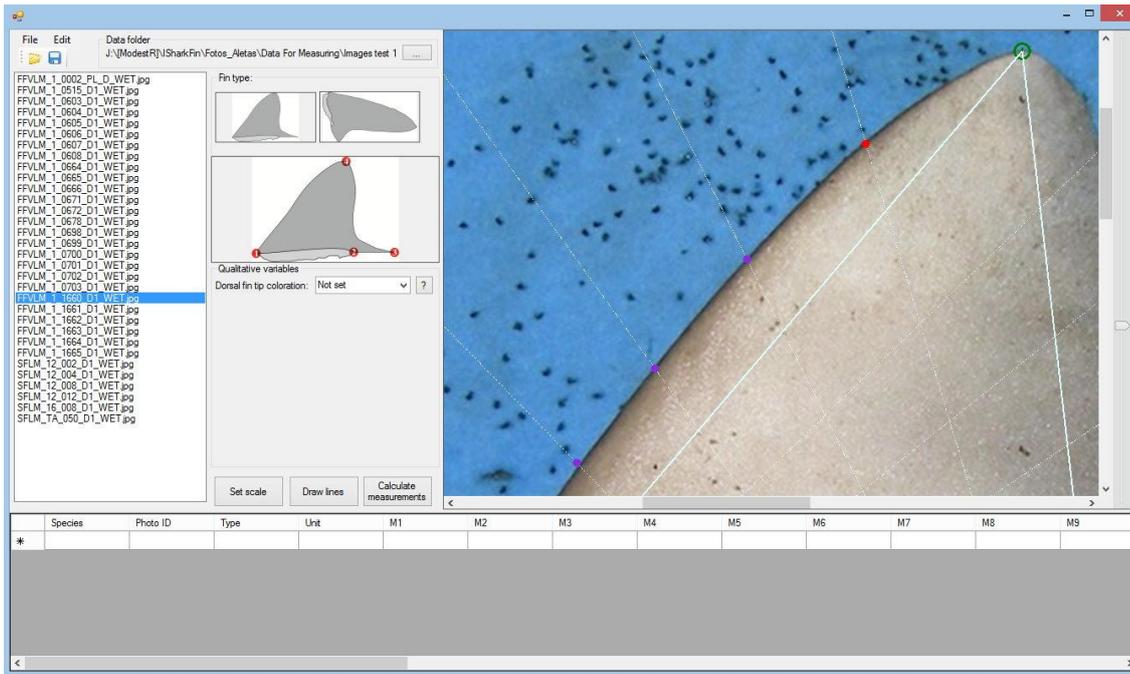


Image 5: After clicking “Draw lines”, use the zoom bar on the right to move the purple points precisely to the fin edge

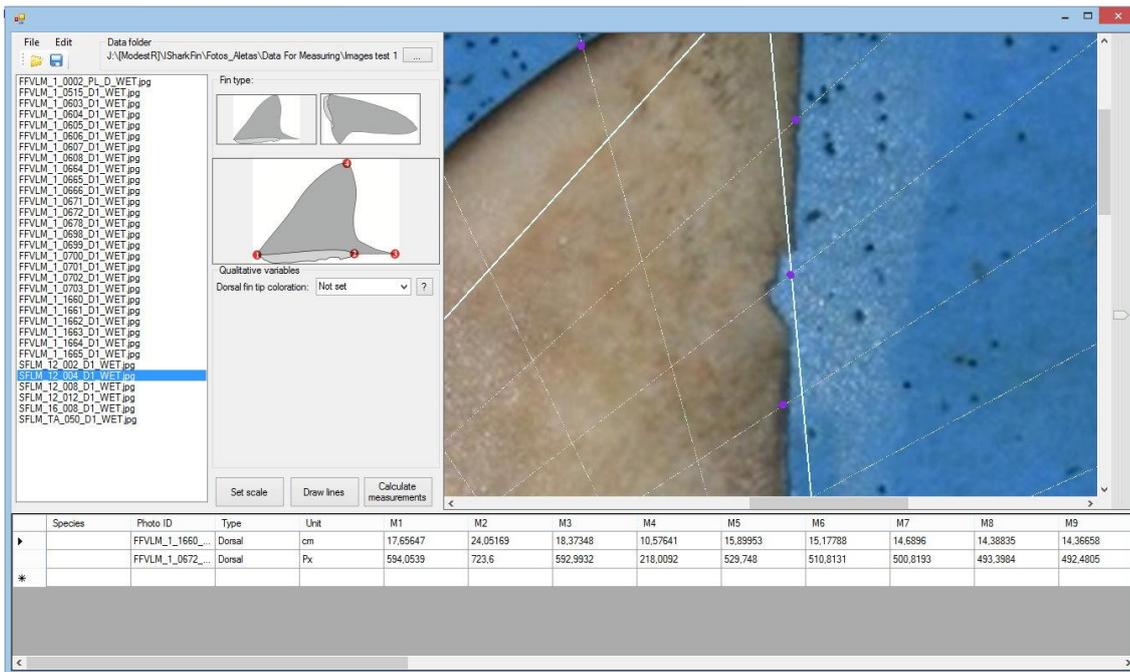


Image 6: In the case of missing skin parts, move the point to the position where the edge is expected to be.

Step 4 (Optional): Set scale

To define a scale, first hit the “Set scale” button. Next, click on the photographs twice, to select the beginning and end points of a known distance (for example, by a ruler that is visible on the photograph). A dialogue will show up, where you can select the unit (centimetres or inches) and insert the measure corresponding to the selected distance on the photographs. If you define a scale, the measures will be converted into that unit.

This function allows the system to memorize the real measurements of the fins, data that can be useful for estimating the total length and the weight of the individual to which the fin belonged.

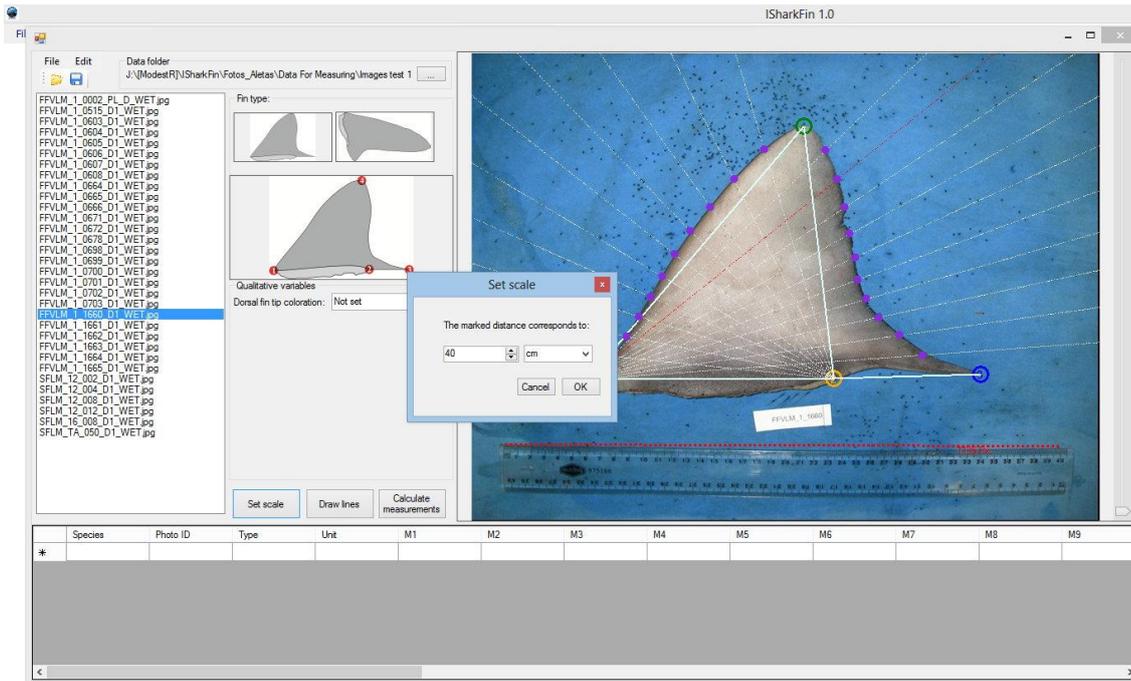


Image 7: If the photograph contains a ruler as reference for the size, you can define a scale for working with measurements in centimetres or inches instead of pixels.

Step 5: Choose qualitative variables

To date, the only qualitative variable used by the identification algorithm is the “Dorsal fin tip coloration”. Use the combo box to select one of the four possibilities: no tip color; decolored fin; white tip or black tip. Click the “?” button to see a description and example photographs of the selected character.

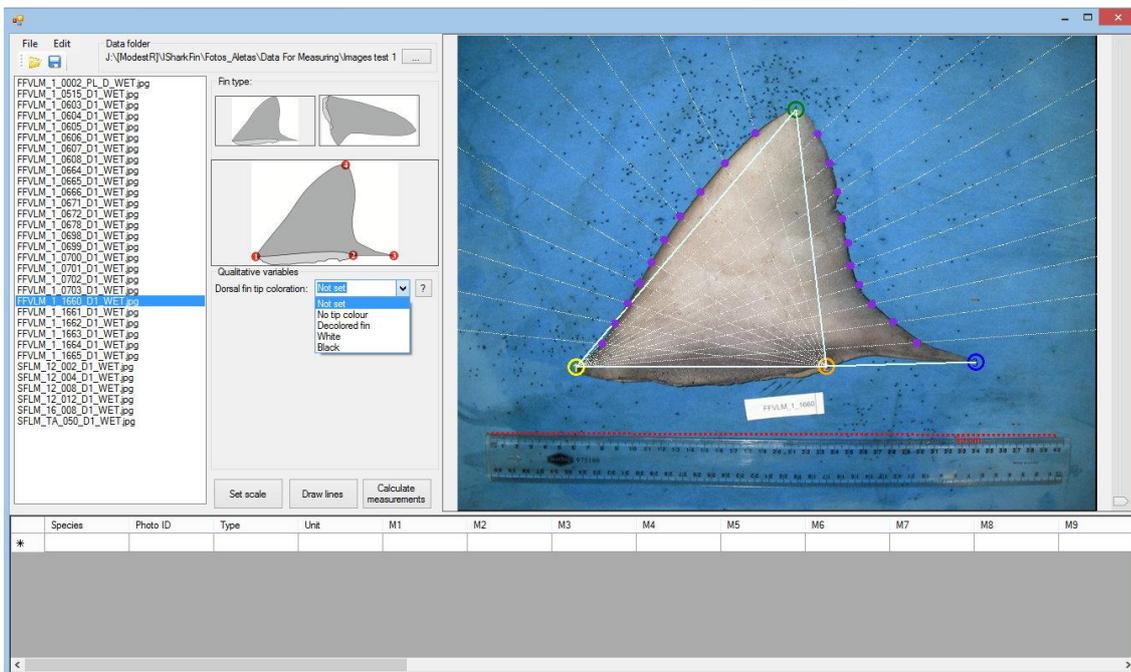


Image 8: Choose a value for the qualitative variables.

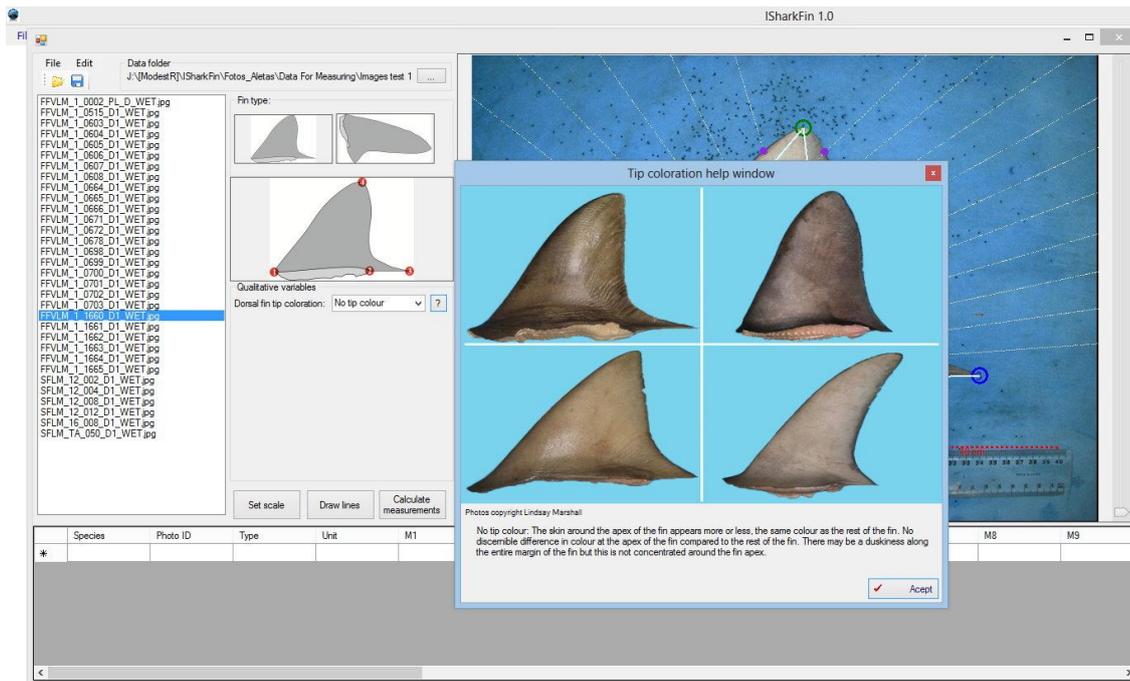


Image 9: Use the help button “?” to see example images for the chosen qualitative variable value.

Step 6: Create measures

Create the measurement values using the button “Calculate measurements”. The measurements will appear in the table in the lower part of the screen. You can copy and paste lines, or edit and delete them manually. If you want to correct measurements that have already been made, click in the leftmost column to select the row and change the position of the points on the photograph. If you click again on “Create measures” while a row is selected in the table, the old values will be overwritten.

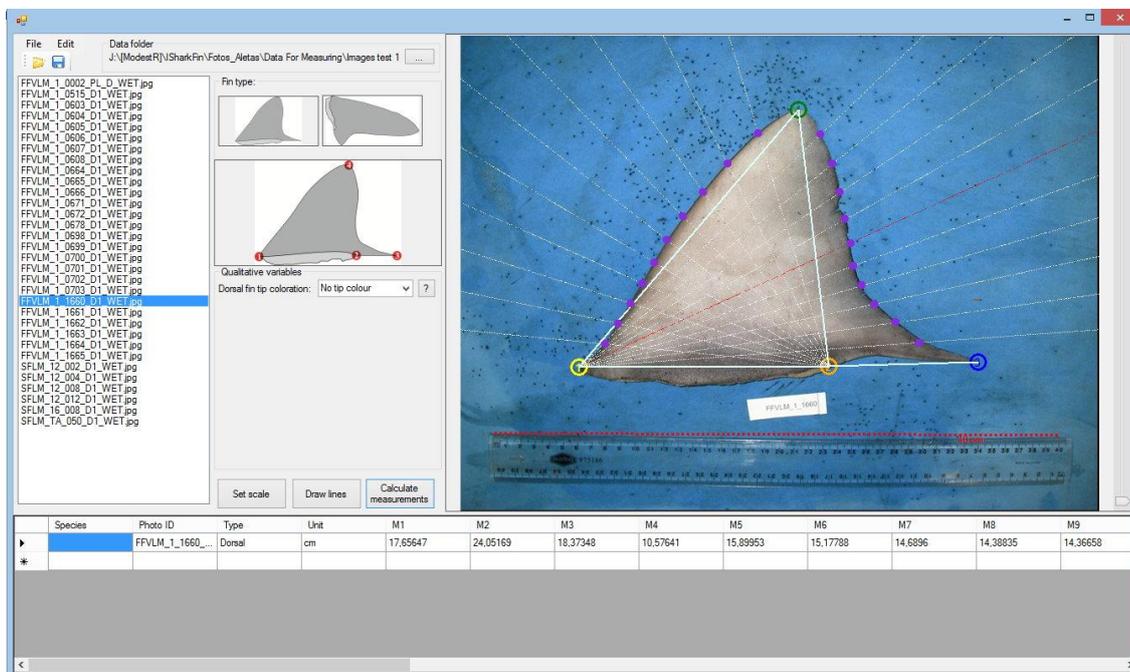


Image 10: Finally create the measurements by hitting the “Calculate measurements” button. The measurements will appear as a new line in the table on the bottom of the window.

Step 7: Save file

Finally save your work as either a “.sfin” or “.txt” file. The “.sfin” files are binary **iSharkFin** project files that contain all information to restore the state of the project in the moment of saving. To be sure the file preserves the information on the position, do not move the file “.sfin” and the folder containing the photographs from the original position. The .txt files are readable text files that contain only the created measurements, but not the location of the points that have been placed on the pictures, thus the text files contain only the information you can see in the table at the bottom of the screen.

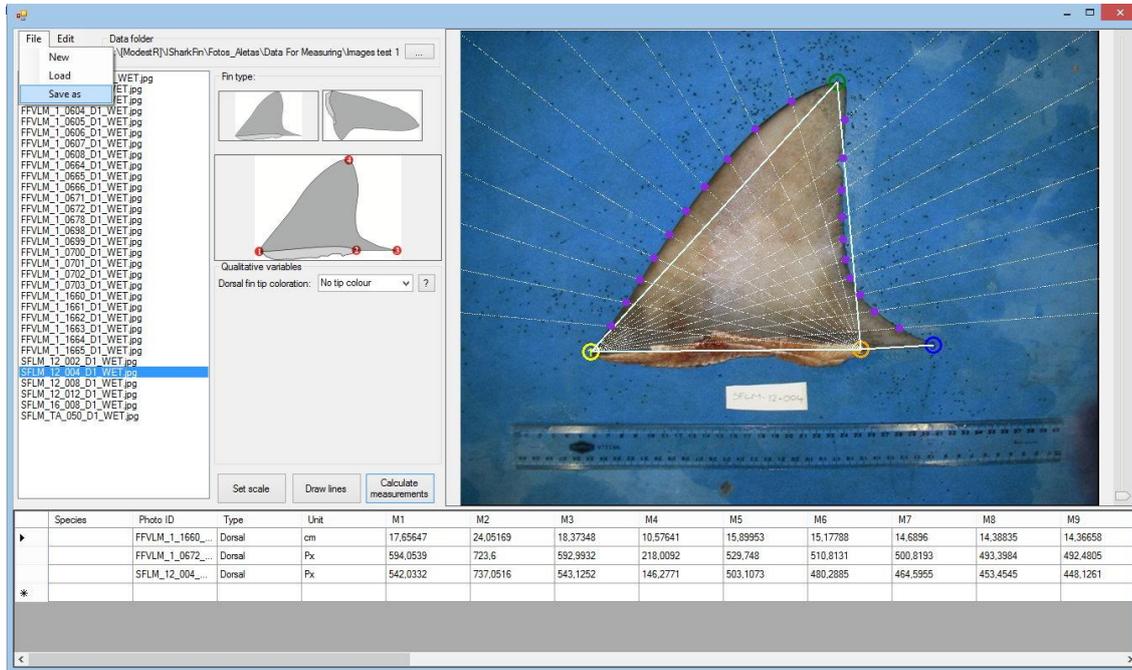


Image 11: Do not forget to save the measurements for use in the identification module.

2.2 Interactive identification

If you would like to identify one fin and you have saved the photograph on your PC, go to “Identification -> Interactive identification” for the identification procedure. Open the “Interactive identification” window and perform all the steps (Steps 1–7) described in the previous section, beginning from the button “...” and searching for the folder where you have saved the photograph. Once you have completed the procedure for taking the measurements, click on the “Identify” button.

From the window “Interactive identification”, you can also load one of the files generated in the previous section. This allows you to identify one by one the fins already measured, selecting the row with the measurements in the table of the fin and then clicking on the “Identify” button.

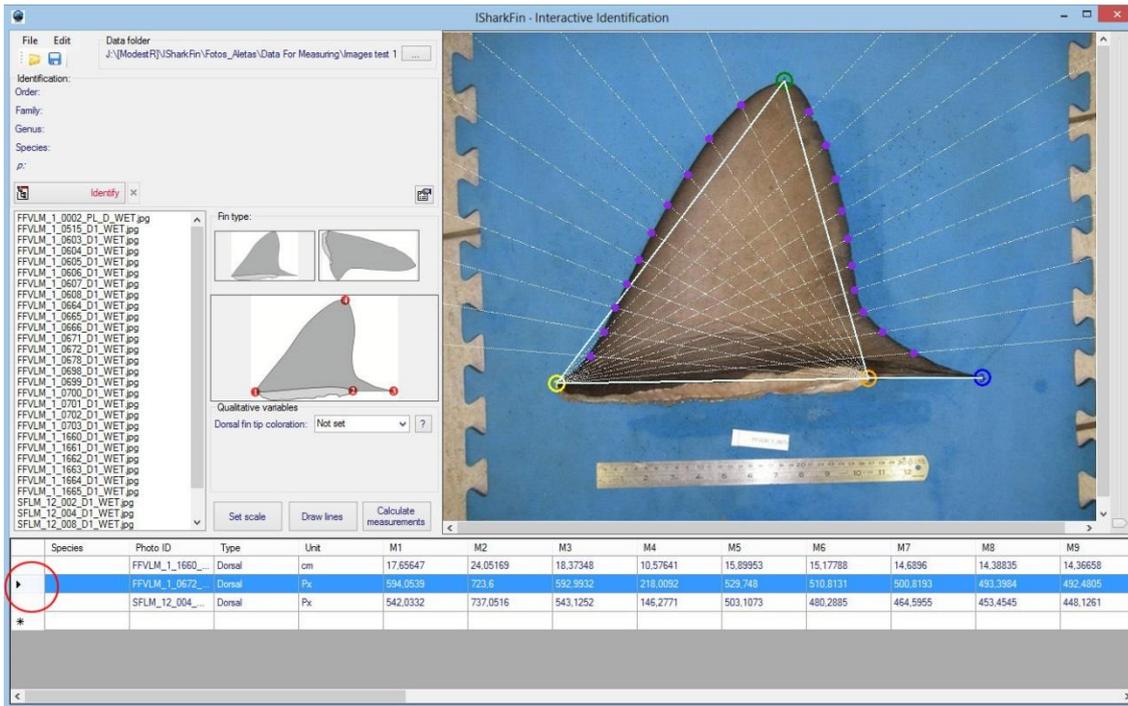


Image 12: Load one of the previously generated files in the “Interactive identification” window and select the row of the fin you wish to identify in the table by clicking in the leftmost column of the table (see picture).

If the program is able to identify the photograph, the order, genus, family and species of the shark will appear on the screen, together with a probability value indicating the level of uncertainty about the identity of the specimen (probability, abbreviated with p , varies from 0 to 1; a p value close to 1 indicates strong evidence that the fin belongs to the taxon identified). If it is not possible to identify the photograph, a message indicating that the photograph is “unidentified” will appear. In this latter case, the system could be able to give some indication about the taxonomic group to which the fin belongs.

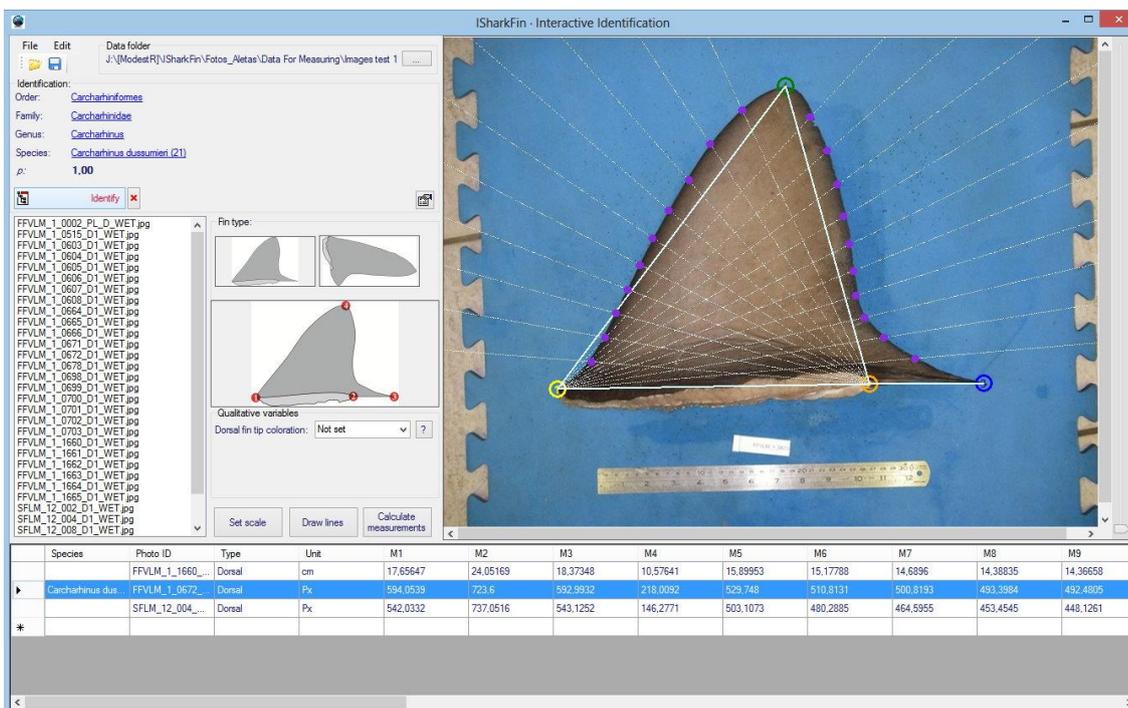


Image 13: Trigger the identification process by hitting the “Identify” button.

If you already have some information about the order, family or genus of the species, it is possible to give hints to the expert system. To do, click the small button “Direct selection” at the bottom right within the identification area. This makes a combo box appear where you can select the known order, genus or family, before triggering the identification process by hitting the “Identify” button.

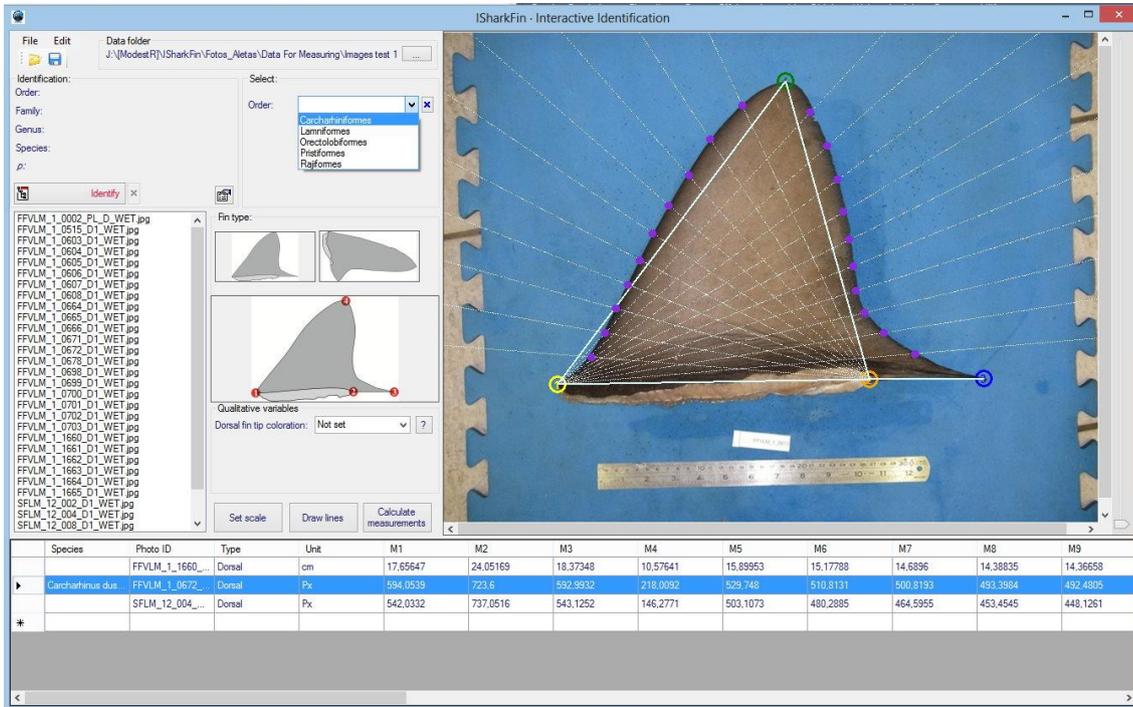


Image 14: You may give hints if you have information about the order, family or genus of the fin on the photograph.

2.3 Identification from file

To follow this procedure, you need to have first created a file with data of the measurements, as explained in the “Preparing photographs” section. If you have already created such files, go to “Identification -> Identification from file” in the menu. Select the input file by using the “Load” button. The input file may be either in the .sfin or .txt format. You can check the data table in an external editor by clicking the buttons with the notepad or Excel icons. Finally, click the button “Identify” and see the result in the table. You can save the results by using the save button.

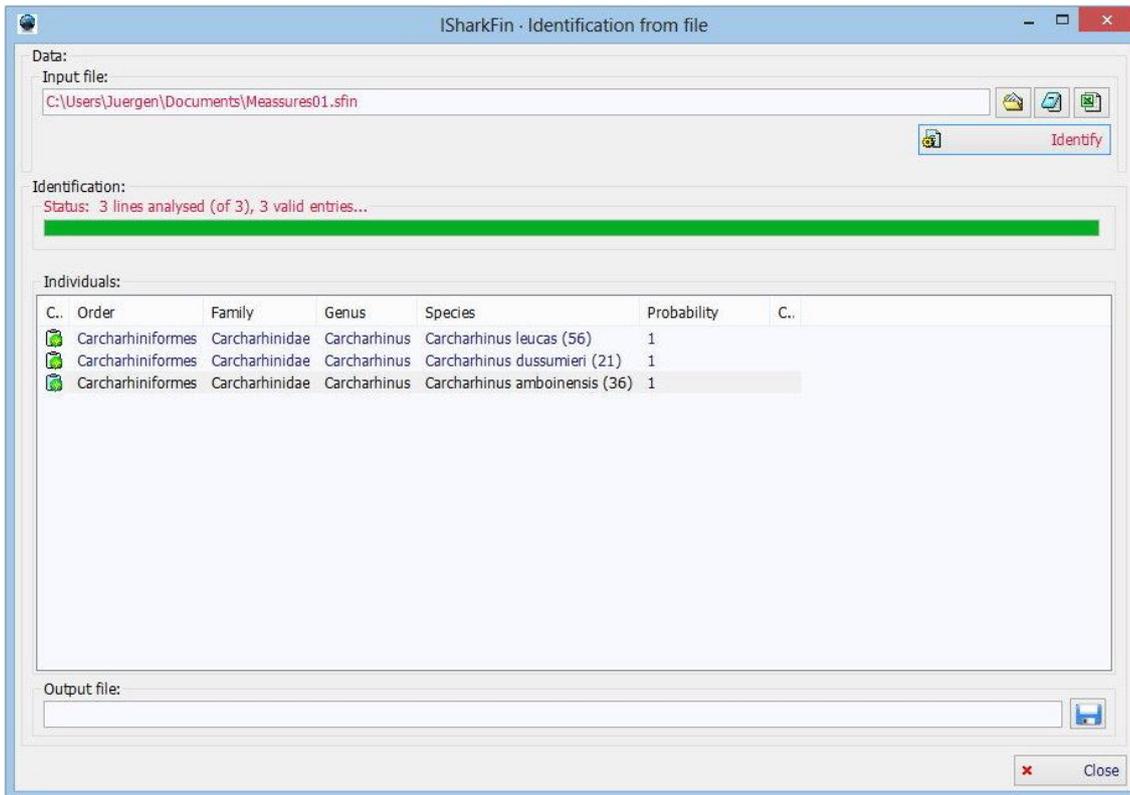


Image 15: The result after identification from file.

You also have the possibility to access further information of the identified species by clicking with the right mouse button on the row of the identified species in the table and selecting "Images", "Common names" or "Map", which will open another window with the respective information. The windows that open are identical to those used in the "List of species" window, so see the following section on how to use them.

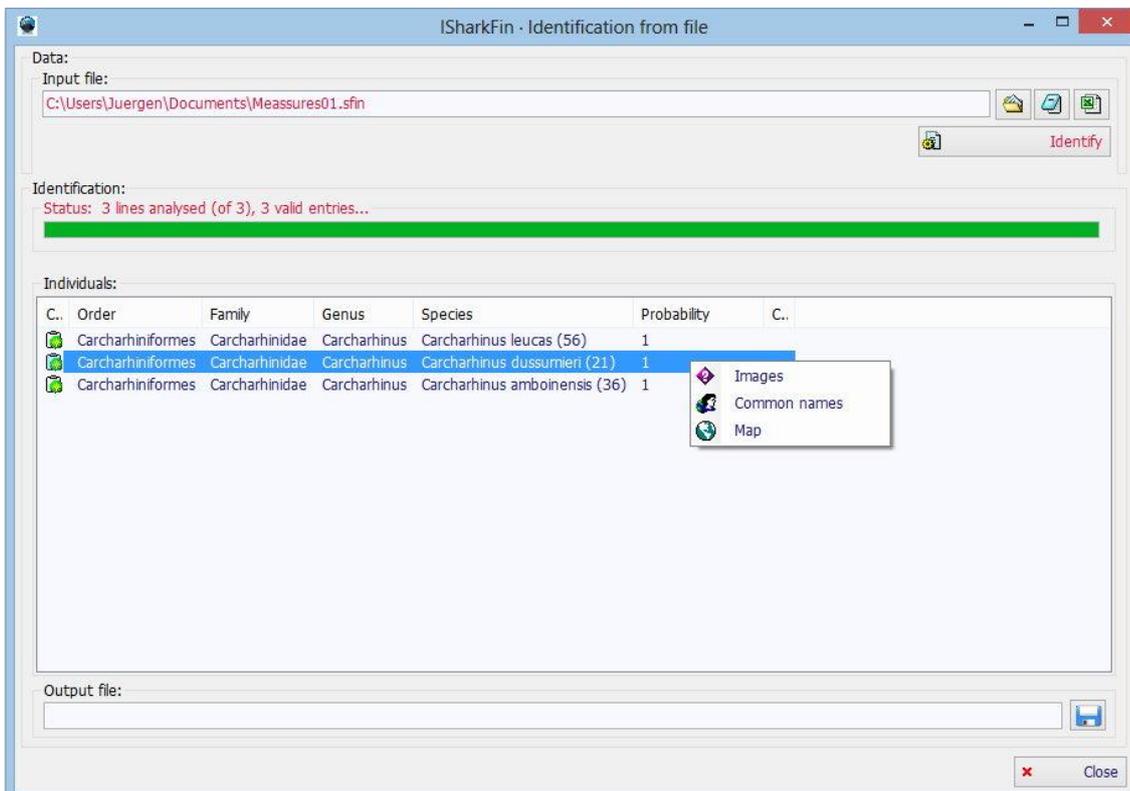


Image 16: Access further information on the identified species by right clicking on the result in the table.

3. Further functionality

Besides identifying sharks, you can browse the database and taxonomy tree used by **iSharkFin**. It contains pictures, distribution maps and Internet links to further information on the different orders, genus, families and shark species.

3.1 List of species

To see the taxonomy tree, go to “Species->List of species” in the main menu. The list of species is not limited to the shark species for which the identification of fins is possible, but contains a complete checklist of sharks (www.ipez.es). A window will show up where you can browse the tree and see further information, pictures and Internet links. Small icons “C”, “O”, “G”, “F” and “E” used in the tree stand for “class”, “order”, “genus”, “family” and “species” (last one appears in red while the rest of them are in blue). At species level, a parenthesis with extra information, for example “(6D,7P)” may appear. This means that for the selected species measures from 6 dorsal and 7 pectoral fins are available in the database and used in the identification algorithm.

The taxonomy tree window also has a search function, and it is possible to search by scientific name, common name and synonym. Use the different search options “Name starts with search term” (B), “Name ends with search term” (E), “Name contains search term” (M) or limit the search to only order, family, genus or species level.

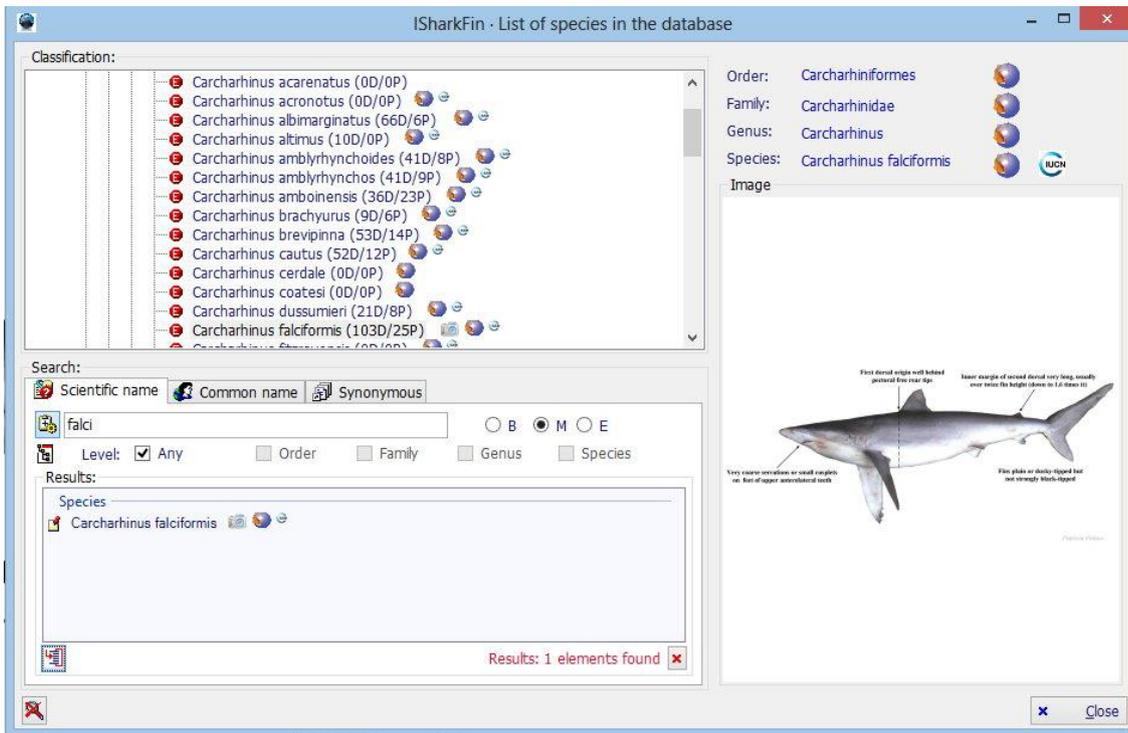


Image 17: The taxonomy tree used by iSharkFin with the possibility to search entries and additional information such as photographs, common names, distribution maps and links.

If no picture of the species is shown in the picture box, this means that there is no picture available on your local hard disk. However, there may be a picture available on the iSharkFin server. To search for pictures on the iSharkFin server, proceed as follows:

- 1) Right click on the picture box and select “Multi language”.

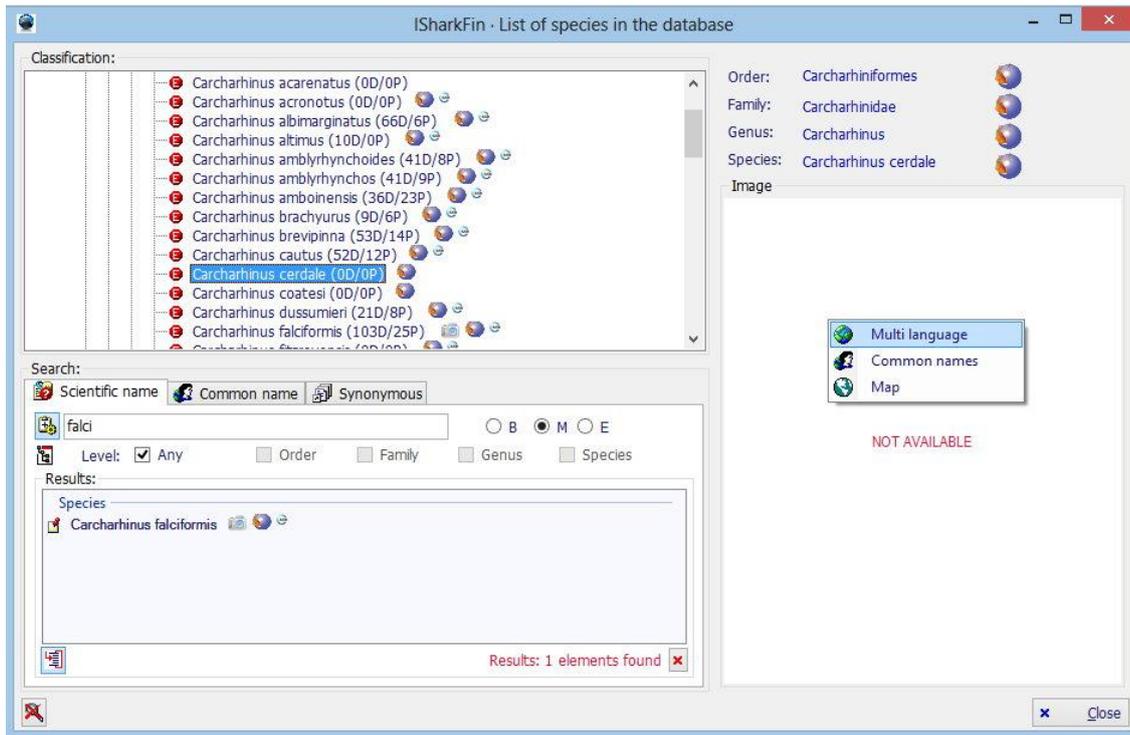


Image 18: Right click on the (empty) picture box to look for pictures on the iSharkFin server or to access further information such as distribution maps or common names.

- 2) A dialogue will appear where you will see a list with information on the availability of the pictures in the different languages. To download one of them, select it and click “Download from iSharkFin server” on the bottom of the window.

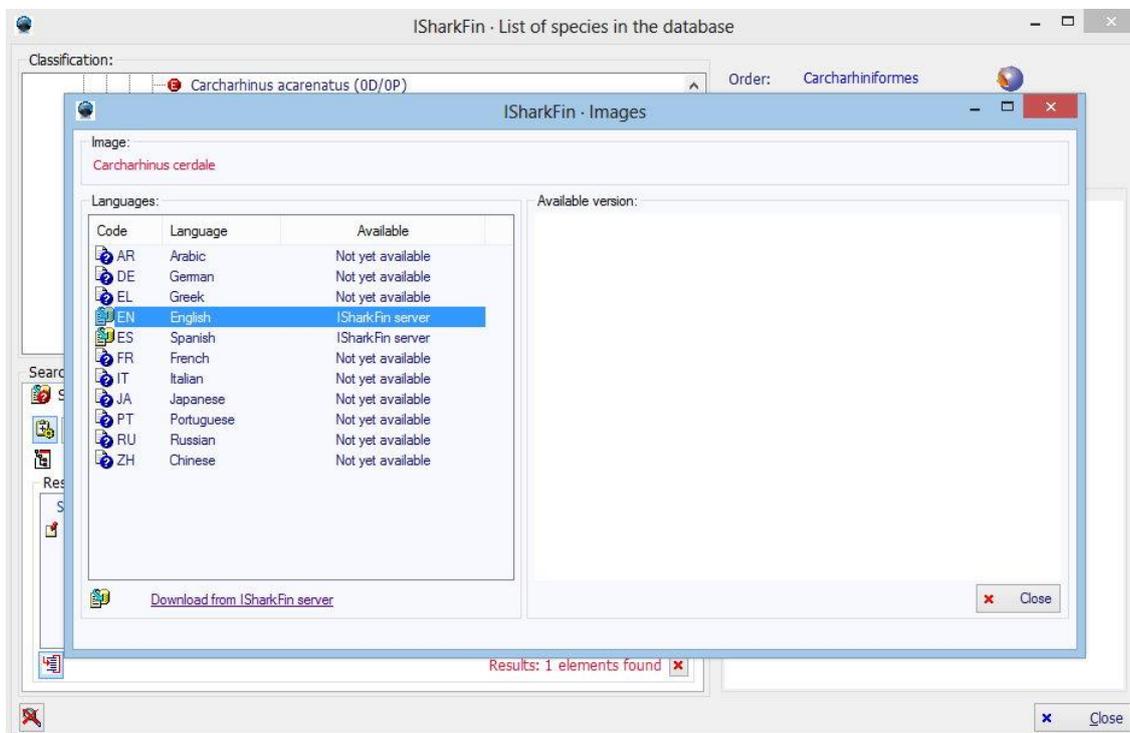


Image 19: Select the picture you want to download and click “Download from iSharkFin server”.

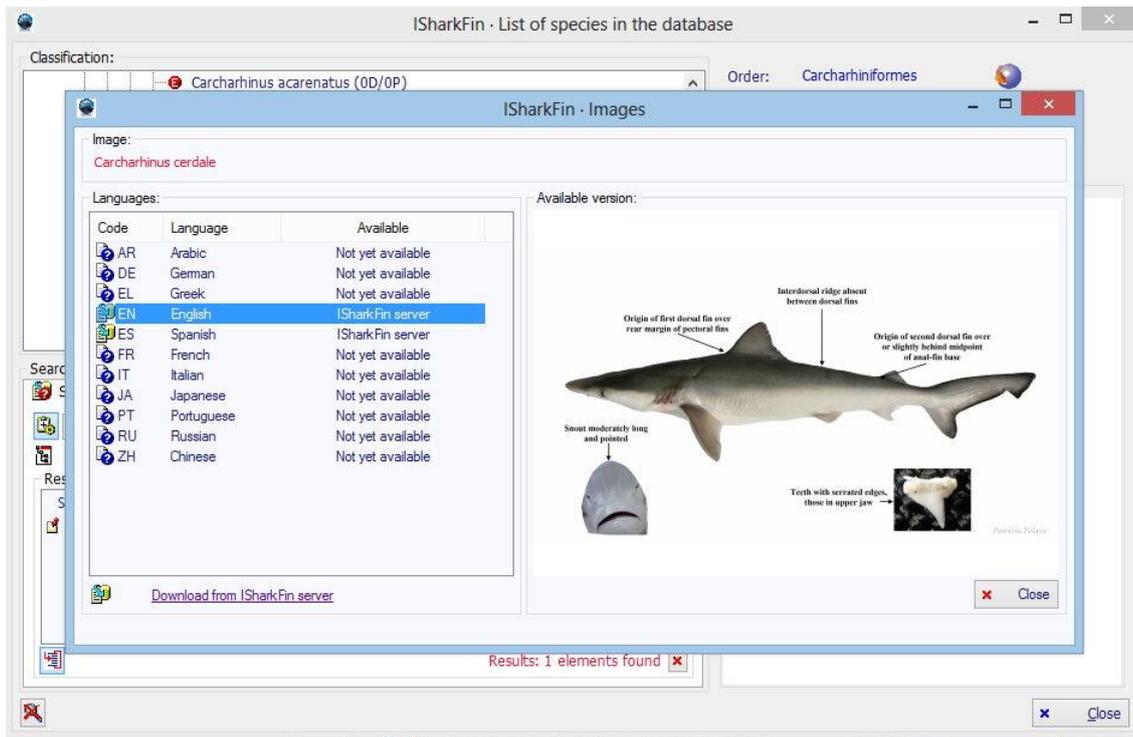


Image 20: Example of picture downloaded from the server.

in addition to downloading pictures, you can use the context menu of the picture box, opening it with a click of the right mouse button, to open a window with information about common names of the species in local languages of the different countries and to see a distribution map of the species, where available. The names can be ordered by common name, by the countries where the name is used, and by language.

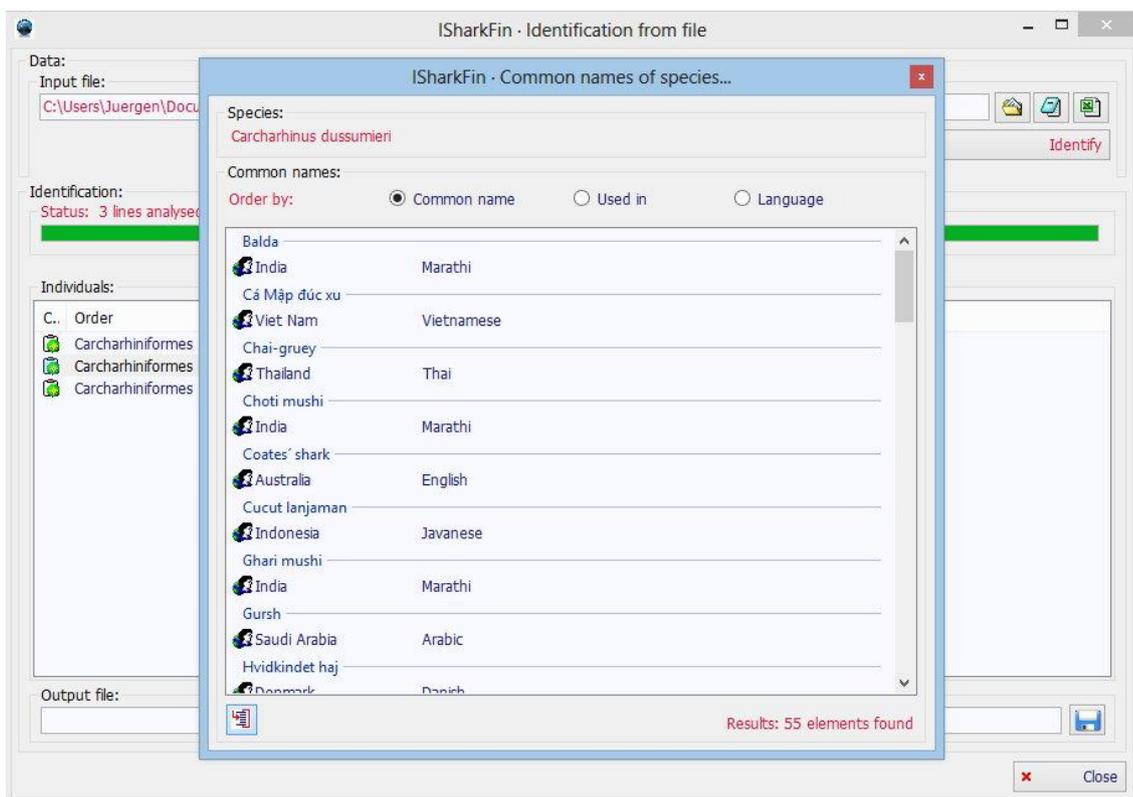


Image 21: Different names of the species used in different countries and in different languages.

The distribution maps work exactly the same way as the species pictures. If available on the local hard disk, it will show up immediately on request; if not, you may look for it on the iSharkFin server and download it with the “Download from iSharkFin server” button.



Image 22: Example of distribution map of the species.

3.2 Export taxonomy

The program allows users to export a full taxonomy tree of the database. There are two ways of exporting the data. “Structured” and “Unstructured”. See the following images for examples of both.

	A	B	C	D	E	F
1	Subclass	Order	Family	Genus	Species	
2	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis americanus	
3	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis donghaiensis	
4	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis folirostris	
5	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis longirostris	
6	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis marmoratus	
7	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis nanhaiensis	
8	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis ori	
9	Elasmobranchii	Rajiformes	Anacanthobatidae	Anacanthobatis	Anacanthobatis stenosoma	
10	Elasmobranchii	Rajiformes	Anacanthobatidae	Sinobatis	Sinobatis borneensis	
11	Elasmobranchii	Rajiformes	Anacanthobatidae	Sinobatis	Sinobatis bulbicauda	
12	Elasmobranchii	Rajiformes	Anacanthobatidae	Sinobatis	Sinobatis caerulea	
13	Elasmobranchii	Rajiformes	Anacanthobatidae	Sinobatis	Sinobatis filicauda	
14	Elasmobranchii	Rajiformes	Anacanthobatidae	Sinobatis	Sinobatis melanosoma	
15	Elasmobranchii	Rajiformes	Arhynchobatidae	Arhynchobatis	Arhynchobatis asperrimus	
16	Elasmobranchii	Rajiformes	Arhynchobatidae	Atlantoraja	Atlantoraja castelnaui	
17	Elasmobranchii	Rajiformes	Arhynchobatidae	Atlantoraja	Atlantoraja cyclophora	
18	Elasmobranchii	Rajiformes	Arhynchobatidae	Atlantoraja	Atlantoraja platana	
19	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja abyssicola	
20	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja aguja	
21	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja albomaculata	
22	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja aleutica	
23	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja andriashevi	
24	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja bergi	
25	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja brachyurops	
26	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja caeluronigricans	
27	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja cousseauae	
28	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja diplotaenia	
29	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja eatonii	
30	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja fedorovi	
31	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja griseocauda	
32	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja hesperaficana	
33	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja interrupta	
34	Elasmobranchii	Rajiformes	Arhynchobatidae	Bathyraja	Bathyraja irrasa	

Image 23: The result of the “Unstructured” taxonomy export.

	A	B	C	D	E	F	G
1	Subclass	Order	Family	Genus	Species	Total Species	
2	Elasmobranchii					1154	
3		Rajiformes				356	
4			Anacanthobatidae			13	
5				Anacanthobatis		8	
6					Anacanthobatis americanus		
7					Anacanthobatis donghaiensis		
8					Anacanthobatis folirostris		
9					Anacanthobatis longirostris		
10					Anacanthobatis marmoratus		
11					Anacanthobatis nanhaiensis		
12					Anacanthobatis ori		
13					Anacanthobatis stenosoma		
14				Sinobatis		5	
15					Sinobatis borneensis		
16					Sinobatis bulbicauda		
17					Sinobatis caerulea		
18					Sinobatis filicauda		
19					Sinobatis melanosoma		
20			Arhynchobatidae			96	
21				Arhynchobatis		1	
22					Arhynchobatis asperrimus		
23				Atlantoraja		3	
24					Atlantoraja castelnaui		
25					Atlantoraja cyclophora		
26					Atlantoraja platana		
27				Bathyraja		51	
28					Bathyraja abyssicola		
29					Bathyraja aguja		
30					Bathyraja albomaculata		
31					Bathyraja aleutica		
32					Bathyraja andriashevi		
33					Bathyraja bergi		
34					Bathyraja brachyurops		

Image 244: The result of the “Structured” taxonomy export.

4. Updates

Auto update

By default, the program is configured to search automatically for updates at each program start. You can change this configuration by using the menu “Configuration->Remote update->Automatic update”. It is possible to define the number of “Downloaded files” for each update. This option is particularly useful when installing iSharkFin for the first time. The program downloaded from the web page does not have the photographs that are in the database. Therefore, if the Internet connection is not very fast, the update process could take a long time, and it is possible to spread the downloading over several days.

Manual update

If you deactivated the automatic update, you can update the program at any time manually by using the menu “Configuration->Remote update ->Update management”. A window will appear where you can see a list of updateable files. You can apply filters for only updating certain file types of certain languages. To update, either hit the “Update all” button, for updating all files in the list, or make a selection of the files you wish to update and use the “Update selection” button instead.

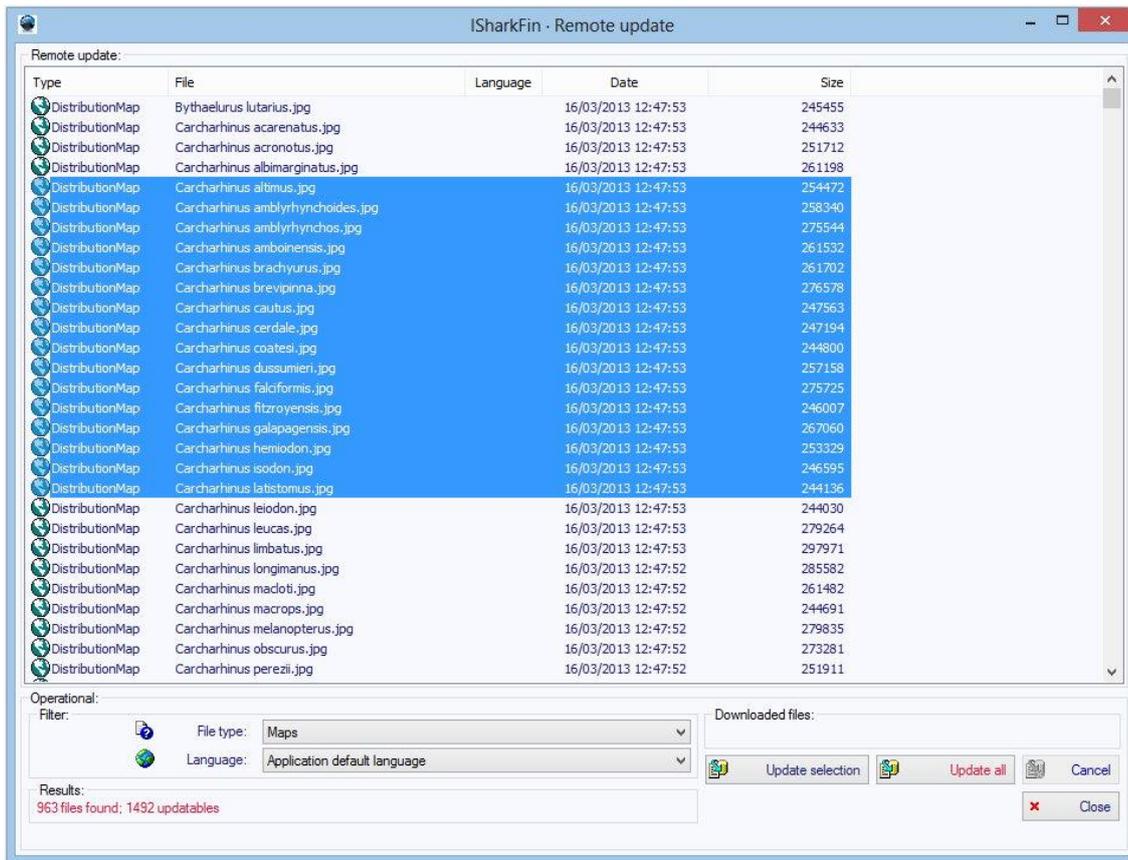


Image 24: The manual update window with a selection of distribution maps that can be downloaded from the iSharkFin server.

PRACTICAL PROTOCOL
STANDARD PHOTOGRAPHS OF SHARK FINS, AND TISSUE SAMPLING FOR GENETIC ANALYSIS

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What you need:

- A camera, smartphone or tablet.
- Background, possibly light blue (e.g. a yoga carpet or a plastic blue sheet, opaque to avoid the reflections).
- A rolling ruler (tape measure) to take length measurements.
- A ruler to be included in the photo as scale reference.
- Labels to include the code of the specimens in the photograph (species, place captured [GPS location or description], sex, total length, date).

1) If you have a whole shark

EXAMPLE IN LABORATORY

1) Photograph of the whole animal with the code label and the ruler on it.



2) Photograph of the ventral side (head and pectoral fins included).



3) Photograph of the first dorsal fin.



4) Photograph of the second dorsal fin.



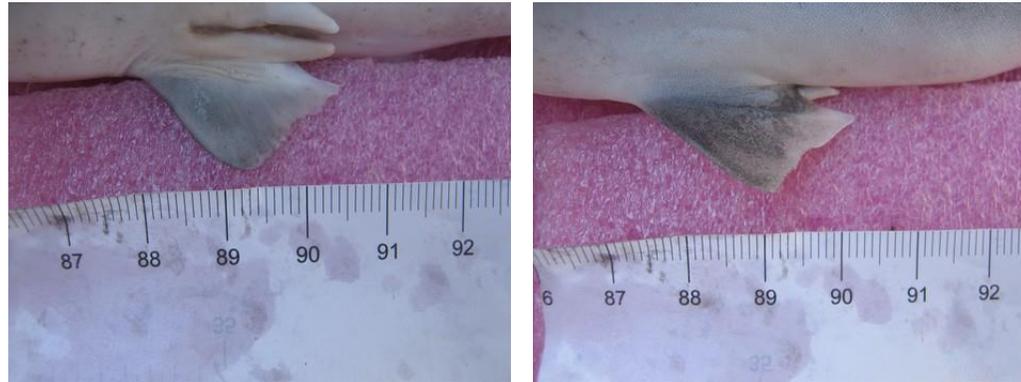
5) and 6) Photographs of both sides of the pectoral fin.



7) Photograph of the caudal fin.



8) and 9) Photographs of both (dorsal and ventral) sides of the pelvic fin.



10) Photograph of the anal fin.



EXAMPLE AT THE LANDING SITE

1) Photograph of the specimen.



2) Photograph of diagnostic characters (underside of head, teeth, caudal peduncle).



NOTES

- Take the photograph perpendicular to the plane of the fin (to avoid large distortions).
- The position of the individual fin should be as natural as possible.
- If the position of the shark, or the time available, does not allow you to take photographs the complete set of fins, give priority to the **first dorsal**, both sides of the **pectoral** and the **caudal**.

3) Photograph of the first dorsal fin. On the left, how to take the photograph; on the right, the resultant photograph.



4) Photograph of the second dorsal fin.



5) and 6) Photographs of both sides of the pectoral fin.





7) Photograph of the caudal fin.



8) Photographs of both sides of the pelvic fin.

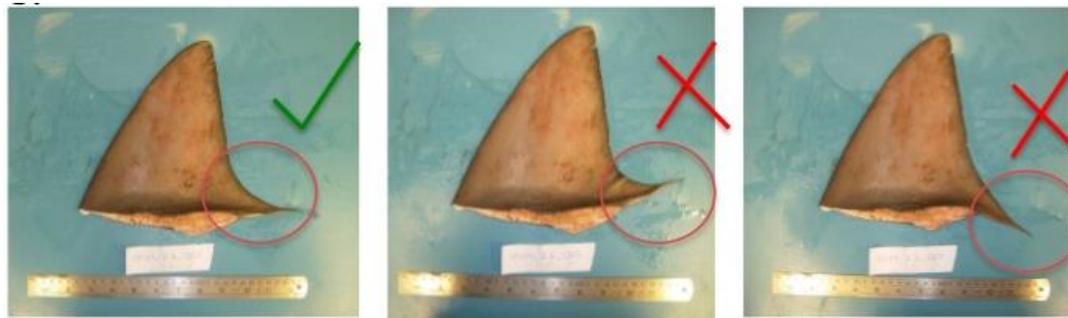


9) Photographs of the anal fin.



2) Examples of photographs of fins removed

Take pictures of the fin on a homogenous background with a ruler and possibly a label with the specimen code in the photograph. Make sure the specimen is in the most natural position possible, e.g.:



For pectoral and pelvic fins (or if you are unsure of which fin type it is), please take a photograph of both sides.



TAKING A TISSUE SAMPLE FOR GENETIC ANALYSIS

What you need:

1. Tools to cut and transfer the tissue, e.g. **scalpel and blades / surgical scissors and forceps**.
2. Vials containing **preservative** (such as 70 percent ethanol or a dimethyl sulphoxide [DMSO solution]) to store the sample, each to be assigned with a unique identifier. A volume of 1.5–2 ml per vial is sufficient. If no preservative is available, use sample bags and freeze the samples as soon as possible.
3. A **naming scheme** to reliably link the data collected for each specimen to its corresponding tissue sample.

Instructions:

Cut a small piece of skin and/or muscle tissue, a ~0.5 cm cube or more is recommended, or not more than one-third of the volume of the preservative in the vial (to ensure adequate preservation). The tissue can come from anywhere on the specimen, but an easy method is to cut a V-shape from the edge of a gill slit (as pictured) using scissors, or through the softer skin under the pelvic fins using a scalpel blade.

Importantly, take the samples in a way that minimizes or prevents cross-contamination among samples. This is of particular importance where samples are intended for forensics. In most cases, taking a sample with skin and some internal tissue is suitable. Best practice would be to use a new scalpel blade for each specimen or to sterilize tools between specimens, and to sample internal parts of the specimen, avoiding exposed surfaces. (Pocket sharps disposal containers and bleach wipes are a useful way to achieve this under field conditions). In any case, it is worth quickly noting the collection protocol used for the genetic analyst. If you feel there is high potential for contamination among specimens under your conditions, cut larger samples to allow the analyst to sample away from the exposed edges of the tissue sample when conducting the DNA extraction.

Include with your collected samples a datasheet linking unique sample identifiers with specimens, and detailing the preservative and dilution. If shipping your samples, ensure they are adequately preserved (do not post frozen material at ambient temperature). Consider the shipping implications before choosing a preservative; for example, many air freighters will not allow ethanol solutions stronger than 70 percent. Including a Material Safety Data Sheet (MSDS) for the preservative can prevent potential delays with some carriers.

Note that CITES-listed species cannot be shipped internationally without a permit.



Image: Taking a V-shaped tissue sample from a gill slit using surgical scissors.