

SpermTree How-To!

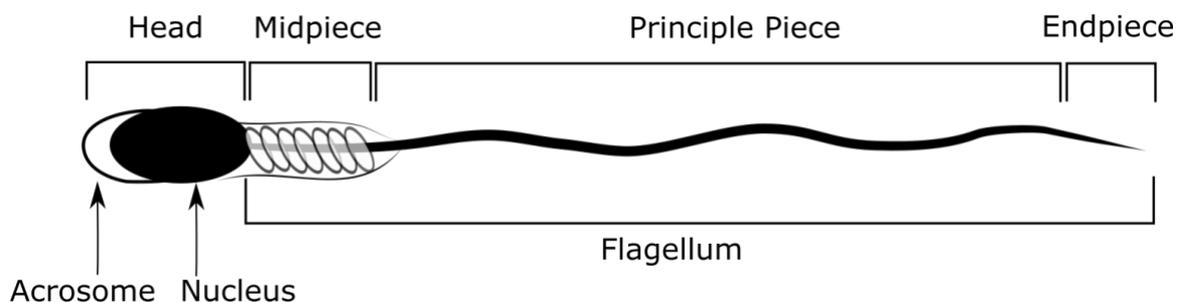
Thanks for your interest in helping the community build a bigger and better SpermTree! We can use your help in many ways to make this dataset a better resource for everyone.

What and how can I contribute?

Currently we are only adding data on sperm morphology to SpermTree (though we hope to add more reproductive data in the future). You can contribute data from measurements you have generated from the taxa you are working on or data that you have found that is currently absent in the database. We have created an xlsx template file with a few rows of examples. You can easily add data to the template and email it to spermtree@zoologi.su.se. If the paper you are citing is a rare source (not easily accessed online), then please include a pdf (if possible) with your email. Once we have vetted the data, we will add it to the database on the next update!

Some details for formatting your data in the template file:

- First, please read the details in the column descriptions tab in the excel file. Information about what should be added to each column is listed there. We have broken the dataset into two sections, the current 'core' data, and 'new' data (data which we hope to add as SpermTree grows). New data are found at the far right of the spread sheet and colored green.
- We ask that you only add information for each line that is specifically discussed or described in the paper that is cited for that line.
- For phylogenetic information, please use taxonomy from the Catalogue of Life: <https://www.catalogueoflife.org/>. If you are unsure of the correct taxonomy, please leave this area blank, and we will fill it out. Do not update the Genus and Species column with new taxonomy, **please use the name used in the original paper**.
- If there is information about where the population was collected, feel free to add this info to the population column.
- In the current database we have combined some measurements of the cell to calculate flagellum length and total length. We ask that you please ONLY include the raw data that is listed in the paper, and do not sum these values when you submit.
- Because research spans over 120 years and this cell can be variable in morphology, the nomenclature used to describe the parts of the cell can vary over time and between taxa. If you are unsure about which part of the cell is being described, you may add these lengths to the notes section instead of the table or send us an email and we can discuss how best to format your data. Below is a diagram of a 'standard' sperm, with the nomenclature that we use in the database.



- Sperm take a wide variety of shapes. To simplify analyses, we have categorized sperm as 'standard' (like the cell above, with or without the midpiece), 'bi- or multiflagellate', 'aflagellate', or 'heteromorphic'. These classifications are listed in the 'Sperm Type' column, and are coded in the 'SpermTypeCode' column. In some cases, the heteromorphic cells can fall into multiple categories. When coding these cells, please use S-HET for sperm where the fertilizing sperm is a standard morphology, and NS-HET when the fertilizing sperm is a 'non-standard' morphology (you can also use AF-HET or other codes in combination). If the fertilizing cell morph is unknown for heteromorphic sperm, please list all lengths in the notes column.
- If there are any details about that species' sperm morphology that seem interesting or important (i.e. number of flagella, lengths that do not fit into the column categories, presence/size of hooks, appendages, or undulating membranes etc.), then please add this information into the notes section.
- Citation format follows that of the journal Evolution. Please list the short format (e.g. Franzen 1956) in the 'Source: Sperm morphology' column, and list the full citation in 'citation_sperm1'. Here's a guide for formatting: <https://paperpile.com/s/evolution-citation-style/>

How do I report an error?

We have done our best to make sure that the data in SpermTree is high quality, but with this much data some errors may have slipped past us. If you find one, then please let us know. You can send us an email at spermtree@zoologi.su.se and give us the details and we will correct it as soon as possible.

Would you like to become a curator?

As the database grows, so does the need for curation. We hope we can build a team of curators to spot-check the database, add new data/traits, and who will be recognized for their hard work on the website and twitter account @SpermTree. If you are interested in becoming a curator, then we would love your help. Send us an email at spermtree@zoologi.su.se and we will get you set up.

How can I use the database?

You can use it however you like. We hope that as many people use this resource as possible to ask new and interesting questions about the evolution of sperm. We just ask that you cite the database in your paper.

What if I have other reproductive traits that I want to submit now?

We hope that we can expand the number of traits in SpermTree to include other reproductive traits in the future (both male and female). If you would like to submit such reproductive traits along with sperm morphology data, feel free. You can add new columns to the right of the 'new' data section in the xlsx file. However, it will take some time for new traits to be added into the main database. There are empty columns available in the excel sheet where these traits can be added.