

# Interpreting your eDNA data

Ka pai – you've taken your first eDNA sample!

After you sent your sample to Wilderlab, they extracted the DNA collected on the filter and the DNA in the sample was sequenced. The DNA sequences detected were then matched to species where possible, and you received an email to say your sample report is available.

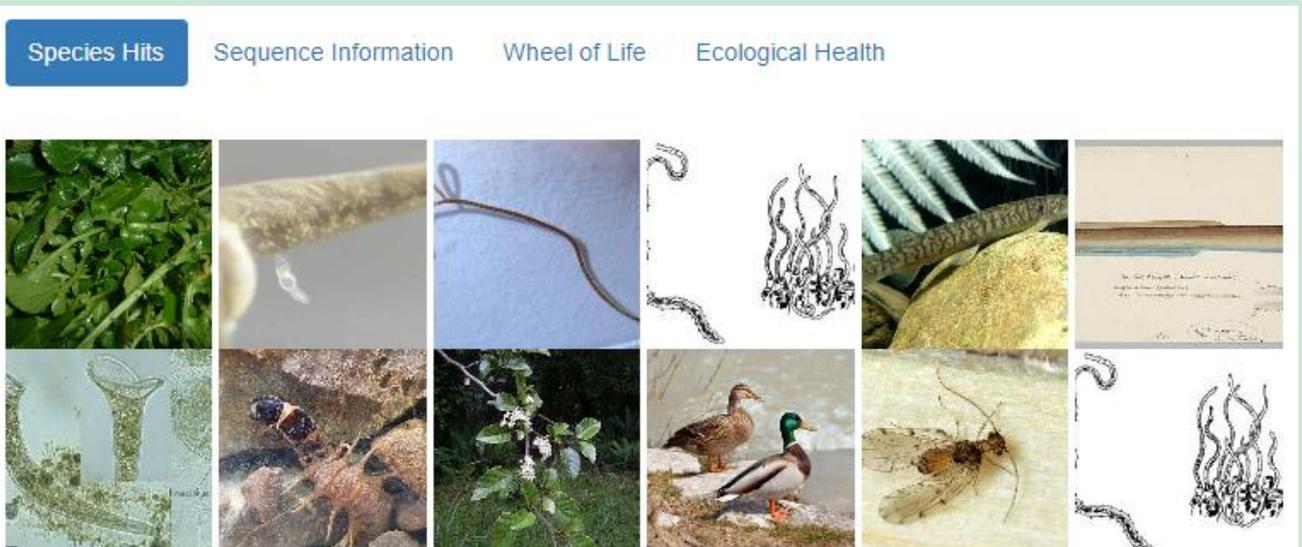
Here, we take you through the different layers of your sample report, ways you can explore the data there, and some information about eDNA data. For more in-depth information on this topic, you're invited to watch our 'Understanding your eDNA data' webinar at [www.epa.govt.nz/eDNA](http://www.epa.govt.nz/eDNA) under 'Resources'.

## Get information from your eDNA sample

Now you've received your results, set aside some time to go over the information on the species you found, eDNA sequences, ecological health and biodiversity.

There is no one-size-fits-all approach to interpreting your data. It comes down to your questions and interests. The context and stories of the place and environment the sample was from are important to keep close as you consider the results.

## Exploring your sample report



### Species hits

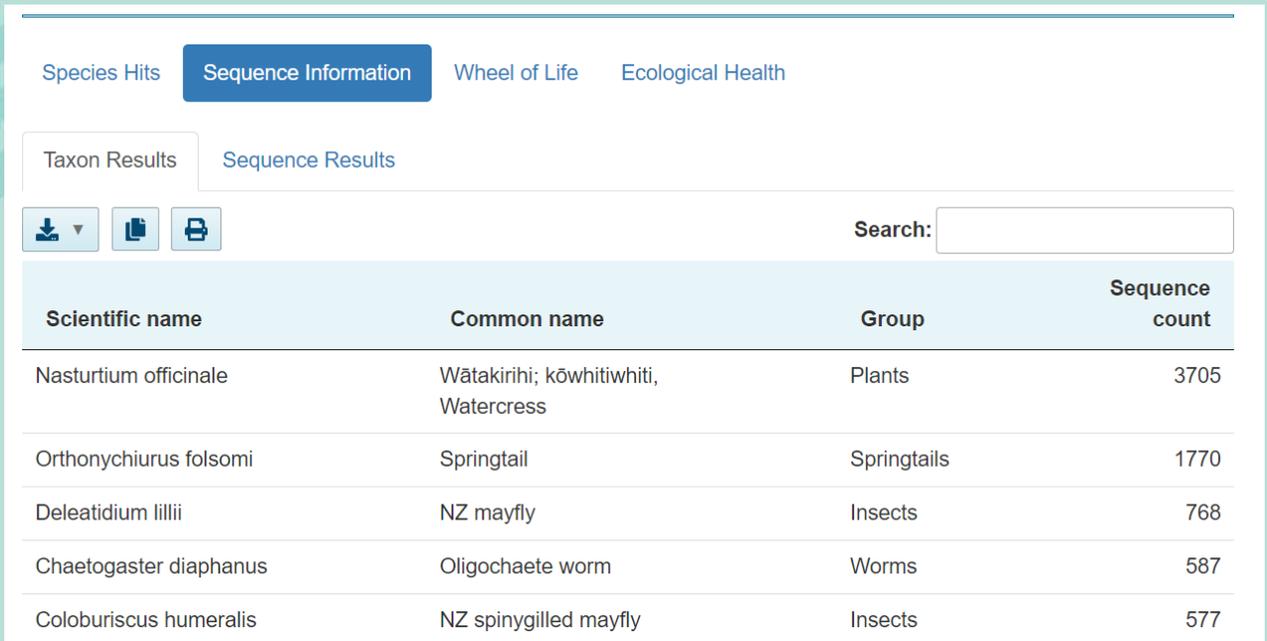
The species hits tab displays images of species found in your sample that link to Wikipedia pages. This is a great place to start.

Get curious, explore, and learn more about the species you might not have heard of.

# Sequence information

The sequence information tabs provide a complete list of all the species detected in your eDNA sample. As you scroll down the list, you'll see names for sequences that don't match to exact species but can be matched to another category, like genus or family. These are listed in order of the number of eDNA sequences counted in the sample for each species. Within this tab, you can:

- search for species or groups of species (eg, fish) that you are interested in
- export as a csv or excel file to sort the data or make graphs
- save as a pdf to share with others, or copy the sample report website address



Scientific name	Common name	Group	Sequence count
Nasturtium officinale	Wātakirihi; kōwhitiwhiti, Watercress	Plants	3705
Orthonychiurus folsomi	Springtail	Springtails	1770
Deleatidium lillii	NZ mayfly	Insects	768
Chaetogaster diaphanus	Oligochaete worm	Worms	587
Coloburiscus humeralis	NZ spinygilled mayfly	Insects	577

## A note on sequence count:

The sequence count is an indication of how many times a DNA sequence matched to a name was counted. It is not an indication of how many individuals with that name were detected.

Although sequence counts can give you a loose indication of what the most dominant things are in your area, Wilderlab recommends you use the data mainly to detect the presence and absence of organisms.

This is because there are lots of things that can influence eDNA sequence counts including:

- the distance of organisms from the sampling point
- the type and size of organisms
- the presence of dead/decaying organisms
- environmental factors that can speed up or slow down eDNA breakdown.

## Unexpected results

Occasionally, some organisms that are not physically living in the area are picked up in your eDNA results.

The DNA of different organisms become introduced to your sample site from other places. Common culprits are gumboots, vehicles, other animal waste (such as dog or shag faeces), and run off from urban and farming areas.

It is also possible to miss species that you expected to see. This can happen because:

- there are insufficient sample replicates – while there are benefits to doing one test at a site, sometimes you might miss things. Wilderlab recommends taking six tests per site at the same time to capture over 90% of the biodiversity present
- the species you expect to see isn't in the reference database or is not in the scope of Wilderlab's tests.

## TICI score – applicable for samples from flowing freshwater

A TICI score and rating from 'very poor' to 'pristine' is included in some sample reports.

Wilderlab developed this ecological health index to use all the sequences from your sample to calculate an overall score.

It is currently only included for samples from rivers or streams.



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o te Taiao**  
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A programme  
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Environmental  
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