**Table S1**: GenBank/ENA accession numbers of published sequences used in the present study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Species | origin | Reference | GenBank/ENA accession number |  |
|  |  |  | COI-5P | *psb*C | *rbc*L  | nrDNA |
| ***Battersia*** |  |  |  |  |  |  |
| *B. arctica* | Sweden  | Draisma *et al*., 2002, 2010 |  | FM957139 | AJ287881 |  |
| *B. plumigera* | Scotland  | Draisma *et al*., 2002, 2010 |  | FM957140 | AJ287878 |  |
|  | Japan (KU687) | Draisma *et al*., 2010 |  | FN667657 | FN667656 |  |
| *B. racemosa* | Scotland | Draisma *et al*., 2002, 2010 |  | FM957138 | AJ287880 | AJ311817 |
| ***Chaetopteris*** |  |  |  |  |  |  |
| *C. plumosa* | Norway | Draisma *et al*., 2002, 2010 |  | FM957109 | AJ287879 |  |
| ***Cladostephus*** |  |  |  |  |  |  |
| *C. spongiosus* | Netherlands | Draisma *et al*., 2001, 2010 |  | FM957136 | AJ287863 |  |
| *C. kuetzingii* (as *'C. spongiosus* f. *hedwigioides'*) | Falkland Is. | Mystikou *et al*., 2016 | LN828731 |  |  |  |
| *C. hirsutus* (as *'C. spongiosus'*) | New Zealand | Draisma *et al*., 2010 |  | FM957146 |  |  |
| *C. hirsutus* (as *'C. spongiosus'*) | Australia | Draisma *et al*., 2010 |  | FN667652 | FN667651 |  |
| *C. hirsutus* (as *'C. spongiosus'*) | France | Bittner *et al.,* 2008 | EU579864 |  |  |  |
| *C. hirsutus* (as *'C. spongiosus'*) | France | Bittner *et al.,* 2008 | EU681396 |  |  |  |
| ***Sphacelorbus*** |  |  |  |  |  |  |
| *S. nanus* |  | Draisma *et al*., 2010 |  | FM957137 | AJ287875 |  |

**Supplementary Table S2**: Uncorrected base pair differences (absolute and percentage) within and between species of *Cladostephus*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | *rbc*L (943 bp) | *psb*C (1038 bp) | COI-5P (543 bp) | ITS (805 bp) |
| *C. spongiosus* (Clade 1) | 0 (3 bp for AJ287863) | 0 bp | 0 bp | 0-3 bp (0-0.4%) |
| *C. hirsutus* (Clade 2; all samples) | 0-3 bp (0-0.3%) | 0-4 bp (0-0.4%) | 0-11 bp (0-2%) | 0-4 bp (0-0.5%) |
| excl. "Mediterranean"\*  | 0 bp | 0 (1 bp for FN667652) | 0 bp | 0-4 bp (0-0.5%) |
| "Mediterranean"\* subclade | 0-3 bp (0-0.3%) | 0-4 bp (0-0.4%) | 0-11 bp (0-2%) | 0-2 bp (0-0.2%) |
| "extra-Mediterranean" vs*.* "Mediterranean"\* subclade | 0-3 bp (0-0.3%) | 1-4 bp (0.1-0.4%) | 2-9 bp (0.4-1.7%) | 0-4 bp (0-0.5%) |
| *C. kuetzingii* (Clade 3) | 0-5 bp (0-0.5%) | 0-3 bp (0-0.3%) | 0-13 bp (0-2.4%) | 1 bp (0.1%)\*\*\* |
| *C. spongiosus* vs. *C. hirsutus* (i.e. Clade 1 vs. Clade 2) | 2-9 bp (0.2-1%) | 8-16 bp (0.7-1.4%) | 34-42 bp (6.3-7.7%) | 14-47 bp (1.7-5.8%)\*\* |
| *C. spongiosus* vs. *C. kuetzingii* (i.e. Clade 1 vs. clade 3) | 5-13 bp (0.5-1.4%) | 8-13 bp (0.7-1.1%) | 29-39 bp (5.3-7.2%) | 14-43 bp (1.7-5.3%)\*\* |
| *C. hirsutus* vs. *C. kuetzingii* (i.e. Clade 2 vs. Clade 3) | 2-8 bp (0.2-0.8%) | 12-21 bp (1.1-1.8%) | 37-48 bp (6.8-8.8%) | 12-34 bp (1.5-4.2%)\*\* |

\* including SBDN 850A from Portugal

\*\* lowest values due to not all sequences covering the whole length of the alignment

\*\*\* only two sequences were included in the ITS alignment