Fig. S1. Neighbour-joining tree reconstructed using the sequences of a fragment (658bp) of the cytochrome c oxidase subunit I gene of specimens currently identified as Lasioglossum villosulum, Lasioglossum medinai and one as Lasioglossum berberum in our sampling and in the public repositories (GenBank and BOLD). The tree is drawn to scale, with branch lengths representing p-distances (proportions of variable sites). AP222 Lasioglossum bluethgeni was used as outgroup. Labels at the end of each branch include our own ID (starting with AP) or GenBank accession number or BOLD process ID or originating country. A. Lasioglossum medinai. B–D. Three supported clusters (a fourth cluster could be defined in C by partitioning in C 1-2) within Lasioglossum villosulum. Labels highlighted in red correspond to possible morphological misidentifications (see Discussion). Label highlighted in blue corresponds to L. berberum. Values at nodes correspond to bootstrap values (%).