Geometric morphometrics of wing shape recover tribe association of fossil and contemporary halictid bees (Hymenoptera: Halictidae: Halictinae).

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Taxonomic attributions of fossils are often difficult because descriptions and phylogenetic analyses are mainly based on a small data set of available morphological characters. By integrating numerous information, shapes of rigid structures can help palaeontologists to support their taxonomic hypothesis. Here we study taxonomic attribution of bee fossils by analysing wing shape of fossil and extant taxa. Compared with other organs, wings show many methodological advantages, such as 2D structure, rigidity, species specificity and good conservation in fossil specimens from amber and compression. Moreover, wing veins and their intersections are unambiguously homologous among bees. In the present study, model taxa are halictid bees (Hymenoptera: Halictidae: Halictinae). Halictinae is a well known cosmopolitan group including more than 2500 species in five tribes described from robust molecular data. We sampled 202 specimens of Halictinae (2 fossils, 110 Halictini, 28 Auglochlorini, 27 Caenohalictini, 22 Sphecodini and 13 Trinchostomini) and 5 specimens from the sister subfamilly (Nomiinae) as comparison group. To analyse wing shape, we adapted the geometric morphometrics method as detailed in Aytekin *et al.* (2007) by using 19 landmarks. Ordination methods as canonical variates analysis (CVA) were used to discriminate the tribe. Wing shape clusters of contemporary taxa were congruent with clade from molecular analysis indicating that the phylogenetic signal is strong in the shape of halictid wings. However the “morphometric affinity” of the two fossil taxa do not confirm their original taxonomic attribution. By re-examining the fossil description we propose new taxonomic attribution. This new method of fossil study could be helpful in fossil calibration in molecular clock analyses.