

Appendix 2:

Networks showing most parsimonious relationships among repeated elements from all nine Belgian *G. olivacea* individuals, inferred using the criterion of parsimony with the program TCS 1.13 from Clement et al. (2000). Each repeat is represented by a rectangle and is named after the individual it comes from followed by a number identifying the position of the repeat in the sequence. For example, "B1-5" refers to repeat number 5 from individual GoliB1. Repeat elements not separated by a branch represent identical sequences (e.g., B2-12 and B3-12). Each branch represents a single mutational step, i.e., one nucleotide substitution or one insertion/deletion event. Empty circles represent missing (i.e., unobserved) intermediate sequences. Only the branches of length ≤ 5 are represented because this is the "parsimony limit" (i.e., a most parsimonious relationship of 5 steps or fewer has a probability of $>95\%$ of being true) that is estimated by the statistical parsimony approach (Templeton et al., 1992).

