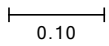


A

B

C



**Figure S9. Maximum Likelihood tree of lepidopteran alpha-amylases, computed and drawn using MEGA7 (Kumar et al., 2016) from an alignment of 47 protein sequences.** Positions with less than 95% site coverage were eliminated, and 473 positions were left for analysis. The tree with the highest log likelihood (-14029.00) is shown. The tree was drawn to scale, branch lengths representing the number of substitutions per site. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.5450)). A, B and C boxes indicate the three amylase types we identified in Lepidoptera.