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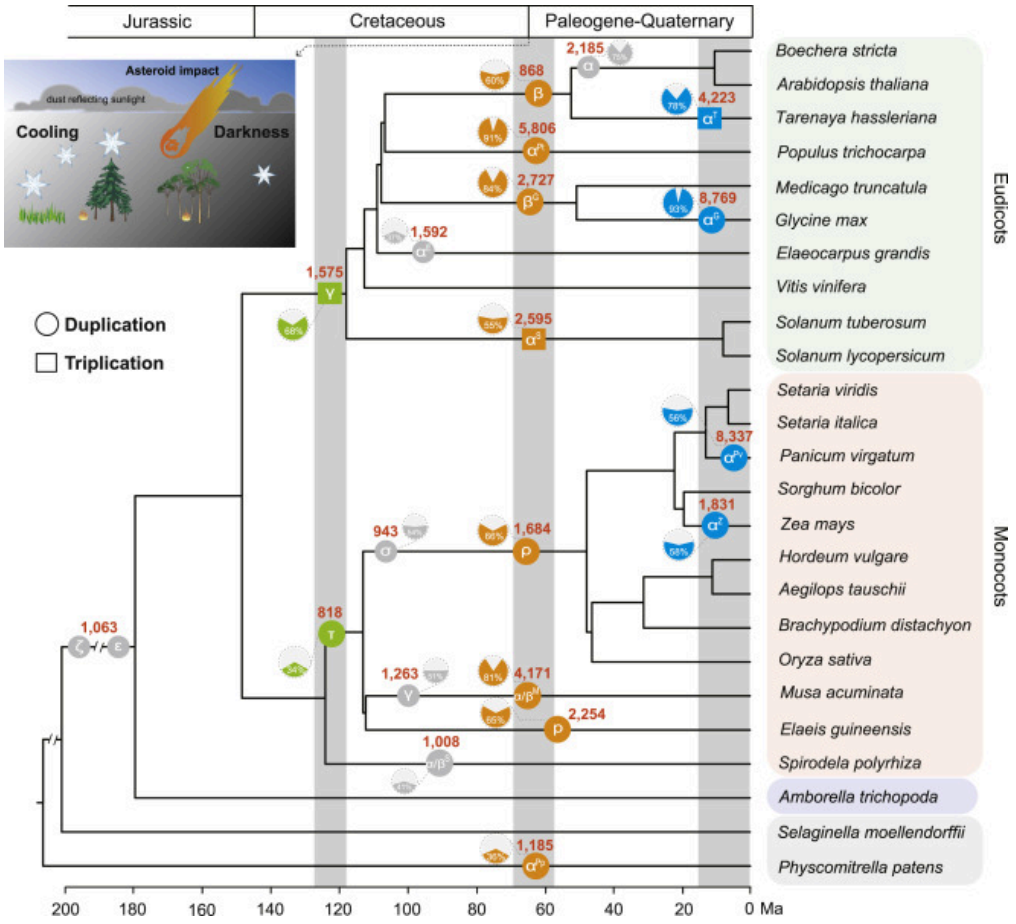
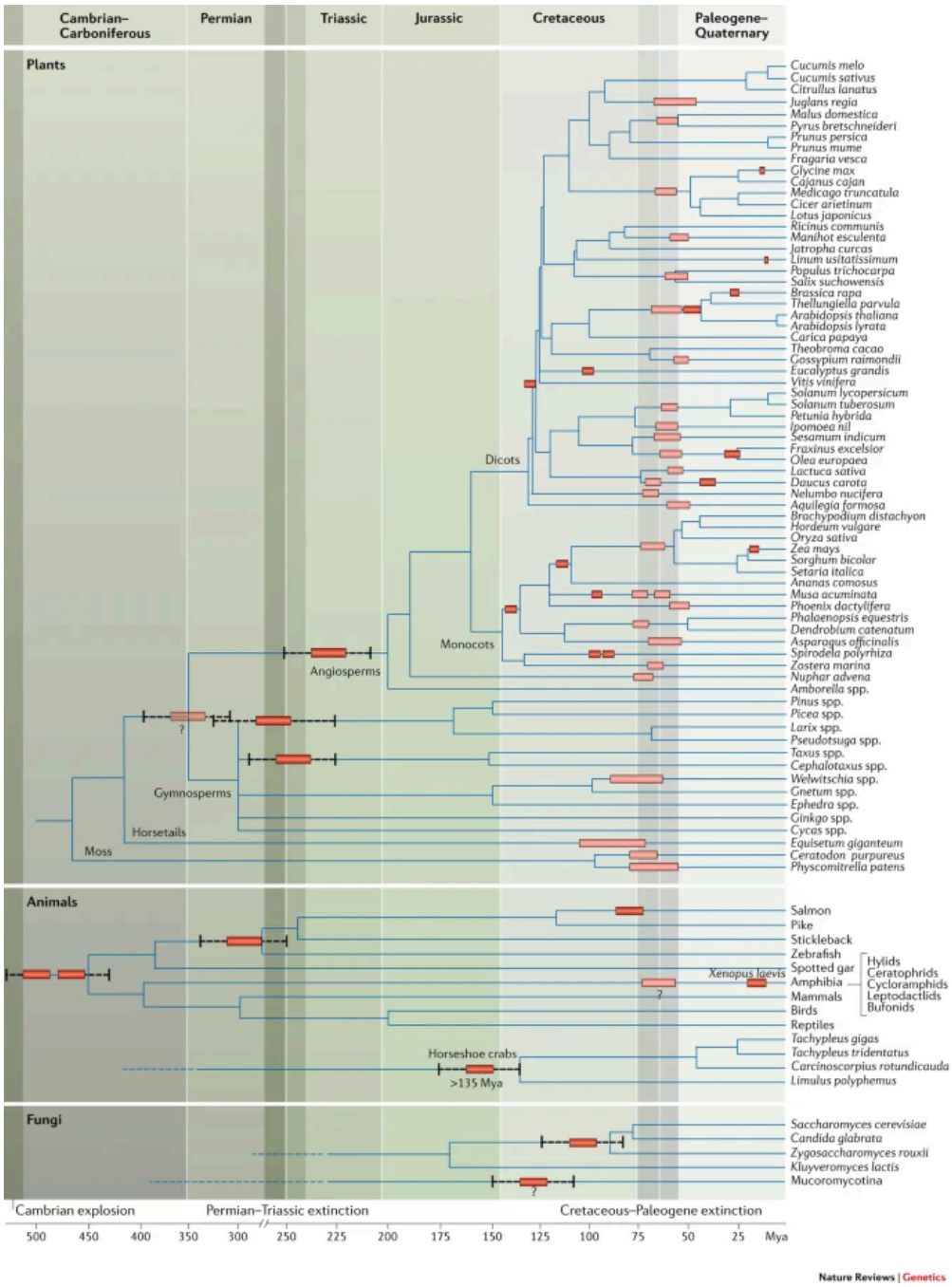


Three periods (~120, ~66, and <20 Ma) with prolific WGDs were recognized, and are denoted in green, orange, and blue, respectively. The number of gene families with duplicates retention following each WGD are shown around the corresponding circle or square. The proportion of the duplications verified by synteny evidence were generated from WGDs, which were indicated in the dashed circles. A sketch map in the upper left shows the major environmental stresses during the Cretaceous-Paleogene extinction period.
https://www.sciencedirect.com/science/article/pii/S1674205219303594



A pruned tree for plants160,161, animals and fungi showing the evolutionary relationship between species for which the genome sequence or extensive transcriptome data are available and which are representative for the topic of polyploidy. Mapping of whole- genome duplications (WGDs) described in previous studies68,73,97,162,163,164,165,166,167,168,169,170,171,172 onto the tree (rectangles) has been performed to the best of our knowledge, with bold black dashed lines reflecting uncertainty in the date of the events. WGDs estimated to be between 55 and 75 million years old (shaded area around the Cretaceous–Paleogene boundary) are indicated by light red rectangles. Mass extinction events are indicated by shaded areas with

boundaries 10 million years either side of the predicted date of the event. Mya, million years ago.

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