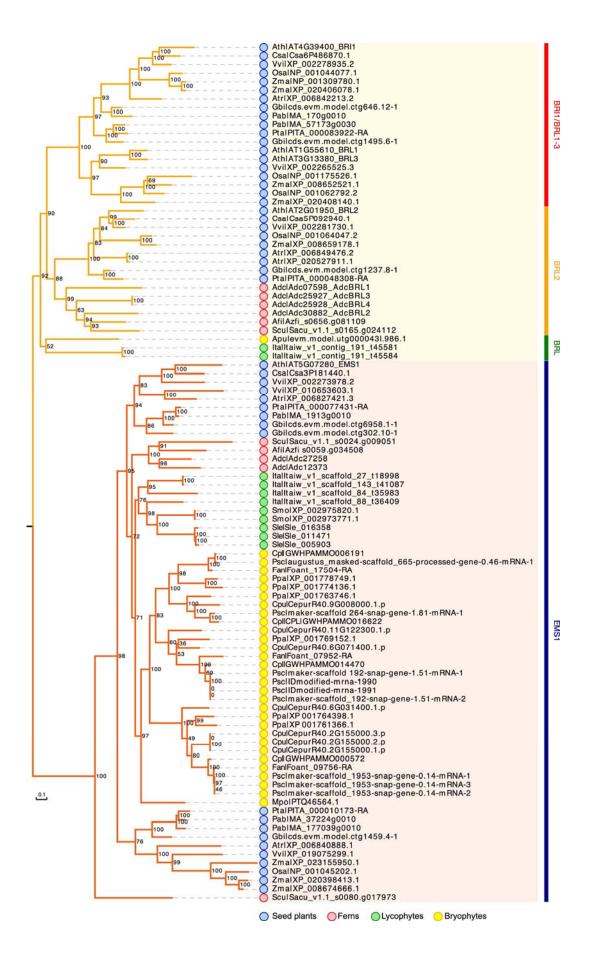
Extended Data Fig. 4: The maximum-likelihood tree of the *BRI1-BRL* and *EMS1* gene family in land plants.

From: The genome of homosporous maidenhair fern sheds light on the euphyllophyte evolution and defences



The domains of *BRI1-BRL* (TM, LRR, ID, and KD) and its closest gene family *EMS1* (TM, LRR, and KD) were identified from all main land plant groups (in different colours). Maximum-likelihood tree was constructed with parameters: WAG + F + R6 model and 1,000 bootstrap replicates. Whole genome assemblies from 24 species were used for identification of *BRI1-BRL* and *EMS1* homologs, including 9 bryophytes (Mpo, *Marchantia polymorpha*; Cpl, *Calohypnum plumiforme*; Fan, *Fontinalis antipyretica*; Cpu, *Ceratodon purpureus*; Ppa, Physcomitrella patens; Psc, Pleurozium schreberi; Aan, *Anthoceros angustus*; Aag, *Anthoceros agrestis*; Apu, *Anthoceros punctatus*), 3 lycophytes (Ita, *Isoetes taiwanensis*; Smo, *Selaginella moellendorffii*; Sle, *Selaginella lepidophylla*), 3 ferns (Adc, *Adiantum capillus-veneris*; Afi, *Azolla filiculoides*; Scu, *Salvinia cucullata*), and 9 seed plants (Pab, *Picea abies*; Pta, *Pinus taeda*; Gbi, *Ginkgo biloba*; Ath, *Arabidopsis thaliana*; Atr, *Amborella trichopoda*; Csa, *Cucumis sativus*; Osa, *Oryza sativa*; Vvi, *Vitis vinifera*; Zma, *Zea mays*). The detailed information is provided in Supplementary Data 19.