Supplementary Figures

(a)

(b) 2001 2004 2007 2010 2013 2016 2019 2020

#0 arabidopsis leave
#1 maize pulvini
#2 specific function
#3 panicum virgatum
#4 secondary metabolite
#5 genome-scale reconstruction
#6 transcriptome analysis
#7 transcriptome characterization
#8 situ freezing tolerance
#9 full-length transcriptome analysis
#10 nmr-based metabolomics
#11 nmr-based metabolomic analysis
#12 individual element
#13 tomato ovaries
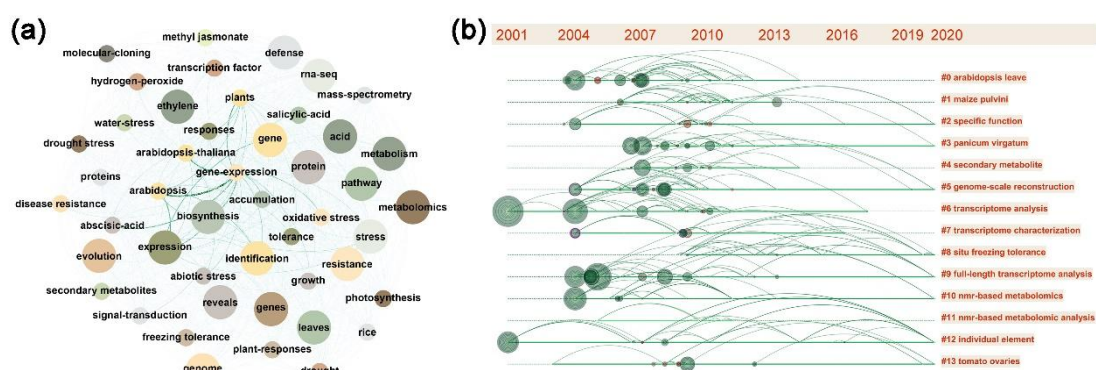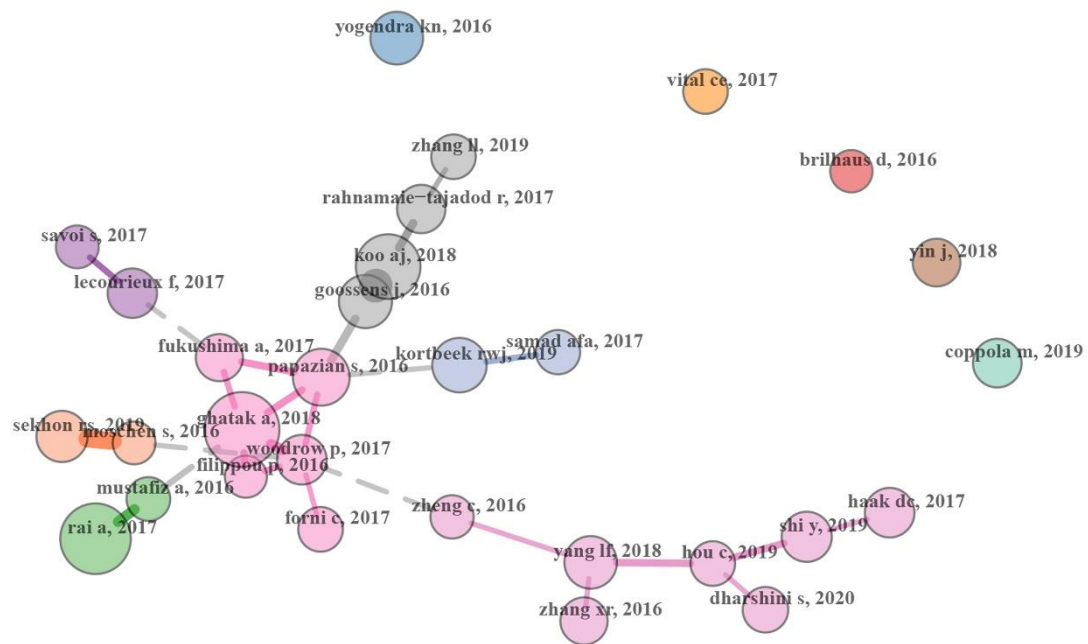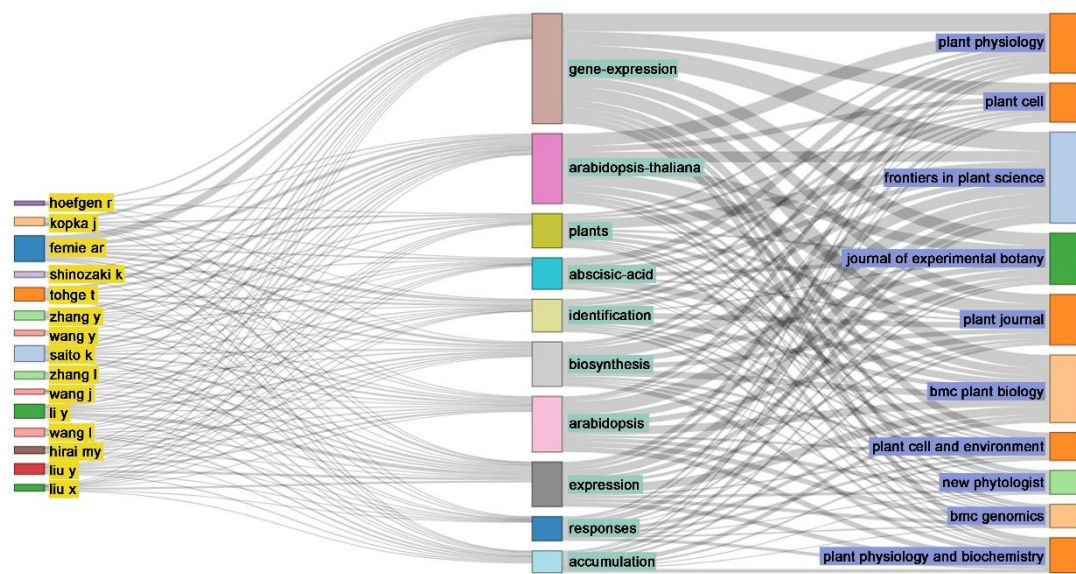
Figure S1 Conceptual structure of TMPQE during 1994–2020.
(a) Major keywords network of co-occurrence. (Nodes represent keywords, edges connect keywords that co-occur, and the width of the edges indicates the frequency of these co-occurrences)
(b) Timeline view for document co-occurrence cluster. (Each circle denotes a cited article, with its size proportional to its citation count, and these citations are chronologically ordered along the horizontal axis. The vertical axis categorizes the citations by broad topics, illustrating the interconnectedness of related research areas)

Figure S2 Bibliographic coupling analysis of the literature of TMPQE in 2016-2020 （Each literature is represented as a node, with the size of the node indicating the local citation counts of the literature. The color of the node signifies the literature's cluster）

Figure S3 Sankey plot of top 20 author-top 10 keyword plus-top 10 journal in research on TMPQE.