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## TeaAS: a comprehensive database for alternative splicing in tea plants (Camellia sinensis)

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### Title

TeaAS: a comprehensive databasefor alternative splicing in tea plants (Camelliasinensis)

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### Abstract

Alternative splicing (AS) increases the diversity of transcripts and proteins through the selection of different splicesites and plays an important role in the growth, development and stress tolerance of plants. With the release of the reference genome of the tea plant (Camellia sinensis) and the development of transcriptome sequencing, researchers have reported the existence of AS in tea plants. However, there is a lack of a platform, centered on different RNA-seqdatasets, that provides comprehensive information on AS. To facilitate access to information on AS and reveal the molecular function of AS in tea plants, we established the first comprehensive AS database for tea plants (TeaAS, [http:// www. teaas. cn/ index. php](http://www.teaas.cn/index.php)). In this study, 3.96 Tb reads from 66 different RNA-seq datasets were collected to identify AS events. TeaAS supports four methods of retrieval of ASinformation based on gene ID, gene name, annotation (non-redundant/Kyoto encyclopedia of genes and genomes/gene ontology annotation or chromosomal location) and RNA-seq data. It integrates data pertaining to genomeannotation, type of AS event, transcript sequence, and isoforms expression levels from 66 RNA-seq datasets. The ASevents resulting from different environmental conditions and that occurring in varied tissue types, and the expression levels of specific transcripts can be clearly identified through this online database. Moreover, it also provides two useful tools, Basic Local Alignment Search Tool and Generic Genome Browser, for sequence alignment and visualization of gene structure. The features of the TeaAS database make it a comprehensive AS bioinformatics platform for researchers, as well as areference for studying AS events in woody crops. It could also be helpful for revealing the novel biological functions of AS in gene regulation in tea plants.

