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A review on the genome-based approaches for the development of stress and climate resilient tea crops

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Abstract

Tea is one of the most significant plantation crops to be emphasized towards research on climate-resilient variants that survive during various environmental stresses, which affects the productivity of crop across the world including India. Recently, the advancements in the tea genome research eased the thought to apply this strategy for various crop improvement programs that addresses biotic, abiotic stresses and productivity. Though the effect of climate change with unpredictable weather conditions on tea crop's resistance is unclear, DNA based, and genomics-assisted breeding techniques might play prominent role in facing future challenges of crop improving set-ups. Transgene based technological advancements and molecular breeding strategies have simplified the progress of elite tea genotypes with robust adaptation to climate change and the genomics-assisted breeding strategies in specific, found to play a substantial part in the advance of climate resilient tea crops. In this review, we briefed the signs of progress in tea genome-based research and their future perspectives needed to address the current challenges we face due to the climate crisis and to breed for the abiotic stress tolerant tea plant.

Keywords

Camellia sinensis; tea genomics; climate-resilient; drought tolerant; stress tolerant.

Introduction

Tea plant (*C. sinensis* (L.) O. Kuntze) is an evergreen, cross- pollinated, perennial, plantation crop of the Theaceae family. It grows up to 15 m but under cultivation, the bush height is 0.6 - 1 m for harvesting the tender leaves . Tea is one of the first non-alcoholic caffeine-containing beverages recorded on this planet.

Tea as a beverage was known for about 3000 years in China, was believed that it originated in south-east Asia. However, it is recently confirmed through genomic sequencing that tea is diverse in origin. Currently, tea is cultivated all over the world and more than 60 countries produce more than 6 million tonnes of tea per annum and the major manufacturers are China, India, Sri Lanka, and Kenya (1).

Suitable environment condition

Tea plants grow normally at 18 and 20°C. The soil should be well-drained, aerated, enriched with a pH from 4.5 to 5.5. Prolonged drought, waterlogged conditions, and low temperature (less than 12°C and above 30°C) are not suitable for the growth of tea. The minimum annual rainfall of 1200 mm and 70-75% average relative humidity is suitable for the growth of tea plant (2).

Seed and clonal propagation in tea plant

Tea plant is propagated through seeds or through clonal propagation (vegetative means by stem cuttings). Vegetatively propagated tea plants are denoted as clones or accessions which exhibit homogeneity in their morphology and physiology. This consistency and flexibility in choices have aided the progress of 'clones', which are high yielding than tea plants raised from seeds. Perhaps, seedling teas offer very valuable genetic diversity required for crop enhancement in many plantations and nurseries.

Types of manufactured tea and their health benefits

The tea plants under cultivation are viz., the short leaved “China” plants, *C. sinensis* (L.) O. Kuntze and the broad-leaved "Assam" cultivar, *C. assamica* (Masters) Wight. The “Cambod” variety, a subspecies of the latter, is considered as *C. assamica* sub sp. *lasiocalyx* (Planchon ex watt) Wight (3).

Tea currently made in the world are six main types based on its processing methods, namely black tea, green tea, white tea, yellow tea, oolong tea, and the reprocessed tea. Green tea is known as unfermented tea, on contrary; black tea is a fully fermented tea with the characteristic colour and taste of black tea. Oolong tea is a half-fermented tea (4).

Tea beverage is the second most commonly drank liquid after water. The black and green tea are produced and consumed mainly, with small amounts of other types. Tea drink is the most preferred refreshing non-alcoholic beverage in almost all countries and used as a both common and healing drink. In Chinese traditional medicine Green tea is used for the treatment viz. headaches, body pain, digestion problems, improvement of the immune system, cleansing, as a stimulant, and to extend life (5). Tea has vital minerals and trace elements required for human well-being apart from Potash, Manganese, Chromium, Nickel, and Zinc (6).

Hybrid status of tea species

Due to widespread hybridization among diverse *Camellia* species, numerous intergrades, introgressants, and putative hybrids were produced. Hybrids have physical characters that cover from China types through intermediates to those of Assam types. The extreme hybridization might have resulted in ambiguity on the presence of true tea archetypes (7). Hence, certain genotypes are propagated vegetative means by stem cuttings and released as clonal assortments.

“China”, “Assam” and “Cambod” type and many of their hybrids are exploited commercially in most of the tea plantations. It is thought that several wild species of *Camellia* have also played a role in the present-day hybrids of cultivated tea florae and Botanists have always been concerned to identify such hybrid tea crops (8).

Hybridization between clones was initiated to develop biclonal seed stocks combining the desirable attributes found in different clones and a handful number of biclonal seed stocks have been found to be highly promising in field trials. But it is largely accepted that at least three taxonomic groups i.e., *C. assamica*, *C. sinensis,* and *C. assamica* sub sp. *lasiocalyx* have mainly contributed to the gene pool of tea cultivars (9). The term ’tea’ should consequently include descendants of these taxa and the hybrids amongst them.

In the tea industry, due to commercial demands, the prospect of making of high-yielding plants has improved but it did not enable broadening the genetic unpredictability of tea, as practices were generally constrained to choosing elite parent bushes or progenitors from natural tea hybrid populations (10).

Tea yield and productivity

Tea yield is determined by the harvested area as well as the total weight of tea leaves plucked. The canopy's stature is preserved at an optimal level for plucking, with two and a bud or three leaves and a bud.

Tea bushes’ young shoots are usually harvested or plucked in seven-to-ten-day cycles. Young buds and shoots rely on a layer of developed leaves, termed as ‘maintenance foliage', for their source of assimilates after harvest due to the poor photosynthetic potential of young tea leaves. The overall photosynthetic rate of the tea leaf increases as it matures, reaching a peak when the young shoots are ready to be harvested. From photosynthetically absorbed carbon, leaves of various ages produce a variety of phytochemicals. A comparatively substantial fraction of assimilated carbon is combined into flavanols, amino acids, and organic acids in young leaves, but most of the integrated carbon is fused into easily translocatable elements such as sugars in mature leaves (11-12). Tea uses C3 type of photosynthetic process, and photorespiration accounts for roughly about 19% of total photosynthesis under typical atmospheric conditions (13).

As the leaf yield is controlled by rates of shoot initiation and extension, rather than the supply of assimilates from current net photosynthesis, the current rate of net photosynthesis is only indirectly connected to leaf yield in tea (14). The rate of tea growth is also regulated by the rate of respiration. Mature tea builds up a lot of biomass and consumes 67-85% of the photo-assimilates for respiration (15).

Climate change, the impacts, and future challenges in tea

Global warming-induced climate change and its impacts on agricultural productivity are one of the most important areas of research and the preparations to face the challenges are huge and vital at the global level.

Like other crops, cultivated tea plants have to face the climate crisis from drought, heat, flood and increased pests and diseases attacks. In India (Assam) over the past several decades’ temperatures have been snowballing andit impacted the tea-growing climate and subsequently, the prevailing temperature . It was observed that due to an increase in every degree above 28^{o}C, there is a reduction of

4 percent in the yield (16). The anticipated average temperatures in the next few decades will be higher by 2°C than the current atmospheric temperature and hence novel solutions to prevent the further yield loss are vital. The water-deficit stress like drought and heat-stress trouble the tea plantations in summer and during monsoon. Erratic rain causes water logging problems. And this can cause shooting up of tea prices in major tea growing countries like India and Sri Lanka, in the coming next few decades (17-18).

Research attention for climate-friendly tea using a genomics approach

To tackle the growing climate change impacts, many tea-growing nations developing climate-friendly tea crop improvement programs and management strategies. Transcriptome analysis would yield the stress-related genes and helps in marker-assisted breeding (MAB) and the development of abiotic and biotic stress-resistant tea clones.

The effective application of the combination of phenotypic and molecular markers such as high throughput precise phenotyping and next generation genomic technology respectively would yield promising results in the development of superior tea crops with quality and yield (19).

The tea genome sequencing facilitated the identification of important trait-specific genes for abiotic and biotic stresses and this aids the tea breeders to evolve climate-smart tea plants that adapt to the specific region and its anticipated climate (20). Hence, this genome-based research out comes helps tea farmers to act appropriately.

Genomics based approaches have aided the breeding programs of many crops while in tea it is limited as the quality of whole-genome sequences of Sinensis (CSS) and Assamica (CSA) varieties have to be improved because chromosome level reference genome of tea species ratifies breeding strategies. Large-scale cultivation of propagated tea clones makes the gene pool less diverse, narrower and this would make the cultivars vulnerable to abiotic and biotic stresses.

More recently, a genome wide analyses were made in tea and reported 14 abiotic stress associated CsSAP genes (CsSAP 1-14) with the help of reference genome database (Camellia sinensis var. sinensis). In this study, CsSAPs were categorised into Group I, containing one AN1 domain and Group II, containing two AN1 domains and/or two C2H2 domains. They further concluded that CsSAP12 might be a promising gene to improve drought tolerance in tea plants (21).

Pure line selection and true- breeding are difficult because tea is a highly cross-pollinating heterozygous plant and exploitation of distinct qualitative agronomic traits like biotic and abiotic stress resistance in tea would be useful for breeding (22).

Generation of QTL for quantitative and qualitative agronomic traits, sequencing of genomes and transcriptomes of other tea species including elite cultivars benefit the pan- genomics studies in tea to develop the gene pool and like in other crops the reference genome will be useful for evolving different stress resistance tea varieties (23).

Cold acclimatization

A study conducted to understand molecular mechanisms underlying cold adaptation of tea cultivars using two varieties SCZ and YH9, cold resistant and susceptible respectively, revealed that improved resistance was connected with previous expression of cold-induced genes (24). SCZ, the variety that can withstand cold temperatures during cold stress was found to have minimal relative electrical conductivity and advanced chlorophyll fluorescence (Fv/Fm) values.

SCZ and YH9 varieties have a total of 6072 and 7749 differentially expressed genes (DEGs), respectively, with 978 DEGs common to both. According to an enrichment study, DEGs were shown to be involved in photosynthesis, hormone signal transduction, and transcriptional regulation of plant-pathogen communication pathways.

According to another study, two mechanisms, carbohydrate metabolism and calcium signalling, play a key role in tea plant cold acclimation (25). In their research, it was found that among 1770 of differentially expressed mRNAs implicated in cold sensor or signal transduction, cold responsive transcription, plasma membrane stability, osmo-sensing responses and enzyme detoxification, 1168 are up-regulated.

Further, study on the *ICE1*-*CBF*-Cold Regulated (COR) Cold Response Pathway, one of the dominant cold-signalling mechanisms arbitrating cold response in plants, revealed that *CsICE1* gene has positive roles in cold tolerance in tea by promoting polyamine accumulation by communicating with *arginine decarboxylase* (ADC), which correspondingly offers an opportunity for improving cold tolerance in tea bushes (26).

Heat/drought

Alternative splicing (AS) of genes in tea plant was reported in response to drought, temperature and their collective stress using a popular tea cultivar ‘Zhongcha108’ which is extensively planted in Shandong province of China. The outcomes showed that the AS of genes in tea leaves was expansively activated by water deficit, heat and their combined stresses and resultant transcriptomic analysis revealed 12,178, 11,912 and 14,413 genes differentially spliced in response to drought, heat and their combined stresses, respectively. All differentially spliced genes (DSGs) considered for 48% of the annotated genes in tea crop genome. The study provides foundation for developing resistant cultivars for water deficit, temperature and collective stress in the future (27).

Recently, a genetic map was built for two segregating populations in tea using morphological data to identify Quantitative Trait Loci (QTL) that influences drought stress related traits with a consensus genetic map created using the DArTseq platform. Similarly, a functional gene annotation of presumed QTL linked with black tea quality and drought tolerance traits was also reported and the presumed candidate proteins identified in this study were related to abiotic/biotic stress response which may benefit breeders in selection of parents for development of novel tea cultivars with specific traits (28-29).

Samarina et al. (2020) revealed 3 robust candidate genes (RHL41, CAU1, Hydrolase22) using qRT-PCR which were upregulated in response to drought in tea plant (30).

Autophagy

Autophagy-related genes in tea crops (CsARGs) were examined, as well as the various roles played by autophagy in response to different growth phases or environmental stress levels. The two available tea plant genomes, '*ShuChaZao*' and '*YunKang10*,' revealed that a total of 35 CsARGs were known. CsATG14 has only been found in tea plants, but the others are well-preserved in homologues from other plant species.

During cold stress, the expression patterns of CsARGs differed between two cultivars, *Longjing-43* and *DaMianBai*, which were cold-tolerant and susceptible, respectively. Except for CsATG101, which revealed the opposite trend, expression levels of 10 CsARGs were more complex in the cold-resistant cultivar than in the cold-susceptible cultivar. In next study, the authors consider the idea of employing some CsARGs as possible molecular markers for the breeding of cold-resistant tea cultivars.

Conclusion

The current research for the development of stress and climate resilient tea crops are need of the hour. Extensive global level strategy development, knowledge exchange and implementation at the micro level would pave ways to face the climate change-based challenges. The scrupulous planning for producing stress tolerant hybrid tea for various tea growing countries and their climatic conditions, experimentation, field trial, and release of tea crops need many years, and planting the newly developed climate-smart tea variants on the field to replace the existing stress susceptible ones need more time. It requires high resourceful planning, progressive approach, and execution. The affordability of adapting such expensive time-consuming measures are mammoth tasks for small tea growers.

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Authors contributions

MR has initiated the manuscript preparation, designed the outline of the review article, drafted genomics-based approaches in tea, tea genome sequencing, manufacturing aspects of tea and allocated the different topics to co-authors. SVN contributed botanical aspects of tea and involved in the preparing final manuscript. LR participated in drafting tea genome sequencing, molecular breeding aspects of the tea. All authors have read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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