agronomy

Editorial

Developing Temperature-Resilient Plants: A Matter of Present and Future Concern for Sustainable Agriculture

Ali Raza [1,*], Daojie Wang [2,*], Xiling Zou [3,*] and Channapatna S. Prakash [4,*]

1 College of Agriculture, Fujian Agriculture and Forestry University (FAFU), Fuzhou 350002, China
2 College of Agriculture, Henan University, Jin Ming Avenue, Kaifeng 475004, China
3 Oil Crops Research Institute, Chinese Academy of Agricultural Sciences (CAAS), Wuhan 430062, China
4 College of Arts & Sciences, Tuskegee University, Tuskegee, AL 36088, USA
* Correspondence: alirazamughal143@gmail.com (A.R.); drdaojiewang@163.com (D.W.); zouxiling01@caas.cn (X.Z.); cprakash@tuskegee.edu (C.S.P.)

1. Introduction

Plants are decisive for nurturing life on Earth, but climate change threatens global food security, poverty decrease, and sustainable agriculture [1,2]. Climate change events, such as altered rainfall patterns, mega-fires, droughts, soil salinity, floods, extreme temperatures, and spreading pests and diseases, are becoming more frequent and severe. These events directly and indirectly influence sustainable agriculture, food security, and people's livelihoods (FAO, Climate Change; https://www.fao.org/climate-change/en/, accessed on 8 March 2023). According to current climate change predictions, extreme temperatures exert a significant risk to the sustainability of major crops globally. These extreme temperatures hinder plant growth and development, trigger damage, and eventually cause yield shortfalls, making it difficult to reach the "ZERO HUNGER (Sustainable Development Goal 2)" (FAO-UN, https://www.fao.org/sustainable-development-goals/goals/goal-2/en/, accessed on 8 March 2023).

Plants cannot avoid temperature stress by relocating as they are immobile [3,4]. Consequently, plants have developed diverse mechanisms to acclimatize to stressful environments by changing their developmental, physio-biochemical, and molecular activities [1,4–8]. To fast-track the development of stress-resilient crops for sustainable agriculture, discovering approaches to improve plant stress tolerance is a vital mission for plant biologists worldwide. Therefore, this Special Issue entitled "Developing Temperature-Resilient Plants: Responses and Mitigation Strategies" (https://www.mdpi.com/journal/agronomy/special_issues/temperature_resilient, accessed on 8 March 2023) was designed at the right time to collect the recent scientific advances on different mitigation strategies as well as stress adaptation and tolerance mechanisms to support the rising population. Twenty papers are published in this Special Issue, including 15 research and 5 review articles authored by a diverse group of scientists worldwide. Based on the published articles, this editorial presented the scientific advances in two sections, i.e., (1) genetics and genomics interventions and (2) agronomic and physiological interventions in developing temperature-resilient plants for the sustainable future.

2. Genetics and Genomics Interventions in Developing Temperature-Resilient Plants

Heat stress at different developmental stages substantially impacts the production of cotton (*Gossypium hirsutum* L.). Recent advances in genetics and genomics tools have revolutionized crop improvement against temperature stress by identifying stress-responsive regions, genes, and pathways. In this context, Rani et al. [9] aimed to discover and map the quantitative trait loci (QTLs) associated with heat tolerance in cotton using a microsatellite marker approach. They used an F2 population originating from a cross of MNH-886

check for updates

Citation: Raza, A.; Wang, D.; Zou, X.; Prakash, C.S. Developing Temperature-Resilient Plants: A Matter of Present and Future Concern for Sustainable Agriculture. *Agronomy* **2023**, *13*, 1006. https://doi.org/10.3390/agronomy13041006

Received: 22 March 2023
Accepted: 26 March 2023
Published: 29 March 2023

(heat-tolerant) and MNH-814 (heat-sensitive) varieties and mapped different heat tolerance-related QTLs during diverse morphological stages in cotton. Authors have identified a total of 17 QTLs which are located on different chromosomes and are associated with other traits, including heat stress. They also discovered that some QTLs were highly significant and accounted for a considerable fraction of the phenotypic variation (7.76%–36.62%). In short, these findings may facilitate marker-assisted breeding on cotton heat tolerance and contribute to developing heat-tolerant cotton varieties [9].

Improving quantitative attributes associated with crop yield, quality, and stress tolerance is the primary objective of breeding programs. Hence, Arslan et al. [10] examine the genetic diversity of grass pea (*Lathyrus sativus* L.) germplasm (94 accessions), a legume crop is grown under low- and high-land conditions in Turkey, to identify genetic markers associated with stress tolerance and yield-related traits. Authors have observed high genetic diversity among the grass pea accessions, and there were significant variations between genotypes for all agronomic attributes in low-land locations. The information on differences in agronomic, quality, and forage attributes identified in this study presented valuable genetic resources. The parental genotypes with preferred traits can be utilized in grass pea improvement programs for developing stress-resilient new cultivars [10].

It is vital to predict approved green super rice (GSR) to uphold the high production of rice (*Oryza sativa* L.) in Pakistan [11]. Zaid et al. [11] analyzed the genetic diversity, heritability, and stability of yield-connected traits of GSR grown under multi-environmental conditions (eight regions) in Pakistan. This research revealed three stable GSR lines (GSR 305, GSR 252, and GSR 112) with the lowest stability values in univariate stability data. It is observed that GSR 48 demonstrated the highest stability than all other lines in the univariate model across the two years for grain yield and associated attributes data. It is also determined that multivariate parametric stability models are suitable for choosing the most appropriate and stable GSR lines for particular and diverse environments. AMMI and GGE biplot analysis classified GSR 305 and GSR 252 as the most stable genotypes across eight examined locations. Furthermore, Swat, Narowal, and Muzaffargarh are the best locations to commercialize GSR lines in Pakistan [11].

Genome-wide identification and characterization of various gene families help to uncover their putative roles in plant growth/development and stress tolerance [12–15]. For instance, Kilwake et al. [12] identified 16 members of S-adenosyl-L-methionine synthetase (SAMS) gene family in upland cotton, named *GhSAMS*. Different bioinformatics tools were used to characterize their properties, and structures and predict their putative functions. Gene expression analysis showed that the *GhSAMS2* gene was highly induced by salinity and drought stress. The *ghSAMS2* gene was knockdown using the virus-induced gene silencing method, and the resultant knock-down plants demonstrated sensitivity to both salinity and drought stresses. The knock-down plants revealed *GhSAMS2* was involved in cotton's growth and physiological performances. These discoveries deliver perceptions into *SAMS* gene structure, classification, and roles in abiotic stress responses in upland cotton [12]. Maize (*Zea mays* L.) is a major cash crop grown globally; however, its growth and yield are impacted by numerous stresses. To get insight into the mechanisms of stress responses by maize, Haider et al. [13] performed a comprehensive genome-wide analysis. They identified 25 Heat shock transcription factors (HSFs) in the maize (*ZmHSFs*) genome. A diverse set of *in silico* tools were used to characterize the *ZmHSFs*, including chromosomal location, gene structure, phylogenetic analysis, motif analysis, localization, protein–protein interaction, and gene ontology. RNA-seq-based expression analysis showed that different *ZmHSFs* are highly expressed in various organs (seed, vegetative, and reproductive development) and upregulated against other abiotic stresses such as temperature, salinity, UV, and drought. This study offers novel visions for functional dissection of the *ZmHSFs* in maize and will benefit breeding programs [13].

Wheat (*Triticum aestivum* L.) is an essential supplier of starch, protein, and minerals in the diet of >35% of the world's population [16,17]. To stabilize wheat production under different conditions, it is crucial to predict novel genes associated with growth and stress tolerance. Altaf et al. [14] identified 40 *TUBBY* genes (*TaTLPs*), and Rasool et al. [15] identified 37 phenylalanine ammonia-lyase genes (*TaPALs*) in the wheat genome. Both studies have used different in silico tools to comprehensively characterize their physio-biochemical properties, gene structures, *cis*-elements, duplication types, etc. qRT-PCR-based expression analysis of *TaTLPs* confirmed that most of the genes were upregulated in response to various hormones, and temperature stress, indicating their vital roles in wheat improvement under extreme temperature [14]. On the other hand, *TaPAL* genes showed higher expression in roots of drought tolerant than in those of drought-sensitive varieties. RNA-seq-based expression analysis showed that all *TaPAL* genes were highly expressed in shoots and roots under abiotic stress conditions [15]. These studies lay the grounds for functional studies of *TaPAL* and *TaTLPs* genes to uncover their roles in wheat growth/development and stress tolerance.

Pervaiz et al. [18] explore cDNA-microarray and miRNAs to understand how plants respond to abiotic stresses and survive in challenging environments. MicroRNA notably impacts the response of plants to environmental stressors, plant growth, and development and controls diverse biological and metabolic functions. Despite the availability of relevant miRNAs, there is still a limited way to identify them and the application of cDNA-microarray. Advanced sequencing and bioinformatics techniques are necessary for miRNA identification and target gene network prediction. This article recommends the application of miRNAs for detecting and organizing new practical genes conferring a significant practical role in stress tolerance [18].

3. Agronomic and Physiological Interventions in Developing Temperature-Resilient Plants

There is rising importance in using chemical approaches to enhance plant growth and productivity in stressful conditions. These approaches involve the exogenous application or seed priming of natural or synthetic substances, such as phytohormones, osmolytes, neurotransmitters, gaseous molecules, amino acids, etc. [6,7,19,20]. A study by Hmmam et al. [21] reported the protective role of salicylic acid (SA, 0, 0.5, 1, and 1.5 mM L^{-1}) in alleviating the harmful consequences of chilling stress (4 ± 1 °C) on “Seddik” mango transplants. Results showed that the application of SA (mainly 1.5 mM L^{-1}) helped to cope with the chilling stress by sustaining the integrity of the cell membrane in the leaves, lessening the electrolyte leakage, enhancing the photosynthetic pigment contents, antioxidant enzyme activities, total sugar contents, 2, 2-diphenyl-1-picrylhydrazyl radical scavenging activity and by decreasing proline and total phenolic contents in the “Seddik” mango transplants’ leaves [21].

In another study, Waraich et al. [22] showed that seed priming with thiourea (500 ppm) improves the efficiency of Camelina (*Camelina sativa* L.) plants under heat stress (32 °C) by regulating several physiological and yield-related traits. Thiourea seed priming increases shoot and root length, biomass, gas exchange rate, water relations, and seed yield, and helps Camelina plants to mitigate the adverse influences of heat stress [22]. A combination of heat, salinity, and waterlogging reduces wheat’s growth and yield-associated attributes, whereas Altaf et al. [23] reported that applying sulfur-coated urea (SCU, 130 kg ha^{-1}) helps boost the grain yield under all three stresses. They found a strong association between soil nitrogen content and growth rate, spike length, yield, and physiological limitations in wheat plants. While the effectiveness of SCU fertilizer was limited under heat stress, it was observed to cause better tolerance of wheat to salinity [23].

Zulfiqar et al. [20] reviewed glycine betaine’s beneficial role in plants’ heat stress tolerance. The exogenous application of glycine betaine has displayed promise in advancing heat stress tolerance by increasing osmolyte contents, protein modifications, photosynthetic mechanisms, stress-responsive gene expression, and oxidative defense. Under heat stress, glycine betaine accumulation in plants varies; consequently, engineering genes for glycine betaine accumulation in non-accumulating plants is an integral approach for increasing heat stress tolerance.

The production of cotton, a fiber crop, is being hindered by the unpredictable increase in temperature caused by rapidly changing climate conditions, as reviewed by Majeed et al. [24]. In this review, the authors comprehensively presented the impacts of heat stress on various traits such as seed germination, development of seedlings at early and lateral vegetative growth phases, yield and quality of fiber, floral components, and physiological aspects. Various breeding and mitigation strategies for heat stress tolerance have been discussed, including conventional and genomics-assisted breeding (QTL mapping, GWAS, and genomic selection), transgenic breeding, and CRISPR/Cas-mediated genome editing. Omics approaches have greatly improved our knowledge of how cotton responds to heat stress by identifying genes, proteins, and metabolites that appear differentially. These novel markers can be utilized for genetic engineering to produce cotton cultivars resilient to heat stress [24].

Rana et al. [25] examined thirteen upland cotton genotypes for variations in physiological and morphological attributes associated with heat stress during the vegetative and reproductive phases. The authors hypothesize that different parts of a single cotton plant may display variable responses to stress, which was tested by observing two flowering positions [25]. They collected data on various traits from different genotypes' top and bottom branches. The bottom branches performed better for most traits except boll weight. AA-933 genotype had the best pollen germination and boll retention, while CYTO-608 had the highest pollen viability. MNH-1016 and CIM-602 had better cell membrane thermostability and chlorophyll content, respectively. This variability within genotypes can be helpful in breeding programs to develop stress-tolerant varieties [25].

In tomato (*Solanum lycopersicum* L.) plants, heat stress causes changes in diverse responses during all vegetative and reproductive growth stages, resulting in poor fruit quality and low yield, as reviewed by Lee et al. [26]. The authors have reviewed past and present research efforts to identify heat-resistant tomato varieties through screening procedures conducted under varying heat stress conditions and temperature thresholds. They have also presented information on the correlation between heat tolerance and physiological and biochemical characteristics at different vegetative and reproductive growth stages. This article has explored the numerous parameters utilized to assess the heat tolerance of tomatoes, which include factors related to both vegetative and reproductive growth, such as leaf growth parameters, plant height, stem size, number of flowers, fruit set, yield, and the development of pollen and ovules, thus suggesting techniques for developing tomato cultivars that are more tolerant to heat stress [26].

When the temperature is too high, plants cannot make or use energy properly through respiration and photosynthesis, which are vital metabolic events for plants to endure and grow [27]. In this context, Sharma et al. [27] explore the mechanistic underpinnings of how heat stress triggers mitochondrial dysfunction, ultimately controlling dark respiration in plants. They also analyze the influence of hormones on the intricate network of processes involved in retrograde signaling. This review suggested various approaches for mitigating carbon loss under heat stress, such as choosing genotypes with lower respiration levels or employing gene editing techniques to modify carbon pathways by relocating, switching, or reorganizing metabolic events.

At the flowering stage, Zafar et al. [28] evaluated the consequences of heat stress on agronomic and physiological attributes of green super rice, such as plant height (PH), tillers per plant (TPP), grain yield per plant (GY), straw yield per plant (SY), harvest index (HI), 1000-grain weight (GW), grain length (GL), cell membrane stability (CMS), normalized difference vegetative index (NDVI), and pollen fertility percentage (PFP). The results explained that GY, TPP, SY, HI, and CMS were substantially impacted by heat stress, while other traits like PH, GW, GL, PFP, and NDVI were altered in only a few genotypes. These findings can aid in preventing and managing heat stress in rice. NGSR-16 and NGSR-18 genotypes performed well under heat stress and can be employed to create heat-tolerant rice.

Thoroughly examining the adaptability mechanisms of short- and long-duration japonica rice cultivars under different temperature circumstances is beneficial for probing improved adaptation and management ways. Given this background, Farooq et al. [29] experimented with two locations in China to examine the adaptability mechanisms of four japonica rice cultivars in response to varying temperature conditions. They concluded that earlier transplantation and anthesis were helpful in stress tolerance, and high temperature at the start of the day aided plants in escaping from high temperatures later in the day. The temperature had a considerable impact on rice, while the precipitation of the growing season did not. The influence of daily sunshine was substantial but less spatially consistent. These discoveries are contributed to sustainable and rewarding rice cultivation in the Northeast China region.

Pea (*Pisum sativum* L.) is frequently cultivated in semi-arid temperate zones. Tafesse et al. [30] examined the role of leaf pigments and surface wax in heat avoidance in pea canopies and their correlation with spectral vegetation indices. Field trials were conducted on 24 pea cultivars with varying leaf traits across six environments in western Canada. Heat stress reduced leaf pigment concentrations but increased chlorophyll a/b ratio, anthocyanin, and wax concentrations. Higher pigment and wax concentrations were linked with cooler canopy temperatures and increased heat tolerance. Spectral vegetation indices, including photochemical reflectance index, green normalized vegetation index, normalized pigment chlorophyll ratio index, and water band index, were revealed to have strong correlations with heat avoidance attributes and heat tolerance index. This report emphasized heat avoidance attributes in crop canopies and spectral lengths for choosing heat-tolerant genotypes.

Creating new varieties that can survive abiotic stresses is vital for meeting the challenge for natural fibers. Thus, Dey et al. [31] aimed to detect cold-tolerant varieties and understand the mechanisms that improve cold tolerance in various jute varieties. Findings revealed that Y49 and M33 varieties had high levels of chlorophyll and carotenoid contents and enzymatic and non-enzymatic antioxidants and phenolics, which helped lessen oxidative damage triggered by cold stress. Furthermore, osmolytes such as soluble sugars and proline were found to play roles in lowering impairment caused by cold stress. This study verified the cold tolerance ability of some chosen varieties, suggesting their perspective as an efficient adaptation strategy and as candidates for cold-resilient breeding programs.

The above-overviewed articles present the latest scientific advancements and developments in the mechanisms of crops' resilience to temperature stress, aimed at ensuring their sustainable production in the future. Consequently, our Special Issue will be a valuable one-stop source for scientists developing temperature-resilient plants to feed the growing population.

Funding: This research was funded by the National Natural Science Foundation of China (NSFC: grant number 32161143021), and by the Key R&D program of Henan province (221111110200).

Acknowledgments: We thank all the authors who have contributed to this Special Issue and the reviewers who have provided valuable feedback to enhance the quality of the articles. We would also like to thank the editorial team for their helpful assistance in compiling this Special Issue.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Zandalinas, S.I.; Fritschi, F.B.; Mittler, R. Global warming, climate change, and environmental pollution: Recipe for a multifactorial stress combination disaster. *Trends Plant Sci.* **2021**, *26*, 588–599. [CrossRef] [PubMed]
2. Fujimori, S.; Wu, W.; Doelman, J.; Frank, S.; Hristov, J.; Kyle, P.; Sands, R.; Van Zeist, W.-J.; Havlik, P.; Domínguez, I.P. Land-based climate change mitigation measures can affect agricultural markets and food security. *Nat. Food* **2022**, *3*, 110–121. [CrossRef]
3. Zandalinas, S.I.; Mittler, R. Plant responses to multifactorial stress combination. *New Phytol.* **2022**, *234*, 1161–1167. [CrossRef] [PubMed]
4. Rivero, R.M.; Mittler, R.; Blumwald, E.; Zandalinas, S.I. Developing climate-resilient crops: Improving plant tolerance to stress combination. *Plant J.* **2022**, *109*, 373–389. [CrossRef] [PubMed]

5. Raza, A.; Tabassum, J.; Kudapa, H.; Varshney, R.K. Can omics deliver temperature resilient ready-to-grow crops? *Crit. Rev. Biotechnol.* **2021**, *41*, 1209–1232. [CrossRef]
6. Raza, A.; Charagh, S.; García-Caparrós, P.; Rahman, M.A.; Ogwugwa, V.H.; Saeed, F.; Jin, W. Melatonin-mediated temperature stress tolerance in plants. *GM Crops Food* **2022**, *13*, 196–217. [CrossRef]
7. Raza, A.; Charagh, S.; Abbas, S.; Hassan, M.U.; Saeed, F.; Haider, S.; Sharif, R.; Anand, A.; Corpas, F.J.; Jin, W. Assessment of proline function in higher plants under extreme temperatures. *Plant Biol.* **2023**, *25*, 379–395. [CrossRef]
8. Saeed, F.; Chaudhry, U.K.; Raza, A.; Charagh, S.; Bakhsh, A.; Bohra, A.; Ali, S.; Chitikineni, A.; Saeed, Y.; Visser, R.G. Developing future heat-resilient vegetable crops. *Funct. Integr. Genom.* **2023**, *23*, 47. [CrossRef]
9. Rani, S.; Baber, M.; Naqqash, T.; Malik, S.A. Identification and Genetic Mapping of Potential QTLs Conferring Heat Tolerance in Cotton (*Gossypium hirsutum* L.) by Using Micro Satellite Marker's Approach. *Agronomy* **2022**, *12*, 1381. [CrossRef]
10. Arslan, M.; Yol, E.; Türk, M. Disentangling the Genetic Diversity of Grass Pea Germplasm Grown under Lowland and Highland Conditions. *Agronomy* **2022**, *12*, 2426. [CrossRef]
11. Zaid, I.U.; Zahra, N.; Habib, M.; Naeem, M.K.; Asghar, U.; Uzair, M.; Latif, A.; Rehman, A.; Ali, G.M.; Khan, M.R. Estimation of genetic variances and stability components of yield-related traits of green super rice at multi-environmental conditions in Pakistan. *Agronomy* **2022**, *12*, 1157. [CrossRef]
12. Kilwake, J.W.; Umer, M.J.; Wei, Y.; Mehari, T.G.; Magwanga, R.O.; Xu, Y.; Hou, Y.; Wang, Y.; Shiraku, M.L.; Kirungu, J.N. Genome-Wide Characterization of the *SAMS* Gene Family in Cotton Unveils the Putative Role of *GhSAMS2* in Enhancing Abiotic Stress Tolerance. *Agronomy* **2023**, *13*, 612. [CrossRef]
13. Haider, S.; Rehman, S.; Ahmad, Y.; Raza, A.; Tabassum, J.; Javed, T.; Osman, H.S.; Mahmood, T. *In silico* characterization and expression profiles of heat shock transcription factors (HSFs) in maize (*Zea mays* L.). *Agronomy* **2021**, *11*, 2335. [CrossRef]
14. Altaf, A.; Zada, A.; Hussain, S.; Gull, S.; Ding, Y.; Tao, R.; Zhu, M.; Zhu, X. Genome-wide identification, characterization, and expression analysis of Tubby gene family in wheat (*Triticum aestivum* L.) under biotic and abiotic stresses. *Agronomy* **2022**, *12*, 1121. [CrossRef]
15. Rasool, F.; Uzair, M.; Naeem, M.K.; Rehman, N.; Afroz, A.; Shah, H.; Khan, M.R. Phenylalanine ammonia-lyase (PAL) genes family in wheat (*Triticum aestivum* L.): Genome-wide characterization and expression profiling. *Agronomy* **2021**, *11*, 2511. [CrossRef]
16. Miransari, M.; Smith, D. Sustainable wheat (*Triticum aestivum* L.) production in saline fields: A review. *Crit. Rev. Biotechnol.* **2019**, *39*, 999–1014. [CrossRef]
17. Singh, J.; Chhabra, B.; Raza, A.; Yang, S.H.; Sandhu, K.S. Important wheat diseases in the US and their management in the 21st century. *Front. Plant Sci.* **2022**, *13*, 1010191. [CrossRef]
18. Pervaiz, T.; Amjid, M.W.; El-kereamy, A.; Niu, S.-H.; Wu, H.X. MicroRNA and cDNA-microarray as potential targets against abiotic stress response in plants: Advances and prospects. *Agronomy* **2021**, *12*, 11. [CrossRef]
19. Raza, A.; Salehi, H.; Rahman, M.A.; Zahid, Z.; Haghjou, M.M.; Najafi-Kakavand, S.; Charagh, S.; Osman, H.S.; Albaqami, M.; Zhuang, Y.; et al. Plant hormones and neurotransmitter interactions mediate antioxidant defenses under induced oxidative stress in plants. *Front. Plant Sci.* **2022**, *13*, 961872. [CrossRef]
20. Zulfiqar, F.; Ashraf, M.; Siddique, K.H. Role of glycine betaine in the thermotolerance of plants. *Agronomy* **2022**, *12*, 276. [CrossRef]
21. Hmmam, I.; Ali, A.E.; Saleh, S.M.; Khedr, N.; Abdellatif, A. The Role of Salicylic Acid in Mitigating the Adverse Effects of Chilling Stress on "Seddik" Mango Transplants. *Agronomy* **2022**, *12*, 1369. [CrossRef]
22. Waraich, E.A.; Ahmad, M.; Soufan, W.; Manzoor, M.T.; Ahmad, Z.; Habib-Ur-Rahman, M.; Sabagh, A.E. Seed priming with sulfhydral thiourea enhances the performance of *Camelina sativa* L. under heat stress conditions. *Agronomy* **2021**, *11*, 1875. [CrossRef]
23. Altaf, A.; Zhu, X.; Zhu, M.; Quan, M.; Irshad, S.; Xu, D.; Aleem, M.; Zhang, X.; Gull, S.; Li, F. Effects of environmental stresses (heat, salt, waterlogging) on grain yield and associated traits of wheat under application of sulfur-coated urea. *Agronomy* **2021**, *11*, 2340. [CrossRef]
24. Majeed, S.; Rana, I.A.; Mubarik, M.S.; Atif, R.M.; Yang, S.-H.; Chung, G.; Jia, Y.; Du, X.; Hinze, L.; Azhar, M.T. Heat stress in cotton: A review on predicted and unpredicted growth-yield anomalies and mitigating breeding strategies. *Agronomy* **2021**, *11*, 1825. [CrossRef]
25. Rana, I.A.; Majeed, S.; Chaudhary, M.T.; Zulfiqar, M.; Yang, S.-H.; Chung, G.; Jia, Y.; Du, X.; Hinze, L.; Azhar, M.T. Intra-Plant Variability for Heat Tolerance Related Attributes in Upland Cotton. *Agronomy* **2021**, *11*, 2375.
26. Lee, K.; Rajametov, S.N.; Jeong, H.-B.; Cho, M.-C.; Lee, O.-J.; Kim, S.-G.; Yang, E.-Y.; Chae, W.-B. Comprehensive understanding of selecting traits for heat tolerance during vegetative and reproductive growth stages in tomato. *Agronomy* **2022**, *12*, 834. [CrossRef]
27. Sharma, N.; Thakur, M.; Suryakumar, P.; Mukherjee, P.; Raza, A.; Prakash, C.S.; Anand, A. 'Breathing Out' under Heat Stress—Respiratory Control of Crop Yield under High Temperature. *Agronomy* **2022**, *12*, 806. [CrossRef]
28. Zafar, S.A.; Arif, M.H.; Uzair, M.; Rashid, U.; Naeem, M.K.; Rehman, O.U.; Rehman, N.; Zaid, I.U.; Farooq, M.S.; Zahra, N. Agronomic and physiological indices for reproductive stage heat stress tolerance in green super rice. *Agronomy* **2022**, *12*, 1907. [CrossRef]
29. Farooq, M.S.; Gyilbag, A.; Virk, A.L.; Xu, Y. Adaptability mechanisms of japonica rice based on the comparative temperature conditions of harbin and qiqihar, heilongjiang province of Northeast China. *Agronomy* **2021**, *11*, 2367. [CrossRef]

30. Tafesse, E.G.; Warkentin, T.D.; Shirtliffe, S.; Noble, S.; Bueckert, R. Leaf Pigments, Surface Wax and Spectral Vegetation Indices for Heat Stress Resistance in Pea. *Agronomy* **2022**, *12*, 739. [CrossRef]
31. Dey, S.; Biswas, A.; Huang, S.; Li, D.; Liu, L.; Deng, Y.; Xiao, A.; Birhanie, Z.M.; Zhang, J.; Li, J. Low temperature effect on different varieties of *Corchorus capsularis* and *Corchorus olitorius* at seedling stage. *Agronomy* **2021**, *11*, 2547. [CrossRef]