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ORIGINAL ARTICLE

Opinion paper: when drought meets Fusarium Head Blight: urgent need to better understand and breed for plant disease resistance under a changing climate

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Abstract
The current alarming trends in global climate development are increasingly threatening agriculture. Extreme weather events, such as prolonged drought and heat waves, put crops under greater stress and alter the occurrence and severity of plant diseases. This article reflects on exemplary Fusarium–drought interaction experiments in barley, providing insights on how researchers can support breeding for disease resistance under future, more unfavourable environmental conditions.

Keywords Fusarium · Drought · Climate change · Disease resistance · Stress combination

Introduction

Global warming increasingly threatens agriculture and food security through extreme weather events such as prolonged drought and heat (Lobell and Di Tommaso 2025; Brás et al. 2021). Despite extensive evidence and calls for climate action, anthropogenic greenhouse gas emissions remain insufficiently reduced and warming continues to intensify (Foster and Rahmstorf 2026). In 2024, the global average temperature exceeded 1.5 °C above the pre-industrial reference period for the first time (Copernicus Climate Change Service 2025), and the eleven warmest years on record have all occurred since 2015 (Berkeley Earth 2026). Europe is warming faster than the global average (van der Schrier et al. 2013), resulting in more frequent and severe droughts (Hanel et al. 2018; Spinoni et al. 2018) that threaten cereal production (Naumann et al. 2015; Brás et al. 2021; Martin et al. 2025). However, breeding a new cereal variety requires approximately nine years from the first cross to market release, which unfortunately is too slow to allow timely adaptation of crop genotypes.

Extreme weather conditions also affect pathogen distribution, abundance and host susceptibility (Delgado-Baquerizo et al. 2020; Bebber 2015; Raza and Bebber 2022; Chakraborty and Newton 2011), raising the risk of epidemic plant disease outbreaks, threatening food security and safety. Appropriate adaptation of cropping systems, and particularly crop genotypes, to simultaneous abiotic and biotic stress is therefore decisive, requiring rapid translation of stress combination research into plant breeding.

The complexity of combined stresses

Multi-stress experiments are conceptually and experimentally challenging. Consequently, plant responses to combined stresses remain poorly understood. Most studies still focus on single stresses or model species (Prasch and Sonnewald 2013; Zandalinas et al. 2021; Tan et al. 2023), limiting their agricultural relevance. Stress severity, frequency, and combination determine the degree of plant damage, with additive, antagonistic, or synergistic effects, depending on the specific stressors (Atkinson et al. 2013; Rivero et al. 2022). Concurrent abiotic and pathogen stress often leads to unpredictable and complex responses through signalling cross-talk, resource trade-offs, and altered defence (Gupta et al. 2016; Karasov et al. 2017; Leisner et al. 2023; Zandalinas

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et al. 2021). Even mild stresses can cause disproportionate impacts on disease severity when combined, depending on their number, timing, sequence, and strength (Pandey and Senthil-Kumar 2019; Zandalinas et al. 2021; Sinha et al. 2024). Emerging evidence suggests that improved understanding of plant physiology under combined stresses could identify key regulatory pathways and hub genes, supporting the breeding of crops with both stress-tolerance and disease resistance. However, this is a complex task, because every crop species may respond differently to various combinations of stress, and complexity in the responses increases with each added stressor (Sinha et al. 2024). Each new study contributes to a more complete understanding of disease resistance under abiotic stress in crop plants. Such knowledge may reveal novel stress-responsive traits and associated genetic markers that can be exploited in breeding programs, either directly through marker-assisted selection or through the identification of quantitative trait loci (QTL) underlying stress adaptation and disease resistance. Alternatively, better understanding of stress physiology may support selection of suitable pre-breeding material and design of training populations for subsequent genomic selection.

Drought-driven shifts in fusarium disease dynamics

Drought and fungal diseases may appear counterintuitive at first, as fungi generally depend on moisture. While fungal diseases can be suppressed under very unfavourable conditions, such as prolonged drought in the field (Hoheneder et al. 2021, 2023a), this simplification fails to capture the complexity of pathogen responses under fluctuating climatic and weather conditions. Global warming is predicted to promote soil-borne fungi (Delgado-Baquerizo et al. 2020), and moisture remains a key factor driving fungal disease outbreaks (Romero et al. 2022). Thus, fungal diseases are not expected to decline generally under dry conditions (Choudhary and Senthil-Kumar 2024), except during extreme, long-lasting droughts.

Some pathogens may persist within specific ecological niches, while others occur less frequently and re-emerge when conditions become favourable (West et al. 2012). For example, under increasingly dry seasonal conditions, *Fusarium* species are likely to cause Fusarium crown rot (FCR) more frequently. This disease is promoted by drought (Liu and Liu 2016) and affects large areas in semi-arid and arid cereals-growing regions (Kazan and Gardiner 2018). In contrast, reduced moisture and rain splash limit infection of the ear and thus might limit Fusarium head blight (FHB) severity. At the same time, sufficient moisture from nighttime dew in the field can provide leaf wetness durations relevant for pathogen infection (Burrage 1972; Huber and Gillespie 1992), and together with occasional individual rainfall events, can enable noticeable head infections with *Fusarium* spp. and foliar diseases, even during prolonged hot and dry seasons (Hoheneder et al. 2021, 2022). This example illustrates the close relationship between diseases caused by agro-ecologically flexible pathogens and both climatic and regional weather conditions. Consequently, depending on future weather conditions, either FHB or FCR could be favoured in cereals. However, fungal pathogens, such as *Fusarium* spp. are highly responsive to changing climatic conditions (Moretti et al. 2019; Madgwick et al. 2011) and are therefore expected to remain relevant under future climate scenarios.

For a detailed insight into the response of plants to multi-stress situations, we require defined stress levels applied under controlled conditions. Although conditions often do not fully represent field conditions, very clear phenotypes can be obtained and reproduced here. In own greenhouse experiments, the application of drought stress before infection of barley heads with *Fusarium culmorum* reduced FHB severity across different genotypes with the most susceptible plants showing the greatest benefit (Hoheneder et al. 2023b). In particular, the drought stress induced accelerated ripening and seed maturation, which might have shortened the time frame to colonize the spikes, when compared to the irrigated control plants. Similarly, (Adamik et al. 2025) found that pre-anthesis water deficit followed by rehydration with simultaneous inoculation reduced FHB severity by inducing persistent physiological and metabolic changes in wheat. This illustrates how decisive the timing of exposure to one stressor is in determining the impact on a second stressor.

Transcriptome analysis in barley revealed that the combination of drought and *Fusarium culmorum* infection resulted in the highest number of differentially regulated genes and reflected a modular composition of the single stress responses (Hoheneder et al. 2023b). The additive gene expression response under combined stress suggests that barley can express a strong response to drought stress and simultaneously shows a strong response to fungal infection. Similar relationships between drought responsiveness and disease resistance have been described for FCR in wheat and barley, where resistant genotypes exhibited reduced drought stress and enhanced defence responses, suggesting that abiotic stress tolerance and pathogen resistance can be co-regulated (Su et al. 2021). It should therefore be possible to select genotypes that optimally allocate resources under combined biotic and abiotic stress.

In a different scenario, the simultaneous application of drought stress and Fusarium head infection increased FHB severity in quantitatively resistant genotypes, but not in

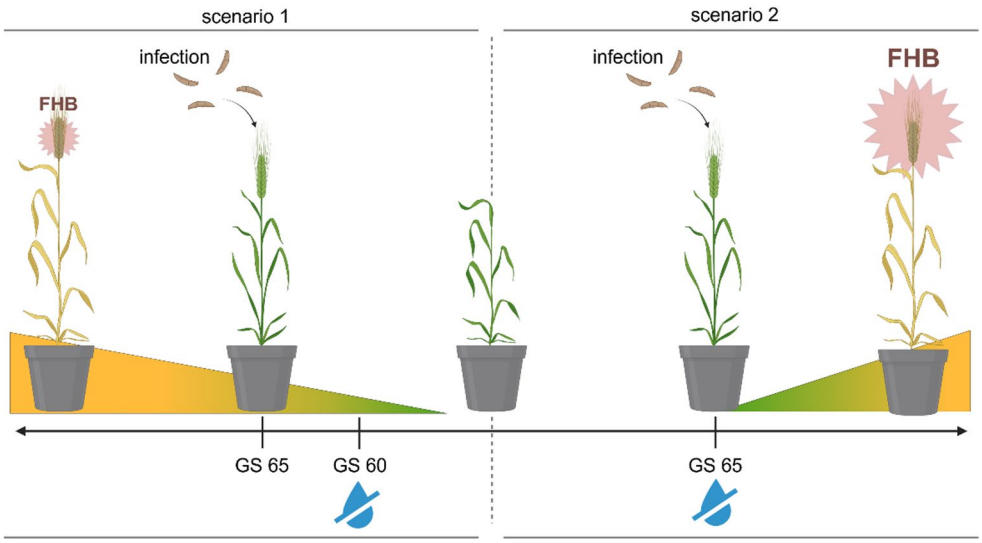


Fig. 1 Effects of drought timing on Fusarium head blight (FHB) severity in barley. Drought applied before inoculation with *Fusarium culmorum* reduced FHB severity across three barley genotypes (scenario 1), whereas simultaneous onset of drought and infection increased FHB severity in a genotype-dependent manner (scenario 2) (Hoheneder et al. 2023b, 2026). Created in BioRender. Hoheneder, F. (2026) https://BioRender.com/wq67tos

the more susceptible ones (Fig. 1). In both scenarios under single stress, barley regulated independent sets of pathogen- and drought stress-responsive genes, which combined into a modular response under combined stress, resulting in the highest number of regulated genes. This clearly reflects the enhanced physiological costs of complex stress situations and underlines that responses to stress combinations in barley largely represent a modular composition of single stress responses (Hoheneder et al. 2023b, 2026). However, species or genotype-specific responses need to be further evaluated. In contrast, studies in wheat have shown that beyond shared responses, combined stress can induce substantial unique transcriptional and metabolic regulation, supporting the concept that stress combinations may constitute a distinct physiological state (Adamik et al. 2025).

Taken together, a strong response to drought stress does not generally limit a high response to fungal infection, and thus selection for drought tolerance appears compatible with durable *Fusarium* resistance in wheat and barley and may also be achievable in other cereals (Su et al. 2021, 2025). However, a subset of co-expressed infection-related barley genes exhibited opposite regulation under drought and predominantly attenuated or reversed responses under combined stress compared with infection alone (Hoheneder et al. 2026). This indicates that drought can partially compromise infection-induced defence outputs by weakening the expression of infection-responsive genes, thereby reflecting a trade-off between *Fusarium* and drought responses. With prolonged drought, drought-related gene regulation became dominant, and the quantitative resistance remained only functional in some individual genotypes. This highlights that conflicting stress signals, e.g. at transcriptional and hormonal levels, elicit contradictory responses that limit the plant's capacity to mitigate combined stress effectively, thereby increasing FHB susceptibility. Conversely, drought tolerant plants may be able to keep upright physiological plasticity under stress allowing them to comprehensively respond to pathogens even under drought, as shown for FCR in wheat and barley (Su et al. 2021). Accordingly, genotypes with higher translational and physiological plasticity may better be able to optimize and prioritize resource allocation under complex stress conditions, keeping resistance and yield stable. Such genotypes must be selected in breeding programs targeting stability of such traits across multiple environments. However, it needs also to be investigated whether this kind of cross-protection of independent stress response pathways can be generalized or a clash of physiological stress responses hinders stacking abiotic and biotic resistance traits in other plant organs, genotypes, species or stress combinations.

Bridging the gap: from controlled conditions to field environments

Moving beyond laboratory and greenhouse experiments toward realistic field conditions is essential to validate plant–environment–pathogen interactions and integrate phytopathological research with stress physiology. Extending transcriptomic and metabolomic analyses to field-grown plants can reveal stress- and infection-responsive regulatory networks under realistic environmental conditions.

To translate these insights into practice, stress physiology needs to be more effectively incorporated into applied (pre-) breeding, prioritizing the key stress response mechanisms, the underlying genetic networks, phenotypic plasticity and traits relevant under combined stress conditions. Closer collaboration between scientists and (pre-)breeders, enables designing targeted experiments and the identification of pheno- and genotypic variation as well as novel traits in

candidate germplasm as genetic resource for breeding programs (e.g. see (Su et al. 2025).

Field-based stress manipulation tools, such as rainout shelters, free-air carbon dioxide enrichment facilities or soil heating cables, enable the simulation of future growth scenarios (Melloy et al. 2010; Tessmann and van Sanford 2018; Hoheneder et al. 2021, 2023a). When combined with an inoculation nursery, these facilities allow targeted comparison and selection of candidates with robust genotype-specific disease resistance under projected climatic conditions. Multi-location testing across stress-prone environments provides realistic selection pressure for identifying robust germplasm, despite being resource-intensive. Together, these approaches bridge the gap between controlled experiments and field realities, enabling breeders to select genotypes that maintain both yield stability and disease resistance under combined stress conditions.

Implications for breeding and future directions

The rapid increase in global temperatures will affect resistance breeding and selection of new varieties (Miedaner and Juroszek 2021) including e.g. low mycotoxin contents in grains, phenological plasticity and resource allocation efficiency. In addition to yield, breeding for high and durable disease resistance is of major importance (Brown 2021) and will become even more critical under future climate scenarios. Addressing combined abiotic and biotic stresses requires integrated approaches that link phytopathology, stress physiology, and breeding.

Technological advances now provide unprecedented opportunities: declining DNA and RNA sequencing costs allow deeper and more accurate SNP detection and deeper transcriptomic studies; pan-genome resources expand genetic reference frameworks; and emerging tools such as digital image-based and hyperspectral phenotyping, combined with artificial intelligence and machine learning, enable high-throughput geno- and phenotyping. Together, these developments increase the resolution of scientific studies and support data-informed breeding decisions, accelerating the identification of robust germplasm under multiple stress scenarios. This could increase selection response and speed, while also allowing for the evaluation of more complex traits.

Conclusions

The intensification of global warming is rapidly altering plant–pathogen interactions, and immediate action is required to adapt crop varieties to multi-stress conditions. As shown here, drought can both suppress and exacerbate FHB in barley depending on its timing, highlighting the complexity and context dependency of combined stress responses.

Coordinated efforts combining advanced phenotyping and genotyping tools, multi-environment testing, new technologies, and close collaboration between scientists and breeders are critical to identify and deploy robust germplasm and favourable traits under complex stress conditions. With increased support from scientists, breeders should increasingly integrate these approaches to accelerate the development of crop varieties with stable yield, high phenotypic plasticity, and durable resistance, ensuring that agriculture can keep pace in the race against evolving pathogen pressures under a changing climate.

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Declarations

Conflict of interest The author declares no conflict of interest.

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