# Differential tolerance to changes in moisture regime during early infection stages in the fungal pathogen *Zymoseptoria tritici*

Anne-Lise Boixel[1], Sandrine Gélisse[1], Thierry C. Marcel[1], Frédéric Suffert[1*]

[1] Université Paris-Saclay, INRAE, AgroParisTech, UMR BIOGER, 78850, Thiverval-Grignon, France

* Corresponding author: Frédéric Suffert (frederic.suffert@inra.fr)

## Abstract

Moisture levels are a crucial meteorological factor affecting all epidemiological stages of foliar diseases, but their effect on pathogen development has been much less studied that of temperature, for example. There has been no detailed investigation of the tolerance or adaptation of pathogen populations to contrasting or changing moisture conditions. We investigated differential tolerance to moisture stress in the wheat fungal pathogen *Zymoseptoria tritici* at the individual and population levels. We retained 48 genetically different isolates from populations originating from two Euro-Mediterranean climatic zones – Ireland and Israel – with very different moisture conditions (annual air relative humidity – RH – of 85.1% *vs.* 69.7%, respectively). We assessed the responses *in planta* of these isolates to four different moisture regimes imposed on wheat seedlings during the first three days after inoculation (RH of 88.3%, 92.2%, 96.1% and 100%). Visual assessments of lesion development conducted at 14, 17 and 20 dpi were performed to establish individual- and population-level moisture reaction norms expressing the sporulating area of the pathogen on inoculated leaves for the mean RH over the three days following inoculation. Our findings highlight: (i) the critical effects of moisture regime on the development of *Z. tritici* during the earliest infection stages (pycnidiospore

germination, epiphytic hyphal growth and penetration) despite the relatively high RH in the driest conditions tested (88.3%); (ii) the considerable individual variation in the phenotypic plasticity of *Z. tritici* with respect to sensitivity to RH; (iii) the greater tolerance of the Israeli population to drier conditions at 14 dpi, together with the absence of genotypic differentiation for neutral microsatellite loci between the two populations, providing the first evidence of a moisture adaptation signature in a fungal pathogen of plants. These findings provide insight into drought stress tolerance and the diversity of its responses between pathogen individuals and populations in terms of the likely effects of climate change on plant disease epidemics.

## Keywords

moisture tolerance, relative humidity, phenotypic responses, reaction norms, individual variation, population differentiation, septoria tritici blotch

# Introduction

Micrometeorological factors within the plant canopy define the physical environment in which fungal pathogens live and develop (Campbell and Norman, 1998; Chelle, 2005). Temperature and moisture are critical physical factors that govern each epidemiological stage of foliar diseases (Agrios, 2005). The presence, abundance and persistence of moisture determine whether the biological processes of infection (Yarwood, 1992), and colonization accelerate, slow or stop altogether, with consequences for the incubation and latent periods (Huber, 1992), spore production (Rotem *et al.*, 1978) and release (Ingold, 1978). The effects of temperature have been studied in detail, but much less is known about the precise effects of moisture levels and thresholds, whether considered in terms of relative humidity (RH) or leaf wetness (presence of water films and droplets), on pathogen and disease development.

This gap in our knowledge may reflect the experimentally greater challenge of controlling, measuring and reporting moisture conditions (Rowlandson *et al.*, 2015). RH is defined in physical terms and can be measured as the ratio of the partial pressure of water vapor to the equilibrium vapor pressure of water at a given temperature. Wetness, by contrast, is not easy to define and is not a standard meteorological measurement. Leaf wetness duration (LWD) is also very difficult to measure as different parts of the leaves may be wet and dry at different times, both in the field and in controlled conditions (Huber & Gillespie, 1992).

Several epidemiological studies have identified prolonged wetness as an important factor, and several disease-forecasting models contain the variable LWD (Rowlandson *et al.*, 2015). Fewer studies have focused on RH requirements for optimal infection; some have established that the RH threshold (the level below which infection does not occur) differs between types of pathogens. RH requirements can be very high for some fungal species (e.g. 90% for *Magnaporthe oryzae*, Li *et al.*, 2014; 95% for *Didymella rabiei*, Jhorar *et al.*, 1998).

Studies of the response of a fungal pathogen to moisture conditions at the leaf scale during the earliest stages of infection (incubation period) are particularly relevant, because this period, together with the spore release and dispersal stages, is one of the most sensitive to LWD and RH in the vast majority of pathogens. Septoria tritici blotch, caused by *Zymoseptoria tritici,* formerly known as *Mycosphaerella graminicola,* is a highly relevant biological model in this context, because of its long latent period (*i.e.* asymptomatic stage), spanning from 15 to 35 dpi, depending on temperature (Shaw, 1990).

The impacts of post-inoculation LWD and of the duration and interruption of the wet period on *Z. tritici* have been analyzed in detail in controlled conditions (Holmes, 1974; Shearer & Zadoks, 1972; Eyal, 1977; Hess *et al.*, 1987; Chungu *et al.*, 2001; Magboul *et al.*, 1992; Shaw, 1990; Shaw, 1991; Fones *et al.*, 2017). Moisture appears to be crucial at all stages of the cycle (Shaner *et al.*, 1975). An increase in RH favors an increase in overall infection rate (penetration of leaf tissues via the stomata; Kema *et al.*, 1996), hyphal growth and pycnidiation intensity (Shaw, 1991; Fones *et al.*, 2017). RH is of particular importance because early penetration (< 24-48 h) is rare, with spores germinating rapidly on the leaf and epiphytic growth occurring over a period of up to 10 days or more (Fones *et al.*, 2017). RH has been inferred to be optimal between 72 and 96 h, at 100% (Shipton *et al.*, 1971; Chungu *et al.*, 2001; Suffert *et al.*, 2013), and pycnidiation has been reported to occur at an RH of 35-100% (Pachinburavan, 1981). However, threshold RH levels have not been formally tested, except for 50%-75%-100% comparisons (Shaw, 1991), probably because it is technically more difficult to generate different RH conditions in parallel than to modulate LWD under the same RH conditions. The RH threshold for *Z. tritici* therefore remains unknown. The duration of leaf wetness has also been shown to have critical effects on infection, pycnidiation and, in some cases, the duration of the latent period (Chungu *et al.*, 2001; Shaw, 1990). These experimental results are supported

by the importance of the presence and duration of moisture (particularly LWD) for the prediction of septoria tritici blotch epidemics in wheat (Hess & Shaner, 1987; Markham, 1992). Reviews on the impact of climate change on plant diseases have stressed the importance of focusing on changes in temperature and rainfall patterns (Garrett *et al.*, 2006). Global climate models (GCMs) predict more frequent and extreme rainfall events and higher atmospheric water vapor concentrations with increasing temperature (Kirk-Davidoff *et al.*, 1999; Huntingford *et al.*, 2003). Until recently, it was difficult to obtain LWD and RH, which critically influence plant pathogen infection and disease development, from GCM outputs (Chakraborty *et al.*, 2000). It had been suggested that higher levels of canopy moisture promoted the development of a range of foliar pathogens, but this factor was never considered essential and was rarely taken into account in discussions on the effects of climate change on plant diseases (e.g. West *et al.*, 2012). However, the changes in RH are likely to be at least as marked as those in temperature in semi-arid zones, such as the area around the Mediterranean basin (Vicente-Serrano, 2007). The predicted slight decrease in the duration of wet periods and slightly warmer conditions will probably have opposite effects, decreasing and promoting infection, respectively, and detailed modeling approaches are therefore required to predict the overall outcome.

This paradigm shift will require an understanding of the diversity of responses and levels of adaptation of pathogen populations to contrasting RH conditions. This understanding can be developed by identifying differences in moisture responses between pathogen genotypes within the same species, and, more generally, by characterizing the intra- *vs.* inter-population phenotypic variability connected to genetic differentiation at neutral marker loci to reveal local adaptation (Merilä & Crnokrak, 2001).

RH may have been much less considered than temperature to date because there are more convenient methods for thermal phenotyping (e.g. Zhan & McDonald, 2011; Boixel *et al.*,

2019a) than for moisture phenotyping (Li *et al.*, 2014; Xu *et al.*, 2016). Assessments of the differences in response to temperature *in vitro* (tests conducted without interaction with the plant) are biologically meaningful and can be reasonably extrapolated (Boixel *et al.*, 2019a). By contrast, differences in the response to humidity must necessarily be performed *in planta* (tests conducted in interaction with the plant), particularly for the early stages of infection (e.g. spore germination, epiphytic growth, stomatal penetration).

We investigated the diversity in moisture responses in *Z. tritici,* at the individual and population levels, for two natural populations collected from contrasting climatic zones (humid *vs.* dry environment). We evaluated the variation of the aggressiveness of the individuals of these populations on wheat seedlings subjected to four moisture regimes.

# Methods

## Fungal material

We chose to investigate two *Z. tritici* populations collected from contrasting Köppen-Geiger Euro-Mediterranean climatic zones (Peel *et al.*, 2007): (i) an Irish population (IR) sampled on cultivar JB Diego from a single field at Carlow (52°83'65'' N - 6°93'41'' E) in July 2016 (Cfb, oceanic climate); (ii) an Israeli population (IS) sampled on cultivar Galil from a single field at Kiryat-Tivon (32°71'62'' N - 35°12'74'' E) in March 2017 (Csa, hot-summer Mediterranean climate). These two populations, which have already been characterized for thermal adaptation and genotyped for 12 neutral genetic markers (Boixel *et al.*, 2019b), originate from environments with different mean RH conditions (85.1% *vs.* 69.7%, respectively), mainly due to marked differences in mean temperature and rainfall regimes over the year (Figure 1). We selected 24 IR and 24 IS *Z. tritici* isolates from these populations for sequential studies in three experimental series in which isolates were screened in a growth chamber under different moisture regimes but in identical temperature conditions.

## Plant material

The 48 isolates were phenotyped on the highly susceptible bread wheat cultivar, 'Taichung 29', commonly used as a susceptible check cultivar (Kema *et al.*, 2000) in the screening of wheat germplasm (Makhdoomi *et al.*, 2015) or in tests of global panels of *Z. tritici* isolates (Zhong *et al.*, 2017). Wheat seeds were sown in 0.4-liter pots, so as to obtain three seedlings per pot. The pots were kept in a growth chamber, under a controlled light/dark cycle (16 hours of light at 300 $\mu mol.m^{-2}.s^{-1}$ - Osram Lumilux L58W/830 - at 22°C / 8 hours of dark at 18 °C).

## Inoculation procedure

Isolates were grown in Petri dishes containing PDA (potato dextrose agar, 39 g $L^{-1}$) at 18°C, in the dark, for five days. Conidial suspensions were prepared by flooding the surface of the five-day-old cultures with sterile distilled water and then scraping the agar surface with a sterilized glass rod to release the conidia. The density of conidia in the suspension was adjusted to $10^5$ conidia.$mL^{-1}$ with a Malassez counting chamber. We added two drops of surfactant (Tween 20, Sigma) to each suspension to ensure adequate coverage of the inoculated leaf surface. A paintbrush was used to inoculate the 7.5 cm mid-length portion of the second leaf of six two-week-old seedlings with each of the isolate suspensions.

**Differential exposure to moisture regimes during the incubation period**

After inoculation, the plants were split into two identical groups assigned to two experimental blocks, under four RH regimes. We decided to modulate RH conditions during the crucial early stages of infection (Fones *et al.*, 2017), and, more specifically, over the first three days post-inoculation, to cover the time required for penetration (Kema *et al.*, 1996; Duncan and Howard, 2000; Cousin *et al.*, 2006). The four RH regimes were obtained by covering plants with transparent polyethylene bags for different periods of time after inoculation (0, 1, 2 and 3 days, respectively; Figure 2). These bags did not maintain visible drops of moisture on leaves, but they favored condensation, as the plant transpired in a closed space. Previous studies have demonstrated that free water on the leaf surface is not required for infection (Shaw *et al.*, 1991; Suffert *et al.*, 2013). Plants were exposed to 100% RH when covered with polyethylene bags, whereas uncovered plants were exposed to 100% RH in the dark and to a RH of about 80% (on average) during light periods.

Air temperature (T) and relative humidity (RH) in the growth chamber were automatically recorded, every 15 minutes, with a ventilated sensor. For characterization of the RH sensitivity of the isolates through comparisons of their moisture reaction norms (see '*Data analyses*'

section below), we summarized the four moisture regimes in terms of the mean RH prevailing during the three-day-post-inoculation period: 88.3% (C0), 92.2% (C1), 96.1% (C2) and 100% (C3). We chose not to characterize each moisture regime by the duration of time for which RH = 100 %. Indeed, there is no evidence to suggest that a RH of 80 %, which is higher than the RH value below which infection is thought to be impossible (RH = 50%; Shaw, 1991) but below the "driest" conditions tested here, can prevent fungal growth and stop infection.

**Disease assessment**

Disease severity was assessed by eye, by the same assessor, at 14, 17 and 20 dpi (days post-inoculation), as the percentage of the inoculated leaf surface (1, 2, 3 and 5%, then increments of 5% up to 100%) displaying chlorosis (chlorotic area), necrosis (necrotic area, including both sporulating and non-sporulating area) and visible fruiting bodies or pycnidia (sporulating area).

**Data analysis**

**Effect of moisture conditions on disease severity –** The experimental and biological main effects on the variability of sporulating area (SPO, expressed as a percentage of the inoculated leaf surface) and their interactions were assessed by a statistical modeling approach. We investigated the partitioning of the variability into eight different components of variation (deviance): series (S), block (B), RH conditions (H), population (P), isolate I(P), RH conditions × population interaction (H×P), RH conditions × isolate interaction (H×I(P)), residuals ($\varepsilon_{sbpih}$). We analyzed these deviance components, by fitting a generalized linear model (GLM) with a log-link function and quasi-Poisson errors to account for overdispersion, according to the following model (R *glm* function; R Core Team, 2018): $SPO_{sbpih} = S + B + P + I(P) + H + H\times P + H\times I(P) + \varepsilon_{sbpih}$. *Post-hoc* comparisons of differences in SPO means (multivariate analysis of

variance) and homoscedasticity (Levene's test) between IR and IS populations were performed to investigate differences in inter- and intra-population responses to moisture conditions.

**Establishment of individual moisture reaction norms –** Individual moisture reaction norms, describing the pattern of SPO as a function of relative humidity, were established for each isolate. Reaction norms were assumed to be linear within the investigated 80-100% RH range and were therefore estimated by a linear regression $y = a.x + b$. Individual reaction norm properties were summarized by three parameters accounting for sensitivity to RH: (i) the intercept '*b'* corresponding to the elevation or the sensitivity to the driest environment; (ii) the steepness of the slope '*a'* corresponding to the response to variation, *i.e.* whether phenotypic responses increased or decreased in extreme environments and to what extent; (iii) the midpoint '$y_{94.2\%}$' corresponding to the average response or the response at the midpoint of the RH range, to consider shifts in the entire reaction norm. The heterogeneity of RH sensitivity across isolates at the individual level and the difference between IR and IS population-level moisture reaction norms were assessed on the basis of these three parameters.

**Differentiation in individual and population responses –** Phenotypic differentiation in terms of the intercept, slope and midpoint was compared to between-population neutral genetic differentiation, to determine the potential for local adaptation of moisture responses ($P_{ST}$ - $F_{ST}$ comparisons performed with the '*Pstat*' R package). Neutral genetic variability, and the structure and distribution of diversity between and within the IR and IS populations were characterized in a previous study (Boixel *et al.*, 2019b) based on microsatellite genotyping data acquired for 12 SSRs (ST1, ST2, ST3A, ST3B, ST3C, ST4, ST5, ST6, ST7, ST9, ST10, ST12 neutral microsatellites; Gautier *et al.*, 2014). In parallel, components of phenotypic variation in the response to the four moisture regimes (C0, C1, C2, C3) were extracted by principal component analysis. We projected all four-fold phenotypes onto a two-dimensional space and

clustered the isolates (hierarchical classification on principal components, HCPC) on the basis of their sensitivities to the four moisture regimes ('*FactoMineR*' and '*factoextra*' R packages).

## Results

### Overall effect of the experimental conditions

The block (B) and series (S) effects were significant. Our experimental design provided strong control over RH conditions (saturation-level application), but these experimental effects are probably due to the spatial and temporal variability of other micrometeorological conditions reported to occur within growth chambers, even under controlled conditions (e.g. gradient in irradiance intensity due to artificial lighting; Poorter *et al.*, 2012). Mean RH had a significant effect on sporulating area at all times of disease assessment (14, 17 or 20 dpi; $p$-value < 0.01; Table 1, Figure 3). The significant differences in sporulating area induced by different *Z. tritici* isolates (I(P)) confirmed the genetic origin of the variability in aggressiveness. The population effect (P) was significant at 14 dpi, when sporulating area was greater for IS than for IR isolates under the C0, C1 and C2 regimes (Figure 4). Significant H×I(P) and H×P interactions highlighted differential individual and population-level tolerance to the four moisture regimes (Table 1). At 14 dpi, differences in the mean sporulating area (*post-hoc* analysis of the H×P interaction, *i.e.* the interaction of moisture regimes and differential population-level response to these conditions) and its intrapopulation variance (Levene's test for homogeneity of variance) between the IR and IS populations were significant ($p$-value < 0.05; Figure 4). At 17 dpi, these differences were small and did not differ significantly between the two populations; they had completely disappeared by 20 dpi.

### Significant effect of moisture during the early stages of infection

The temporal dynamics of the effect of moisture regimes justified the sequential fitting of GLMs at 14, 17, and 20 dpi (Figure 3): at 14 dpi, the differences in sporulating area between C0-C1 and C2-C3 highlighted a dichotomy between unfavorable and favorable RH conditions, probably separated by a threshold at about 94% RH. At 17 dpi, the differences between the four moisture regimes C0, C1, C2 and C3 were larger and significant. At 20 dpi, there were no longer any differences, due to saturation being reached for sporulating area (100%). In summary, from 0 to 3 dpi, the closer the RH to 100%, the more intense the development of lesions. Indeed, a slight difference in moisture regime during the very early stages of *Z. tritici* infection, despite the relatively high RH value of the driest conditions tested (88.3%), had a strong impact on the dynamics of lesion development. Any increase in average RH bringing it closer to 100% favored the development of the isolate during the early stages of infection.

**Comparisons of tolerance to drier conditions are best performed at 14 dpi**

Sporulating areas at 14 dpi were significantly larger for IS isolates on wheat plants subjected to the C0-C1-C2 regimes, whereas no significant difference was observed for C3 (Figure 4), highlighting the greater tolerance of drier conditions in the IS population. No difference was observed between the populations at 17 and 20 dpi (no statistically significant H×P interaction, although this interaction was close to significance at 17 dpi; $p$-value < 0.1), suggesting that the driest regimes delayed infection processes but did not prevent *Z. tritici* development. These results led us to perform further analyses at 14 dpi, through comparisons of 'moisture reaction norms' or 'response curves', to assess the differences between isolates within these two pathogen populations in more detail.

**Interindividual differences in moisture adaptation within the two populations at 14 dpi**

The comparison of individual reaction norms (Figure S1), particularly for density distributions, and the ranges of values for the three parameters capturing the general characteristics of the

response (intercept, slope, midpoint), highlighted high levels of interindividual variation in moisture sensitivity (Figure 5). Mean phenotypes did not differ significantly between the two populations (Wilcoxon rank sum test; differences in mean response assessed for the intercept: *p*-value = 0.33; slope: *p*-value = 0.39; midpoint: *p*-value = 0.92), but individual variation was greater for the midpoint coefficient in the IS population (Bartlett test of homogeneity of variance; *p*-value < 0.01). For the population-level linear moisture reaction norm, a significant difference in sporulating area was observed between the IS and IR populations for C1 (Wilcoxon rank sum test, *p*-value = 0.03), but not for the other three moisture regimes (*p*-value > 0.05). This suggest that RH conditions may have been too restrictive or detrimental for the expression of biological differences and variance for the trait under the C0 regime, whereas they were not limiting for C2 and C3. Neutral markers highlighted no differences in genetic structure between the IR and IS populations (Figure S2). $P_{ST}$ values (computed at the critical $c/h^2$ ratio of 1) and their confidence intervals at $c/h^2 = 1$ indicated a robust difference between $P_{ST}$ and $F_{ST}$ (Figure S3). Thus, any phenotypic difference can be interpreted as a result of adaptation, suggesting that interindividual differences in moisture adaptation within the two populations may conceal signatures of local adaptation.

### Classification of *Z. tritici* sensitivity to the four moisture regimes

Based on a PCA of phenotypic variation, we were able to classify the 48 *Z. tritici* isolates according to their sensitivity to the four moisture regimes (Figure 6). At 14 dpi, the C2 and C3 regimes did not discriminate between individual responses in terms of sporulating area. Cluster 4 consisted of isolates with a particularly large sporulating area (extreme phenotypes of is16, is19 and is34; Figure S1) that were less affected by the C0 and C1 regimes.

## Discussion

**Effect of moisture conditions during the early stages of *Z. tritici* infection**

In this experimental study, we established individual- and population-level moisture reaction norms, expressed as the area of *Z. tritici* sporulation on inoculated leaves for a RH averaged over the three days following inoculation. By this approach, we were able to assess the critical effects of moisture regime on the development of septoria tritici blotch during the earliest stages of infection (pycnidiospore germination, epiphytic hyphal growth and stomatal penetration) despite the relatively high RH value of the driest regime tested (88.3%). It also made it possible to refine the findings of several previous studies performed in our range of experimental conditions (Holmes, 1974; Shearer & Zadoks, 1972; Eyal, 1977; Hess *et al.*, 1987; Chungu *et al.*, 2001; Magboul *et al.*, 1992; Shaw, 1990; Shaw, 1991; Fones *et al.*, 2017). The effects of moisture conditions were more pronounced at 14 dpi than at 17 and 20 dpi. Based on these results, we analyzed the data acquired at 14 dpi in more detail, to determine moisture sensitivity at both the individual and population levels. These findings also raise the question as to why the effects of moisture conditions are less pronounced at 17 and 20 dpi. Fones *et al.* (2017) previously showed that increasing leaf moisture is associated with increasing disease severity (number of pycnidia per leaf), because it decreases the time required for *Z. tritici* to penetrate into leaf tissues. This finding is consistent with our results, suggesting that moisture conditions have a greater impact on the rate at which symptoms appear than on their final intensity. We may hypothesize that suboptimal moisture regimes have slowed epiphytic hyphal growth and penetration into the leaf tissues via the stomata, but that they did not ultimately reduce the germination rate or infection efficiency, at least for the RH values which were tested here. Epiphytic development was probably slower during the daytime periods, when wheat leaves were not bagged, resulting in a ‘delay’ in the infection process rather than an ‘irreversible’ ending of this process. This hypothesis could be tested with direct experimental approaches based on cytological observations or indirect approaches measuring infection efficiency,

defined as the proportion of pathogen spores able to infect susceptible plant tissues once they have landed on them, which could be assessed by methods based on the time-resolved imaging of disease progress (Karisto *et al.*, 2019).

**Technical limitations: moving towards *in vitro* tests for minimizing background noise?**

Even under controlled conditions, growth chambers are subject to spatiotemporal fluctuations in within-chamber conditions, particularly as concerns the distribution of light intensity (Potvin & Tardif, 1988; Poorter *et al.*, 2012). Such spatial patterns of heterogeneity may have contributed to the block effect we detected in our experimental design, whereas differences in inoculation conditions (e.g. abiotic factors, spore virulence levels) might also explain the differences in symptom expression between series (Kay *et al.*, 2019). One possible improvement to experimental methods, making it possible to screen larger numbers of isolates in a more standardized way (making it easier to separate environmental and physiological responses), would be to control and test moisture conditions *in vitro*, with the experimental devices proposed by Li *et al.* (2014; different RH conditions formed within humidity chambers obtained with different glycerol solution concentrations) or Xu *et al.* (2016; discrete RH gradient formed in spatially separated wells of a modified multiwell plate), for example. This would have the advantage of countering the effect of the host resistance × environmental response interaction on the expression of aggressiveness in isolates (Ahmed *et al.*, 1996), although, in our experiment, the two *Z. tritici* populations were similarly aggressive on the cultivar 'Taichung 29'. *In vitro* approaches may be particularly relevant for *Z. tritici,* as they have been shown to be a reliable *proxy* for the assessment of differences in thermal sensitivity (Boixel *et al*., 2019a).

**First evidence of moisture adaptation in a fungal plant pathogen**

Our results highlight strong individual variations in the phenotypic plasticity of *Z. tritici* with respect to sensitivity to RH conditions. Notwithstanding the relatively limited sample size (48 isolates) and number of populations ($n$ = 2) investigated here, this study revealed, for the first time in a fungal plant pathogen, the existence of individual variation in responses to moisture conditions. Moreover, the Israeli population was shown to be more tolerant to drier conditions at 14 dpi and we found no genotypic differentiation for neutral microsatellite loci between the two populations. This result highlights a moisture adaptation signature, again, the first to be reported for a fungal plant pathogen, and is consistent with the climatic conditions of the areas from which the two populations were collected.

The interaction between RH and isolate effects was significant, whenever disease was assessed, highlighting the importance of taking the interindividual variation in response to moisture conditions into account. Differences in moisture sensitivity were analyzed at both the population and individual levels. The moisture performance curves highlighted sensitivity variations between the two populations. The differences in the mean values of the parameters characterizing this sensitivity were not significant. However, the interindividual analysis revealed significant differences in moisture sensitivity between isolates, suggesting that it would be possible to quantify such differences more accurately in future experiments. This would require the study of larger numbers of individuals and more stringent moisture conditions.

**The estimation of interactions between moisture and temperature adaptation at both population and individual levels is ambitious, but technically possible**

The Israeli and Irish *Z. tritici* populations studied here are part of a Euro-Mediterranean set of eight populations included in a broader study on thermal adaptation (Boixel *et al.*, 2019b). General ecological concepts, knowledge and methods have been developed to a greater extent

for thermal biology than for moisture biology (Angiletta, 2009). The estimation of interactions between moisture and temperature adaptation would also be relevant at both population and individual level. For this purpose, *Z. tritici* is an interesting case, both because a physical relationship between the two microclimatic variables, temperature and moisture, has been established (Shaw & Royle, 1993; Pietravalle *et al.*, 2003), and because the development of septoria tritici blotch is known to be strongly influenced by both variables (Markham, 1992). The interactions between temperature and moisture effects could be studied from a mechanistic angle (for instance, testing pleiotropy *vs*. co-selection hypotheses in the genetic determinism of such a dual adaptation) but also from an epidemiological angle (predicting the consequences of climate changes affecting plant disease development in a more holistic way). The comparison of differences between temperature and moisture responses in different pathogen populations, starting with the Israeli and Irish populations, is particularly interesting because moisture adaptation is already interconnected with thermal adaptation in some models (e.g. Shinozaki & Yamaguchi-Shinozaki, 2000; Mutamiswa *et al.*, 2019).

**How best to characterize individual variations of phenotypic plasticity and sensitivity to RH conditions in *Z. tritici*?**

This study did not aim to determine the moisture limit below which *Z. tritici* isolates cannot infect wheat, but we can nevertheless unambiguously conclude that a "RH as close as possible to 100% is best for *Z. tritici*". The minimal RH threshold for *Z. tritici* remains unknown. Shaw (1991) previously showed that breaks at 50% relative humidity had large effects but nevertheless enabled infection to occur. We can assume that there is a threshold moisture (a lethal condition definitively blocking the infectious process), like that for temperature, but previous studies in *Z. tritici* and general knowledge about the epidemiology of fungal disease suggest that a minimum threshold, rather than a maximum, must be taken into account (as RH, by definition, cannot exceed 100%), together with a time period during which RH remains

below this minimum threshold. Conversely, for temperature, the lethal threshold that should be considered is a maximum value, because *Z. tritici* can survive the thermal conditions of winter and freezing at -80°C in laboratory conditions.

We used averaged RH conditions to describe the moisture regimes, which limits comparisons with published data, as most previous studies focused on the duration of moisture periods rather than variations of RH values *sensu stricto* (Shaw, 1991; Magboul *et al.*, 1992; Chungu *et al.*, 2001). However, we found that this was the most pragmatic approach to the establishment and comparison of moisture performance curves. As mentioned above, in addition to RH, leaf wetness duration is crucial, as different parts of the leaves may be wet and dry at different times (Huber & Gillespie, 1992). More generally, the question of how best to describe RH conditions remains unresolved: averaging, intermittent favorable/unfavorable conditions, etc. How can the effect of the putative minimum moisture threshold (still unknown) be linked to the effect of the duration of dry periods? To which microclimatic variables are the individuals and populations really (mal)adapted? These questions should be addressed. As for moisture, it has been experimentally demonstrated that *Z. tritici* responds to 'leaf temperature' (similar to 'body temperature' for animals) rather than 'air temperature' (Bernard *et al.*, 2012), and that the time step for measurement is important (Bernard, 2012). These conclusions can also be extended to moisture.

Additional studies on adaptation to very suboptimal moisture regimes (e.g. 50-75% RH) rather than regimes close to the optimum (e.g. 85-100% RH) should be considered: (i) for methodological reasons, because this would probably maximize the expression of adaptation, making it easier to characterize experimentally, with populations contrasting less than the Israeli and Irish populations studied here; (ii) for epidemiological reasons, because it would provide knowledge to improve predictions of the adaptation of *Z. tritici* populations on bread and durum wheat in dryland farming areas (e.g. in Middle East and North Africa) in response

to climate change. Such aims are ambitious and the studies will need to take into account the difficulties involved in experimental studies of the effects of moisture.

The exploitation of relevant analyses based on biological data requires attention to the issue of 'drought stress tolerance' and an extension of reflections to the ecology of communities (Sheik *et al.*, 2011). Our study provides preliminary insight into such drought stress tolerance and the diversity of its responses across individuals and populations when considering the effects of climate change on plant disease epidemics. A knowledge of the microclimatic requirements for fungal pathogen development is essential for prospective studies of the impact of climate change with a solid experimental basis. To date, such studies have mostly focused on temperature, but climate change in the global context will also include large changes in moisture conditions with pronounced domino effects (Siepielski *et al.*, 2017).

## Data Availability Statement

The data that support the findings of this study are openly available in the INRA Dataverse online data repository (https://data.inra.fr/) at https://doi.org/10.15454/FK7WHW.

## Author Contributions

FS conceived the study and was in charge of overall direction and planning, with substantial input from ALB. SG performed the experiments according to a protocol developed jointly by FS and TM. ALB and FS analyzed the data, prepared the figures and wrote the manuscript. TM provided critical feedback. All authors approved the final version of the manuscript.

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## Conflict of Interest Statement

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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## Supplementary Material

Supplementary material is available in the online version of this article.

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**Table 1 - Analysis of the deviance of sporulating area (SPO in %) induced by 48 *Zymoseptoria tritici* isolates on wheat seedlings exposed to four RH regimes (see Figure 2) at 14, 17 and 20 dpi**. A quasi-Poisson generalized linear model with a log-link function was fitted to experimental data, to assess the relative importance of the factors considered for the observed variation: series (S), block (B), RH conditions (H), population (P), isolate I(P), RH conditions × population interaction (H×P), RH conditions × isolate interaction (H×I(P)). The values reported in the table correspond to the components of deviance and their corresponding *p*-values (*P*).

| | $SPO_{14dpi}$ | | $SPO_{17dpi}$ | | $SPO_{20dpi}$ | |
|---|---|---|---|---|---|---|
| | Deviance | *P* | Deviance | *P* | Deviance | *P* |
| Series (S) | 2480.1 | < 0.01 | 4899.5 | < 0.01 | 3917.4 | < 0.01 |
| Block (B) | 49.5 | < 0.01 | 87.5 | < 0.01 | 94.9 | < 0.01 |
| Population (P) | 87.5 | < 0.01 | 2.5 | 0.56 | 0.2 | 0.83 |
| Isolate I(P) | 7368.6 | < 0.01 | 10033.2 | < 0.01 | 7772.5 | < 0.01 |
| RH conditions (H) | 5283.0 | < 0.01 | 7426.8 | < 0.01 | 3851.1 | < 0.01 |
| H×P | 224.0 | < 0.01 | 51.4 | 0.08 | 2.8 | 0.91 |
| H×I(P) | 2241.0 | < 0.01 | 4047.8 | < 0.01 | 4091.8 | < 0.01 |

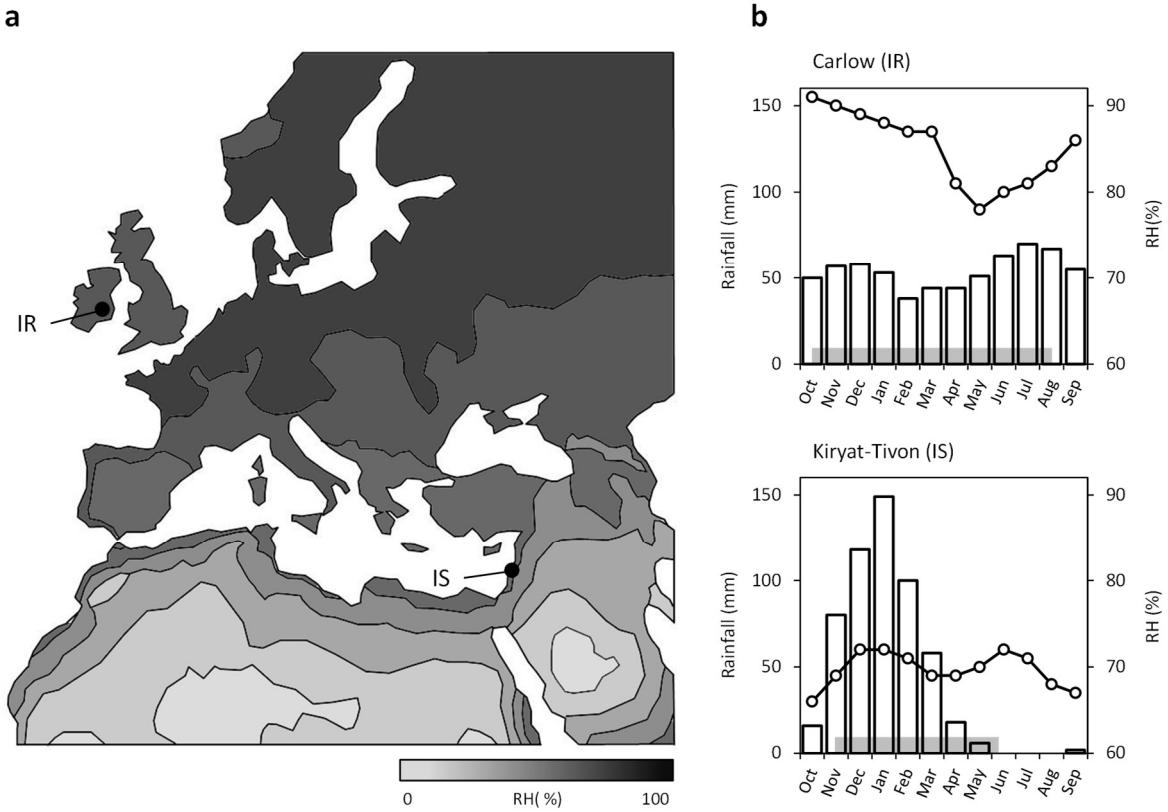



**Fig. 1 - Relative humidity (RH) conditions and precipitation at the two sampling sites.** (a) Mean annual RH in the Euro-Mediterranean area (data from the Atlas of the Biosphere, http://atlas.sage.wisc.edu/; New *et al.*, 1999); (b) mean monthly RH and rainfall distribution (1982-2012 data from the World Climate Database, https://en.climate-data.org/) at the sites from which the two *Zymoseptoria tritici* populations were collected (Carlow in Ireland for the IR population; Kyriat-Tivon in Israel for the IS population). The horizontal gray bar indicates the standard wheat-growing period (from sowing to harvest).

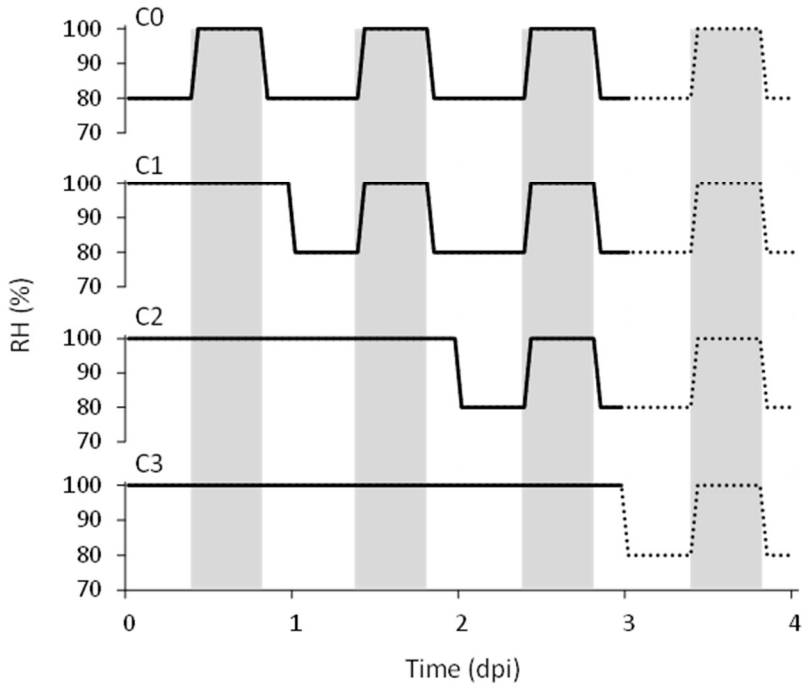



**Fig. 2** - **Moisture regimes investigated over the three first days post-inoculation (dpi).** Solid (from 0 to 3 dpi) and dotted (after 3 dpi) lines depict the four post-inoculation moisture regimes to which the wheat seedlings were subjected in the early stages of infection: C0 = without bagging (mean RH = 88.3%); C1 = bagged for one day (mean RH = 92.2%); C2 = bagged for two days (mean RH = 96.1%); C3 = bagged for three days (mean RH = 100%). White and gray areas indicate successive light and dark periods, respectively.

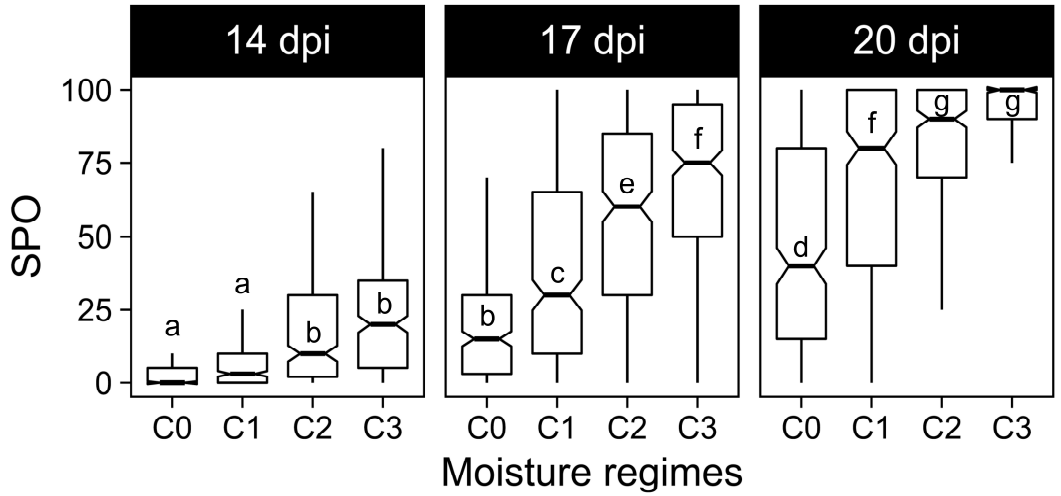



**Fig. 3 - Effect of moisture regime (C0, C1, C2, C3; see Figure 2) on the percentage of sporulating area (SPO) induced by *Zymoseptoria tritici*, by disease assessment time (14, 17, 20 dpi).** Medians are indicated by the lines at which the notches converge, and different letters indicate significant difference in SPO between experimental conditions in *post-hoc* tests.

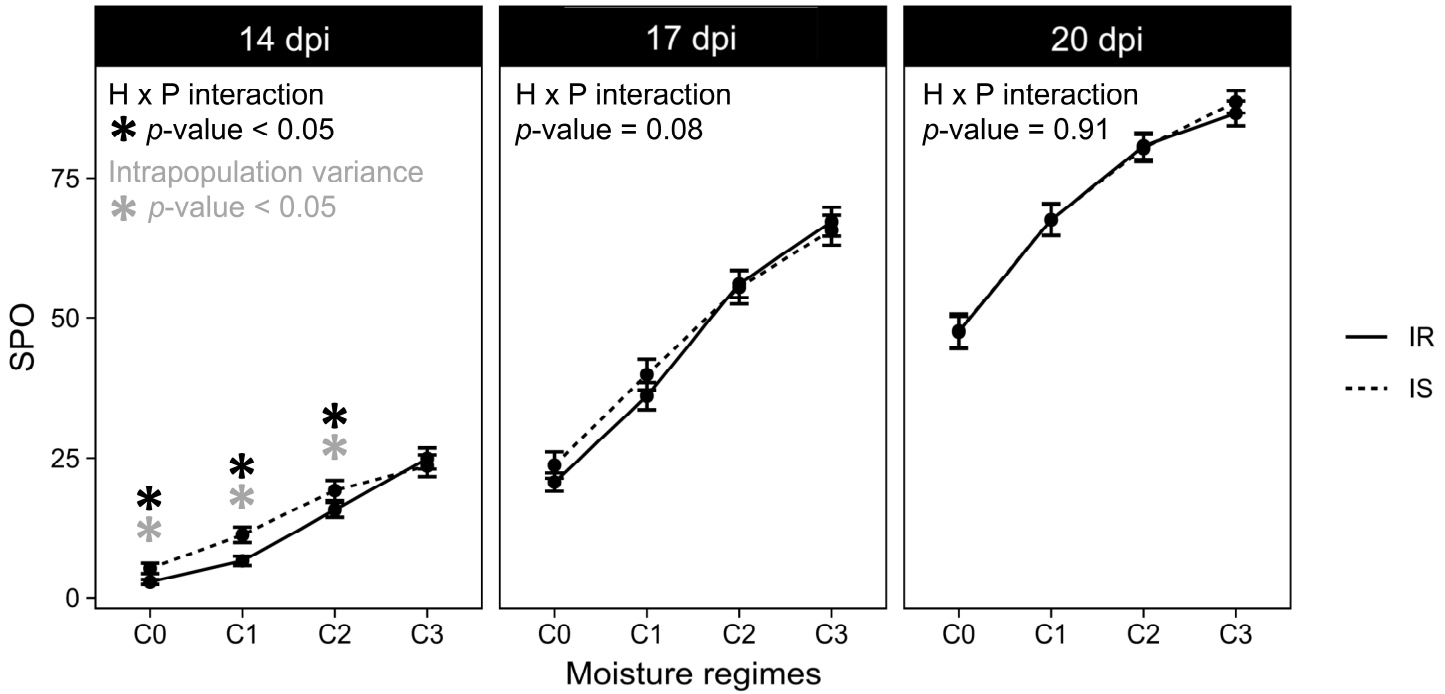



**Fig. 4 - Dynamics of the effect of moisture regime (C0, C1, C2, C3; see Figure 2) on the percentage of sporulating area (SPO expressed as the mean ± SEM) in the early stages of *Zymoseptoria tritici* infection, by isolate origin - Ireland (IR; solid line) or Israel (IS; dashed line) - and the timing of disease assessment (14, 17, 20 dpi).** Significant differences in the mean (*post-hoc* analysis of the H × P interaction, *i.e.* the interaction of moisture regimes and differential population-level response to these conditions) and the intrapopulation variance (Levene's test for homogeneity of variance) of SPO between IR and IS populations are highlighted by black and gray stars, respectively ($p$-value < 0.05).

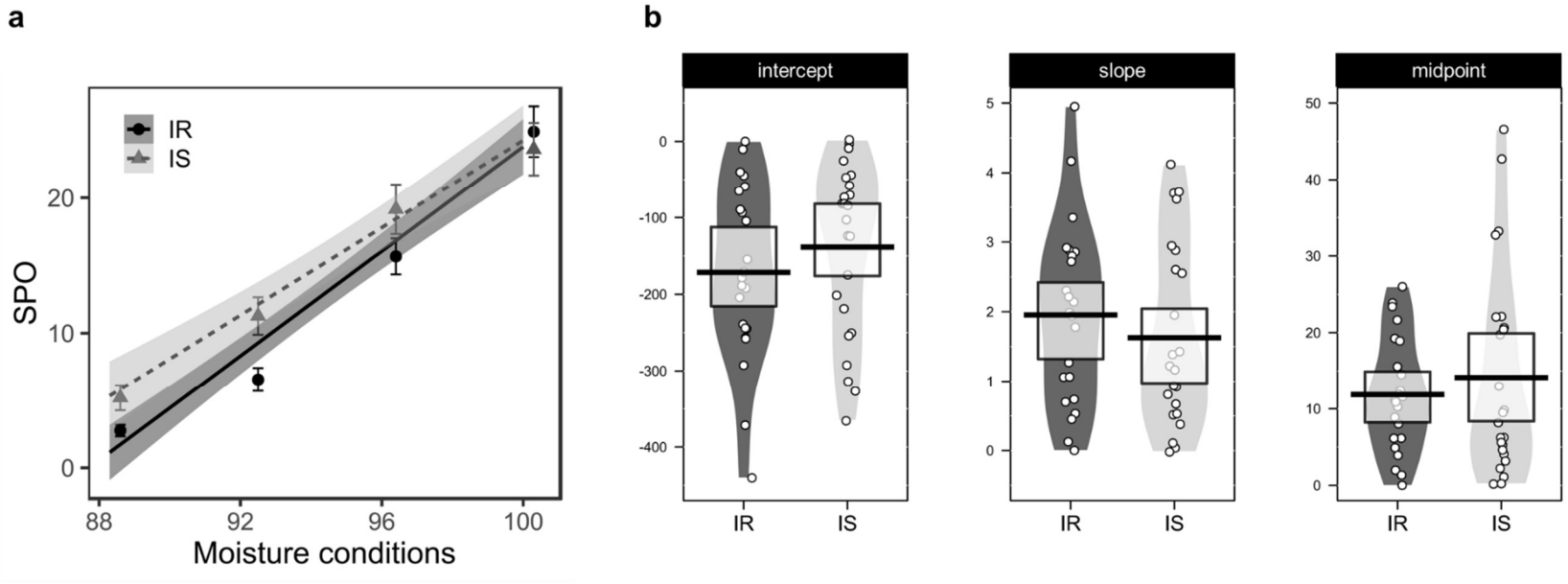



**Fig. 5 - Variation of *Zymoseptoria tritici* response to moisture conditions at the population (IR: Irish population, IS: Israeli population) and individual levels, at 14 dpi.** (a) Population-level moisture reaction norms (mean RH prevailing over the first three days after inoculation, expressed as a %) for the IR (black circles/solid line) and IS (gray triangles/dashed line) populations. The corresponding linear regression lines fitted to the percentage of sporulating area (SPO, expressed as the mean ± SEM) are displayed with their 95% confidence intervals. (b) Interindividual variation of the three chosen descriptors of individual moisture reaction norms: intercept (*b*), slope (*a*) and midpoint ($y_{94.2\%}$). Crude individual values (open circles), means (horizontal black thick lines), distributions (smoothed density curves) and 95% Bayesian highest density intervals (central rectangular boxes enclosing the means) are shown for each descriptor for which interindividual variation is displayed by population (IR, IS).

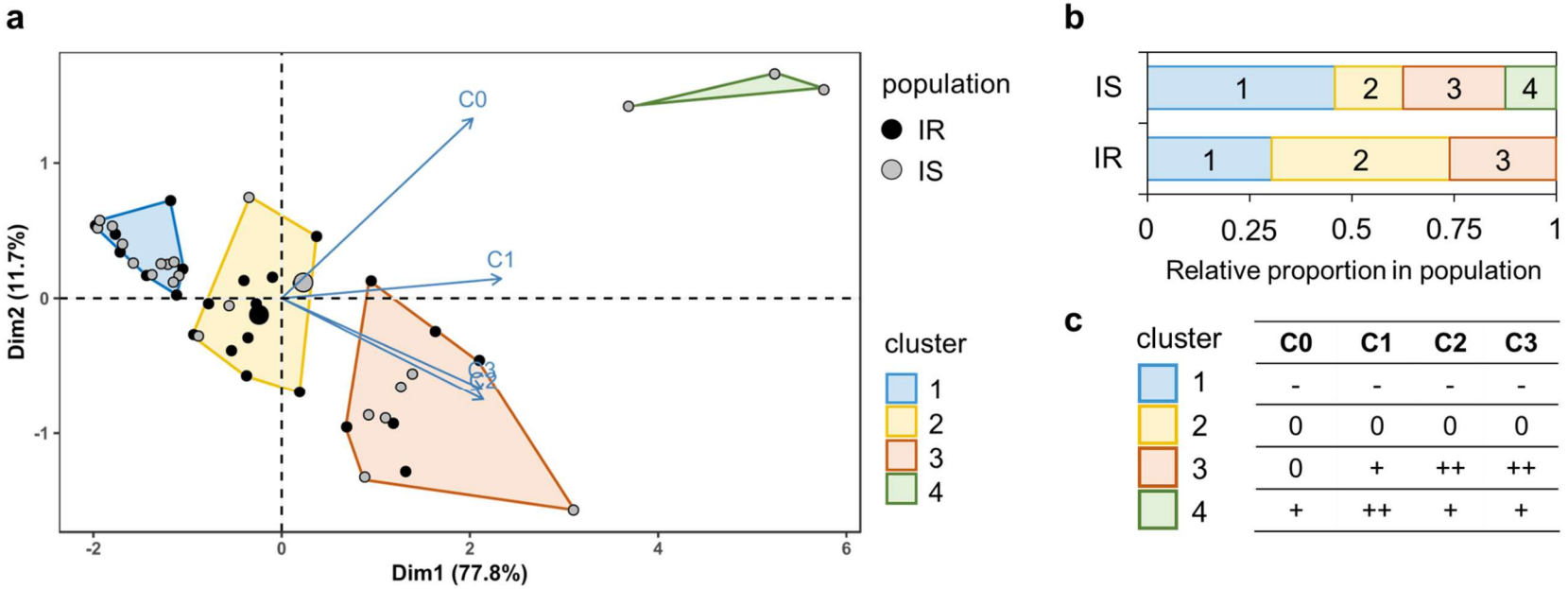
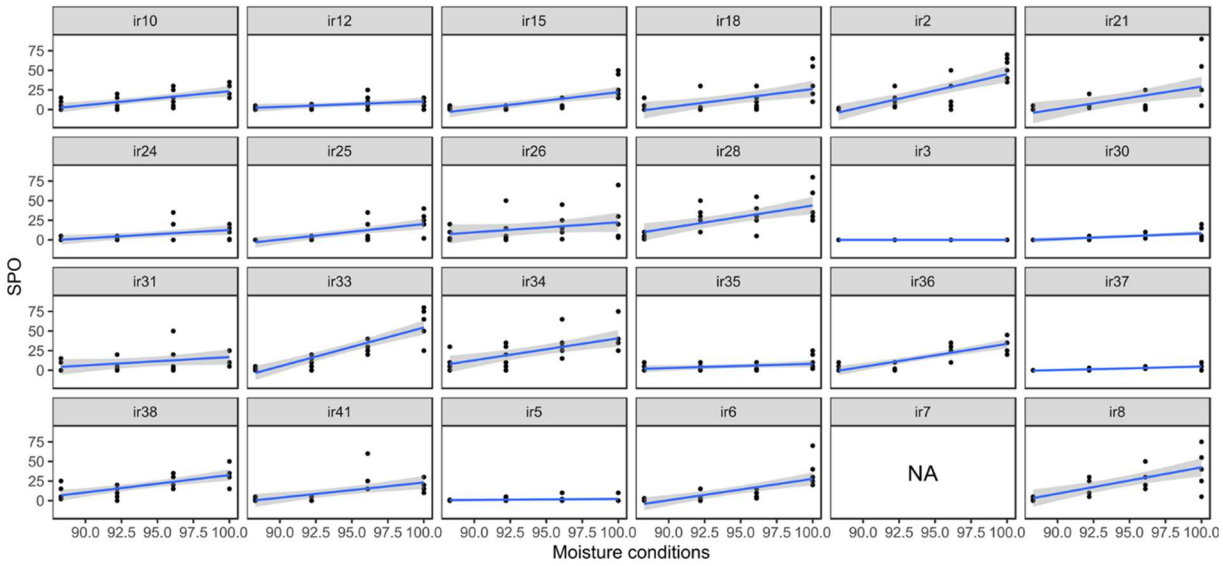



**Fig. 6 - Classification of *Zymoseptoria tritici* sensitivity to the four moisture regimes (C0, C1, C2, C3; see Figure 2) at 14 dpi.** (a) Principal component analysis (PCA) biplot showing Irish (IR, black points) and Israeli (IS, gray points) isolates plotted in two dimensions, using their projections onto the first two principal components to summarize their response (SPO, *i.e.* percentage of sporulating area) under the four moisture regimes. HCPC clusters of individual responses are shown as colored areas on the factorial plane. (b) Relative proportions of the four identified clusters in the IR and IS populations. (c) Reading grid for the clustering of isolates based on their responses to the four moisture regimes: SPO significantly lower (-) or higher (+) than the dataset mean (0).

**(a)**




**(b)**

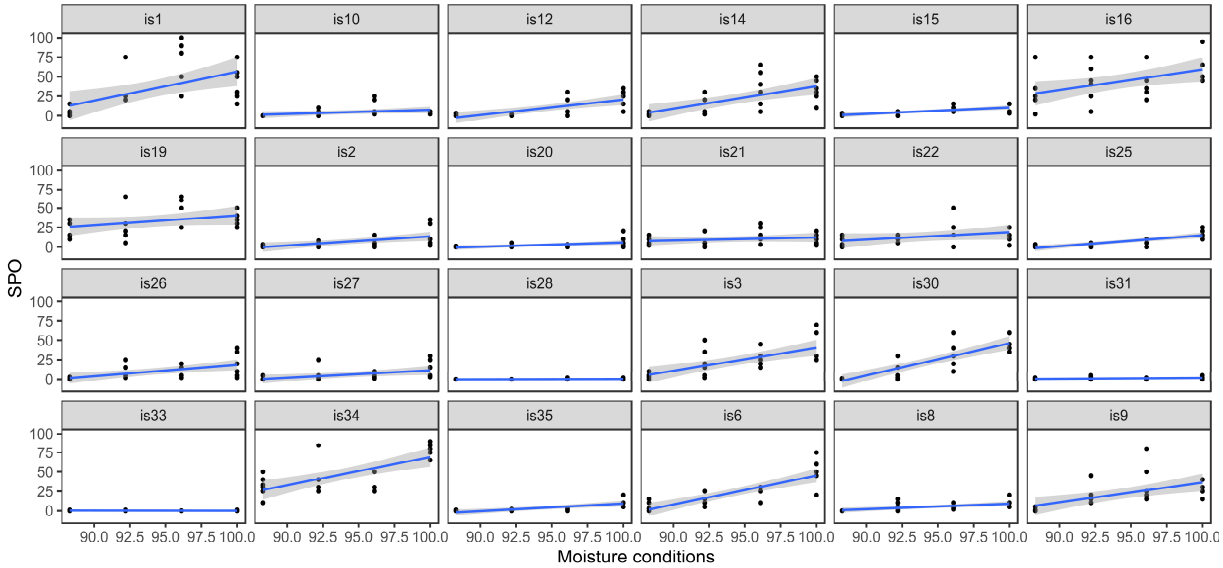



**Fig. S1 - Individual moisture reaction norms at 14 dpi for (a) the 24 Irish (IR) and the (b) 24 Israeli (IS) *Zymoseptoria tritici* isolates.** Sporulating areas (SPO) are expressed as a percentage of the inoculated leaf area for each isolate (except ir7, due to unsuccessful inoculation), in response to four moisture conditions characterized by the mean RH prevailing during the three-day period immediately after inoculation (see Figure 2). Linear regression lines (in blue) and their 95% confidence intervals were fitted independently to experimental observations (dark points corresponding to six seedling wheat leaves per isolate × moisture conditions).

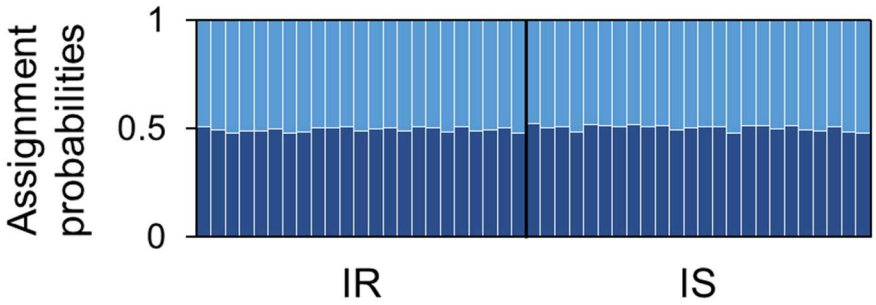



**Fig. S2 - Genetic subdivision of the 48 *Zymoseptoria tritici* isolates composing the Irish (IR) and Israeli (IS) populations.** Bar plot displaying the Bayesian genetic clustering of IR and IS populations according to 12 SSR markers. The STRUCTURE algorithm was applied under the admixture and correlated allele frequencies model (500,000 iterations of the Markov chain followed by a run phase of 1,000,000 iterations with 10 independent replicates for each tested number of clusters). Each isolate is represented by a single vertical bar broken into two color segments, the lengths of which are proportional to the probability of to the isolate being assigned to the inferred genetic clusters ($K = 2$). No population structure was detected because each individual was affected to the three genetic clusters with similar probabilities.

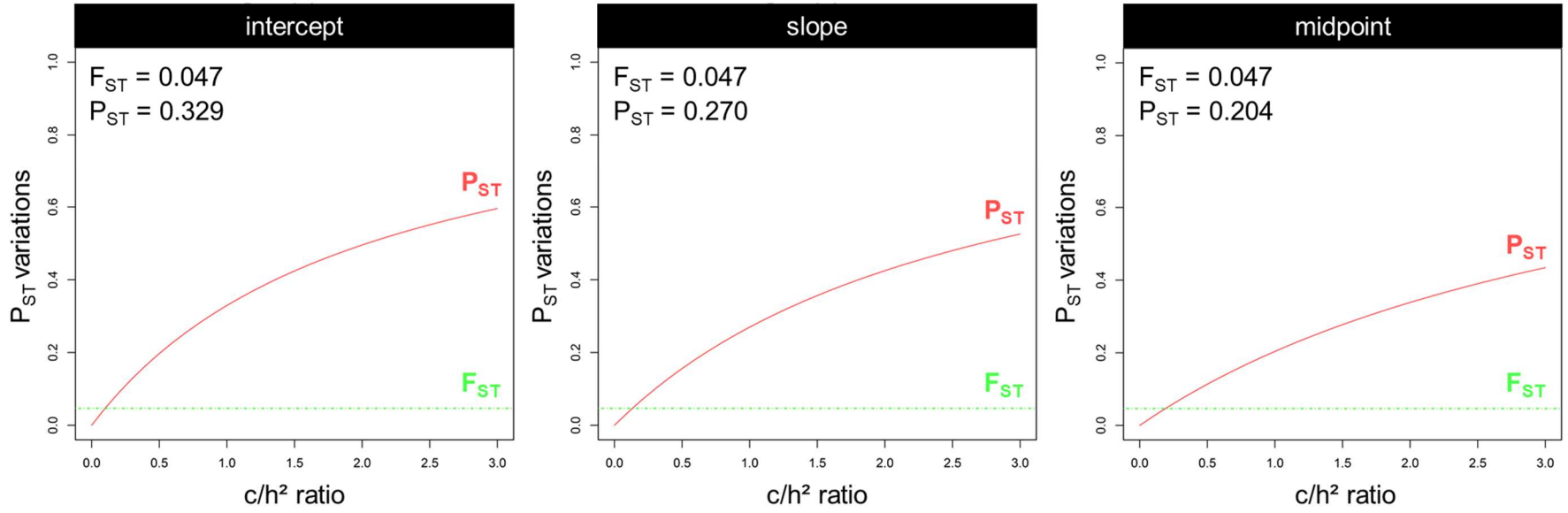



**Fig. S3 - Phenotypic divergence in moisture reaction norms between the IR and IS populations.** Sensitivity analyses exploring the robustness of $P_{ST}$–$F_{ST}$ comparisons over variations in the $c/h^2$ ratio, which determines the accuracy of the approximation of $Q_{ST}$ by $P_{ST}$. Phenotypic divergence in individual moisture reaction norms between populations ($P_{ST}$) was investigated for the intercept, slope and midpoint parameters. On each plot, estimates of $P_{ST}$ (solid line in red) and $F_{ST}$ (dashed line in green) are shown, to reveal the contrasting patterns of phenotypic responses to moisture conditions and neutral genetic divergence. The $P_{ST}$ values displayed (computed at the critical $c/h^2$ ratio of 1) and their confidence intervals at $c/h^2 = 1$ indicate the occurrence of a robust difference between $P_{ST}$ and $F_{ST}$, suggesting the existence of signatures of local adaptation.