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Contrasting nutrient-disease relationships: Potassium gradients in barley leaves have opposite effects on two fungal pathogens with different sensitivities to jasmonic acid

Jayne L. Davis[1,2,+], Patrick Armengaud[1++], Tony R. Larson[3], Ian A. Graham[3], Philip J. White[2*], Adrian C. Newton[2], Anna Amtmann[1*]

[1]Plant Science Group, Institute for Molecular, Cell and Systems Biology, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow G128QQ, UK

[2]The James Hutton Institute, Invergowrie, Dundee DD2 5DA, UK

[3] Department of Biology, Centre for Novel Agricultural Products, University of York, York YO10 5DD, UK

[+] Current address: NIAB, Huntingdon Road, Cambridge CB3 0LE UK

[++]Current address: ITK, Montpellier Agglomeration Business Innovation Center, Cap Alpha, Avenue de l'Europe, 34830 Clapiers, France

*Corresponding author:
Anna Amtmann
E-mail: anna.amtmann@glasgow.ac.uk
Tel +44 (0)141.3305393

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Summary statement
Jasmonic acid (JA) is a plant hormone with important roles in leaf senescence and pathogen defense. Our finding that JA-biosynthesis is up-regulated by low concentrations of potassium (K) in leaves suggests that JA may provide the molecular link between plant K status and fungal disease. This hypothesis was further supported by the finding that disease symptoms on barley leaves were positively correlated with leaf K content for the JA-sensitive powdery mildew (*Blumeria graminis*) but negatively correlated with leaf K content for the JA-insensitive leaf scald (*Rhynchosporium commune*).

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ABSTRACT

Understanding the interactions between mineral nutrition and disease is essential for crop management. Our previous studies with *Arabidopsis thaliana* demonstrated that potassium (K) deprivation induced the biosynthesis of jasmonate (JA) and increased the plant's resistance to herbivorous insects. Here we addressed the question how tissue K affects the development of fungal pathogens and whether sensitivity of the pathogens to JA could play a role for the K-disease relationship in barley (*Hordeum vulgare* cv. Optic). We report that K-deprived barley plants showed increased leaf concentrations of JA and other oxylipins. Furthermore, a natural tip-to base K-concentrations gradient within leaves of K-sufficient plants was quantitatively mirrored by the transcript levels of JA-responsive genes. The local leaf tissue K concentrations affected the development of two economically important fungi in opposite ways, showing a positive correlation with powdery mildew (*Blumeria graminis*) and a negative correlation with leaf scald (*Rhynchosporium commune*) disease symptoms. *B. graminis* induced a JA-response in the plant and was sensitive to methyl-JA treatment while *R. commune* initiated no JA-response and was JA-insensitive. Our study challenges the view that high K generally improves plant health and suggests that JA-sensitivity of pathogens could be an important factor determining the exact K-disease relationship.

Keywords: Potassium, Jasmonic acid, *Blumeria graminis, Rhynchosporium commune*

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INTRODUCTION

Reducing the amount of excess mineral fertilizer applied to crops is an essential step towards sustainable food production (White, Broadley & Gregory 2012). It is therefore important to understand how food crops respond to changes in nutrient supply. High-throughput methods for the analysis of transcripts, metabolites, proteins and enzyme activities have already provided us with detailed information about the molecular responses of plants to varying nutrient supply under controlled conditions, and about the integration of these responses with plant growth (Amtmann & Armengaud 2009; Tschoep *et al.* 2009; Sulpice *et al.* 2009, 2010; Wang & Wu 2013; Chérel, Lefoulon, Boeglin & Sentenac 2014). In the field, nutrient deficiencies are accompanied by other stress factors, most importantly pathogens and pests. Combating disease in crops is already a major drain on agricultural budgets with expenditure ranking third after those for energy and fertilization (Tegtmeier & Duffy 2004; Pimentel 2005; Savary, Ficke, Aubertot & Hollier 2012). Thus, a more detailed understanding of the relationships between plant responses to nutritional and biotic stresses is needed for rapid progress towards low-input agriculture.

Availability of mineral nutrients can affect plant susceptibility to pathogens in a variety of ways (Datnoff & Elmer 2007; Huber, Römheld & Weinmann 2012; Gupta, Debnath, Sharma, Sharma & Purohit 2017). Some mineral elements, such as nitrogen and sulphur, are constituents of organic compounds that feed, attract or deter pathogens, whereas others, like calcium and silicon, determine the mechanical properties of cell walls and influence physical barriers or palatability (Halkier & Gershenzon 2006; Datnoff & Elmer 2007; Bloem, Haneklaus, Salac, Wickenhäuser & Schnug 2007; Huber *et al.* 2012). Potassium (K) fertilization is generally advertised as improving plant health (Imas & Magen 2000; Wang & Wu 2013; Wakeel, Gul & Zörb 2016) but a close look at the published studies shows that the effect of K on disease is much less predictable. Evidence from over 2000 laboratory, glasshouse and field trials indicates that the effect of K fertilization is most beneficial in ameliorating fungal diseases and pests, whereas less benefit is seen for bacterial and viral infections (Perrenoud 1990; Prabhu, Fageria, Huber & Rodrigues 2007). For all classes of pathogen some studies report no benefit or even a negative impact of K fertilization. As the mode of pathogenicity does not correlate with taxonomic grouping, this might be expected. A correlation with mode of pathogenicity or trophic state that shows more correspondence with mode of recognition or defence might be more significant in determining infection success

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(Newton, Fitt, Atkins, Walters & Daniell 2010). The exact relationship between K supply and disease incidence and severity depends not only on the specific host-pathogen interaction but also on accompanying mechanistic and environmental factors, but these vary between studies and are often poorly documented. There is no shortage of possible mechanistic links between K-deficiency and disease. The 'usual suspects' include: increased sugar content, lack of stomatal control, decreased turgor and mechanical stability (Amtmann, Troufflard & Armengaud 2008). However, it is important to note that experimental studies proving a relationship or even a correlation between K-induced physiological changes and disease severity are lacking.

Previous work in our laboratories identified K-dependent changes in metabolites of arabidopsis (*Arabidopsis thaliana* [L.] Heynh.), such as increases in reducing sugars and accumulation of glucosinolates, that are potentially of relevance to pathogens and pests in K-deficient plants (Armengaud *et al.* 2009; Troufflard *et al.* 2010). K-deficient arabidopsis plants were found to have greater expression of genes related to the biosynthesis of the phytohormone jasmonic acid (JA) and of genes related to defence, the latter being dependent on the function of the JA-receptor COI1 (Armengaud, Breitling & Amtmann 2004, 2010; Yan *et al.* 2009) . *AtLOX2*, encoding lipoxygenase 2 which catalyses the first committed step in JA biosynthesis (Delker *et al.* 2006; Wasternack & Hause 2013), responded to low K prior to any visible symptoms (e.g. senescence and growth retardation), demonstrating that the induction of the JA pathway was not a secondary effect of stress symptoms (Troufflard *et al.* 2010). In agreement with the transcriptional regulation of JA biosynthesis genes, levels of JA, as well as its precursors 12-oxo-phytodienoic acid (OPDA) and hydroxyl-12-oxo-octadecadienoic acids (HODs), were elevated in K-deficient plants (Troufflard *et al.* 2010). Although extensive research on JA signalling has been carried out in dicots such as arabidopsis and tomato (Kazan & Manners 2008; Wasternack & Hause 2013; Yan *et al.* 2016; Pathak, Baunthiyal, Pandey, Pandey & Kumar 2017), JA signalling pathways in monocots are relatively unexplored (Lyons, Manners & Kazan 2013; Shyu & Brutnell 2015; Ding, Yang, Yang, Cao & Zhou 2016). A number of genes induced in response to JA treatment have been identified in barley, but little is known about their function. They are referred to collectively as jasmonate-induced proteins (JIPs) and known by their molecular weight (Wasternack 1997; Andresen *et al.*, 1992; Weidhase *et al.*, 1987).

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In light of the relationship between low plant K status and JA, it is possible that some of the variation in the effects of K nutrition on plant disease evident in the literature is due to different sensitivity of pathogens to JA. Thus, high concentrations of JA or related oxylipins in K-deficient plants might positively or negatively modulate plant-inherent defence responses. It has been proposed that necrotrophic pathogens induce plant defences through JA (Glazebrook 2005; Thaler, Humphrey & Whiteman 2012; Kazan & Lyons 2014; Dar, Uddin, Khan, Hakeem & Jaleel 2015) whereas biotrophic pathogens induce plant defences through the JA-antagonist salicylic acid (SA). However, this generalisation does not always hold true. For example, treatment of tomato plants with methyl-jasmonate (Me-JA) increased resistance to a range of pathogens with both lifestyles (Thaler, Owen & Higgins 2004). The issue is further complicated by a complex cross-talk between JA and SA signalling-pathways; while antagonistic interactions prevail in early signalling events, synergistic interactions have been reported for systemic responses (Devoto & Turner 2005; Mur, Kenton, Atzorn, Miersch & Wasternack 2006; Loake & Grant 2007; Truman, Bennett, Kubigsteltig, Turnbull & Grant 2007; Wasternack & Hause 2013; Berens, Berry, Mine, Argueso & Tsuda 2017; Per *et al.* 2018). Finally, crop varieties display a continuous spectrum of resistance to a given pathogen due to allelic variation in many different genetic loci that determine pathogen recognition and inducible defence responses (Piffanelli *et al.* 2004; Wise, Lauter, Szabo & Schweizer 2009; Zellerhoff *et al.* 2010; Seeholzer *et al.* 2010; Moscou, Lauter, Steffenson, Wise & Soller 2011). Clearly, the effect of low-K induced up-regulation of the JA-pathway on disease needs to be investigated in individual, well-defined host-pathogen systems before we can understand (and predict) the effects of K supply on disease incidence.

To test the hypothesis that JA is an important factor for the K-disease relationship in crops, we measured K concentrations in leaves of barley (*Hordeum vulgare* L. cv Optic) plants grown under different K regimes, and related them to transcript levels of JA-biosynthesis and JA-responsive genes, and the development of two fungal pathogens. Based on agricultural importance and different lifestyles we selected the obligate biotroph *Blumeria graminis* f.sp. *hordei* (powdery mildew, *B. graminis*) and the hemi-biotroph *Rhynchosporium commune* (rhynchosporium, *R. commune*). The UK malting barley variety Optic was selected due to its susceptibility to both fungi. Infection with *B. graminis* initiates no hypersensitive response or lesion formation, thereby allowing the fungus to spread across the leaf and to obtain nutrients from epidermal leaf cells (Glawe 2008). The life cycle of *R. commune* (scald or leaf blotch) includes an early biotrophic phase during which the fungus grows asymptomatic under the

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cuticle, and a necrotrophic phase during which conidia are formed normally and necrotic lesions become visible on the leaf surface (Avrova & Knogge 2012). The results obtained suggest that jasmonate-signaling links plant K-status with disease development.

MATERIAL and METHODS

Plant material and growth conditions

Barley (*Hordeum vulgare* L. cv Optic) seeds were germinated on water-saturated paper towels in an environmentally controlled growth chamber with 9h light (270 µmol m-2 s-1 at 22°C and 15 h dark at 18°C and constant 70% relative humidity). After 4 days, seedlings were transferred to hydroponic solution, supported by corrugated plastic sheets, each holding 60 plants, suspended above 10 litres of nutrient solution. The control nutrient solution was composed of (in mM) 1.25 KNO_3, 0.5 $Ca(NO_3)_2$, 0.5 MgSO4, 0.625 KH_2PO_4, 2 NaCl. A solution with no added K (-K) was composed of (in mM) 1.0 $Ca(NO_3)_2$, 0.5 $MgSO_4$, 0.625 NaH_2PO_4, 1.375 NaCl. Both media contained the following micronutrients (in µM): 42.5 FeNaEDTA, 0.16 $CuSO_4$, 45 H_3BO_3, 0.015 $(NH_4)6Mo_7O_2$, 0.01 $CoCl_2$, 0.38 $ZnSO_4$, 1.8 $MnSO_4$. The nutrient solution in the plant growth containers was replaced every 7 days. Shoots and roots were harvested at the indicated intervals, weighed, frozen in liquid nitrogen and stored at -80°C.

Preparation of detached leaf segments

Barley seedlings were grown for 14 days in control or -K solutions. 40 mm long segments were cut from the tip, middle and base parts of the emerged blade of the second leaf Supplemental Figure 1. For subsequent analysis of K content, RNA or oxylipins the tissue was frozen immediately after cutting. Treatment of the leaf segments with methyl-jasmonate or fungal pathogens is described below.

Determination of tissue water, K and oxylipin contents

Approximately 100 mg of frozen shoots, roots or leaf segments were weighed and freeze-dried overnight. Water content was determined as the loss of weight by drying, and expressed as percentage of fresh weight. To determine K content, freeze dried tissue from shoots, roots or leaf segments was incubated in 2 M HCl (100 µl for 1 mg of dry tissue) at room temperature for 48 hours. Tissue debris was removed by centrifugation and the extracts were diluted 1:500 in ddH_2O. K was detected using a flame photometer (Sherwood flame photometer 410). K concentrations in the diluted extracts were determined from a standard

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curve established with solutions containing 15 to 250 µM KCl in 4 mM HCl. Tissue K concentrations were then calculated by multiplication with the dilution factor and the incubated dry weights. Oxylipins were measured in triplicate 50 mg samples of lyophilised leaf tissue from leaf segments of plants grown for 14 days in control or -K media (20 plants each). Extraction and LC-MS analysis was carried out according to previously described procedures (Dave *et al.* 2011). Initial analysis showed that the variation was too large to resolve differences between leaf segments. Therefore data from all leaf segments grown in either control or -K media were pooled for statistical analysis.

Measurement of transcript levels using quantitative PCR

Total RNA was extracted from leaf tissue using Trizol® Reagent (Invitrogen, Cat. 15596-026) and cDNA prepared using the Superscript III™ Reverse Transcriptase kit (Invitrogen, Cat. 18080-044). A 1/10 dilution of the reverse transcription final reaction was prepared, 1 µl of the dilution was used as template for the qPCR reaction consisting of 0.4 µM of each primer and 1× SYBR green mastermix (QuantiTech®SYBR® Green PCR Kit; Qiagen, Cat 2041453), using a Bio-Rad Chromo 4 with Opticon Monitor 3 software (Bio-Rad Laboratories, Inc., California, USA.). Serial dilutions of corresponding amplification product were used to monitor the amplification efficiency and to transform threshold cycles into concentrations. The PCR conditions were 15 min at 95°C, then 40 cycles of 15 s at 95°C, 30 s at 58°C, and 30 s at 72°C. Transcript levels were normalized to the expression level of α-tublin (U40042). Primers were as follows. Lipoxygenase 2.A (HvLOX2, gene bank AK362687): AGTACCTGGGAGGGATGGAG (forward) and TGGTTTCATGAGCTGGTACG (reverse); allene oxide cyclase (HvAOC, gene bank AJ308488) GCTACGAGGCCATCTACAGC (forward) and AAGGGGAAGACGATCTGGTT (reverse); 60 kD jasmonate-induced protein (HvJIP60, gene bank BM815987): CAGCAGCGACTTCATTTACA (forward) and ATGGTGTCGCAGACTATCCT (reverse); α-tubulin (Hvα-TUB, gene bank U40042): AGTGTCCTGTCCACCCACTC (forward) and AGCATGAAGTGGATCCTTGG (reverse).

Treatment with methyl-jasmonate

For treatment with methyl-jasmonate (Me-JA) the middle segments from the second leaf of 14 day old seedlings grown in control nutrient solution were floated on 45 µM Me-JA (from 0.1 M stock solution in ethanol) dissolved in water or water with the same final concentration of ethanol (control), and incubated for 24h in a lit incubator (LEEC) at 17°C. Detached leaf

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segments were blotted dry on paper towel and transferred to 0.5% agar/120 mg l^{-1} benzimidazole plates for subsequent inoculation.

Treatment with pathogens

Barley leaf segments were placed on 0.5% agar/120 mg l-1 benzimidazole plates (Newton 1989; Newton, Hackett & Guy 1998) and incubated in a lit incubator (LEEC) with continuous light (light intensity 200 µmol m-2 s-1at 17°C) for 24 h before inoculation with the fugal pathogens. *Rhynchosporium commune* isolate 13-13 from the culture collection at The James Hutton Institute was grown on CZV8CM agar medium (Newton *et al.*, 1998) at 17°C in the dark. The mycelia were scraped from 14 day old cultures using a sterile spatula and transferred to a homogenizer containing sterile water and homogenized for approximately 30 sec. The suspension was filtered through glass wool and re-suspended in sterile distilled water at a concentration of 10^6 spores ml^{-1}. The leaf area to be inoculated was brushed gently with a trimmed-down paint brush to disrupt the cuticle (Newton *et al.*, 2001). 10 µl of 10^6 spores ml^{-1}solution were dispensed on to each leaf segment. The plates were returned to the 17°C incubator. The severity of infection was assessed by measuring the length of the lesions (Supplemental Figure 2A). *Blumeria graminis* f.sp. *hordei* was isolated from infected barley leaves. Spores from individual colonies were used to inoculate detached leaf segments with a paint brush and the fungus was allowed to grow for approximately 2 weeks. To ensure a pure culture individual colonies where selected twice more. To inoculate the leaf segments uniformly an inoculation tower was used (Supplemental Figure 2B). The plate containing the spores was inverted over a sheet of paper and tapped to dislodge the spores. A cone was formed from the paper and the spores were blown into the inoculation column. The spores were allowed to settle on the leaf segments for 5 min, before the lids were replaced, and plates were returned to the lit incubator at 17°C. The level of infection was assessed by counting the number of visible colonies on each leaf segment (Supplemental Figure 2C), and dividing by the leaf area (measured from photographs using image J). Non-inoculated leaf segments kept in the same conditions as the inoculated leaf segments showed no visible signs of deterioration (Supplemental Figure 2D).

Statistical analysis

Statistical analysis was performed using ANOVA with Genstat version 15.1 and calculation of Pearson correlation between parameters measured over time and across the leaf using

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Minitab 15 statistical software. Correlation coefficients are shown in Table 1 and p-values for all correlations tested are given in Supplemental Table1.

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RESULTS

Leaves of K-deprived barley plants reach critically low tissue K concentrations

Barley seedlings were transferred to hydroponic culture four days after germination and grown on a minimal nutrient solution with either 2 mM (control) or no added K (-K). No differences in plant size or development were apparent between treatments until 10-12 days after transfer to hydroponics (Figure 1). Subsequently, K-deprived plants displayed constantly lower shoot fresh weights (Day 12, n=3, p=0.005) and shoot lengths (Day 12, n=3, p=0.013) than control plants (Figure 1A, B). The time point at which K deprivation started to impact visually on growth coincided with the emergence of the third leaf (Figure 1C-E). At this time, seed K reserves for leaf growth will have been exhausted (White & Veneklaas 2012). The first leaf of K-deprived plants grew to its full length and the second leaf showed only a minor reduction in length at the end of its growth period (Figure 1C,D). The third leaf, however, was shorter in K-deprived plants than in control plants from the beginning of its emergence on day 10 (Figure 1E). The root fresh weight of K-deprived plants was also less than the control plants grown in full nutrient medium after 10 days (Supplemental Figure 2A) although the roots were longer than those in control medium (Supplemental Figure 3B).
The K concentration in the medium had an impact on tissue K concentrations, expressed on a dry weight (DW) basis, before a difference in fresh weight was apparent (Figure 2, Supplemental Fig. 3). Three days after transfer to hydroponics, K-deprived plants already had lower shoot K concentrations than control plants (1.4% compared to 2.5% DW). Over the following 12 days, shoot K concentrations increased in the control plants and decreased in K-deprived plants (n=3, p=0.012; Figure 2A). The root K concentration in K-deprived plants was also lower than in control plants on day 3 (n=3, p=0.043), and remained constant thereafter whilst root K concentrations of control plants increased (Supplemental Fig. 3C). On day 12, the shoot K concentration of K-deprived plants was only 14% (n=3, p=0.044) and the root K concentration was 22% (n=3, p=0.010) of that of control plants. From this time point onwards, shoot growth was no longer sustained in K-deprived plants (Figure1A, B). Nevertheless the overall shoot water content was maintained (Table 1).

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Leaf K concentration displays a gradient across the emerged blade

Potassium is mobile in the plant and is preferentially allocated to growing and metabolically active tissues (White & Karley 2010). Barley leaves are particularly well characterized in this respect; differential allocation of K has been reported in epidermis and mesophyll, in the elongation zone (inside the sheath of the previous leaf) and the emerged leaf blade , and in different sections in the emerged leaf blade has been reported (Leigh, Chater, Storey & Johnston 1986; Fricke, Leigh & Deri Tomos 1994a; Fricke, Hinde, Leigh & Tomos 1995; Karley, Leigh & Sanders 2000; Karley & White 2009; Volkov *et al.* 2009). To investigate spatial differences of tissue K concentrations within the leaf area that is most accessible to air-borne pathogens we measured K concentrations in three zones of the emerged part of the second leaf (base, middle and tip as shown in Supplemental Figure 1). In control plants, the K concentration decreased significantly from the base to the tip of the leaf blade (n=3, p=0.012), with the K concentration at the tip being 70% of the K concentration at the base (Figure 3). This is consistent with the observations of Fricke *et al.* (1994b). A decreasing base-to-tip leaf K concentration trend was also apparent in K-deprived plants although the differences were not statistically significant (Figure 3A). In accordance with the function of K as a major osmoticum, K-deprived plants showed a significant decrease in water content (expressed as percentage of fresh weight) from the base to the tip of the leaf (n=3, p=0.004; Table 1), and the tip of the leaf was the first part of the plant to show chlorosis and necrosis (Supplemental Figure 3F). Pearson correlation analysis of the data confirmed a positive correlation between K and water content within the second leaf (n=9, R=0.507, p=0.032; Table 2). In summary, the experimental system allowed us not only to manipulate leaf K concentrations by varying external K supply but also to take advantage of natural differences between local leaf K concentrations within leaves of K-sufficient plants.

Transcript levels of JA-related genes are inversely related to leaf K concentration

Previous research had shown that K deprivation of arabidopsis plants led to increased transcript levels of genes encoding enzymes of jasmonate (JA) biosynthesis, such as *AtLOX2*, *AtAOS*, *AtAOC1* and *AtOPR3* (encoding lipoxygenase, allene oxide synthase, allene oxide cyclase and OPDA reductase respectively), as well as well-known JA targets such as AtVSP2 (encoding vegetative storage protein) (Armengaud *et al.* 2004, 2010; Troufflard *et al.* 2010). To monitor JA-response in barley we used a barley homologue of *AOC1* (AJ308488) and a barley homologue of *LOX2* (gene bank number AK32687). In order to select the most appropriate sequence for LOX2, three *LOX2* genes were investigated. All three sequences

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have higher similarity to the arabidopsis *LOX2* gene than to any other arabidopsis genes encoding lipoxygenases. *LOX2.2* and *LOX2.3* were identified by Bachmann *et al.* (2002) as *LOX2* genes and shown to be responsive to JA treatment. Our BLAST searches identified a third *LOX2* gene (AK32687, *LOX2.A*). Its closest homolog was the rice *LOX2* gene and its closest homolog in arabidopsis was *LOX2*. The dendrogram in Supplemental Figure 4 shows that it is difficult to identify the most likely functional homologue of arabidopsis LOX2 among the three barley genes based on sequence similarity alone. In a preliminary expression analysis with all three genes we found that *LOX2.A* displayed a more consistent response to -K than the other *HvLOX2* genes identified, and therefore selected it for further study. No *VSP* homologue was found in the available barley nucleotide or protein sequence databases, but a number of Me-JA induced genes ("JA-induced proteins", JIPs) have been identified (Weidhase *et al.* 1987; Andresen *et al.* 1992). *HvJIP60* (BM815987), used here, encodes a ribosome inactivating protein with glycosidase activity (Reinbothe *et al.* 1994; Chaudhry *et al.* 1994; Dunaeva, Goebel, Wasternack, Parthier & Goerschen 1999). Three barley genes, encoding α-tubulin (*Hvα-TUB*, U40042), glyceraldehyde 3-phosphate dehydrogenase (*HvGAPDH*, M36650) and ubiquitin (*HvUBQ*, M60175), were tested for their suitability as reference genes by determining the variation of Ct values and the frequency distribution of transcript levels obtained by qPCR across a number of different conditions (Supplemental Figure 5). From this analysis, *Hvα-TUB* emerged as a robust constitutive reference and was used for normalization of transcript levels.

Transcript levels of *HvLOX2*, *HvAOC* and *HvJIP60* in shoots of barley plants varied during the experimental period (3 – 15 days after transfer of the plants to hydroponics) but they were consistently higher in shoots of K-deprived plants than in shoots of control plants from day 9 onwards (n=3, LOX2, $p=0.027$; AOC, $p=0.007$; JIP60, $p=0.002$; Figure 2B-D). To establish whether the transcripts responded to tissue K concentration, we analysed different leaf zones of the second leaf. Not only were transcript levels of *HvLOX2*, *HvAOC* and *HvJIP60* higher in all zones of K-deprived plants ($p<0.001$ for all genes) compared to control plants but they also increased significantly from the base to the tip of the leaf (n=3, $p=0.002$, $p=0.044$, $p=0.005$ respectively; Figure 3B-D), thus showing the contrasting gradient to that observed for tissue K concentration within the leaf (Figure 3A). In summary, the expression of genes in the JA-pathway was inversely related to shoot K concentration whether comparisons were made between K-replete and K-deprived plants, over the experimental period, or within individual leaves. Indeed, Pearson correlation analysis identified transcript levels of LOX2

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(R=0.696, p<0.001), AOC (R=0.731, p<0.001) and JIP60 (R=0.548, p=0.019) as reliable reporters of the overall shoot K concentration, and of local K and water concentrations within the leaf (Table 2).

To test whether the increase in gene expression observed in response to K deficiency was associated with an increase in the concentrations of JA and related compounds, the tissue concentration of several oxylipins were determined (Figure 4) in leaf tissue from plants grown in control or -K media. These included 12-oxo-dodecenoic acid (12-ODD), 13-hydroxyoctadecatrienoic acid (13-HOD), 3-oxo-2-(29-pentenyl)-cyclopen-tane-1-octanoic (OPC-8), *12*-oxo-phytodienoic acid (OPDA) and JA, which are formed in the 13-LOX pathway. This pathway starts with the conversion of linoleic acid into 13-hydroperoxy-9,11,15-octadecatrienoic acid (13-HPOT), which is catalysed by LOX2 (Figure 4B, Wasternack and Strnad, 2016). We also measured 9-hydroxyoctadecatrienoic acid (9-HOD) and 10-octadecenoic acid (10-ODA), which are produced in the 9-LOX pathway (Figure 4B, Wasternack and Strnad, 2016). The measured oxylipin concentrations were considerably (5-50 times) lower than those previously determined in arabidopsis leaves using the same protocols (Troufflard et al. 2010), and we could not resolve statistically significant differences between the leaf segments (data for all leaf segments are shown in Supplemental Figure 6). However, clear differences were apparent between control and –K (Figure 4). With the exception of 10-ODA, all oxylipins measured were found in significantly greater concentrations in the second leaf of K-deprived plants than in the second leaf of K-replete plants (Figure 4A, n=3, p<0.05 for JA and 12ODD, p< 0.01 for all others). Strong positive correlations were found between the transcript levels of the selected JA-marker genes and the concentrations of JA and other oxylipins (Table 2).

Low tissue K has contrasting effects on powdery mildew and rhynchosporium

Typical disease symptoms from *B. graminis* and *R. commune* infection on barley leaves are shown in Supplemental Figure 2. *B. graminis* colonies form 'fluffy' patches (Supplemental Fig. 2B) while *R. commune* causes necrotic lesions only visible during this necrotrophic phase (Supplemental Fig. 2A). Development of the fungal pathogens on the leaves was scored by assessing occurrence, number of colonies (*B. graminis*) or size of lesions (*R. commune*) after inoculation of leaf segments from the second leaf, harvested 14 days after transfer of the plants to hydroponics.

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Disease symptoms caused by *B. graminis* were delayed in leaf segments obtained from K-deprived plants compared to leaf segments from control plants (Figure 5A). In all leaf zones obtained from K-deprived plants the number of *B. graminis* colonies was significantly lower than in leaf zones from control plants ($p<0.001$; Figure 5B-D). Furthermore, the number of *B. graminis* colonies was always significantly lower at the leaf tip than at the leaf base ($p<0.001$), both for K-deprived and for control plants. Pearson correlation analysis showed that *B. graminis* infection (percentage of segments inoculated with visible colonies) was positively correlated with the local tissue K concentration measured before inoculation (e.g. $R=0.687$, $p=0.003$ for D9; Table 2). Thus, a low tissue K concentration in the leaves seems to protect barley against powdery mildew. Correlation analysis also revealed a significant negative correlation between *B. graminis* and transcript levels of JA-related genes or oxylipin concentrations (Table 2).

Low tissue K concentrations had the opposite effect on disease symptoms caused by *R. commune*. Necrotic lesions appeared earlier in leaf segments obtained from K-deprived plants than in segments from control plants (Figure 5E) and the individual lesions were significantly larger ($p<0.001$; Figure 5F-H). In accordance with an effect of local tissue K concentration on *R. commune* infection, lesions were smaller at the base of the leaf than at the tip of the leaf for both control and K-deprived plants. Pearson correlation analysis showed that the severity of *R. commune* symptoms was directly and negatively correlated with the K concentration measured before inoculation (Table 2). Thus, a low tissue K concentration in barley leaves seems to promote the development of *R. commune*.

B. graminis, but not _R. commune_, is sensitive to Me-JA, and induces JA-related genes

The preceding results suggest that induction of the JA-signalling pathway by low K nutritional status may protect barley plants against powdery mildew but not against *R. commune*. It is consistent with reports that external application of methyl-jasmonate (Me-JA) or other oxylipins to barley inhibited powdery mildew development both locally and systemically (Schweizer, Gees & Mosinger 1993; Walters, Cowley & Mitchell 2002; Cowley & Walters 2005) , but had variable effects on infection by *R. commune* (Weiskorn, Kramer, Ordon & Friedt 2002; Steiner-Lange *et al.* 2003; Walters *et al.* 2014). These previous studies used different barley varieties and growth conditions, therefore we compared JA-sensitivity of the two fungal pathogens in our experimental system directly (Figure 6A, B). Plants were grown in hydroponics with control medium for 14 days, and middle leaf segments were

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floated on a solution with or without Me-JA prior to inoculation with the fungi. The Me-JA treatment reduced the number of *B. graminis* colonies (n=3, $p<0.001$, Figure 6A) but had little effect on *R. commune* symptoms (Figure 6B). Thus, Me-JA treatment mimicked the effect of low tissue K concentration on powdery mildew, but was ineffective on *R. commune*. Furthermore, transcript levels of *HvLOX2* and *HvJIP60* were increased after inoculation with *B. graminis* (n=3, $p<0.001$ for both genes) but not after inoculation with *R. commune* (Figure 6C-F). These data suggest that barley uses a JA-based defense against JA-sensitive powdery mildew but not against JA-insensitive rhynchosporium.

In summary, using defined growth and treatment protocols of barley, and taking advantage of an inherent K gradient within the emerged blade of the second leaf, we have shown opposite effects of low tissue K concentrations on *B. graminis* and *R. commune* (decreased/increased), different sensitivity of the fungi to JA (sensitive/insensitive), and different inducibility of the JA pathway by the fungi (induced/not induced).

Discussion

Barley leaves are an excellent system to study nutrient-pathogen interactions

Understanding the interactions between mineral nutrition and disease in plants is essential for good crop management and for making agriculture more sustainable in the future. Molecular plant science has made important contributions to understanding how plants respond to nutritional or biotic stresses but it is now necessary to (a) design experiments that allow us to assess combined stress, and (b) translate knowledge gained in model organisms to crops. In this study we have done both; using a controlled hydroponics system, we have assessed the effects of plant nutritional status on fungal infection in barley. Measurement of several parameters (ions, transcripts, hormones and disease symptoms) allowed us to relate these parameters to each other directly. In addition, we have exploited the differential allocation of nutrients within leaves of barley to relate disease symptoms to tissue nutrient concentrations independent of the amount of nutrient supplied in the growth solution. The second leaf was selected for the latter experiments because it grew similarly well in control and K-deprived plants over most of its growth period, but reached critically low K concentrations in its tip towards the end of this time. The experimental system developed here provides a useful tool for studying nutrient-pathogen interactions in barley and other cereal crops.

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The K-JA relationship; possible signals and physiological functions

Previous work by our groups had discovered a strong effect of K-deficiency on the JA biosynthesis and signalling pathways in arabidopsis (Armengaud *et al.* 2004, 2010; Troufflard *et al.* 2010). Many of the downstream targets of JA signalling (e.g. production of glucosinolates) are particularly prominent in Brassicaceae, and it was therefore conceivable that the JA-response to K deprivation was limited to species of this angiosperm family. The results presented here show that this is not the case. Transcript levels of *HvLOX2* and *HvAOC*, encoding JA-biosynthetic enzymes that underlie positive feedback regulation by JA in arabidopsis (Delker *et al.* 2006), and of *HvJIP60*, previously identified in a screen for Me-JA inducible genes in barley (Weidhase *et al.* 1987; Andresen *et al.* 1992; Wasternack *et al.* 1997), were consistently increased in K-deprived barley plants (Figure 2). More strikingly, the relative levels of these three transcripts increased from the base to the tip of the emerged blade of the second leaf and thus displayed a gradient that was the inverse of the tissue K concentration gradient, even in plants that were grown in K-sufficient conditions (Figure 3). We conclude that the expression of the genes is quantitatively determined by variation in tissue K concentration, whether the latter is the result of external supply or of endogenous tissue allocation. At this stage we cannot distinguish whether the local K signal for JA metabolism is apoplastic or intracellular, and we can only speculate about the down-stream events. A number of early signals in wounding and pathogen responses, e.g. change in membrane potential, rise of cytoplasmic calcium and H_2O_2 production (Thordal-Christensen, Zhang, Wei & Collinge 1997; Yang, Shah & Klessig 1997; Maffei, Mithöfer & Boland 2007), also occur in response to reduced apoplastic K (Allen *et al.* 2001; Shin & Schachtman 2004; Amtmann *et al.* 2008; Armengaud *et al.* 2009). However, whether these signals can be quantitative and can persist long enough to explain a continuous dose-response gradient within the leaf is uncertain.

More intriguing is the observation that constitutively high activity of the vacuolar cation channel TPC1 in the arabidopsis *fou2* mutant results in high *LOX2* activities (Bonaventure *et al.* 2007). The vacuole plays an essential role in cellular K homeostasis because it is used as a reversible K reservoir to maintain stable cytoplasmic K over a wide range of external K concentrations (Walker, Leigh & Miller 1996; Carden, Walker, Flowers & Miller 2003; White & Karley 2010). Trans-tonoplast K fluxes through vacuolar channels will therefore reflect tissue K status in a quantitative manner. Indeed, TPC1 is permeable to K and has been

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implicated in K homeostasis (Peiter *et al.* 2005; Amtmann & Armengaud 2007; Ranf *et al.* 2007; Beyhl *et al.* 2009), although it is not clear whether the link is direct (K transport through TPC1) or indirect.

A good candidate for mediating between cellular K status and defense responses would be calcium. Single-cell measurements of ion concentrations in different parts of barley leaves have shown a negative correlation between vacuolar concentrations of K and Ca (Fricke *et al.* 1995). It has also been shown before for Arabidopsis leaves that a decrease of tissue K under K starvation is compensated by a rise of Ca (Armengaud *et al.* 2009). While is unlikely that a change of the vacuolar Ca concentration directly impacts on the development of fungal pathogens, it could alter the signature of intracellular Ca signals in response to pathogens and thus impact on defense responses. Genetic manipulation of vacuolar K and Ca transporters in barley needs now to be undertaken to investigate whether it is possible to uncouple cellular K and/or Ca homeostasis from JA-signalling and whether fluxes of K and/or Ca across the tonopast underpin the effect of K on pathogen development.

The highest expression of *HvLOX2*, *HvAOC* and *HvJIP60* was measured in the tips of leaves of K-deprived plants, which not only had the lowest K-concentration but also were the first parts of plants to show chlorosis and a significant drop in water content. It has been shown for arabidopsis that induction of two senescence-associated genes, At*SAG12* and At*SAG13*, by K deprivation no longer occurred when JA-antagonists SA and acetyl salicylic acid were applied (Cao, Su & Fang 2006). These findings raise the possibility that JA-related genes inform the plant about local tissue concentrations of the most important cellular osmoticum, K^+, and induce senescence when tissue K concentration falls below a critical threshold.

What underlies the differential effect of leaf K on *B. graminis* and *R. commune*?

The question of how K deprivation affects the susceptibility of barley to different fungal pathogens was addressed by infecting leaves from control and K-deprived plants with *B. graminis* and *R. commune*, two economically-important pathogens with biotrophic and hemi-biotrophic (with a necrotrophic phase) lifestyles respectively. Inoculation with the fungi requires different techniques, which impacts on symptom assessment. An equal number of *B. graminis* spores are blown over the leaf segment allowing quantification of fungal invasion by counting colonies. By contrast, *R. commune* is point-inoculated as a spore suspension and therefore all infection sites potentially produce symptoms. Accordingly, the time it takes for

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visible symptoms to appear and the size of the necrotic lesions formed were scored. In the future it would be interesting to dissect, at the microscopic level, the effects of tissue K on different phases of fungal invasion and development.

The protocols used here for inoculation and disease scoring followed established techniques in the pathogen field (Newton 1989), but potential problems for combined nutrient-pathogen studies should be discussed. The extended incubation of the leaf segments did not lead to any visible deterioration of the tissues apart from chlorosis in a small area adjacent to the cut (see un-inoculated segments after 15 days on plates shown in Supplemental Figure 1D). However, it is possible that the segments loose some K during the incubation period. Therefore our K-disease results strictly relate to the differences of K/JA status before inoculation. Any potential changes occurring in the segments during the incubation period should be monitored in more detail in the future, and controlled plate experiments should be complemented with whole-plant experiments on soil.

Compared with control plants, K-deprived plants showed less disease caused by the biotroph *B. graminis* and more by the necrotrpohic life stages of *R. commune*. This finding was surprising in the light of the conventional assignment of biotrophic and necrotrophic pathogens to SA and JA-based defence pathways respectively. However, it agrees with previous reports of increased resistance against biotrophic pathogens (including powdery mildews) of the arabidopsis mutant *cev1*, which has constitutively high endogenous JA levels (Ellis & Turner 2001; Ellis, Karafyllidis & Turner 2002). External application of jasmonate has also been shown before to reduce *B. graminis* infection in barley both directly and systemically, under controlled conditions (Schweizer *et al.* 1993; Walters *et al.* 2002).

Further information on the K-disease relationship came from analysing disease symptoms in different leaf regions. Interestingly, occurrence and severity of disease symptoms caused by *B. graminis* and *R. commune* were directly (positively and negatively, respectively) correlated with the local tissue K concentration in leaves even in plants that were K-sufficient (control plants). To visualize the leaf profiles of potentially relevant parameters, we assigned a semi-quantitative score between --- (much lower than the median) and +++ (much higher than the median) to the measured absolute values, and plotted this score against the leaf zones for both K-replete and K-deprived plants. As can be seen in Figure 7, *R. commune* and *B. graminis*

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symptoms display almost continuous gradients across zones and treatments as do tissue K concentrations and transcript levels of *HvLOX2*, *HvAOC* and *HvJIP60*.

Promotion of *B. graminis* by increasing tissue K concentration meant that this biotroph developed better in K-rich tissues, particularly at the base of the emerged leaf blade of K-replete plants. While this could be due to a direct beneficial role of K as an essential nutrient, it is difficult to conceive that the small differences of K concentration found in K-replete would cause nutritional deficiency in the fungus. It is more likely that the increased JA level in low-K tissues leads to enhanced plant defence preventing successful development of *B. graminis*. The opposite effect of K on the JA-insensitive fungus *R. commune* (inhibition by high tissue K concentrations) is in line with the general view that K protects plants against disease, but it still requires identification of the underlying mechanism(s). It has been reported that *R. commune* infection leads to increased transpiration and K accumulation around stomata (Ayres & Owen 1971), indicating that stomatal function is modulated either as part of the fungal infection strategy or as a downstream effect. Lowering K may interact with this process and facilitate infection.

The results from this study strongly motivate a new hypothesis that links the effect of tissue K on disease development with the sensitivity of the pathogen to plant JA-signalling , but alternative explanations are still possible and should be examined in more targeted studies. For example, K starvation might increase not only vacuolar but also apoplastic Ca, leading to increased rigidity of cell wall and membranes, which in turn could differentially inhibit pathogens depending on their infection paths. Furthermore, the allocation of K and Ca into individual cell-types (Fricke *et al.* 1995) could change under K-starvation, which again might differentially affect pathogens with specific invasion patterns. Taking into account reported effects of JA on ion fluxes (Evans, Gottlieb & Bach 2003; Yan *et al.* 2015) it is also possible that an initial rise in JA leads to re-distribution of K and/or Ca between cellular compartments and cell-types. Monitoring ion concentrations and pathogen development at a much higher spatial resolution would be a good way forward to test these hypotheses. The experimental protocols developed here to score K-disease interaction provide a good basis for such studies.

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A working model for the K-JA-disease interaction

The results from this study can be summarized in a simple working model (Supplemental Figure 7) in which a low K concentration in leaf tissue induces JA-signalling, which in turn enhances the inducible defence response of the plant against *B. graminis*. In this case the effect seems to be strong enough to overcome any other effects of low K status that may increase plant susceptibility. By contrast, *R. commune* does not induce a JA-based defence response and this pathogen is not sensitive to JA. Induction of JA-signalling by low-K has therefore no consequence on pathogen development. The observed effect of K on *R. commune* is in accordance with the conventional view that K-deficiency promotes disease, but the exact cause still remains to be identified. Our finding that the effect is local and continuous over a range of K tissue concentrations narrows the spectrum of potential causes. For example, levels of sugars increased in -K conditions but were not correlated with K-concentrations in the leaf segments (Supplemental Figure 8).

Interestingly, it has been reported that soil-grown barley plants exposed to a combination of elicitors (including *cis*-jasmonate) after pre-infection with *R. commune* down-regulate *LOX2* (although in this case the transcript measured differed from the one assessed here; Walters *et al.*, 2011). This raises the possibility that *R. commune* infection may cancel the protective effect of low K on *B. graminis*, observed here. Future experiments should assess the effect of K on simultaneous or successive infection by both pathogens. Depending on which pathogen is more damaging there might be scope for fine-tuning K fertilizer applications. Furthermore, the observed differential development of the two fungi in different parts of the leaf could open the possibility of a more targeted application of fungicides.

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Table 1 Water content (% fresh weight) of barley plants grown in control or K-free (-K) media

Day[1]	**Shoot water content (% FW)**		
	Control	**-K**	*P-value*[2]
3	90.6	92.6	*0.196*
6	91.5	89.5	*0.169*
9	91.9	90.5	*0.342*
12	92.7	92.0	*0.499*
15	91.7	90.3	*0.444*

Leaf region[3]	**Tissue water content (% FW)**		
	Control	**-K**	*P-value*[2]
Tip	90.1	86.4	*0.043*
Middle	91.4	90.7	*0.334*
Base	92.1	91.5	*0.225*
P-value[4]	*0.217*	*0.004*	

[1] After transfer to hydroponics.

[2] Difference of water content in different media.

[3] 2nd leaf, as described in Materials and Methods.

[4] Difference of water content in different leaf segments.

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Table 2: Pearson correlation coefficients for parameters measured in whole leaves and different leaf zones of plants grown in control and K-free (-K) media.

Significant positive (green) and negative (red) correlations are shaded according to p-value (< 0.05 light, < 0.01 medium, < 0.005 dark)[1]. D: Day after inoculation.

				GENE EXPRESSION						OXYLIPINS							*Rc* LENGTH of LESIONS			% *Rc* INFECTION			*Bgh* NUMBER of COLONIES			% B*gh* INFECTION		
		% K in DW	% water	LOX2A	AOS	AOC	JIP23	JIP37	JIP60	JA	OPDA	12ODD	9HOD	13HOD	10ODA	OPC8	D 6	D 9	D 12	D 6	D 9	D 12	D 6	D 9	D 12	D 6	D 9	D 12
K	% K in DW		0.51	-0.70	-0.78	-0.86	-0.93	-0.90	-0.55	-0.49	-0.51	-0.41	-0.64	-0.68	-0.32	-0.50	-0.76	-0.74	-0.56	-0.73	-0.72	-0.44	0.51	0.39	0.34	0.59	0.67	0.63
WATER	% water			-0.74	-0.67	-0.54	-0.60	-0.64	-0.59	-0.21	-0.41	-0.68	-0.41	-0.49	-0.60	-0.39	-0.30	-0.46	-0.69	-0.48	-0.47	-0.55	0.41	0.19	0.13	0.39	0.40	0.51
GENE EXPRESSION	LOX2A				0.79	0.74	0.71	0.74	0.75	0.44	0.55	0.46	0.64	0.66	0.54	0.56	0.54	0.45	0.52	0.60	0.43	0.42	-0.74	-0.43	-0.41	-0.63	-0.71	-0.70
	AOS					0.87	0.91	0.91	0.85	0.67	0.70	0.67	0.73	0.77	0.24	0.75	0.46	0.59	0.49	0.49	0.57	0.34	-0.67	-0.54	-0.53	-0.66	-0.80	-0.85
	AOC						0.93	0.90	0.69	0.52	0.63	0.46	0.73	0.76	0.22	0.62	0.57	0.69	0.59	0.59	0.70	0.46	-0.57	-0.44	-0.41	-0.60	-0.73	-0.70
	JIP23							0.97	0.70	0.61	0.62	0.59	0.69	0.76	0.25	0.62	0.61	0.73	0.56	0.63	0.71	0.43	-0.55	-0.44	-0.41	-0.58	-0.72	-0.74
	JIP37								0.75	0.60	0.59	0.64	0.70	0.72	0.30	0.59	0.62	0.75	0.62	0.65	0.73	0.52	-0.58	-0.52	-0.51	-0.63	-0.75	-0.79
	JIP60									0.68	0.61	0.66	0.62	0.64	0.25	0.68	0.25	0.32	0.46	0.26	0.30	0.33	-0.75	-0.66	-0.65	-0.63	-0.79	-0.83
OXYLIPINS	JA										0.28	0.59	0.48	0.41	0.08	0.56	0.16	0.16	0.04	0.07	0.12	-0.13	-0.50	-0.60	-0.56	-0.64	-0.71	-0.67
	OPDA											0.40	0.85	0.92	0.17	0.87	0.15	0.25	0.38	0.19	0.24	0.20	-0.44	-0.24	-0.26	-0.52	-0.50	-0.50
	12ODD												0.47	0.53	0.30	0.55	0.08	0.28	0.30	0.13	0.27	0.11	-0.25	-0.37	-0.30	-0.46	-0.40	-0.50
	9HOD													0.91	0.20	0.92	0.25	0.36	0.31	0.26	0.35	0.15	-0.54	-0.47	-0.47	-0.80	-0.69	-0.64
	13HOD														0.29	0.88	0.35	0.44	0.41	0.36	0.42	0.21	-0.46	-0.32	-0.28	-0.66	-0.59	-0.56
	10ODA															0.03	0.36	0.26	0.59	0.38	0.24	0.52	0.00	0.26	0.28	-0.12	0.01	-0.03
	OPC8																0.03	0.17	0.15	0.05	0.17	-0.06	-0.57	-0.50	-0.49	-0.74	-0.69	-0.67
Rc LENGTH of LESIONS	D 6																	0.82	0.46	0.95	0.78	0.48	-0.35	-0.28	-0.24	-0.36	-0.43	-0.35
	D 9																		0.59	0.86	1.00	0.62	-0.31	-0.32	-0.30	-0.39	-0.48	-0.50
	D 12																			0.53	0.60	0.93	-0.28	-0.04	-0.02	-0.19	-0.26	-0.34
% *Rc* INFECTION	D 6																				0.83	0.56	-0.38	-0.28	-0.24	-0.36	-0.45	-0.39
	D 9																					0.64	-0.29	-0.30	-0.28	-0.37	-0.46	-0.49
	D 12																						-0.26	-0.05	-0.07	-0.09	-0.19	-0.30
Bgh NUMBER of COLONIES	D 6																							0.81	0.80	0.73	0.90	0.86
	D 9																								0.97	0.79	0.87	0.81
	D 12																									0.73	0.85	0.82
% B*gh* INFECTION	D 6																										0.86	0.77
	D 9																											0.95
	D 12																											

[1] For exact p-values see Supplemental Table 1.

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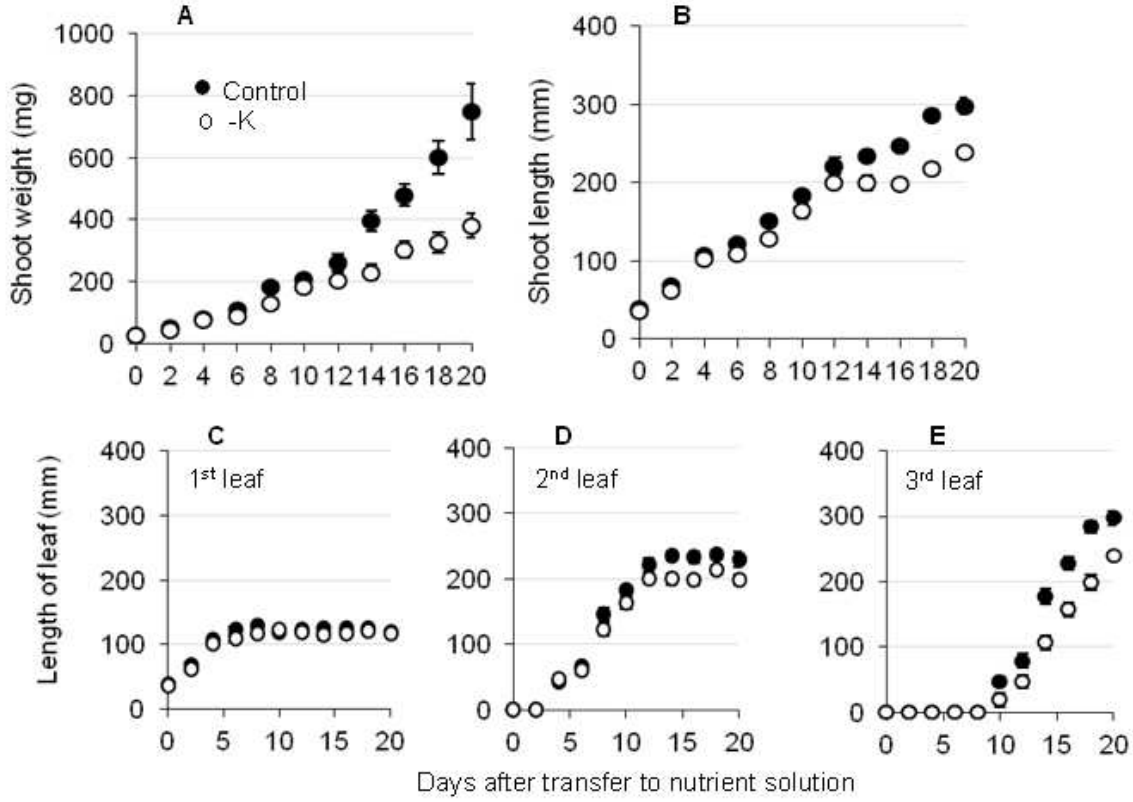

Figure 1. Barley shoot growth in control and -K media.

Shoot fresh weight (A), shoot length (B) and length of individual leaves (C-E) of barley plants grown in control (black symbols) or -K (open symbols) media. Five plants were harvested at each time point, and the mean (± SE) of three independently grown and treated batches of plants is shown (n=3).

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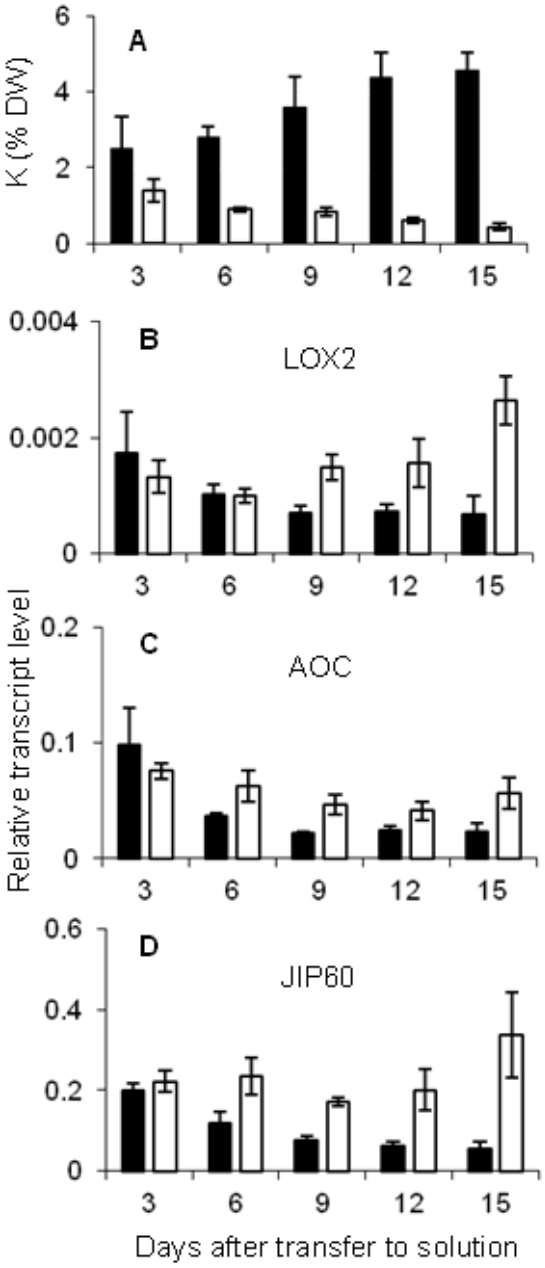

Figure 2. K concentration and JA-related gene expression in barley grown in control or -K media

Shoot K concentration (A) and relative transcript levels of *HvLOX2* (B), *HvAOC* (C) and *HvJIP60* (C) in barley plants grown in control (black bars) or K-free (open bars) media. Five plants were pooled for each sample, and the mean (± SE) of four independently grown and treated batches of plants is shown. α-TUB was used as reference gene.

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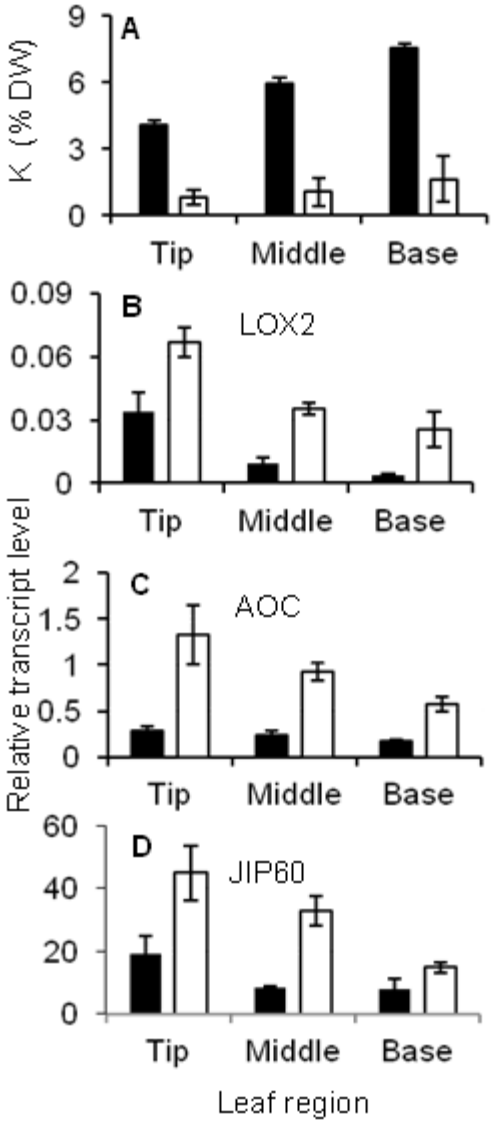

Figure 3 K-concentration and transcript levels of JA-related genes within leaves of barley plants grown in control or -K media

Potassium concentration (A) and relative transcript levels of *HvLOX2* (B), *HvAOC* (C) and *HvJIP60* (D) in different zones of the second leaf of barley plants grown for 14 days in control (black bars) or -K (open bars) media. Corresponding leaf segments from six plants were pooled for each sample, and the mean (± SE) of three independently grown and treated batches of plants is shown. *α-TUB* was used as reference gene.

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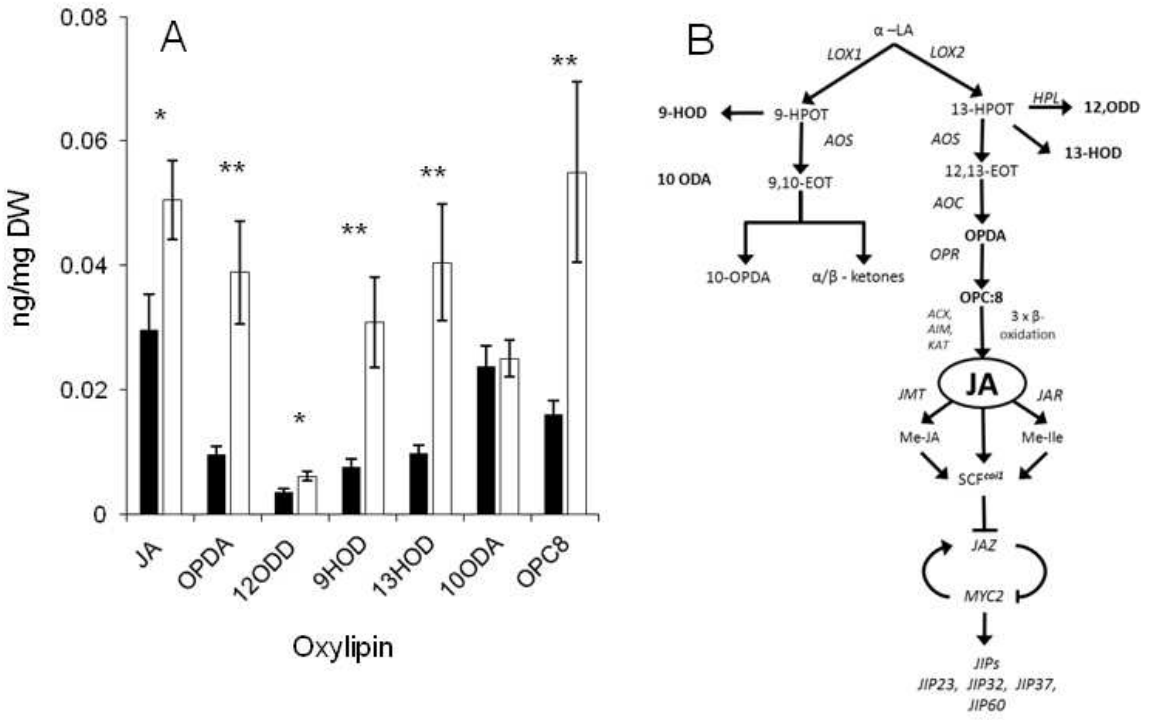

Figure 4 Oxylipin concentrations in leaves of barley plants grown in control or -K media

A: Oxylipin concentrations in leaves of barley plants grown in control (black bars) or K-free (open bars) media. Results from tip, middle and base segments from the emerged blade of the second leaf of 20 plants was pooled for each sample, and means (± SE) of three independently grown and treated batches of plants are shown (n=3). B: Position of oxylipins in the JA biosynthesis pathway. Compounds measured are shown in bold, genes encoding enzymes or downstream targets are shown in italics.

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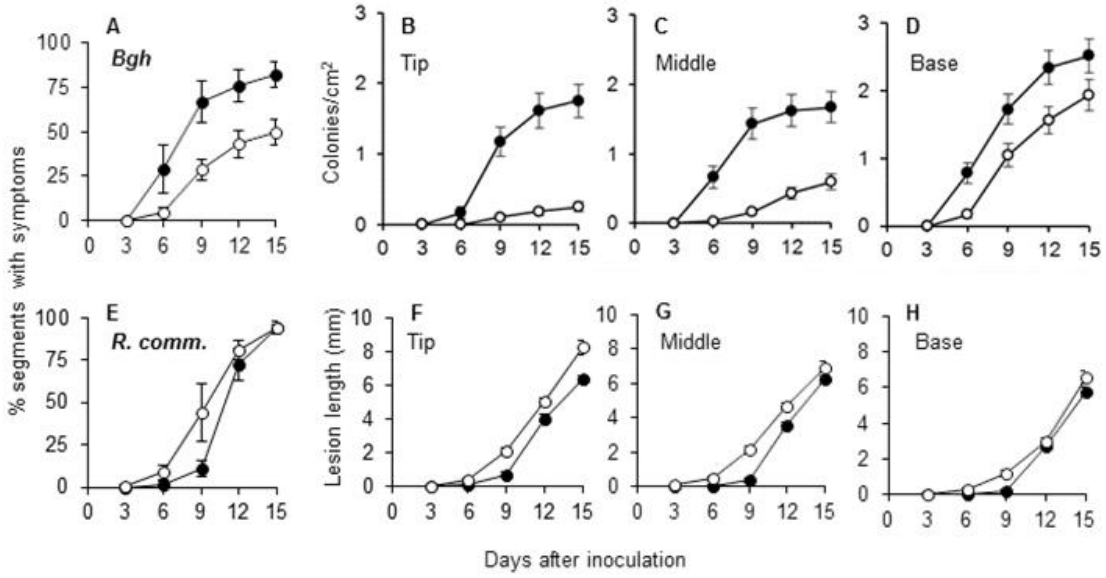

Figure 5 Effect of tissue K concentration on infection by *Blumeria graminis* and *Rhynchosporium commune*

A, E: Number of barley leaf segments (in % of total number of inoculated leaf segments) showing symptoms after inoculation with *B. graminis* (A) or *R. commune* (E). B-D: Number of *B. graminis* colonies on segments derived from tip (B), middle (C) or base (D) of the second leaf. F-G: Length of *R. commune* lesions on segments derived from tip (F), middle (G) or base (H) of the second leaf. Leaf segments were harvested from barley plants grown for 14 days in control (black symbols) or -K (open symbols) media. Means (± SE) from three replicate experiments are shown (n=3).

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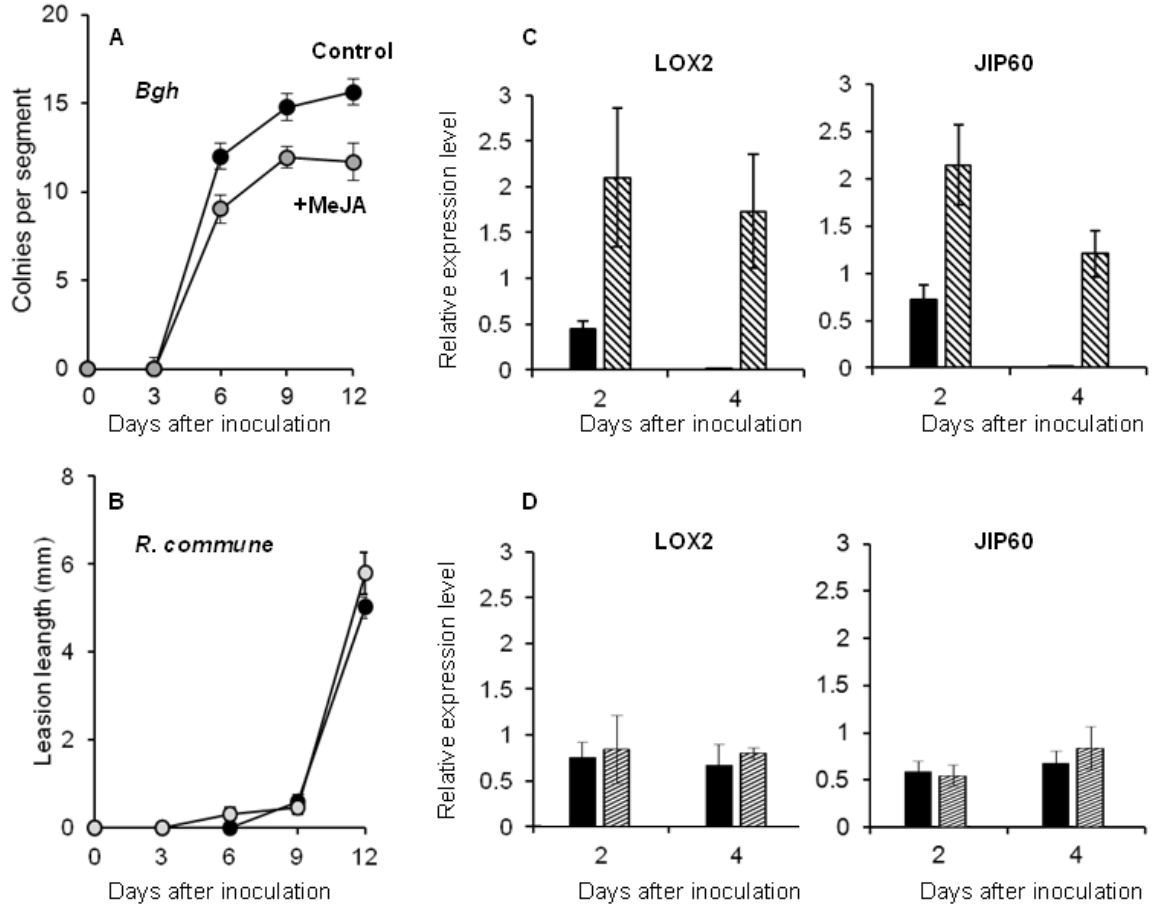

Figure 6 Sensitivity of *Blumeria graminis* and *Rhynchosporium commune* to Me-JA treatment and inducibility of JA-related genes.

A, B: Number of *B. graminis* (*Bgh*) colonies (A) and length of *R. commune* lesions (B) on barley leaf segments pre-treated for 24 hours with 45 µM Me-JA (black circles) or water (control, grey circles). C-F: Relative transcript levels of *HvLOX2* (C,D) and *HvJIP60* (E,F) in uninoculated leaf segments (black bars) or leaf segments inoculated (patterned bars) with *B. graminis* (C,E) or *R. commune* (D,F). α-TUB was used as reference gene. Experiments were performed on middle segments of the second leaves of plants grown for 14 days in control conditions. Means (± SE) from three replicate experiments (n=3).

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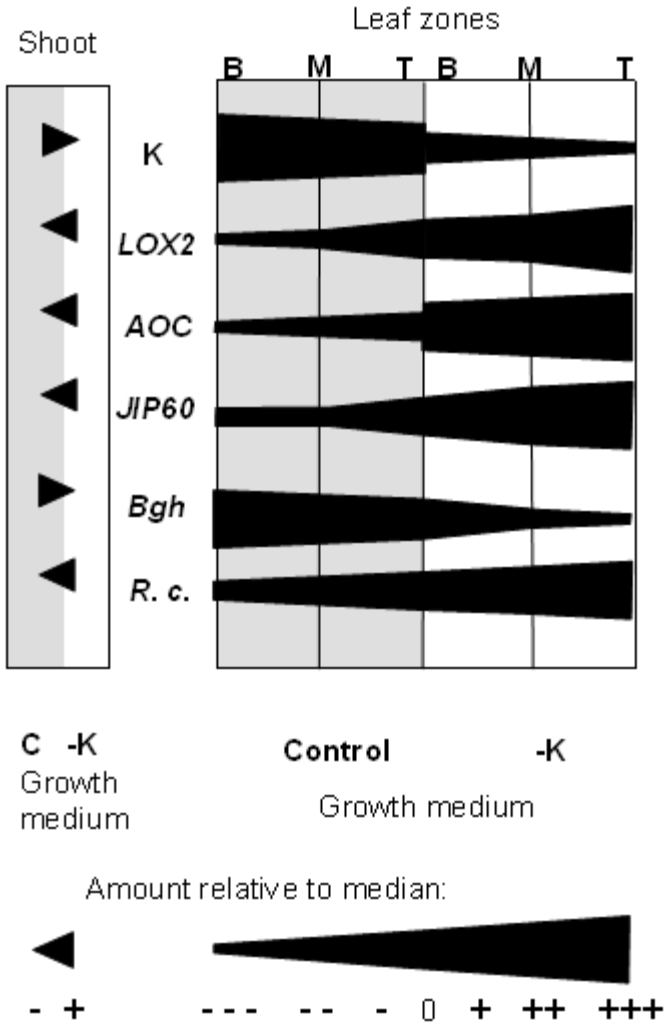

Figure 7 Gradients in tissue K concentration, transcript levels and disease symptoms across leaf zones and K treatments

Semi-quantitative representation of tissue K concentrations (K), transcript levels of JA-related genes (*HvLOX2*, *HvAOC*, *Hv JIP60*) and disease symptoms of *Blumeria graminis* (*Bgh*) and *Rhynchosporium commune* (*R. c.*) in whole shoots (left) as well as base (B), middle (M) and tip (T) regions of the second leaves of plants grown in control (grey background) or -K (white background) media. To build the profiles, measured values were classified into two levels (+, -) for whole shoots or into seven levels for leaf segments, ranging from much lower (---) to much higher (+++) than the median (0) across all samples (see scale bar). If amounts differed between adjacent segments a continuous gradient within the segments was assumed.

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