# This is a postprint of

Iglesias-García R, Rubiales D, Fondevilla S, 2014.

Penetration resistance to Erysiphe pisi in pea mediated by er1 gene is

associated with protein cross-linking but not with callose apposition or

hypersensitive response.

Euphytica 201(3): 381-387.

# DOI 10.1007/s10681-014-1221-2

# The published pdf can be downloaded at:

https://link.springer.com/article/10.1007/s10681-014-1221-2

Penetration resistance to *Erysiphe pisi* in pea mediated by *er1* gene is associated with protein cross–linking but not with callose apposition or hypersensitive response.

R Iglesias–García<sup>1</sup>, D Rubiales<sup>1</sup>, S Fondevilla<sup>2</sup>

<sup>1</sup> Institute for Sustainable Agriculture, CSIC, Apdo.4084, 14080 Córdoba, Spain.

<sup>2</sup> University of Frankfurt, Institute for Molecular Bioscience Max–von Laue Str. 9, D–60438 Frankfurt am Main, Germany.

\*For correspondence E-mail: rbkig@ias.csic.es Phone: +44 (0) 7597811178 Fax: +44 (0) 1206872592

# ABSTRACT

Powdery mildew caused by *Erysiphe pisi* DC is an important pea disease which causes high yield and quality losses. The most efficient way to control this disease is the use of resistant cultivars. Three genes of resistance are known so far in pea, namely er1, er2 and Er3. The most widely deployed gene in pea cultivars worldwide is er1. Resistance conferred by er1 is complete and considered to be durable, being recently demonstrated that er1 is in fact a member of the mlo gene family. Resistance is caused by colony abortion albeit the responsible cellular mechanisms causing this colony abortion are not known. In this study, the presence of different mechanisms related with colony abortion, such as callose apposition, protein cross–linking and hypersensitive response was quantified in a resistant pea er1 line compared to a susceptible check. Our histological studies showed that protein cross–linking, plays a determinant role in the penetration resistance conferred by er1, whereas callose apposition or hypersensitive response played little role.

Keywords: MLO gene family, Powdery mildew, Protein cross-linking, Resistance

### **INTRODUCTION**

*Erysiphe pisi* DC, causing powdery mildew in pea, is a widespread pathogen of *Pisum sativum* L. all over the world. This disease causes up to 50% yield losses and reduces total biomass, plant height, node number, pod number per plant, seeds per pod, pod quality and seeds weight (Fondevilla and Rubiales, 2012).

The infection process begins when asexual spores of *E. pisi* dispersed by wind land and germinate on a suitable host, forming a single germ tube that elongates before differentiating into an appressorium (Smith *et al.*, 1996). An infection peg then attempts to breach the plant epidermal host cell through the cuticle and cell wall. If successful, a biotrophic haustorium is invaginated within the epidermal cell that extracts nutrients to support growth of ectophytic secondary hyphae (Singh and Singh, 1983; Smith *et al.*, 1996). Secondary appressoria are then formed in secondary hyphae from which secondary haustoria will be produced, allowing successful establishment of colonies that sporulate to complete the infection cycle.

The most efficient strategy to control this biotrophic fungus is the use of resistant cultivars. Disease control through inherent plant resistance eliminates dependence on costly fungicides, with their potential and perceived threats to the environment and consumers. Therefore, host resistance to powdery mildew is a vital component in sustainable pea crop production.

Only three genes conferring resistance to *E. pisi* in pea, named *er1*, *er2* and *Er3* have been described so far (Fondevilla et al. 2011). Unlike the other two genes, gene *er1* is widely used in pea breeding programmes. Resistance conferred by this gene has been proven to be stable and is caused by a low success in colony establishment. In *er1* lines the vast majority of *E. pisi* conidia germinate and form appressoria. However, the pathogen is stopped soon after, and no secondary hyphae are formed. In contrast, resistance governed by *er2* and *Er3* is mainly expressed as a post–penetration Hypersensitive Response (HR) that stops the colony growth (Fondevilla et al., 2006a, 2006b, 2007, 2008, 2011).

The *er1* gene has recently been proven to be a member of the *MLO* (*Mildew Resistance Locus* O) gene family and called *PsMLO1* (Humphry et al., 2011). Loss–off function mutations of *MLO* genes confer highly effective broad–spectrum powdery mildew resistance through penetration resistance (Stolzenburg *et al.*, 1984; Gold *et al.*, 1986; Russo and Bushnell, 1989; Bayles *et al.*, 1990; Wolter *et al.*, 1993; Lyngkjær *et al.*, 1998; Consonni *et al.*, 2006; Bai *et al.*, 2008). *Mlo* resistance was originally discovered in barley (*Hordeum vulgare* L.) (Freisleben et al., 1942) and has been successfully employed

in agriculture for more than 40 years (Lyngkjaer et al., 2000). Later on, *mlo* resistance to powdery mildew has also been reported in the dicotylenous plants *Arabidopsis thaliana* L. and tomato (*Solanum lycopersicum* L.), indicating that *mlo*-based powdery mildew resistance was not a barley-specific phenomenon and was probably existing in many higher plant species (Consonni *et al.*, 2006). Nowadays, *MLO* genes have been identified in other plant species such as rice (*Oryza sativa* L.), maize (*Zea mays* L.), grapevine (*Vitis vinifera* L.), wheat (*Triticum aestivum* L.) or soybean (*Glycine max* L. Merr.) (Büschges *et al.*, 1997; Consonni *et al.*, 2006; Bai *et al.*, 2008; Liu *et al.*, 2008; Konishi *et al.*, 2010; Shen *et al.*, 2012). In barley, *Arabidopsis* and tomato, penetration resistance conferred by *MLO* mutations is associated with the formation of papillae in the penetration sites. Papillae are formed by the deposition of a callose matrix containing various inorganic and organic constituents and constitute a physical and chemical barrier to pathogen penetration (Hückelhoven, 2007).

In addition to callose apposition, another mechanism that can delay or stop colony growth is the formation of protein cross–linking in the host cell walls that acts as a physical barrier. This mechanism has proved to be an effective and fast defensive response against pathogens, through the insolubilization of proteins (extensins and other glycoproteins rich in hydroxyproline or HRGPs), which would take place before callose apposition and increase cell wall resistance only a few minutes after pathogen attack (Bradley et al., 1992; Showalter, 1993; Brisson et al., 1994; Hammond–Kosack and Jones, 1996; Brown et al., 2002).

HR, based on death of the invaded epidermal cell after penetration of the host, is a common mechanism of resistance against biotrophic pathogens. This defensive reaction is characterized by the accumulation of reactive oxygen species (ROS), antimicrobial proteins and phytoalexins, culminating in a local cellular suicide (Huckelhoven, 2007). HR typically occurs after the pathogen has penetrated the plant cell wall and has started to produce a haustorium (Aist and Bushnell, 1991). Cell death can occur very fast so no haustorium can be observed, or rather slow, allowing formation of some haustoria and secondary hyphae (Prats et al., 2007). HR is frequently described in resistance to powdery mildews (Boyd *et al.*, 1995; Niks and Rubiales, 2002) and is the main mechanism of resistance in *er2* and *Er3* lines of pea (Fondevilla *et al.*, 2006b).

A low success in colony establishment has been reported in er1 pea lines (Fondevilla et al. 2006a), but the cellular mechanism responsible for this colony abortion is not known. The objective of this work was to identify the mechanism that avoids colony establishment in er1 lines. With this aim, the

presence of different mechanisms that could cause colony abolishment such as formation of callose apposition, HR and protein cross–linking was studied in a *er1* line compared to a susceptible check.

#### MATERIAL AND METHODS

### Plant and fungal material

The resistant pea accession JI2302 (*er1er1*) (Heringa et al., 1969), kindly provided by Jonh Innes Centre (Norwich, UK), and the susceptible pea cv. Messire (*Er1Er1*) were used in this study.

The *E. pisi* isolate CO–01 was used in the inoculations. This isolate, avirulent in absence of a functional *Er1* gene, was obtained from a population collected from naturally infected pea plants in a field at Córdoba (Spain) in 2001 and maintained on the susceptible pea cv. Messire (Fondevilla et al., 2006b).

#### Inoculation and incubation

A total amount of 16 plants per line was grown in pots, one plant per pot, containing 250 cm3 of 1:1 sand-peat mixture in a growth chamber at  $20 \pm 0.5$  °C with a threshold photons flux density at plant level around 250 µmol m<sup>-2</sup> s<sup>-1</sup>. The fourth leaf (two leaflets) of four plants per line at the fifth leaf stage was excised and carefully laid in Petri dishes containing a medium consisting of technical agar (4 g/l) and benzimidazole (62.5 mg/l) (Rubiales et al., 1993). Leaves were inoculated using a settling tower to obtain an inoculum density of about 5 conidia mm<sup>-2</sup>. Two independent inoculations, each containing 8 leaves per line were performed. After inoculation, lids were fitted to the Petri dishes, which were placed back in the same growth chamber and conditions. Incubation lasted 48 hours and was initiated with a 6 h light period, followed by cycles of 12 h darkness/12 h light.

#### Histological studies

Leaflets were sampled at 48 hours after inoculation and subjected to different stains. Two leaflets from each of the two independent inoculations (considered replicates) were examined per line to measure the incidence of each of the resistance mechanisms studied.

To identify the presence of protein cross–linking in cell walls underlying *E. pisi* appressoria, we used the method described by Mellersh et al. (2002) with some modifications. Thus, fresh leaflets from each replicate were submerged in 1% sodium dodecyl sulphate (SDS) for 20 hours at 75 °C to remove soluble proteins. After that, they were left for 3–5 min in 0.1% Coomassie blue in 4:1 (v/v) ethanol: acetic acid to stain proteins covalently linked, rinsed in a solution of 4: 1 ethanol: acetic acid, and kept in

distilled water till they were finally mounted in lactoglycerol. Using this method, the presence of protein cross–linking is marked with a deep blue colour. One hundred epidermal cells underlying *E. pisi* appressoria per leaflet and genotype were examined for the presence of protein cross–linking. In addition, it was also scored whether a colony had been established (spores showing secondary hyphae) or not (absence of secondary hyphae). In order to stain fungal structures a drop of Uvitex staining (Ciba) was placed over the leaflets.

To assess host cell death, indicating a HR as a result of pathogen attack, leaflets were laid, adaxial surface up, on filter paper moistened with a 1:3 (v/v) mixture of glacial acetic acid:absolute ethanol for fixation. When bleached, leaflets were transferred to filter paper moistened with distillate water, left for 1 h to soften the tissues and then transferred to filter paper moistened with lactoglycerol (1:1:1, lactic acid:glycerol:water, v/v) until cleared (2 h) and for storage (Rubiales and Carver, 2000). The epidermal cell underlying 100 appressoria per leaflet and line were examined. Leaflets were observed using bright field and differential interference contrast (DIC) microscopy. The walls and contents of dead cells were discoloured yellow or brown by bright field microscopy, and by DIC the cell contents appeared granular and disorganised. To stain fungal structures and score whether a colony was established or not as described above, a drop of aniline blue in lactoglycerol (0.1%) was deposited on the leaves.

To detect the presence of callose, leaflets were stained with aniline blue and with the aniline blue fluorocrom pure (Underwood and Somerville, 2008). Aniline blue in lactoglycerol (0.1%) was applied by spraying the stain over the samples, which were observed under visible wavelengths. In the case of the aniline blue fluorocrom pure the samples were stained by depositing a drop of a solution of 0.1% aniline blue fluorochrom in water and waiting for 15–30 min before observations (Bordallo et al., 2002). After staining samples were observed under UV fluorescence (340–380 nm) to avoid blue staining and preserve fluorescence of callose.

## Statistical analyses

Analysis of variance was performed according to a completely randomized block design, considering each inoculation as a block. Statistical analyses were performed using Statistix 8.0 statistical package (Analytical Software, Tallahase, USA).

## **RESULTS**

Most sporelings (95.5%) succeeded in establishing a colony on the susceptible cv. Messire (*Er1Er1*) (Table 1). No penetration attempts were associated with protein cross–linking (Fig.1. a, c) and very few (11%) with HR.



**Figure 1.** Leaflets of cv. Messire (a, c) and JI2302 (b,d) infected by *Erisiphe pisi* and stained with Uvitex (a, b) or Coomassie blue (c, d) 48 hai. External fungal structures show autofluorescence under UV–light excitation after staining by Uvitex. Protein cross–linking, stained blue by Coomassie blue, can be observed in JI2302 around the penetration point and slightly on the epidermal cell wall, whereas in Messire there is not such staining.

In contrast, very few (2.3%) sporelings succeeded in establishing a colony in JI2302 (*er1er1*), with 63% of the invaded epidermal cells showing protein cross–linking in the point of penetration (Fig.1. b, d). Both HR and protein cross–linking resulted in the abolishment of colony establishment.

 Table 1. Mean percentages for infection progress of *E. pisi* (isolate CO-01) and host defence responses

 on pea accessions JI2302 and cv. Messire 48 hai.

| Genotype | % Infection units<br>successfully<br>establishing a<br>colony | % Infection units<br>triggering protein<br>cross-linking | % Infection units<br>triggering protein<br>cross-linking<br>resulting in aborted<br>colony | % Infection units<br>triggering<br>Hypersensitive<br>Response | % Infection units<br>triggering<br>Hypersensitive<br>Response<br>resulting in<br>aborted colony |
|----------|---|--|--|---|---|
| JI2302   | 2.3 * <sup>a</sup>  | 63.0 *   | 100.0 *  | 21.3  | 100.0   |
| Messire  | 95.5  | 0  | 0  | 11.0  | 83.2  |

<sup>a</sup> Values with \* by columns differs significantly (ANOVA p< 0.05).

No statistical differences were found between the analyzed genotypes for the percentage of spores with appressorium which triggered HR (ANOVA p>0.05).

Callose deposition was not observed in any of the lines with the staining techniques used.

### **DISCUSSION**

Resistance conferred by *er1* has been reported to be associated with low success in colony establishment (Fondevilla et al., 2006a). However, the cellular mechanism behind this colony abortion was not fully understood. In this study we performed a detailed quantification of the presence of three mechanisms that could cause this colony abortion: callose apposition, protein cross–linking and HR.

In our previous histological study (Fondevilla et al., 2006a), haustoria were not observed in *er1* lines, suggesting a penetration resistance. However, a fast hypersensitive response, immediately after penetration, when the haustoria have just started to be formed, could also stop haustoria development so soon that these structures could not be observed under the appressoria. The so–called HR is a common mechanism of resistance against biotrophic pathogens that need to get their nutrients from living cells. This mechanism has also been reported to be the main cause of the resistance to *E. pisi* mediated by *er2* and *Er3* pea genes (Fondevilla et al., 2006a; 2007; 2011). In the present study, in order to do an accurate and better estimation of the role of HR in *er1* lines, we scored the percentage of penetration attempts associated with HR (no matter whether resulted in aborted or established colonies) in an *er1* line and a susceptible one. Results showed that *circa* 20 per cent of the epidermal cells that were attacked by *E. pisi* died in the *er1* genotype studied. Our present work confirms the effectiveness of HR, since the vast majority of host cells showing this response resulted in aborted colonies of the fungus in both the resistant

and the susceptible lines. However, while most spores were not able to establish colonies in the *er1* genotype, the percentage of infected epidermal cells presenting HR was low and did not differ from that observed in the susceptible cv. Messire. Therefore, although HR is an effective mechanism against *E. pisi* on pea, in this study we confirm that HR is not the primary cause of colonies abortion mediated by *er1*.

Resistance to powdery mildew penetration conferred by mutations in the MLO genes is characterized in other plant species by formation of papillae, complex structures which can even be seen using visible light microscopy and formed among other compounds by callose apposition. In Fondevilla et al., 2006a using light miscroscopy papilla were not observed in erl lines. However, no sstaining was applied to specifically detect the components of papilla. In this study, to definitively discard or confirm the presence of papilla, we applied dyes that specifically stain callose, the main component of papillae. Finally, we did not observe the presence of callose in JI2302 or Messire albeit using specific stains. These results suggested that callose apposition is not associated with the resistance to E. pisi conferred by PsMLO1 loss of function. Interestingly, Consonni et al. (2010) found that resistance against the powdery mildew pathogen Golovinomyces orontii conferred by the MLO mutant allele mlo2 in Arabidopsis is independent of callose apposition, but not of papilla formation. Thereby, mlo2 lines defective in callose formation remained resistant to powdery mildew. Similarly, Perumalla and Health (1989) outlined that callose deposition was not a prerequisite for other cell wall modifications observed in the bean (Phaseolus vulgaris L.) and cowpea rust (Uromyces vignae Barcl.) interactions, supporting the fact that callose is not a requirement for successful penetration resistance of the host plant (Jacobs et al., 2003; Nishimura et al., 2003). Our results support these hypotheses.

Probably the best studied example of prehaustorial resistance is the mlo-based resistance of cultivated barley to *B. graminis* f.sp. *graminis* (Lyngkjær et al., 2000). Other major genes for prehaustorial resistance, with more quantitative effects, occur in wheat against *Puccinia triticina*, i.e. the *Lr34* gene, associated with reduced haustorium formation that was not associated with papillae neither with hypersensitivity (Rubiales and Niks, 1995).

Instead of callose apposition, a high percentage of infected epidermal cells showed protein cross– linking on the *er1* line JI2302. This reaction was not observed in the susceptible cv. Messire, indicating that protein cross–linking is associated with *PsMLO1* mutation mediated resistance. Protein cross– linking has been observed to be a defence mechanism in pea against *Didymella pinodes* (Carrillo *et al.*, 2013) or parasitic plants such as broomrape (Pérez–de–Luque *et al.*, 2006). In our study, the presence of protein cross–linking was in all cases associated with colony abortion, which pointed towards protein cross–linking as the effective mechanism to avoid penetration by *E. pisi* in pea *Psmlo1* lines.

As we have previously mentioned, *MLO* genes codify membrane proteins. Although its precise function has not been unravelled yet, it is thought that these genes act as suppressors of defence mechanisms against powdery mildew (Consonni *et al*; 2006). In *mlo* mutants this defensive reaction is not repressed and mildew attack would result in the activation of mechanisms of resistance that could differ between plant species. Thus, in some plant species the activation of the defensive response could lead to callose apposition while in pea it could result in protein cross–linking.

In conclusion, our study demonstrates that *E. pisi* resistance mediated by loss of function in *Er1* gene is associated with protein cross–linking formation in the attacked host epidermal cells but not with callose apposition or HR. To our knowledge this is the first report of a *mlo* type resistance not associated with callose apposition. This study increases our knowledge about *MLO* genes and suggests that the mutation in these genes may result in different cellular mechanisms of resistance depending on the plant species.

#### REFERENCES

Aist JR, Bushnell WR (1991) Invasion of plants by powdery mildew fungi, and cellular mechanisms of resistance. In: G.T. Cole and H.C. Hoch (eds.) The fungal spore and disease initiation in plants and animals. Plenum Press, New York, pp 321–345

Bai Y, Pavan S, Zheng Z (2008) Naturally occurring broad spectrum powdery mildew resistance in a Central American tomato accession is caused by loss of *Mlo* function. Mol Plant Microbe In 21: 30–39. doi: 10.1094/MPMI2110030

Bayles CJ, Ghemawat MS, Aist JR (1990) Inhibition by 2–deoxy–D–glucose of callose formation, papilla deposition, and resistance to powdery mildew in an ml–o barley mutant. Physiol Mol Plant Pathol 36: 63–72. doi: 10.1016/08855765(90)90092C

Boyd LA, Smith PH, Foster EM, Brown JKM (1995) The effects of allelic variation at the Mla resistance locus in barley on the early development of *Erysiphe graminis* f. sp. hordei and host responses. Plant J 7: 959–968. doi: 10.1046/j.1365-313X.1995.07060959.x

Bradley DJ, Kjellbom P, Lamb CJ (1992) Elicitor– and wound–induced oxidative crosslinking of a proline–rich plant cell wall protein: a novel rapid defense response. Cell 70: 21–30. doi: 10.1016/0092-8674(92)90530-P

Brisson LF, Tenhaken R, Lamb C (1994) Function of oxidative cross–linking of cell–wall structural proteins in plant–disease resistance. Plant Cell 6: 1703–1712. doi: 10.1105/tpc.6.12.1703

Brown I, Trethowan J, Kerry M, Mansfield J, Bolwell P (2002) Localization of components of the oxidative crosslinking of glycoproteins and of callose synthesis in papillae formed during the interaction between non–pathogenic strains of *Xanthomonas campestris* and french bean mesophyll cells. Plant J 15: 333–343. doi: 10.1046/j.1365-313X.1998.00215.x

Büschges R, Hollricher K, Panstruga R, Simons G, Wolter M, Frijters A, van Daelen R, van der Lee T, Diergaarde P, Groenendijk J, Töpsch S, Vos P, Salamini F, Schulze–Lefert P (1997) The barley *Mlo* gene: a novel control element of plant pathogen resistance. Cell 88: 695–705. doi: 10.1016/S0092-8674(00)81912-1

Carrillo E, Rubiales D, Pérez-de-Luque A, Fondevilla S (2013) Characterization of mechanisms of resistance against *Didymella pinodes* in *Pisum* spp. Eur J Plant Pathol 135: 761–769. doi: 10.1007/s10658-012-0116-0

Consonni C, Humphry ME, Hartmann HA (2006) Conserved requirement for a plant host cell protein in powdery mildew pathogenesis. Nat Genet 38: 716–720. doi: 10.1038/ng1806

Consonni C, Bednarek P, Humphry M, Francocci F, Ferrari S, Harzen A, Ver Loren van Themaat E, Panstruga R (2010) Tryptophan–derived metabolites are required for antifungal defense in the Arabidopsis *mlo2* mutant. Plant Physiol 152: 1544–1561. doi: 10.1104/pp.109.147660

Lyngkjær MF, Newton AC, Atzema JL, Baker SJ (2000) The barley mlo-gene: an important powdery mildew resistance source. Agronomie 20: 745–756. doi: 10.1051/agro:2000173

Fondevilla S, Carver TLW, Moreno MT, Rubiales D (2006a) Macroscopic and histological characterisation of genes er1 and er2 for powdery mildew resistance in pea. Eur J Plant Pathol 115: 309–321. doi: 10.1007/s10658-006-9015-6

Fondevilla S, Carver TLW, Moreno MT, Rubiales D (2006b) Identification and characterisation of sources of resistance to *Erysiphe pisi* Syd. in *Pisum* spp. Plant Breeding. doi/10.1111/j.1439–0523.2006.01312.x

Fondevilla S, Cubero, JI, Rubiales D (2011) Confirmation that the *Er3* gene, conferring resistance to *Erysiphe pisi* in pea, is a different gene from *er1* and *er2* genes. Plant Breeding 130: 281–282. doi: 10.1111/j.1439-0523.2010.01769.x

Fondevilla S, Rubiales D (2012) Powdery mildew control in Pea. A review. Agron Sustain Dev 32: 401–409. doi: 10.1007/13593-011-0033-1

Fondevilla S, Rubiales D, Moreno MT, Torres AM (2008) Identification and validation of RAPD and SCAR markers linked to the gene *Er3* conferring resistance to *Erysiphe pisi* DC in pea. Mol Breeding 22: 193–200. doi: 10.1007/s11032-008-9166-6

Fondevilla S, Torres AM, Moreno MT, Rubiales, D (2007) Identification of a new gene for resistance to powdery mildew in *Pisum fulvum*, a wild relative of pea. Breeding Sci 57: 181–184. doi: 10.1270/jsbbs.57.181

Gold R, Aist E, Hazen R, Stolzenburg BE, Marshall MC and Israel HW (1986) Effects of calcium nitrate and chlortetracycline on papilla formation, ml–o resistance, and susceptibility of barley to powdery mildew. Physiol Mol Plant Pathol 29: 115–129. doi: 10.1016/S0048-4059(86)80043-1

Hammond–Kosack KE, Jones JDG (1996) Resistance gene–dependent plant defense responses. Plant Cell 8: 1773–1791. doi: 10.1105/tpc.8.10.1773

Humphry M, Reinstädler A, Ivanow S, Bisseling T, Panstruga R (2011) Durable broad–spectrum powdery mildew resistance in pea *er1* plants is conferred by natural loss–of–function mutations in *PsMLO1*. MolPlant Pathol. doi: 10.1111/j.1364–3703.2011.00718.x

Jacobs AK, Lipka V, Burton RA, Panstruga R, Strizhov N, Schulze–Lefert P, Fincher GB (2003) An *Arabidopsis* callose synthase, GSL5, is required for wound and papillary callose formation. Plant Cell 15: 2503–2513. doi: 10.1105/tpc.016097

Konishi S, Sasakuma T, Sasanuma, T (2010) Identification of novel *Mlo* family members in wheat and their genetic characterization. Gene Genet Syst. 85: 167–175. doi: 10.1266/ggs.85.167

Mellersh DG, Foulds IV, Higgins VJ, Heath MC (2002)  $H_2O_2$  plays different roles in determining penetration failure in three diverse plant-fungal interactions. Plant J 29: 257–268. doi: 10.1046/j.0960-7412.2001.01215.x

Niks RE, Rubiales D (2002) Potentially durable resistance mechanisms in plants to specialised fungal pathogens. Euphytica 124: 201–216. doi: 10.1023/A:1015634617334.

Nishimura MT, Stein M, Hou BH, Vogel JP, Edwards H, Somerville SC (2003) Loss of a callose synthase results in salicylic acid–dependent disease resistance. Science 301: 969–972. doi: 10.1126/science.1086716

Pérez–de–Luque A, González–Verdejo CI, Lozano MD, Dita MA, Cubero, JI, González–Melendi P, Rubiales, D (2006) Protein cross–linking, peroxidase and β–1, 3–endoglucanase involved in resistance of pea against *Orobanche crenata*. J Exp Bot 57: 1461–1469. doi: 10.1093/jxb/erj127

Perumalla CJ, Health M (1989) Effect of callose inhibition on haustorium formation by the cowpea rust fungus in the non-host bean plant. Physiol Mol Plant Pathol 35: 375–382. doi: 10.1016/0885-5765(89)90042-8

Prats E, Llamas M J, Rubiales D (2007) Characterization of resistance mechanisms to *Erysiphe pisi* in *Medicago truncatula*. Phytopathology 97: 1049–1053. doi: 10.1094/PHYTO-97-9-1049

Rubiales D, Brown JKM, Martín A (1993) *Hordeum chilense* resistance to powdery mildew and its potential use in cereal breeding. Euphytica 67: 215–220. doi: 10.1007/BF00040623

Rubiales D, Carver TLW (2000) Cellular responses of *Hordeum chilense* genotypes to inappropriate formae specialis of the cereals powdery mildew fungus. Can J Bot 78: 1561–1570. doi: 10.1111/j.1601-5223.2001.t01-1-00271.x

Rubiales D, Niks RE (1995) Characterization of *Lr34*, a major gene conferring nonhypersensitive resistance to wheat leaf rust. Plant Dis 79: 1208–1212. doi: /doi/10.1111/j.1601-5223.2001.00111.x

Shen Q, Zhao J, Du C, Xiang Y, Cao J, Qin X (2012) Genome-scale identification of MLO domaincontaining genes in soybean (Glycine max L. Merr.). Genes Genet Syst 87: 89–98. doi: 10.1266/ggs.87.89

Singh UP, Singh HB (1983) Development of *Erysiphe pisi* on susceptible and resistant cultivars of pea. T Brit Mycol Soc 81: 275–278. doi: 10.1016/S0007-1536(83)80079-5

Smith PH, Foster EM, Boyd LA, Brown JKM (1996) The early development of *Erysiphe pisi* on *Pisum* sativum L. Plant Pathol 45: 302–309. doi: 10.1046/j.1365-3059.1996.d01-111.x

Showalter AM (1993) Structure and function of plant-cell wall proteins. Plant Cell 5: 9–23. doi: 10.1105/ tpc.5.1.9

Stolzenburg MC, Aist JR, Israel HW (1984) The role of papillae in resistance to powdery mildew conditioned by the *ml-o* gene in barley. I correlative evidence. Physiol Plant Pathol 25: 337–346. doi: 10.1016/0048-4059(84)90041-9

Underwood W, Somerville SC (2008) Focal accumulation of defences at sites of fungal pathogen attack. J Exp Bot 59, 3501–3508. doi: 10.1093/jxb/ern205 Wolter M, Hollricher K, Salamini F, Schulze–Lefert P (1993) The *mlo* resistance alleles to powdery mildew infection in barley trigger a developmentally controlled defense mimic phenotype. *Mol Gen Genet* 239:122–128. doi: 10.1007/BF00281610