

Role of chlorophyll degradation pathway in photosynthetic dysfunctions of *mlo* barleys during resistance responses to powdery mildew

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Powdery mildew disease caused by *Blumeria graminis* DC (Speer) ff. spp., constrain cereal production in temperate regions. A durable resistance mechanism that prevents powdery mildew cell penetration is the formation of papillae, localized cell wall appositions at attack sites. Papillae provide a race non-specific defense conferring broad-spectrum resistance. Barley genotypes carrying the *mlo* gene display highly effective papilla-based penetration resistance to powdery mildew that has proved durable for over 30 years. However, the *mlo* barleys shows adverse pleiotropic effects such as large necrotic/chlorotic flecks on leaves, accelerated leaf senescence and reduced grain yield. These adverse effects are particularly dramatic under stress conditions and for this reason, *mlo* cannot be used in winter barleys. Despite its importance for crop production, the mechanism(s) leading to these pleiotropic effects are still not understood nor are its molecular and cellular bases. In a previous work, we observed that the damages related to the resistance responses were associated with particular genetic backgrounds and were linked to stomatal and photosynthetic dysfunctions but did not relay in the generation of reactive oxygen species. In this work we studied the role of xanthophyll cycle metabolites and chlorophyll degradation pathway in two sets of *mlo*-isogenic lines with different genetic background. Data showed a decrease in chlorophyll a and b and in pheophitin in the resistant isolate characterized by necrotic flecking. Overall, xanthophyll metabolites increased following pathogen inoculation in the resistant *mlo* line lacking lesions. Furthermore, antheroxanthin increased in all genotypes following pathogen challenge but with higher increases in the resistant *mlo* genotype lacking lesions.

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