Proc. Fla. State Hort. Soc. 134:137. 2021.

—Scientific Note—

Lettuce Downy Mildew Differential Cultivars Are Resistant to Other Important Diseases

Lis Natali R. Porto, Richard N. Raid, and Germán V. Sandoya-Miranda*

Everglades Research and Education Center, University of Florida, IFAS, Belle Glade, FL

Additional index words. Breeding, common disease resistance, *Lactuca sativa*

Lettuce (*Lactuca sativa* L.) is planted on 10,000 acres in the Everglades Agricultural Area (EAA), generating over 80 million dollars revenue. The crop is susceptible to diseases due to the region's unique environmental conditions. Lettuce downy mildew (LDM) is caused by the oomycete *Bremia lactucae,* that infects the leaves causing chlorotic yellow spots that eventually coalesce and turn necrotic (Michelmore et al., 2009). *Bremia lactucae* is genetically diverse with 10 races identified in the western United States and 15 races in Europe (van Treuren et al., 2011). Race structure of *B. lactucae* is established utilizing differential cultivars that have known resistant and susceptible reactions. Another disease problem for EAA lettuce growers is bacterial leaf spot (BLS) caused by *Xanthomonas hortorum* pv. *vitians* (*Xhv*). The pathogen produces water-soaked lesions delimitated by veins that progress to tissue collapse, becoming dry with a papery appearance. A newly discovered disease in Florida is fusarium wilt of lettuce (FWL) caused by *Fusarium oxysporum* forma *specialis* (f.sp.) *lactucae* (*Fol*). *Fol* is a soil-borne fungus that produces taproot discoloration, usually pink to reddish-brown. Lettuce infested with *Fol* exhibits stunting, chlorosis, and wilting until plant death due to water and nutrient transport blockage. Host resistance is the preferred method to fight these diseases but breeding for resistance is time consuming. Considering that plant breeders must develop multi-disease resistant cultivars, the process could become exponential if only one disease is considered at a time. Previous studies indicate that resistant gene candidates (RGCs) to many diseases are grouped in clades in the lettuce genome. Four RGCs families were found to provide resistance to at least 16 different diseases (Christopoulou et al., 2016). Therefore, a lettuce accession could be resistant to several diseases. This study aimed to identify common resistance lettuce accessions to BLS and FWL in an LDM differential cultivar set that already possesses race-specific resistance to *B. lactucae*.

Four independent greenhouse experiments were conducted to test 17 differentials and controls (depending on the pathogen) with inoculations of isolates L7, L44, and Sc8B of *Xhv* and #51 of *Fol*. Each experiment was planted in a randomized complete-block design with three replicates and was conducted twice. Trays of 30-day-old lettuce seedlings were inoculated with a hand sprayer containing a suspension of $10^6 \cdot mL^{-1}$ CFU of each *Xhv* isolate. Plants were maintained in a growth chamber for 48 hours and then were transferred to a greenhouse. After 10 days, foliar damage was assessed using a rating scale of 0 (no symptoms) to 5 (> 75% of total foliage infected). FWL trials were conducted using the same cultivars. Plant roots were submerged in a *Fol* suspension of 1×10^6 spores/mL and transplanted into 4-inch pots. Plants were evaluated for foliar damage weekly and root discoloration was evaluated after 30 days using the rating scale described above. Statistical analyses were computed using SAS statistical software (ver. 9.4; SAS Institute Inc., Cary, NC) and analysis of variance was performed following a nonparametric statistic to obtain relative marginal effects (RME) and their confidence intervals.

Significant differences were found among the tested accessions ($P < 0.001$) for foliar damage. No differences were detected between experiments ($P > 0.05$) when inoculated with isolates L7, L44, and Sc8B. 'Muraires' and 'Silvinas' were as resistant as the controls PI 358001-1 and PI 667690 when tested with all *Xhv* isolates. Fifteen cultivars showed similar disease severity as the susceptible control 'Okeechobee'. Likewise, significant differences were found between the tested accessions ($P < 0.001$) for foliar (FDS) and root (RDS) disease severity in the experiment with *Fol*. 'Balesta', 'Colorado', and 'Silvinas' had low FDS and RDS similar to the resistant controls PI 667690 and 60182. Fourteen cultivars were as susceptible as the control 'Chosen' for both parameters evaluated. The aforementioned differentials are likewise resistant to *B. lactucae* races 7, 8, and 9. Therefore, it was possible to identify a lettuce accession resistant to several diseases, creating the possibility of improving lettuce resistance to LDM, FWL, and BLS at the same time.

Literature Cited

Christopoulou, M., S.R. Wo, A .Kozik, L.K. McHale, M.J. Truco, T.Wroblewski, and R.W. Michelmore. 2016. Genome-wide architecture of disease resistance genes in lettuce. G3 (Bethesda). 2015 Oct 8; 5(12):2655-69. https://doi.org/10.1534/g3.115.020818. *Erratum* in: G3 (Bethesda). 6(3):773. https://doi.org/10.1534/g3.116.027144.

Michelmore, R., O. Ochoa, J. Wong. 2009. *Bremia Lactucae* and lettuce downy mildew. p. 241–262. In: Kurt Lamour and Sophien Kamoun (eds.) Oomycete Genetics and Genomics: Diversity, Interactions, and Research Tools. John Wiley & Sons, Inc. Hoboken, NJ.

van Treuren, R., A.J.M. van der Arend, J.W. Schut. 2011. Distribution of downy mildew (*Bremia lactucae* Regel) resistances in a genebank collection of lettuce and its wild relatives. Plant Genetic Resources, 11:15–25. https://doi.org/10.1017/S1479262111000761.

*Corresponding author. Email: gsandoyamiranda@ufl.edu