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Disease Notes

First Report of *Xanthomonas euvesicatoria* Causing Bacterial Spot Disease in Pepper in Northwestern Nigeria

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Bacterial spot (BS) has been reported as an important disease on pepper in Nigeria (4). *Xanthomonas campestris* pv. *vesicatoria* was identified as the causal agent using phenotypic and pathogenicity tests; however, *X. campestris* pv. *vesicatoria* is a synonym for two genetically distinct groups that have been elevated to the species *X. euvesicatoria* and *X. vesicatoria* (2). Furthermore, the latter two species and *X. gardneri* cause similar diseases on pepper (2). In order to determine the species associated with BS on pepper, leaves with irregular, dark brown lesions were collected from pepper plants in fields from northwestern Nigeria, and isolations were made on nutrient agar (NA). Yellow, mucoid colonies typical of *Xanthomonas* were isolated. Six strains isolated from pepper were determined to be non-amylolytic. For race determinations, bacterial suspensions of the pepper strains, derived from 24-h cultures grown on NA at 28°C, were adjusted to 10^8 CFU/ml and infiltrated into leaves of tomato and pepper differential genotypes (5). The six pepper strains elicited HRs on the tomato differential genotypes. The strains produced a susceptible reaction on all pepper differentials and were designated as pepper race 6 (5). Multilocus sequence analysis (MLSA) using six housekeeping genes (*fusA*, *lacF*, *gyrB*, *gltA*, *gapA*, and *lepA*) was used to further analyze the strains (1) (GenBank Accession Nos. KJ938585 to KJ938587, KJ938592 to KJ938594, KJ938599 to KJ938601, KJ938606 to KJ938608, KJ938633 to KJ938635, and KJ938640 to KJ938642). A partial sequence of *hrpB2* was also sequenced since the four *Xanthomonas* species associated with BS can be differentiated based on sequence divergence (3) (KJ938622 to KJ938627). The housekeeping gene sequences were aligned along with other *Xanthomonas* sequences imported from the NCBI database using muscle tool from MEGA software, 5.2.2. Maximum likelihood phylogenetic trees constructed for the six housekeeping gene sequences individually and in concatenation revealed that the Nigerian pepper strains were identical to the *X. euvesicatoria* reference strain 85-10. Although BS is common in Nigeria, to our knowledge, this represents the first report for this pepper pathogen in Nigeria.

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