

Genetic Variability of *Xanthomonas euvesicatoria* pv. *allii*, Associated with Leaf Blight Outbreaks on Onion Crops at Central Region of Brazil.

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Xanthomonas leaf blight, caused by *Xanthomonas euvesicatoria* pv. *allii* (XEA) has been a yield-limiting onion (*Allium cepa*) disease in certain regions. In Brazil, no remarkable outbreaks of the disease had been described until the recent occurrences observed on onion crops cultivated during the summer periods of 2018 and 2019, under sprinkle irrigation, at the central regions of the country. In order to better understand these occurrences and drive future research on the disease management, a genetic study on the pathogen has then been initiated, and its preliminary results on the variability of BOX-PCR (primer BOX-A1R) patterns are reported. A collection of 30 isolates was obtained from symptomatic onion leaf samples, representing three hybrid cultivars, and *Euphorbia heterophylla* (three isolates), a weed species spontaneously grown among the onion plants in one of the sampled fields. Reference isolates IBSBF 1770 (XEA) and EH 2010-60 (*X. euvesicatoria* pv. *perforans*) were included. Eight haplotypes were visually resolved. Ten isolates belonged to the same haplotype of IBSBF 1770. Each cultivar presented a predominant haplotype, even if they had been grown in different places at the same year, the cultivars do not share haplotypes among them, with one exception. These facts lead to a hypothesis of a possible association of the pathogen with the imported seeds of the cultivars used at that time. The isolates of *E. heterophylla* and of onion at the same site shared common haplotypes. Besides, the role of alternative hosts as primary inoculum source should also be addressed.