

Differences in virulence of *Phytophthora capsici* isolates from a worldwide collection on tomato fruits

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Phytophthora capsici causes root, crown, and fruit rot of tomato as well as other vegetable crops in the Solanaceae, Cucurbitaceae, and Fabaceae. To evaluate the virulence of 126 *P. capsici sensu stricto* isolates to 4 to 5 cm diameter green tomato fruits, each fruit was inoculated with one 6-mm-diameter agar plug of *P. capsici* and incubated in a clear plastic box at room temperature ($25 \pm 2^\circ\text{C}$ and 100% relative humidity) for four days. Virulence was estimated by measuring the lesion diameter, pathogen growth diameter, and pathogen sporulation density four days later. Isolates were grouped by host family of origin, geography, and genetic cluster membership for statistical analyses to investigate whether differences in virulence could be observed amongst isolates grouped by these factors. Differences in mean lesion diameter were not apparent when isolates were grouped by genetic cluster membership ($P=0.4542$), but differences were observed when isolates were grouped by host family of origin ($P=0.0041$) and geography ($P=0.0075$). Isolates from fabaceous and solanaceous hosts resulted in larger lesions than the isolate from a sterculiaceae host. When isolates from vegetable hosts were compared with isolates from non-vegetable hosts, isolates from vegetable hosts resulted in significantly larger lesions, pathogen growth diameter, and sporulation density ($P<0.0321$). When isolates were grouped by continent of origin, isolates from Asia and S. America resulted in larger lesions than African isolates. Differences in pathogen growth and sporulation density were not apparent when isolates were grouped by host family of origin, geography, or genetic cluster membership. Our results suggest that isolates used for host resistance screenings in tomato should incorporate the phenotypic and genetic diversity of *P. capsici*, including isolates with differing virulence.