

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

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Vegetable hosts of *P. capsici*

- *P. capsici* is distributed worldwide
 - Causes root, crown and fruit rot of tomato and other vegetables (cucurbits, snap and lima bean, eggplant)
 - Also, tropical hosts (macadamia, cacao, black pepper)
- In Michigan, susceptible vegetables are worth at least \$160 million

- Tomato \$30+ million

≡ <http://www.nass.usda.gov/QuickStats/>



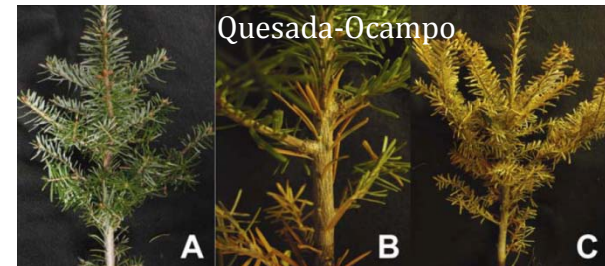
Management Challenges

- Long-term survival of oospores in the soil



- Long-distance spread via irrigation water and human activity (movement of equipment and cull fruits)

- Growing list of susceptible hosts



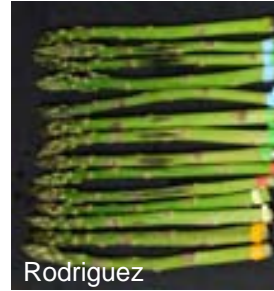
- Limited number of fungicides that provide effective control

- Lack of commercially acceptable resistant cultivars



Differences in virulence in *P. capsici*

12889
OP97
SP98
SFF3

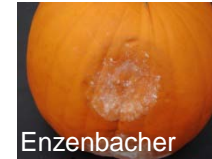


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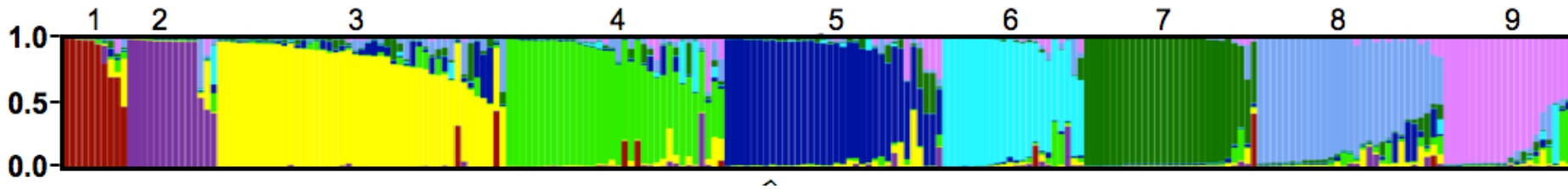
12889
OP97
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SFF3



Population structure of *P. capsici* isolates from a worldwide collection

L. M. Quesada-Ocampo, L. L. Granke et al., *Phytopathology* 101:1061-1073

- Classified 236 isolates in clusters using 10 sequenced genes

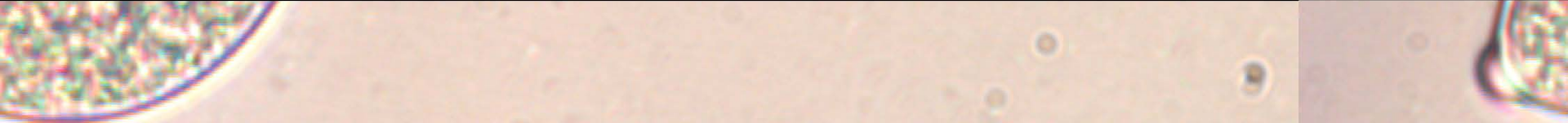


- Clusters are not evidence of physiological race since we did not include virulence data
- Previous study (Islam et al. 2004) found virulence groups corresponded directly with RAPD groups

Is virulence associated with other isolate characteristics?

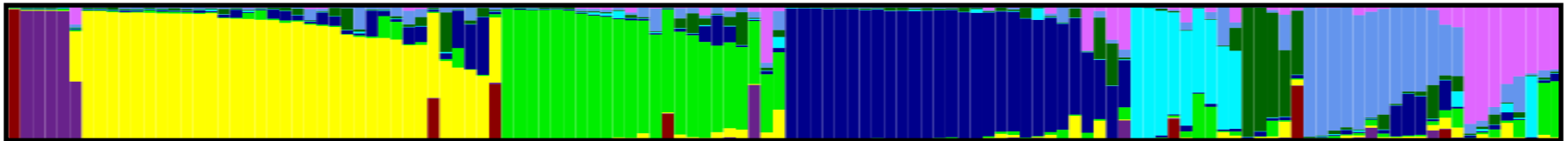
- **Geographic origin**
- **Host family of origin**
- **Genetic cluster membership**

Can we use isolate characteristics to guide isolate selection for host resistance screening?

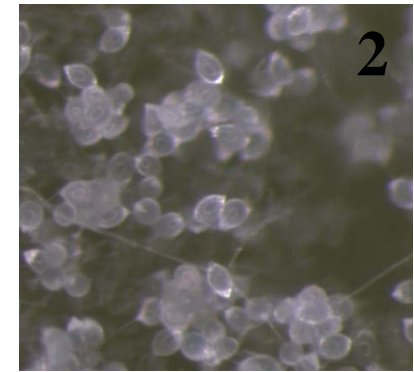
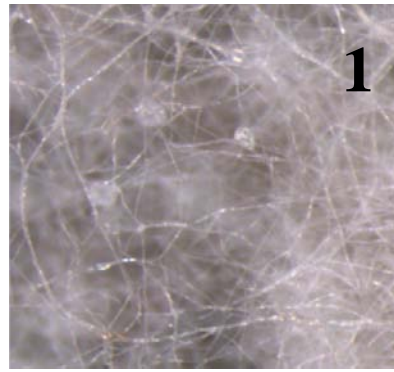
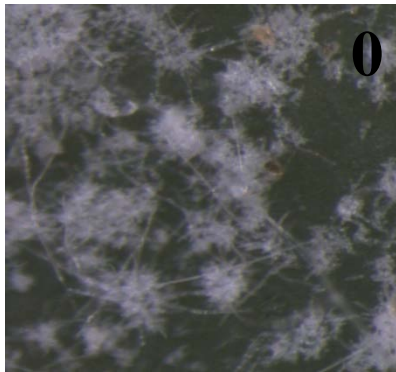


Differences in virulence of *Phytophthora capsici* isolates

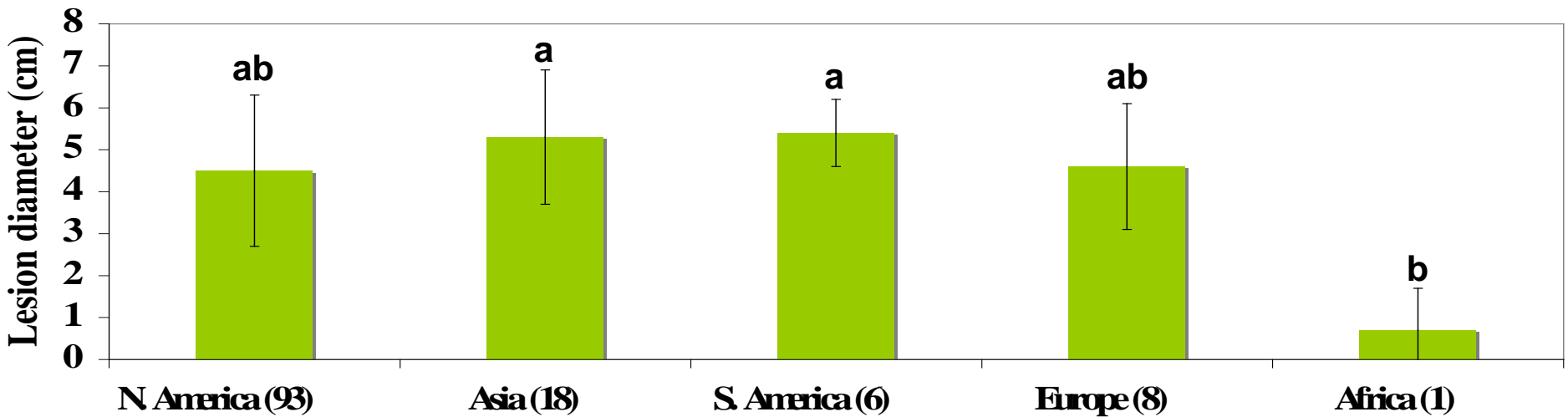
- 126 *P. capsici* isolates
 - 12 countries (Cameroon, Italy, Japan, Korea, Mexico, Norway, Peru, Spain, Taiwan, Thailand, Uruguay, and United States)
 - 6 host families (Cucurbitaceae, Solanaceae, Fabaceae, Piperaceae, Proteaceae, Sterculiaceae)
 - 17 host species



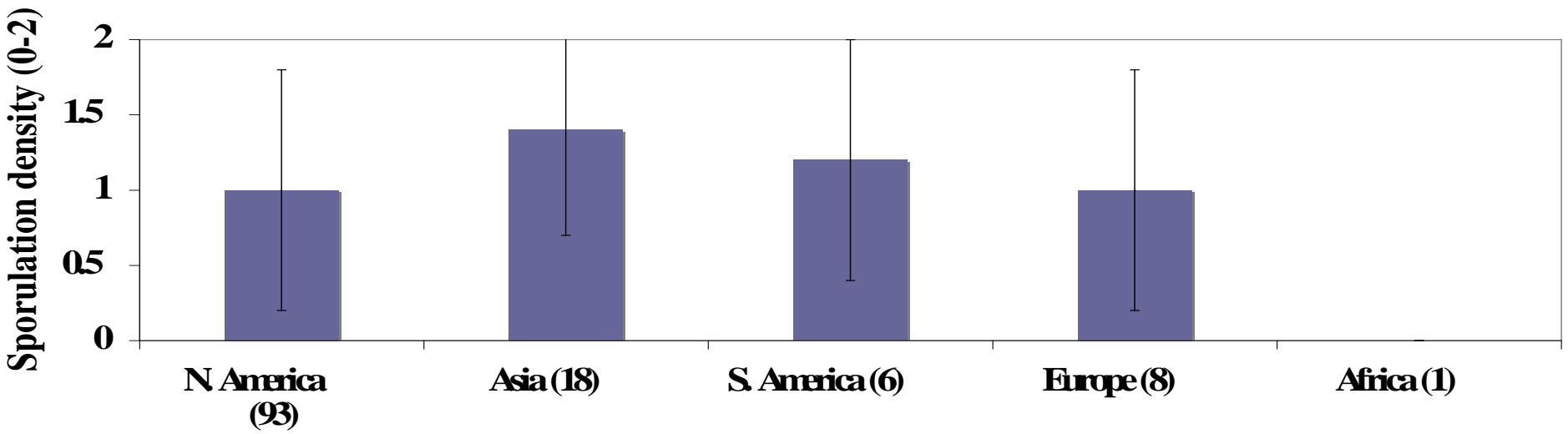
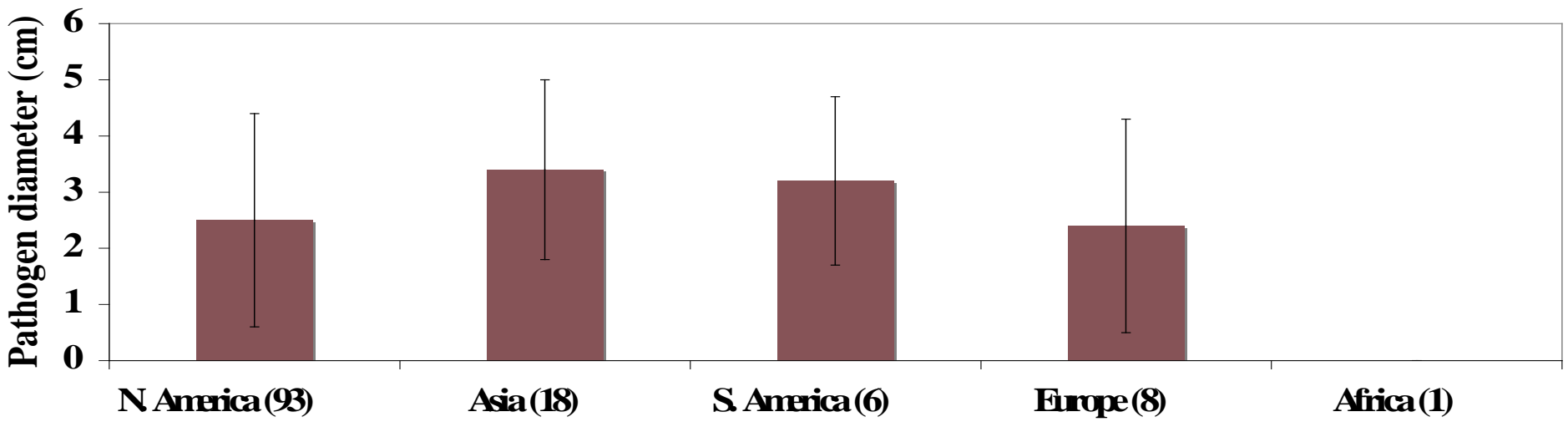
Estimating virulence on fruits



Results: geographic origin

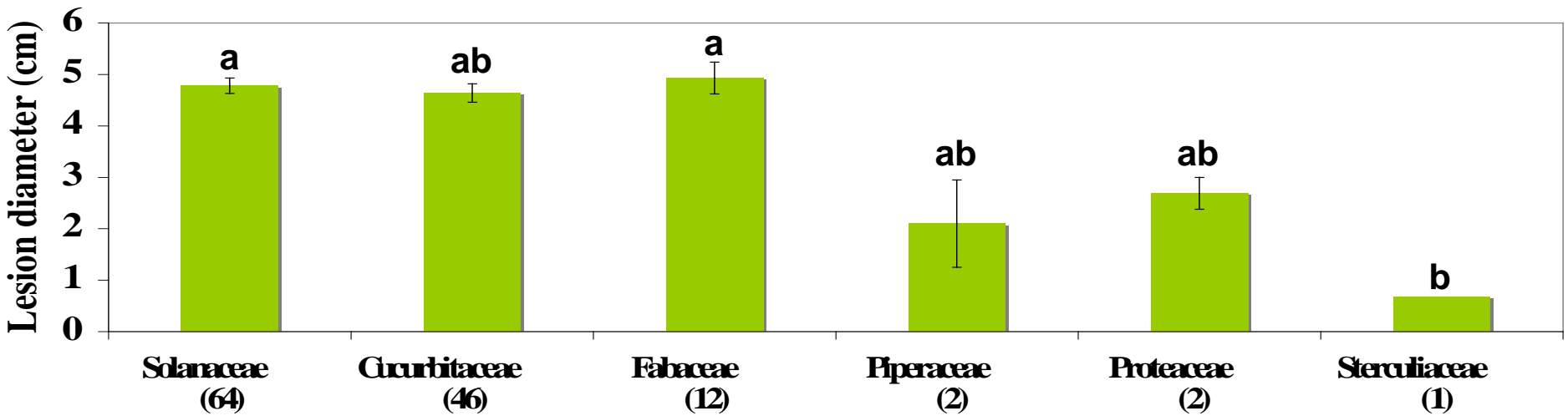


- Differences in isolate virulence by geographic origin was minimal
- The one African isolate (red cluster, cacao) was less virulent than isolates from other continents

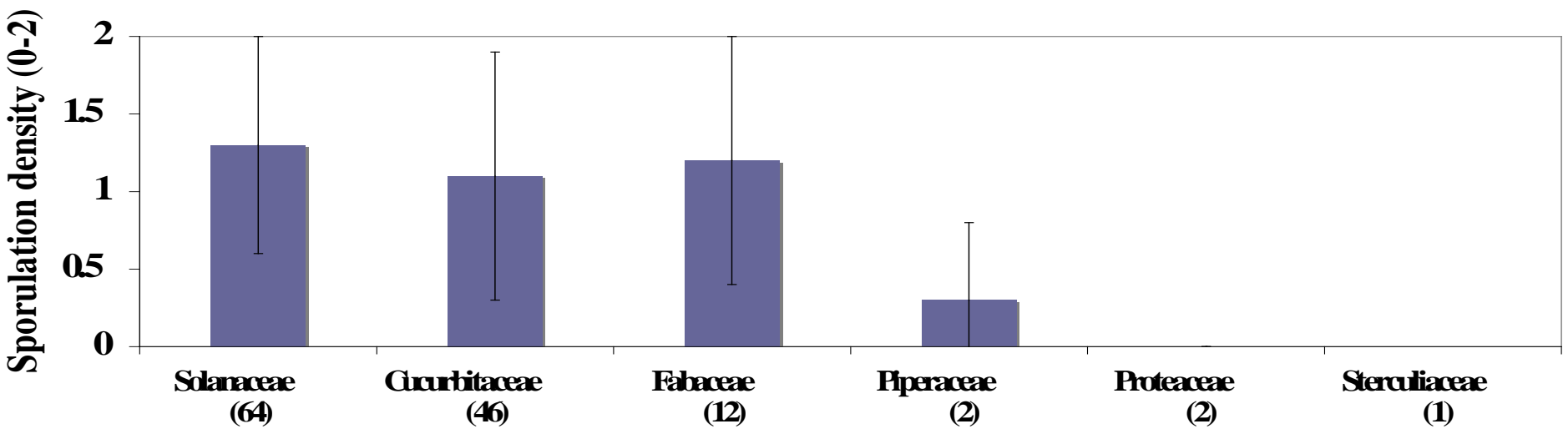
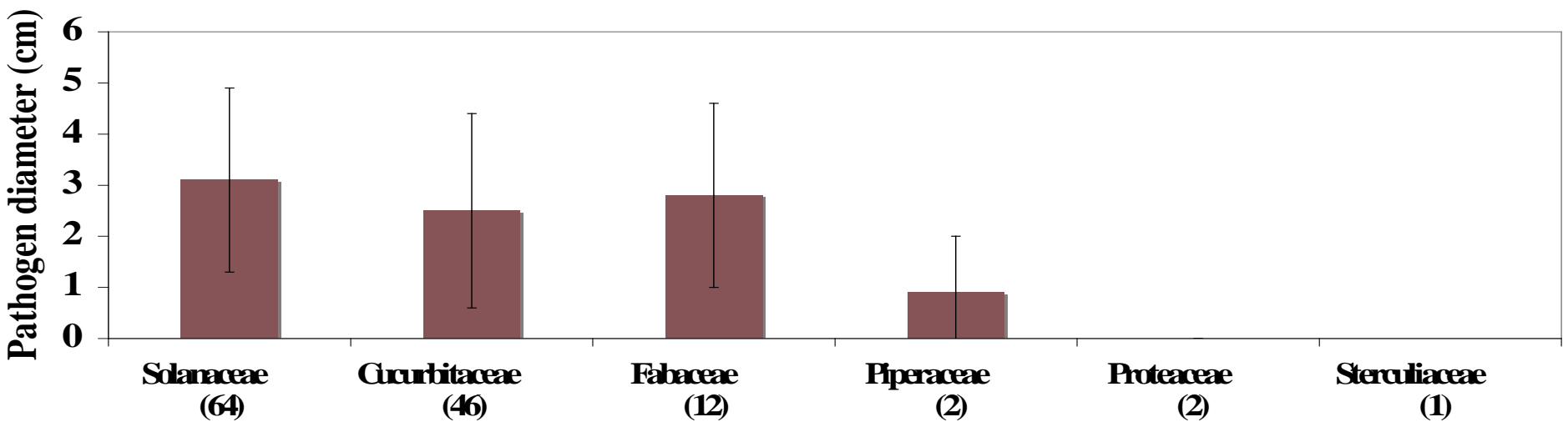


- No significant differences in pathogen growth and sporulation by geography

Results: host family of origin

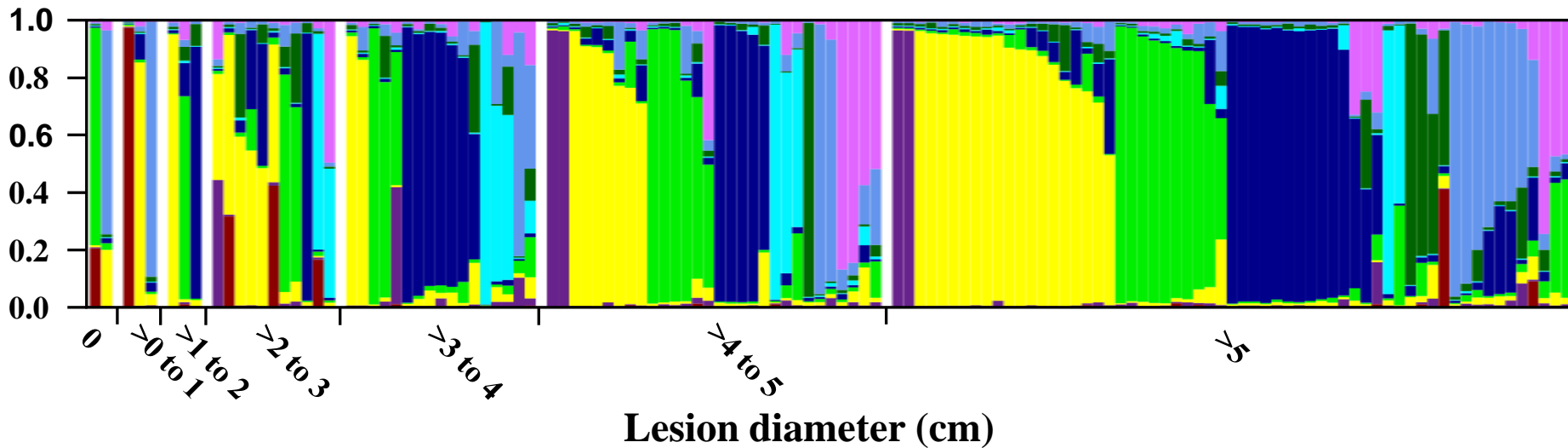


- No significant differences between isolates from vegetable crops
- Isolates from vegetable crops more virulent than isolates from tropical hosts

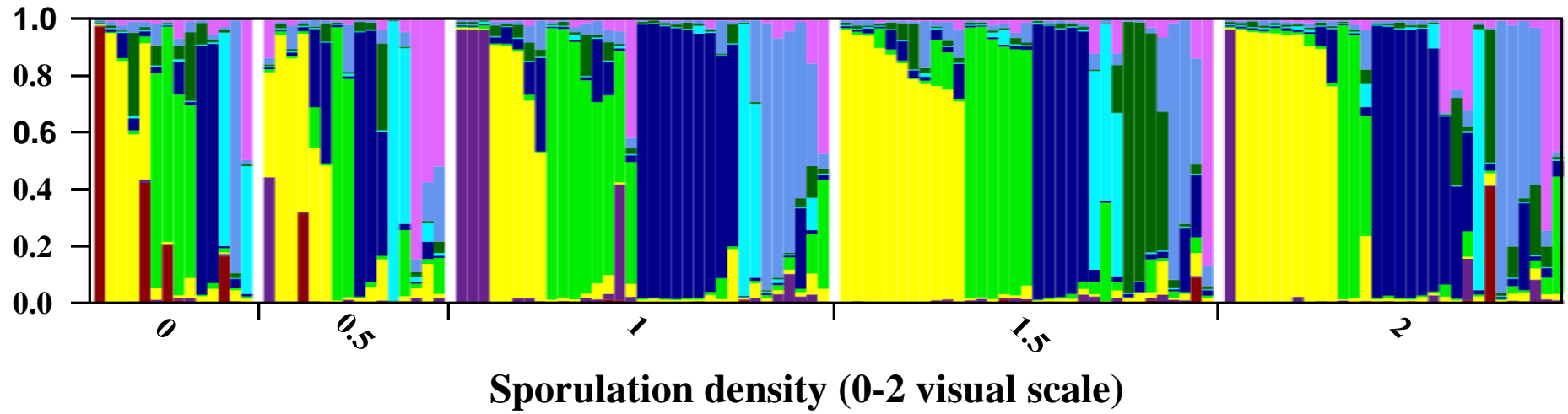
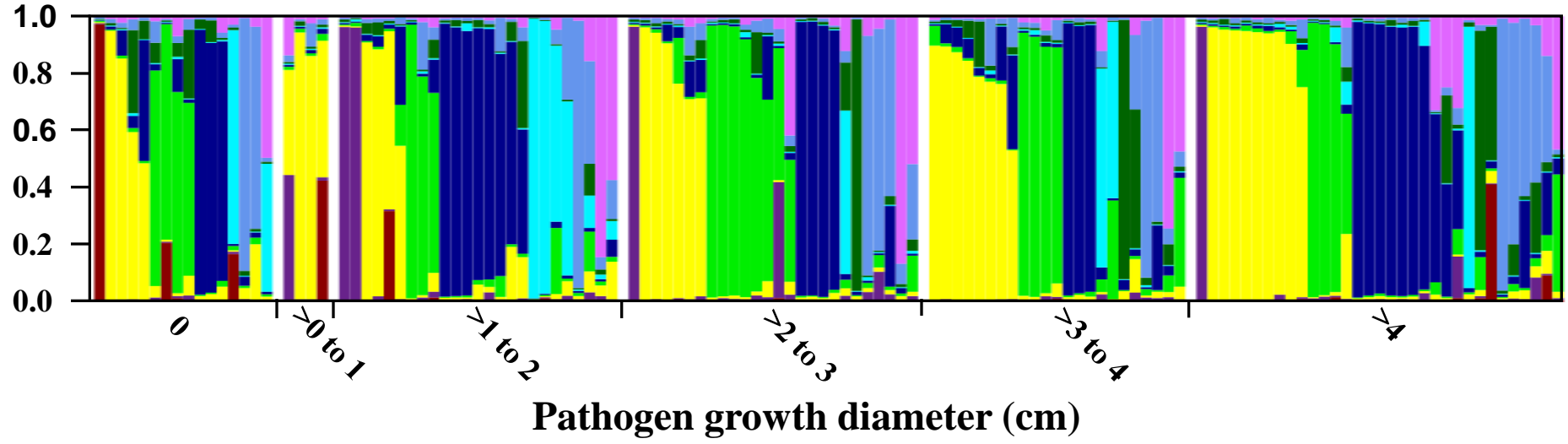


- No significant differences by host family
- Isolates from vegetable crops grew and sporulated better than isolates from tropical hosts

Results: Genetic clusters



- No direct correspondence between virulence and genetic cluster
- Some clusters were more likely to yield virulent isolates
 - Purple, blue, and dark green clusters=large lesions
 - Other clusters showed a range of response
 - Red cluster isolate=small lesions



- No direct correspondence between growth and genetic cluster
- Dark green cluster=good growth and sporulation on fruit
- Red cluster=no growth or sporulation

Summary

- No obvious differences by geography
- Isolates from vegetable crops were generally more virulent than isolates from tropical hosts
 - Bean isolates are highly virulent
- No direct correspondence between clusters and virulence
 - Isolates from purple, blue, and dark green clusters generally were more virulent
- Variation within *P. capsici*
 - Robust host screening should include isolates that represent the variation within *P. capsici*

Acknowledgements

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