

Is the central-marginal hypothesis a general rule?

Evidence from three distributions of an expanding mangrove species, *Avicennia germinans* (L.) L.



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Central-marginal hypothesis (CMH) – range margins =

- ↓ genetic diversity, ↑ genetic differentiation
- ↓ evolutionary potential, inhibited adaptation

CMH **assumes** ecological conditions & abundances decline towards range margins – not true for all species

West and East Florida conform to CMH assumptions, Texas-Louisiana does not

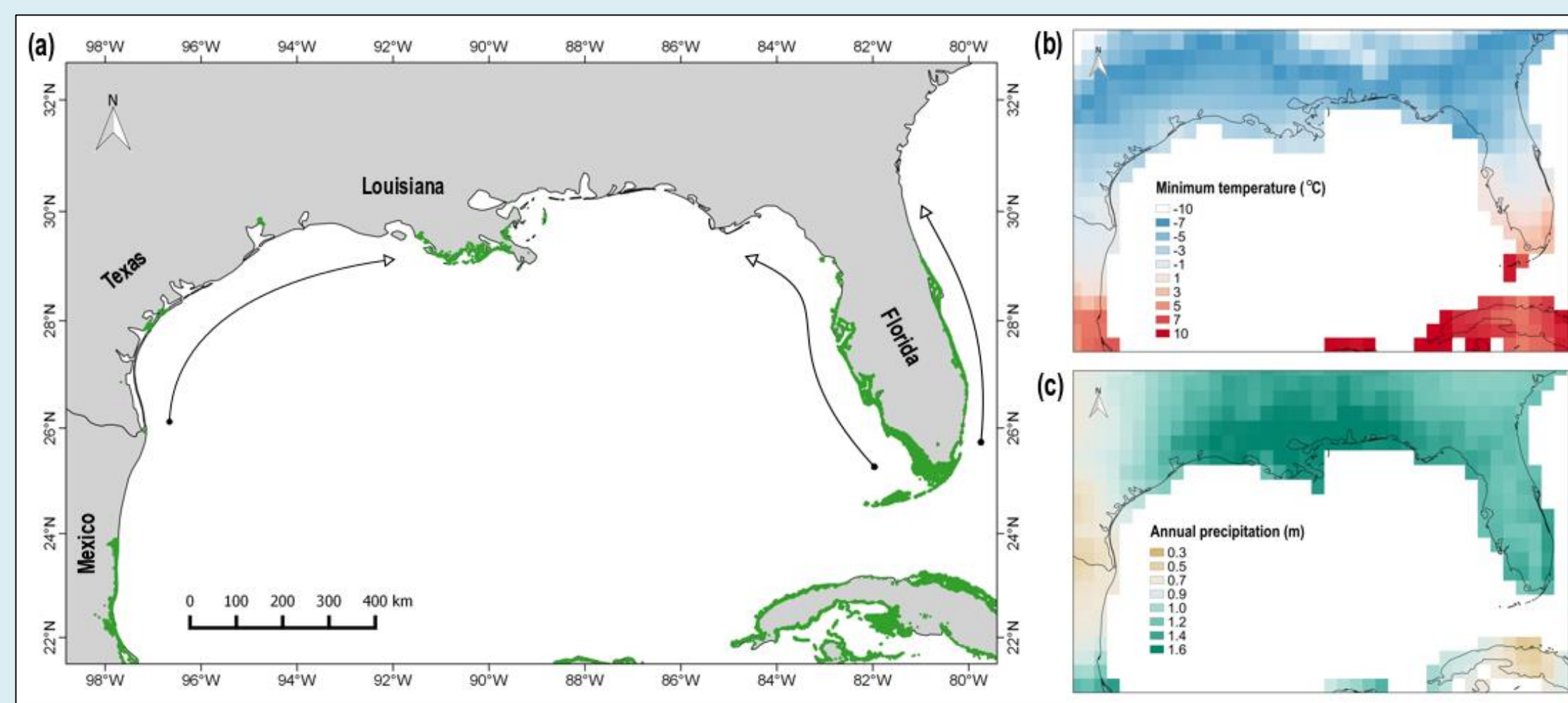


Figure 1. (a) Mangrove distribution in the United States (Giri et al., 2011 Global Ecol Biogeogr). Arrows show three core to margin distribution ranges. (b, c) Climatic factors that control mangrove abundance and range limits: mean annual (b) coldest day and (c) precipitation from 1980-2017 (Cavanaugh et al., 2018 Global Ecol Biogeogr).

USA *A. germinans* genetic diversity and structure

- Sample collection (n = 41 sites; n = 1,083 trees)

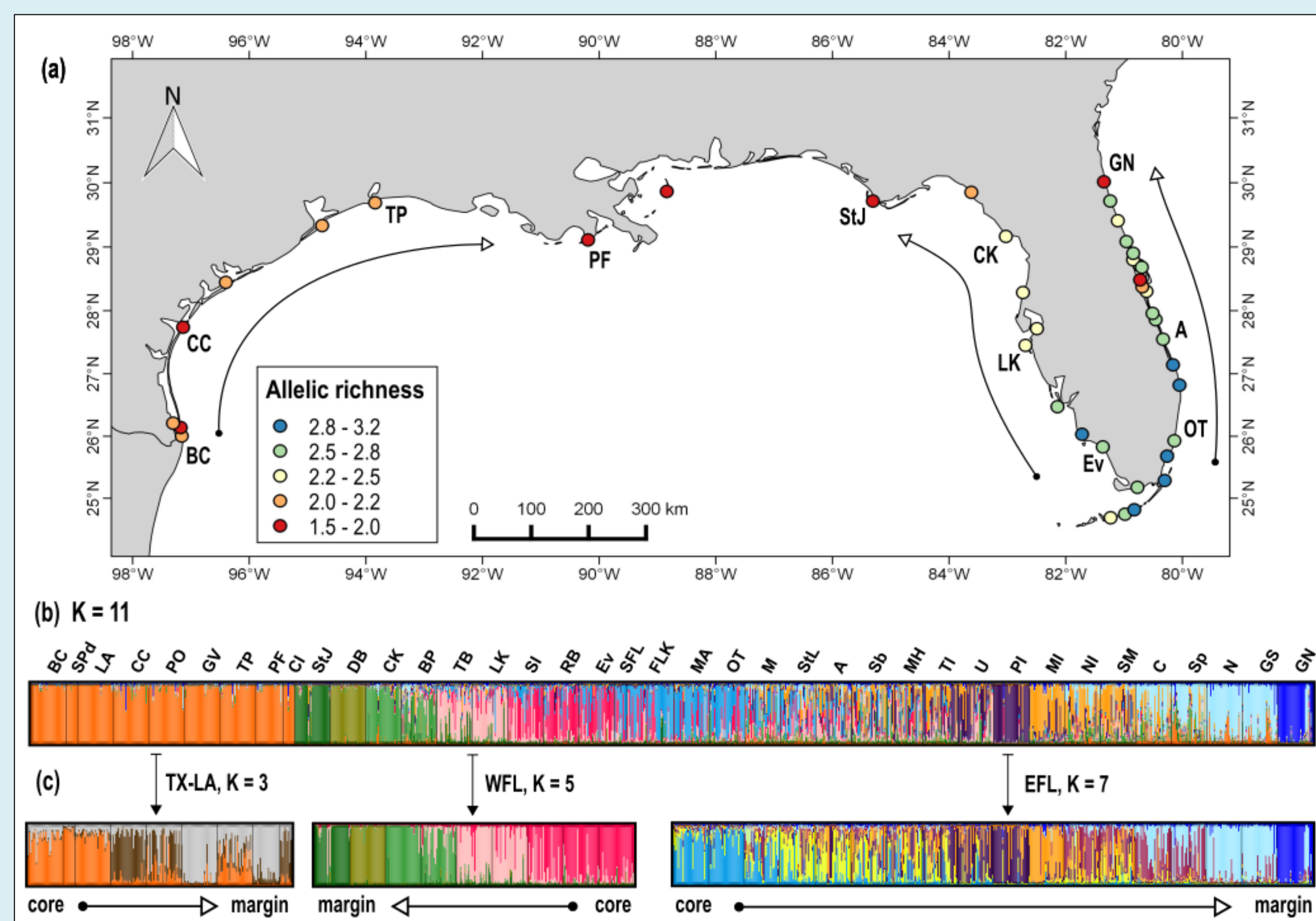


Figure 2. (a) Allelic richness in Texas-Louisiana (TX-LA), West Florida (WFL), and East Florida (EFL) (from left to right). (b) Genetic structure across the USA and (c) for each distribution range separately. K, number of population clusters.

West and East Florida conform to genetic predictions, Texas-Louisiana does not.

- Genotype with 12 nuclear microsatellite loci

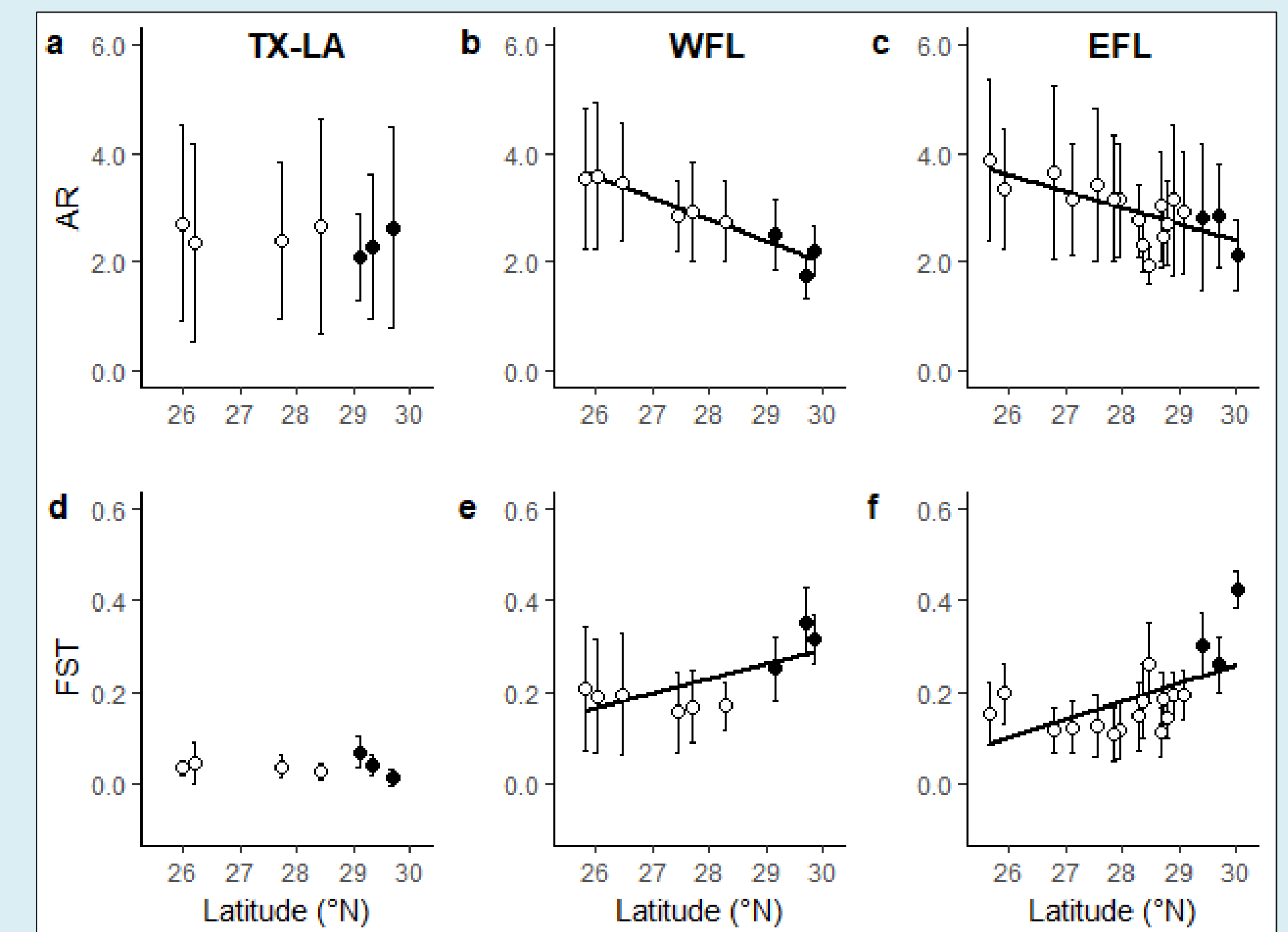


Figure 3. Changes in genetic diversity (allelic richness; AR) and differentiation (fixation index; FST) in (a, d) Texas-Louisiana (TX-LA), (b, e) West Florida (WFL), and (c, f) East Florida (EFL). Solid lines = significant correlations ($p < 0.05$). Range core sites = white; margin sites = black. Error bars = 95% CI.

In contrast to theory – range margin functional traits consistent with greater cold tolerance

- Measure functional traits of leaves – area, length, width, length:width, specific leaf area

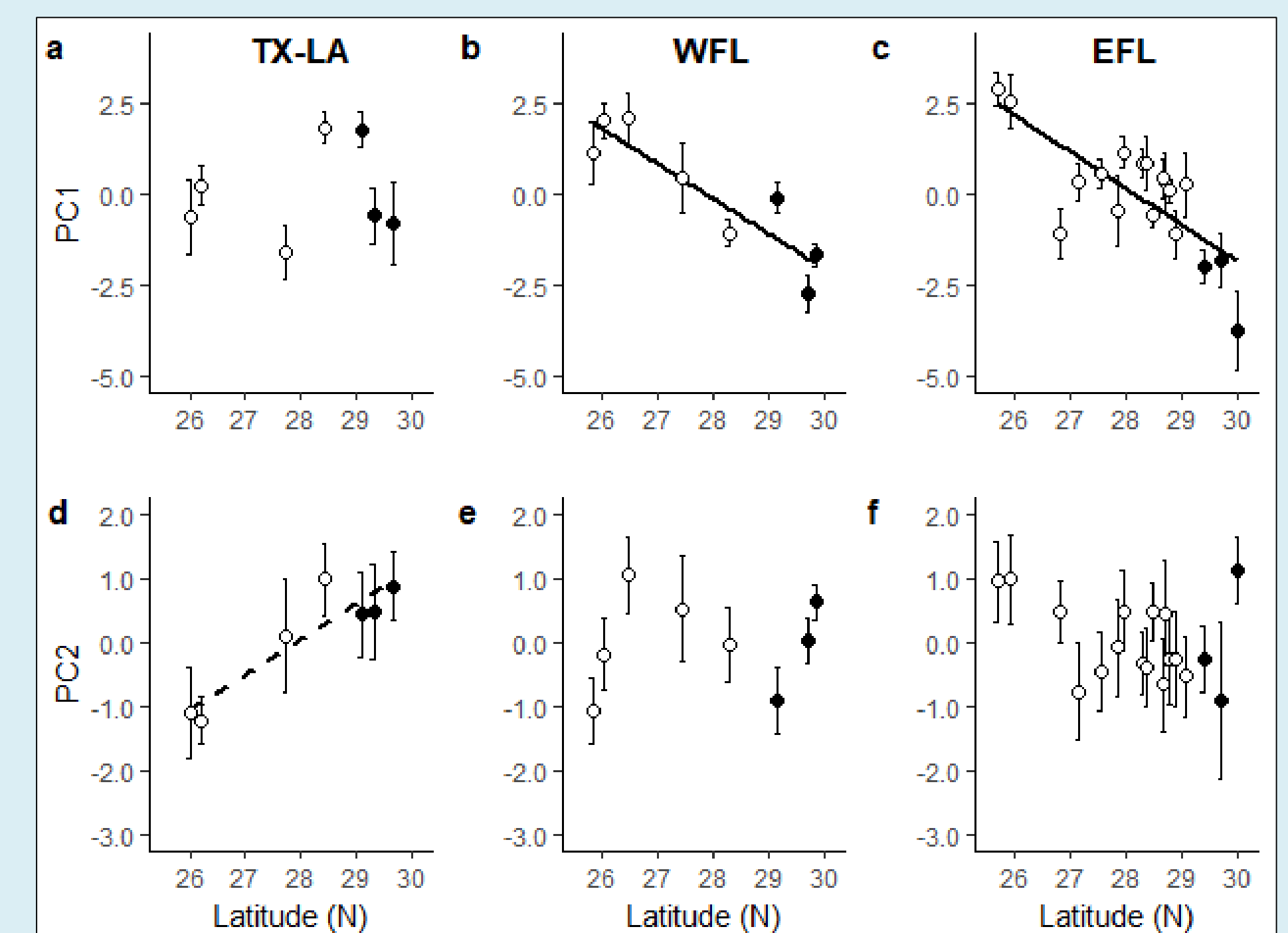


Figure 4. Changes in principal components (PC1: leaf size & specific leaf area; PC2: leaf shape) in (a, d) Texas-Louisiana (TX-LA), (b, e) West Florida (WFL), and (c, f) East Florida (EFL). Solid lines = significant correlations ($p < 0.05$); dashed = marginal non-significance ($p = 0.052$). Range core sites = white; margin sites = black. Error bars = 95% CI.

Conclusions – findings support that CMH is not a general rule
Subsequent research – identify mechanisms shaping patterns

Subsequent research

Hurricane-driven dispersal past the East Florida range margin is almost exclusively from NEARBY sources

- Genotype drift propagules (n = 900)
- Assign to potential sources from across Florida

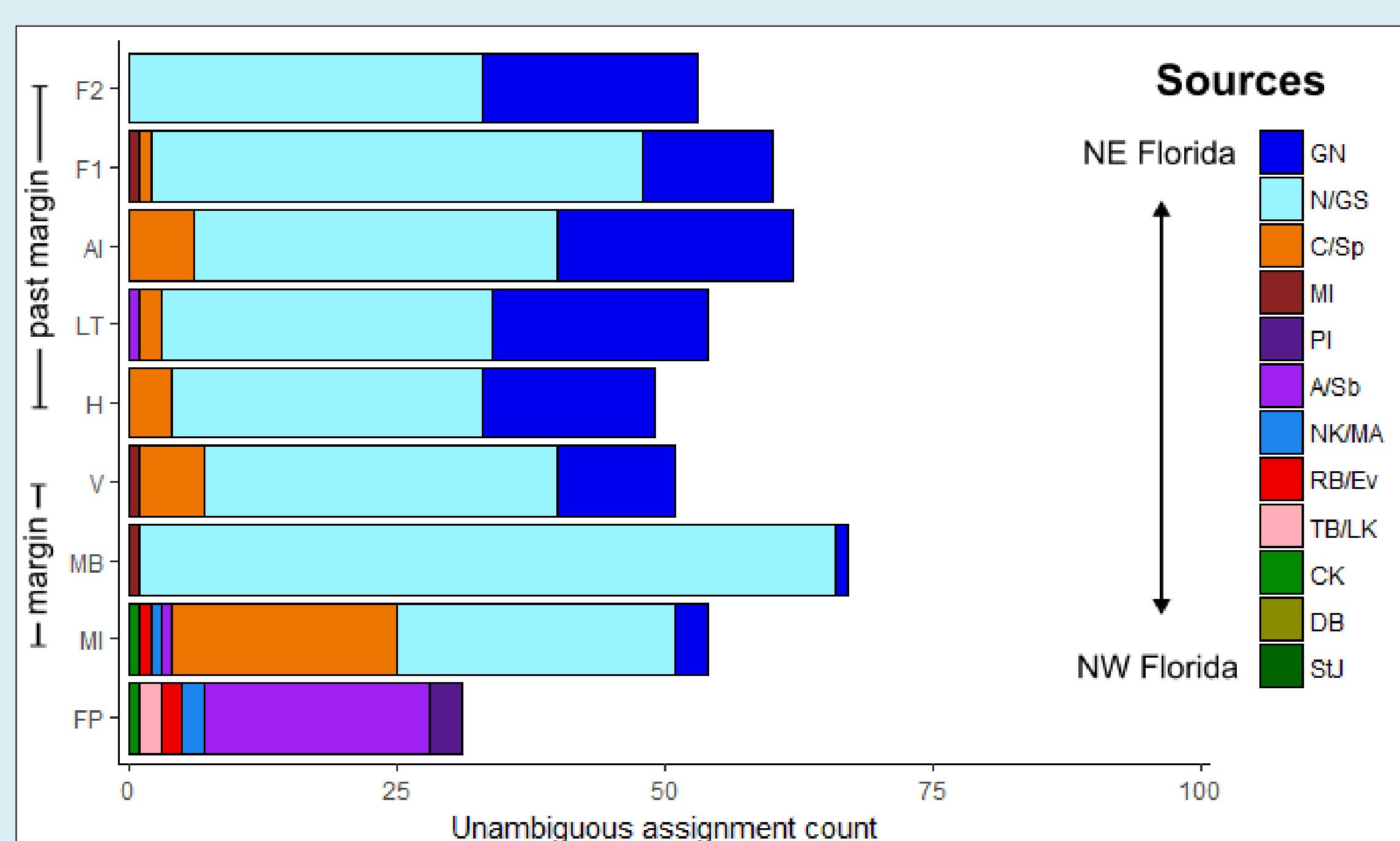


Figure 5. Genetic assignment of propagules collected after Hurricane Irma (Oct, 2017). Sites include beaches at the range margin (MI, MB, V) and past (H, LT, AI, F1, F2), and a range core control site (FP). Potential sources (n = 12) are a subset of Florida collection sites (see Figure 2b).

Reduced outcrossing in East Florida compared to conspecifics in Mexico and congeners in Brazil

- Genotype progeny arrays (n = 1,612)
- Calculate outcrossing rates at 6 East Florida sites

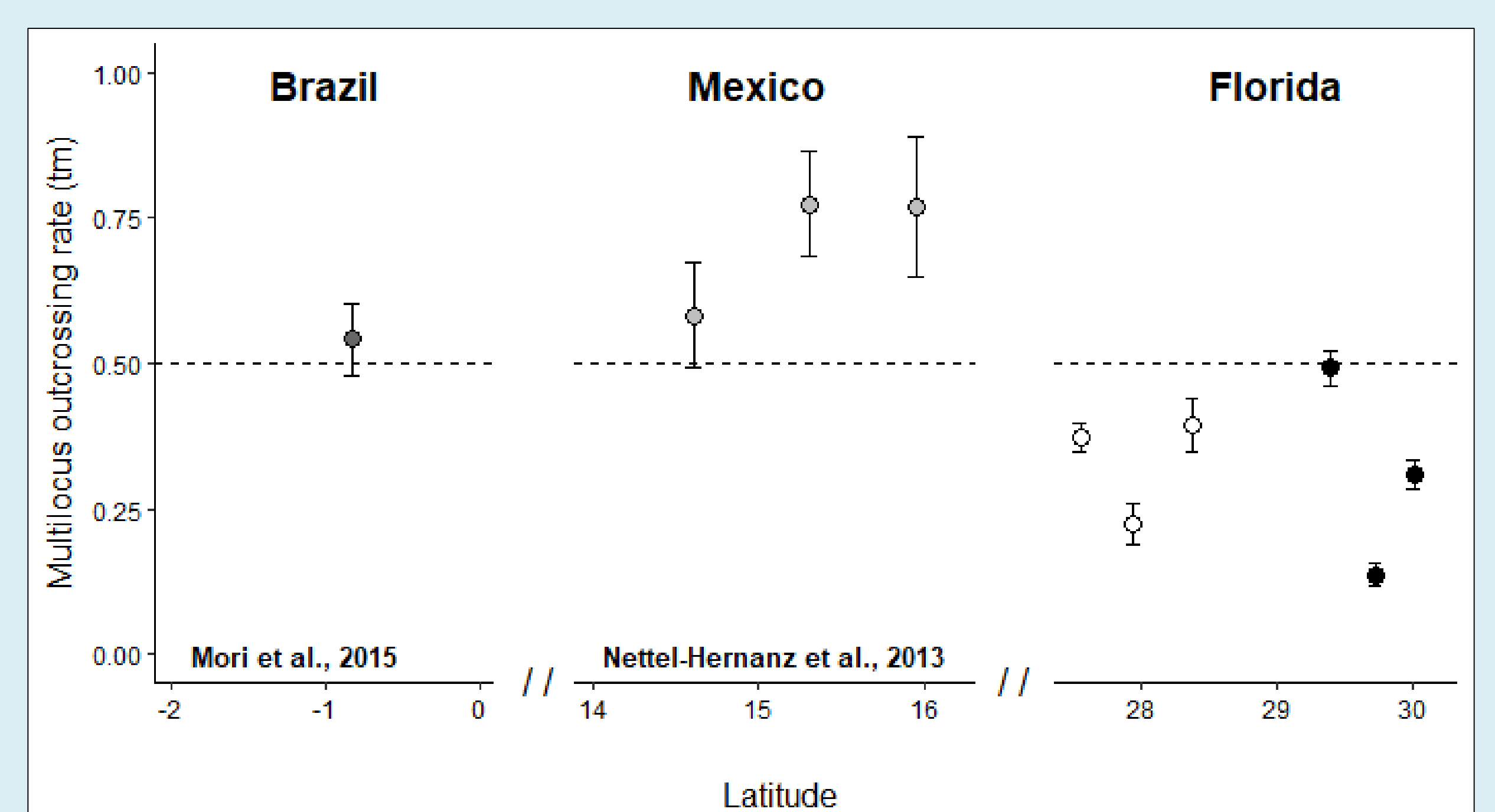


Figure 6. Outcrossing rates for *A. schaueriana* in Brazil (0.8 °S; Mori et al., 2015 PLoS ONE); and for *A. germinans* in Mexico (14-16 °N; Nettel-Hernanz et al., 2013 Botanical Sciences) and East Florida (27-30 °N). Error bars = standard deviation.