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Predator-prey interactions and venom composition in a high elevation lizard specialist, Crotalus pricei(Twin-spotted Rattlesnake)

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ABSTRACT

The Twin-spotted Rattlesnake (Crotalus price) is a small lizard specialist restricted to higher montane habitat in the Sky Islands of Arizona and México. Though this species is restricted to high elevations and dispersal between mountaintops is impossible, few studies have investigated venom composition or the predator-prey relationship between C. p. priceiand its primary prey source, Yarrow's Spiny Lizard (Sceloporus jarrovi). Because of current isolation of popu

clarkia, S. jarrovii, S. magister and S. slevini) having a distribution overlap with C. p. pricei in Arizona (Jones and Lovich, 2009). Sceloporus jarrovii often occurs at high population densities and is most common at

primarily in the presence of unique PLA_2 toxins in Mexican snakes (Figs. 3 and 5). The biological activities and functional signi cance of these PLA_2 toxins have yet to be determined, but these di erences may be related to phylogeographic distribution patterns of *C. pricei*. Sky Island habitats allow for little, if any, current gene exchange between mountain ranges (Favé et al., 2015; Lomolino et al., 1989; Thompson and Anderson, 2000), and based on predicted historical distribution patterns, fragmentation of *C. pricei* populations likely occurred after the LGM, when pine-oak corridors connecting the Mexican Plateau were present (Metcalfe et al., 2000). During this time, it is estimated that dominant vegetation communities were approximately 1000 m lower than present day, associated with the cooler, wetter montane climate and more aligned with apparent physiological needs of *C. p. pricei* and other high elevation herpetofauna (Bryson et al., 2011a; McDonald, 1993; Prival and Schro , 2012; Thompson and Anderson, 2000). Bryson et al. (2011a) found that *C. p. pricei* from Durango and *C. p. miquihuanus* from the northern Sierra Madre Occidental (Nuevo Léon) were genetically more similar, based on a mixed-model Bayesian approach. This apparent genetic similarity, inconsistent with current taxonomy, could account for the venom similarities between *C. p. pricei* from Durango and *C. p. miquihuanus* and di erences between these groups and *C. p. pricei* from Arizona. Additional samples from the Pinaleño, Santa Rita, and Huachuca Mountain ranges are needed to provide substantial support for levels of toxin variation and di erentiation within Arizona populations of *C. p. pricei*, though no consistent di erences were apparent from the samples analyzed in the present study. Furthermore, many of the venom samples collected from snakes originating in the Chiricahua Mountains were located in only two distinct areas, and sampling multiple areas within each mountain range could reveal local variation in venom composition. However, multiple sampling visits to other Arizona Sky Island habitats for *C. p. pricei* in two distinct seasons in 2018 yielded no specimens, so the vicariant nature of

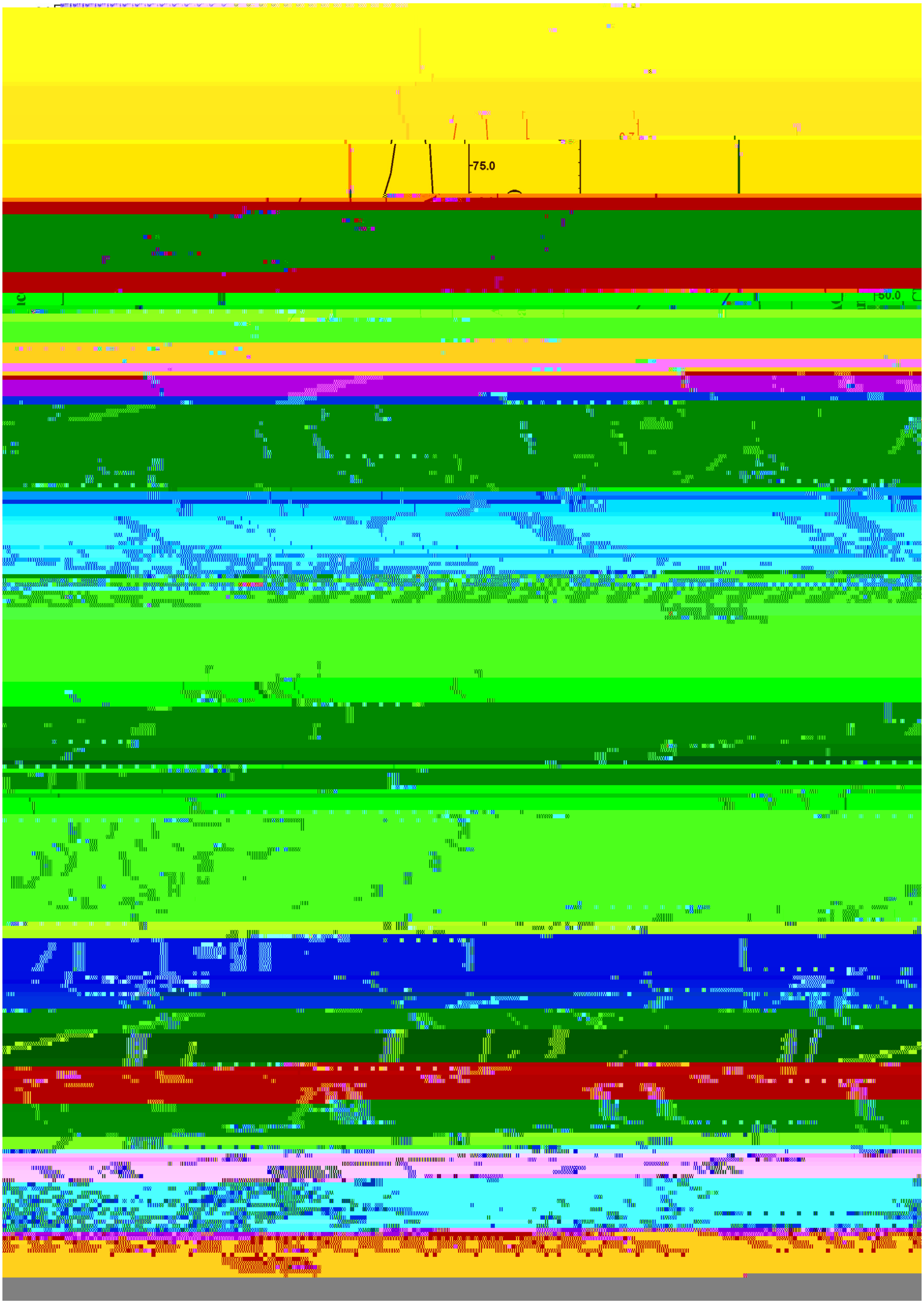


Fig. 4. Reverse-phase HPLC chromatogram overlays and peak elution times of 2.0 mg crude *C. pricei* venom samples. A. Samples from ve individuals from the Chiricahua Mountains; note similarities in elution pro les. B. Samples from the Pinaleño Mountains (green), Chiricahua Mountains (black), and Santa Rita Mountains (blue). Elution gradient is indicated by the black line, with concentrations displayed on the right side of the chromatograms. (For interpretation of the references to

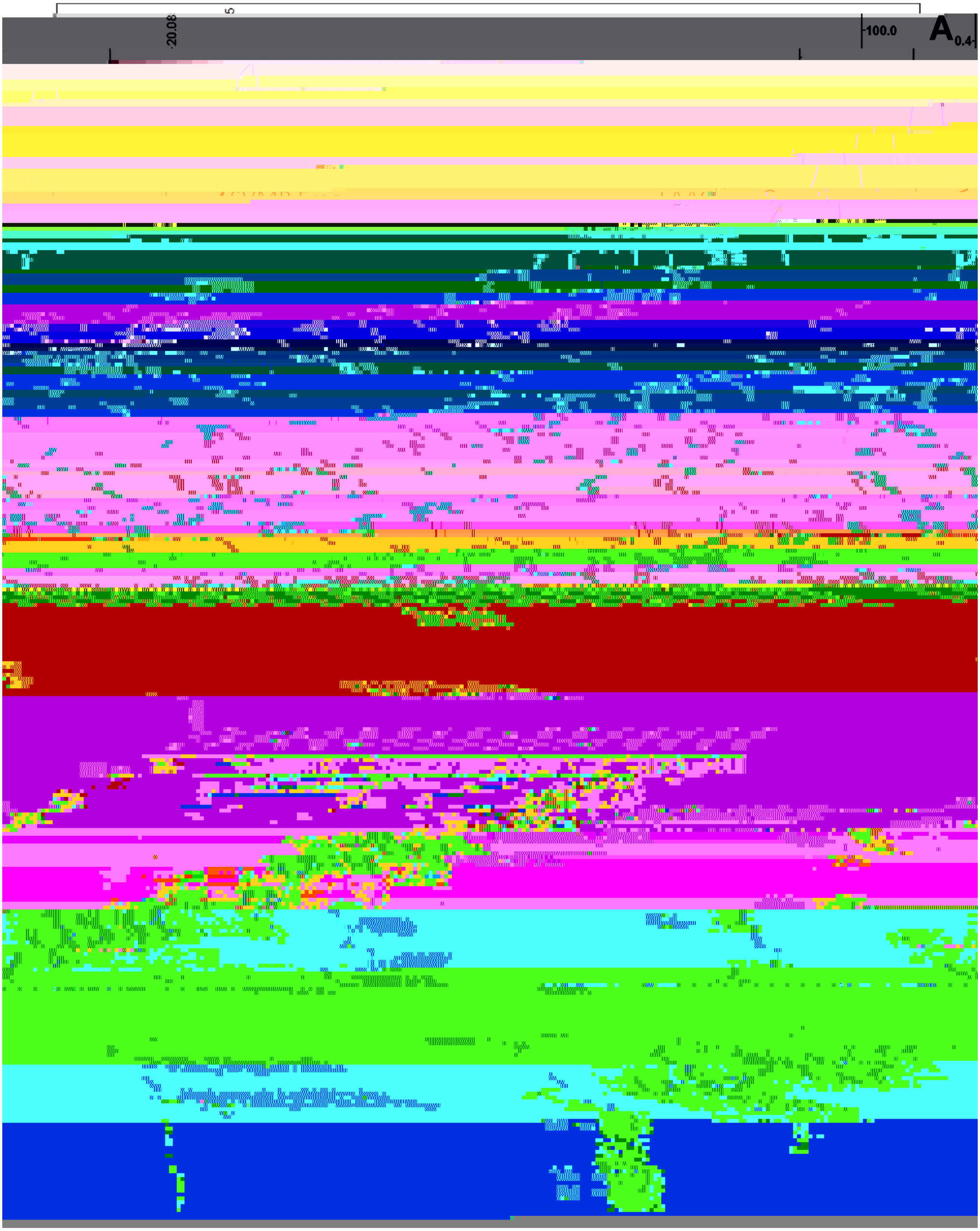
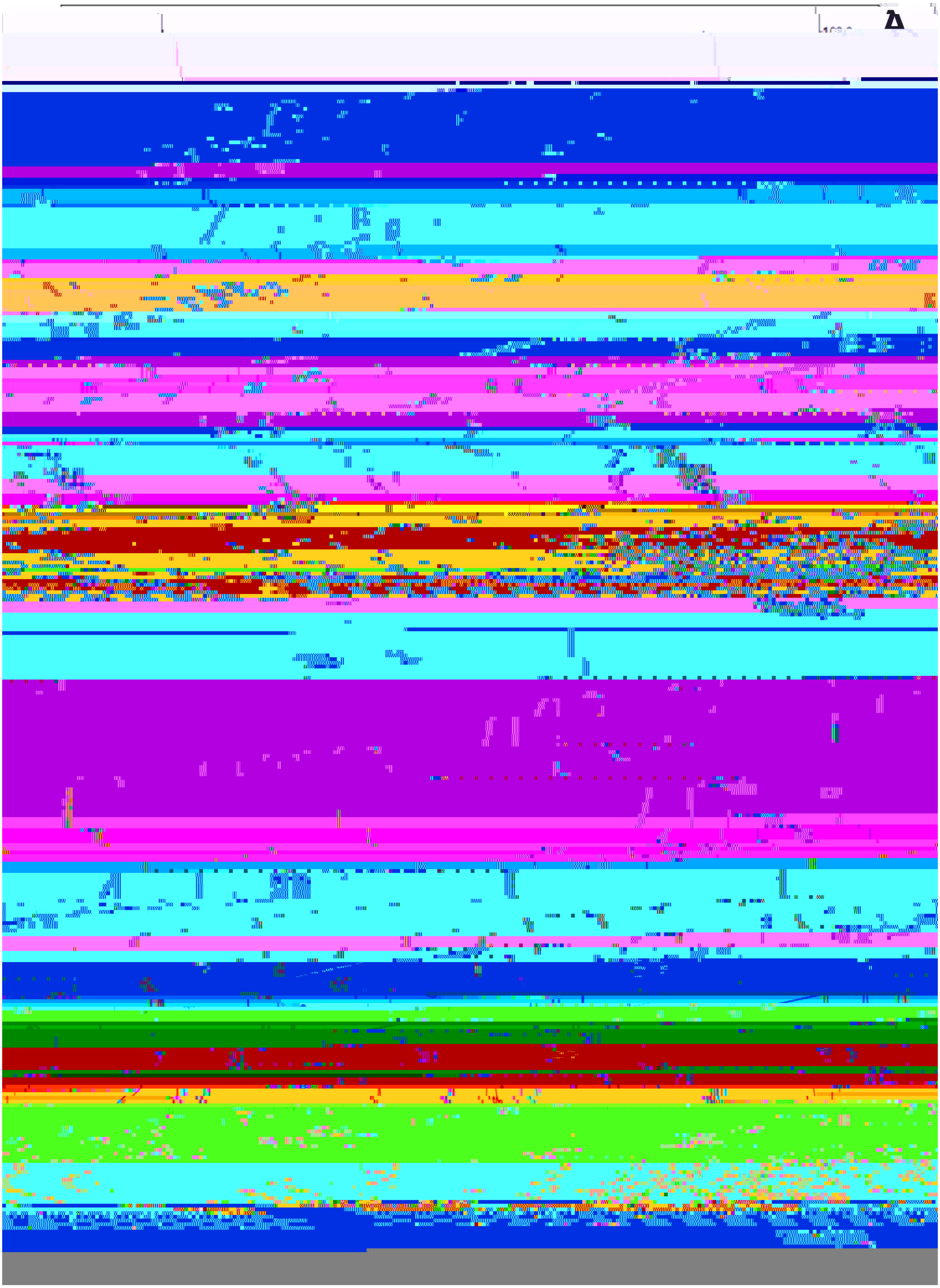


Fig. 5. A. Reverse-phase HPLC chromatogram and peak elution times of 2.0 mg crude C. p. pricei venom from Durango, México (#2) and B. SDS-PAGE of each fraction peak. Elution gradient is displayed to the right of chromatogram. Typical protein families are displayed to the right of the gel and numbers displayed at the top represent peak fractions.



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; Holycross and Mackessy, 2002), a species with a similar diet and body size to that of C. p. pricei.

4.1. Conclusions

Overall, there are well-de