

Population genomics and phylogeography of the boll weevil, *Anthonomus grandis* Boheman (Coleoptera: Curculionidae), in the United States, northern Mexico, and Argentina

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Abstract

Despite the success of the United States (US) Boll Weevil Eradication Program, the boll weevil, *Anthonomus grandis* Boheman (Coleoptera: Curculionidae), remains a threat to cotton production in the southern US and is arguably the most important cotton pest in Central and South America. Management of this species is complicated by the existence of morphologically similar variants and re-infestations of areas where eradication had been successful. To date, no study has applied a high-throughput sequencing approach to better understand the population genetic structure of the boll weevil. Furthermore, only a single study has investigated genetic relationships between populations in North and South America. Here, we used double digest restriction site-associated DNA sequencing (ddRADseq) to resolve the population genomic structure of the boll weevil in the southern US, northern Mexico, and Argentina, test the two-form and three-form hypotheses of boll weevil variation in North America using a phylogeographic approach, and determine the relationship of the South American populations to the North. Our results supported the two-form hypothesis of boll weevil variation in North America wherein there are two major genetic lineages – one consisting of populations found geographically west of the Sierra Madre Occidental mountain range and the second consisting of populations found to the east – both are highly sub-structured across space and time. Boll weevil populations from Argentina were more closely related to the eastern lineage, suggesting a range expansion by the eastern lineage, but additional sampling across Central and South America is needed to determine a probable origin.

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