
Contagious asexuality in the pea aphid and its evolutionary consequences

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Abstract

Asexual lineages occur in most groups of organisms and arise from loss of sex in sexual species. Yet, the genomic basis of these transitions in reproductive modes remains largely unknown. We addressed this issue in the pea aphid where both sexual and obligate asexual lineages coexist in natural populations. These lineages may occasionally interbreed because some asexual lineages maintain a residual production of males potentially able to mate with the females produced by sexual lineages. We combined quantitative genetic and population genomic approaches to unravel the genetic control of shifts towards permanent asexuality in the pea aphid. We found that permanent asexuality was determined as a recessive character by a single locus and identified a 2.5 Mb genomic region responsible for this transition located on the X chromosome. Also, our population genetic data indicated substantial gene exchange between these reproductively distinct lineages, potentially leading to the conversion of some sexual lineages into asexual ones in a contagious manner. We are currently narrowing down the size of the control region and investigating patterns of coding and non-coding polymorphisms within and outside the causal locus in sexual and asexual lineages. This genetic system provides insight into the mechanisms of coexistence of sexual and asexual aphid lineages and on the genomic footprints of reproductive mode variation.

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