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Genetic mapping of *aphicarus* – a sex-linked locus controlling a wing polymorphism in the pea aphid (*Acyrthosiphon pisum*)

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We have initiated research to determine the genetic basis of a male wing polymorphism in the pea aphid *Acyrthosiphon pisum* (Hemiptera: Aphididae). Previous studies showed that this polymorphism is controlled by a single biallelic locus, which we name *aphicarus* (*api*), on the X chromosome. Our objectives were to confirm that *api* segregates as a polymorphism of a single gene on the X chromosome, and to obtain molecular markers flanking *api* that can be used as a starting point for high-resolution genetic and physical mapping of the target region, which will ultimately allow the cloning of *api*. We have established an F_2 population segregating for *api* and have generated X-linked AFLP markers. The segregation pattern of *api* in the F_2 population shows that the male wing polymorphism segregates as a polymorphism of a single gene, or set of closely linked genes on the X chromosome. Using a subset of 78 F_2 males, we have constructed a linkage map of the chromosomal region encompassing *api* using seven AFLP markers. The map spans 74.1 cM and we have mapped *api* to an interval of 10 cM. In addition, we confirmed X linkage of our AFLP markers and *api* by using one X-linked marker developed in an earlier study. Our study presents the first mapping of a gene with known function in aphids, and the results indicate that target gene mapping in aphids is feasible.
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