

Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

The complete mitochondrial genome of the flea beetle *Agasicles hygrophila*

Na Li, Jia-Ning Wei, Dong Jia, Shuang Li & Rui-Yan Ma

To cite this article: Na Li, Jia-Ning Wei, Dong Jia, Shuang Li & Rui-Yan Ma (2015): The complete mitochondrial genome of the flea beetle *Agasicles hygrophila*, Mitochondrial DNA

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1079848>



Published online: 14 Sep 2015.



Submit your article to this journal [↗](#)



View related articles [↗](#)



View Crossmark data [↗](#)

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the flea beetle *Agasicles hygrophila*

Na Li¹, Jia-Ning Wei², Dong Jia¹, Shuang Li¹, and Rui-Yan Ma¹¹Department of Biosafety, College of Agriculture, Shanxi Agricultural University, Taigu, Shanxi, China and ²State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, Beijing, China**Abstract**

To provide molecular markers for population genetic analysis of the flea beetle *Agasicles hygrophila*, we determined its mitochondrial genome (mitogenome) for the first time. The mitogenome of *A. hygrophila* was 15 917 bp in length with an AT content of 75.15%. It had the typical set of 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and an AT-rich control region. Compared with the ancestral mitogenome of insects, no gene rearrangement occurred in *A. hygrophila*. Incomplete stop codons were present in PCGs of *A. hygrophila*. All tRNA genes except for *trnS(AGN)* could form the typical clover-leaf secondary structures. The phylogenetic analysis indicated that *A. hygrophila* was close to other species belonging to the same family of Chrysomelidae.

Keywords

Agasicles hygrophila, flea beetle,
mitochondrial genome

History

Received 21 May 2015

Revised 24 July 2015

Accepted 29 July 2015

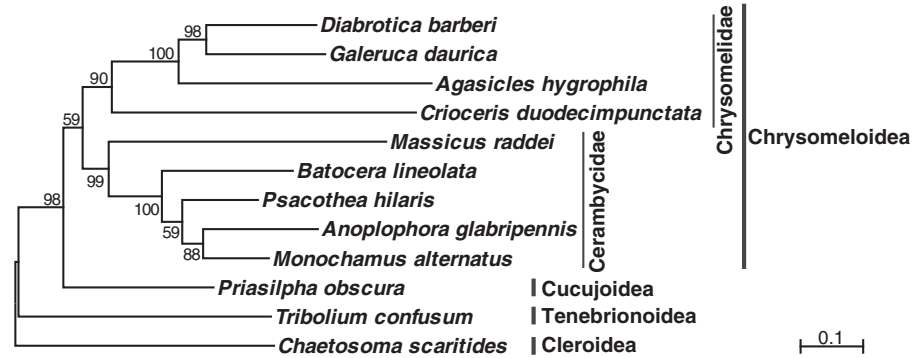
Published online 11 September 2015

Alligator weed (*Alternanthera philoxeroides*) is an amphibious perennial plant native to South America (Holm et al., 1977). It has spread in Asia, Europe, and Australia and has been regarded as one of the serious invasive weeds in ecosystems worldwide (Julien et al., 1995). As a successful biological control agent of alligator weed, the flea beetle *Agasicles hygrophila* (Coleoptera: Chrysomelidae) has been introduced into many countries. In the success of biological control introductions, genetic diversity within populations of biological control agents may play an important role (Roderick & Navajas, 2003). However, the number of molecular markers for determining the genetic diversity of *A. hygrophila* is still limited (Ma et al., 2013). To address this question, we sequenced the complete mitogenome of *A. hygrophila* in this study.

The full-length mitogenome of *A. hygrophila* was 15 917 bp in size (GenBank accession no. KR494279). This mitogenome was comprised of 13 PCGs, 22 tRNA genes, two rRNA genes,

and an AT-rich control region. These genes were arranged in the same order as the inferred ancestral mitogenome of insects (Cameron, 2014). Consistent with other insects, *A. hygrophila* had an AT-biased nucleotide composition (75.15%). Nine overlaps, totaling 36 bp, between adjacent genes were detected. A total of six non-coding regions involving 1365 bp were present in *A. hygrophila* mitogenome. The largest non-coding region was the control region possessing a size of 1335 bp and an AT content of 83.07%. Tandem repeats with a repeat unit of larger than 50 bp were not detected in the control region. The second largest non-coding region (17 bp), located between *trnS(UCN)* and *nad1*, contained a 7-bp conserved motif across insects (Cameron & Whiting, 2008), serving as a binding site of mitochondrial transcription termination factor. All PCGs started with typical ATN codons, and nine out of the 13 PCGs terminated with incomplete stop codons (TA or T). The third codon positions (80.04%) exhibited a higher AT content compared with the first (68.93%) and second (68.38%) codon positions. All the 22 tRNA genes, ranging in size from 60 bp (*trnC*) to 70 bp (*trnK*), had an overall AT content of 78.20%. These tRNA genes could be folded into typical clover-leaf secondary structures with the exception of *trnS(AGN)*, of which the dihydrouridine stem was replaced by a 12-bp loop. The large and small rRNA subunits (*rrnL* and *rrnS*) were located at *trnL(CUN)* to *trnV* and *trnV* to the control region, respectively. The *rrnL* gene was 1273 bp long with an AT content of 83.19%; the corresponding values were 803 bp and 80.45% for *rrnS*. The phylogenetic tree indicated the close relationship of *A. hygrophila* and three other species belonging to the same family of Chrysomelidae (Figure 1).

Figure 1. The maximum likelihood tree inferred from concatenated amino acid sequences of the 13 PCGs. The numbers at nodes refer to bootstrap support values in percent (1000 replicates). *Diabrotica barberi*, NC_022935; *Galeruca daurica*, NC_027114; *Agasicles hygrophila*, KR494279; *Crioceris duodecimpunctata*, NC_003372; *Massicus raddei*, NC_023937; *Batocera lineolata*, NC_022671; *Psacotha hilaris*, NC_013070; *Anoplophora glabripennis*, NC_008221; *Monochamus alternatus*, NC_024652; *Priasilpha obscura*, NC_011326; *Tribolium confusum*, NC_026702; *Chaetosoma scaritides*, NC_011324.



Declaration of interest

This research was supported by grants NSFC (No. 31070480), Ph.D. supervisor's Fund of Ministry of Education of China (No. 20111403110004), the state key laboratory of integrated management of pest insects and rodents research (No. Chinese IPM1206) and Graduate student excellent innovation project in Shanxi Province (No. 20143011). The authors declare no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

References

- Cameron SL. (2014). Insect mitochondrial genomics: Implications for evolution and phylogeny. *Annu Rev Entomol* 59:95–117.
- Cameron SL, Whiting MF. (2008). The complete mitochondrial genome of the tobacco hornworm, *Manduca sexta*, (Insecta: Lepidoptera: Sphingidae), and an examination of mitochondrial gene variability within butterflies and moths. *Gene* 408:112–23.
- Holm LG, Plucknett DL, Pancho JV, Herberger JP. (1977). The world's worst weeds: Distribution and biology. Hawaii, USA: University Press of Hawaii.
- Julien MH, Skarratt B, Maywald GF. (1995). Potential geographical distribution of alligator weed and its biological control by *Agasicles hygrophila*. *J Aquat Plant Manage* 33:55–60.
- Ma RY, Jia XY, Liu WZ, Laushman RH, Zhao LL, Jia D, Wang R. (2013). Sequential loss of genetic variation in flea beetle *Agasicles hygrophila* (Coleoptera: Chrysomelidae) following introduction into China. *Insect Sci* 20:655–61.
- Roderick GK, Navajas M. (2003). Genes in new environments: Genetics and evolution in biological control. *Nat Rev Genet* 4: 889–99.