



parasitoids are found in Irano Anatolian hotspots. As a result, we can say that if these parasitoids are in two regions, may be they can arrive at Caucasus hotspot.

*Lissonota lineata*, *Pion fortipes*, *Syrphophilus bizonarius* spread three in hotspots. According to Yu *et al.*, 2006, these ichneumonids were found first in Mediterranean hotspot, second in Irano Anatolian hotspot and lastly in Caucasus hotspot. Consequently, we can say that these ichneumonids may have followed these routes.

*Lathrolestes unguaris*, *Diaparsis nitida*, *Gelanes fuscus*, *Gelanes simillimus*, *Tersilochus nitens*, which are in Palearctic region, did not find in three hotspots. These species reach to Mediterranean hotspot.

---

### Investigating the genetic control of gall induction in Cynipid gallwasps

Jack Hearn<sup>1\*</sup>, Graham N. Stone<sup>1</sup>, Mark Blaxter<sup>1</sup>, Joseph Shorthouse<sup>2</sup> & The GenePool<sup>1</sup>

<sup>1</sup> Institute of Evolutionary Biology, University of Edinburgh, King's Buildings, West Mains Road, Edinburgh, EH9 3JF United Kingdom; J.Hearn@sms.ed.ac.uk; Graham.Stone@ed.ac.uk; mark.blaxter@ed.ac.uk

<sup>2</sup> Department of Biology, Laurentian University, Sudbury, Ontario, P3E 2C6 Canada; jshorthouse@laurentian.ca

Cynipid gallwasps induce complex and morphologically diverse galls on highly-conserved host plants, the mechanism utilized is a long-standing entomological mystery. With the advent of new high-throughput sequencing technologies traits of non-model organisms with complex life-histories have become amenable to study. We are using a combination of Illumina GAIIx and Roche 454 sequencing to generate genomic data and expressed transcripts at key larval plus adult life stages to determine the genetic control of gall induction. Genomic data will be used for Cynipid genes of viral origin, analogous to virus-like-particle structural genes previously identified in some Polydnavirus utilizing Ichneumonoidea wasp genomes. It will also aid transcriptome assembly. Transcriptome sequencing of larvae during the initial gall induction phase will provide a set of candidate genes for control of gall-induction when controlled for by expression in other life-stage. A comparative approach using two species from different cynipid clades will test for a common conserved mechanism. The Palearctic oak apple forming *Biorhiza pallida* and the Nearctic rose galler *Diplolepis spinosa* have been selected for this purpose. Results from initial genome sequencing, assembly and analysis are presented as is the plan for transcriptome sequencing.

---

### Relationships of Chalcidoidea: a molecular and morphological approach

John Heraty<sup>1</sup>, Roger Burks<sup>2</sup>, James Munro<sup>3</sup>, Johan Liljeblad<sup>4</sup>, Matthew Yoder<sup>5</sup> & Elizabeth Murray<sup>6\*</sup>

<sup>1</sup> Department of Entomology, University of California, Riverside, CA 92521 USA; john.heraty@ucr.edu,

<sup>2</sup> burks.roger@gmail.com, <sup>3</sup> jbmunro@gmail.com, <sup>4</sup> cynips@gmail.com; <sup>6</sup> elizabeth.murray@email.ucr.edu

<sup>5</sup> Department of Entomology, North Carolina State University, Raleigh, NC, 27695 USA; diapriid@gmail.com

Chalcidoidea are economically and ecologically one of the most important groups of Hymenoptera. They are a hyperdiverse group of insects with more than 500,000 estimated species currently allocated to about 89 subfamilies in 19 families. Perhaps not surprisingly, there is little consensus on relationships in the group, and there has never been a comprehensive phylogenetic analysis of the superfamily. We address their relationships using two approaches. First, a molecular phylogeny of 720 taxa including 51 outgroups using a secondary structure alignment for partial 18S and 28S sequences. Second, a morphological



approach based on scoring 243 characters for more than 200 representative taxa using MX, an on-line content management system, with the help of numerous collaborators worldwide. Results of the independent and combined results will be presented in an attempt to resolve the family level relationships in the superfamily.

---

## Evolution of egg parasitism under water in parasitoid Hymenoptera

Yoshimi Hirose

Faculty of Agriculture, Kyushu University, Fukuoka 812-8581, Japan; hirosey@jcom.home.ne.jp

Parasitoid Hymenoptera are species-rich in nearly all terrestrial ecosystems, but the richness of hymenopterous parasitoids of aquatic insects is rather limited, given the species richness of potential aquatic hosts. Clearly, the aquatic habitat has been a barrier to parasitism by parasitoid Hymenoptera. However, subsurface egg parasitism of aquatic insects is not so rare. In the evolution of this type of egg parasitism, there are four reproductive strategies for parasitoid females that lack adaptations to dive and attack eggs of aquatic insects. Such parasitoids can exploit aquatic hosts in the following ways: (1) when the host's eggs are laid on plants and other substrates above water, (2) when the host's eggs are exposed above water at some point in their life cycle, (3) if the females walk down among the plants bearing these hosts under water (i.e., when the hosts are always under water), and (4) by swimming in search of hosts that are always under water. The last step is highly evolved, and is found in at least three families, Trichogrammatidae, Mymaridae and Scelionidae. Thus, females of species of some genera belonging to these families are well adapted to searching the hosts under water, but their searching by swimming might be largely limited to the hosts in ponds rather than those in streams. Such parasitoid females must have a difficulty in searching the hosts in flowing water because of their small size. Evolution of egg parasitoids also is under the ecological constraints of their small size since their hosts are usually smaller than those of larval or pupal parasitoids.

---

## Parasitoids of *Choristoneura* spp. (Lepidoptera: Tortricidae) in the Nearctic region

John T. Huber<sup>1</sup>\* & José Fernández-Triana<sup>2</sup>

<sup>1</sup> Natural Resources Canada, Canadian Forest Service, Ottawa, Ontario, Canada; john.huber@agr.gc.ca

<sup>2</sup> Biodiversity Institute of Ontario, Guelph, ON and Canadian National Collection of Insects, Ottawa, ON, Canada; jftriana@uoguelph.ca

The genus *Choristoneura* (Lepidoptera: Tortricidae) includes several economically important pests in North America. The Eastern spruce budworm, *C. fumiferanae* is the most devastating pest of conifers in eastern North America but six others are also important in forestry (*C. biennis*, *C. conflictana*, *C. pinus*, *C. occidentalis*) or agriculture (*C. rosaceana*, *C. parallela*) in many parts of the continent. Decades of biological studies have resulted in literature records for 230 parasitoids in 106 genera from 11 of the 16 Nearctic species, including 50 species of Braconidae in 18 genera, 113 species of Ichneumonidae in 45 genera, 51 species of Chalcidoidea in 29 genera (9 families), 1 species of Bethyidae, and 15 species (13 genera) of Tachinidae. Illustrated identification keys to most of the species and all of the genera were produced over the past 15 years by four taxonomists (J. Huber, A. Bennett, J. O'Hara, J. Fernández-Triana) based at the CNC, Ottawa. An additional 36 species (14%) of parasitoids are erroneous associations.