

Chalcid Forum

A Forum to Promote Communication Among Chalcid Workers

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Editor's Notes

Welcome to the 23rd edition of **Chalcid Forum**. This issue's masthead is *Perissocentrus striatululus* created by Natalia Florenskaya. This issue is also available on the Systematic Ent. Lab. web site at: <http://www.sel.barc.usda.gov>. We also now have available all the past issues of Chalcid Forum available as PDF documents. Check it out!!

Research News

Michael W. Gates

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During two separate trips to southeastern Arizona in July, 1997 and August, 1999, I was fortunate to witness behaviors of *Acanthochalcis nigricans* Cameron (Chalcididae) and *Orasema tolteca* Mann (Eucharitidae), respectively. My observations of *A. nigricans* began as a chance encounter with another entomologist during a field foray. I had parked my vehicle beside highway 80 near Granite Gap, an interesting erosional formation ~15 miles north of Rodeo, New Mexico. Some time had passed as I swept various shrubs when I heard a distant "Hello?". I turned to see Tim Alten, an instructor at Chaffey College in southern California approaching, net in hand. After brief introductions, he mentioned that, while collecting *Chalcolepidius smaragdinus* LeConte (Elateridae), he had collected about a dozen large, black wasps that were walking up and down stems of *Baccharis sarothroides* Gray (Asteraceae). After determining that these beasts were definitely *A. nigricans*, I proceeded to the locality, a rest stop ~15 miles south of Safford, AZ. Sure enough, 3-4 *A. nigricans* were visible at any one time along the roadside. One female I watched for approximately 15

minutes as she paced up and down *B. sarothroides* stems (both living and partially dead) antennating as she progressed. Every 20-30 seconds, she would briefly pause to raise then lower her body, the chalcidoid analog of a push-up. Upon approaching the branch tips, 1-2 resident males would approach and hover in the vicinity of the female. Unfortunately, no pre-copulatory or copulatory behaviors were observed. Naturally, the female wound up leaving with me.

The second behavior observed took place at Harshaw Creek, ~7 miles southeast of Patagonia in 1999. Jeremiah George (a lepidopterist, but don't hold that against him) and I pulled off in our favorite camping site near the intersection of FR 139 and FR 58 and began sweeping. I knew that this area was productive for the large and brilliant green-blue *O. tolteca*, a parasitoid of *Pheidole vasleti* Wheeler (Formicidae) brood. After netting a few on *Baccharis glutinosa* Pers. (Asteraceae), we began looking on unopened and partially opened flower buds for ovipositing females. The active first instars of these beasts (planidia) are highly motile and seek to gain access to ant brood by hitchhiking on foraging ants or, possibly, ant prey items (e.g. thrips). Within minutes we spotted our first female and began recording observations. While Jeremiah set up his macro camera, I watched the *O. tolteca* female search for suitable unopened buds in which to oviposit. Before ovipositing, the female oriented herself head down and used her serrate, recurved ovipositor to insert eggs into the plant tissue. Eggs were deposited into floret bracts near the middle of the bud initially and continued uninterrupted as she progressed toward the peduncle. At this point, the female would either repeat this process on the same floret (albeit on a different track), or proceed to a new floret. At least 4-5 florets were utilized in each panicle before she proceeded to the next inflorescence by taking flight and hovering around nearby inflorescences searching for a suitable landing site. We watched her repeat the procedure several times in ~50 minutes, whereupon she and several egg-bearing panicles were collected for reference. We captured numerous *O. tolteca* that day, both on film and in our vials.

S. N. Myartseva

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In March 1997, the Institute of Zoology, Academy of Sciences of Turkmenistan celebrated a jubilee. It turned forty. This commemoration is an excellent opportunity to summarize investigations of chalcid wasps in Turkmenistan.

Studies on entomophagous insects, including Chalcidoidea, began in the institute of Zoology in 1966. Prior to 1966, only Sphecidae received the attention of taxonomists. In Turkmenistan alone, approximately 200 species of sphecid wasps were known (Myartseva, 1962-1965). Although no specialists on Chalcidoidea were working in Turkmenistan at the time, the institute initiated taxonomic and biological studies on Chalcidoids that parasitized Homoptera, mainly Coccoidea.

I received the degree of Candidate of Biological Sciences and maintained contact with hymenopterists of the Laboratory of Taxonomy of Insecta at the Zoological Institute of Academy of Sciences of the former USSR. I met Dr. M.N. Nikolskaya, the founder of the scientific school of soviet chalcidologists. One from my first independently described new species of aphelinid wasps was named in honor of Dr. N.M. Nikolskaya (Myartseva 1973). Since then, I have continued to study Chalcidoidea, especially the family Encyrtidae. My first teachers on chalcid studies were professors V.A. Trjapitzin, E.S. Sugonjaev, and V.A. Yasnosh from Georgia.

I have collected and reared parasitic chalcid wasps from numerous hosts on several plants in different landscapes both in Turkmenistan and Middle Asia. In 1984, I defended a thesis dissertation entitled "Encyrtidae of deserts and semi-deserts of Middle Asia" in St. Petersburg. V.A. Trjapitzin, a professor of the Zoological Institute stated that "this study is discovery of new fauna of

Encyrtidae". Three-hundred twenty species in 111 genera of Encyrtidae were recorded in this study. Of these, 125 spp. and 3 genera were new to science. Included in the study, were keys for principal genera i.e. *Discodes*, *Ooencyrtus*, *Anagyrus*, *Copidosoma*, *Microterys*, and species of the Middle Asian Encyrtidae. Subsequent articles, (about 80) described new taxa not only from Middle Asia, but also from the Caucasus region, the Middle East, Iran, Mongolia, Vietnam, and Thailand. Two monographs and 2 brochures on Encyrtidae investigated trophic connections, distribution, ecology, origins of desert fauna, and parasitoid complexes attacking important mealybugs.

About 20 articles were devoted to Aphelinidae, parasitoids of scales and whitefly. Separate groups of aphelinid wasps were studied starting in 1971. In the latest article (Myartseva 1995), 3 new species of Aphelinidae reared from saltcedar in Turkmenistan are described.

Serious attention was given to the family Eulophidae, beginning in 1988 when my students began to study parasitoids of different families of Lepidoptera in orchards of southern Turkmenistan. Over 50% of parasitoids attacking these pests are members of the Eulophidae. Over 20 articles came out of this work, mainly descriptions of new species and complexes of eulophid wasps in Turkmenistan (Myartseva, Kurashev, 1990, 1991; Myartseva, Efremova, 1993, 1994 etc).

Durdyev and Saparmamedova (1989) reared 51 species of chalcid wasps from larvae and pupae of butterflies in orchards of Turkmenistan. E.O. Kokanova later reared and collected 53 species of chalcidoids, including 27 species of Eulophidae, from several host plants in forest shelter belts. They studied biology, ecology, and host relationships of important eulophid species for biological control. In 1992, a monograph on the entomophagous Hymenoptera attacking Lepidoptera in orchards of southern Turkmenistan was published.

Presently, entomologists of the Institute of Zoology study entomophagous insects (particularly Aphelinidae) attacking whiteflies which are serious pests in Turkmenistan. I have compiled a full bibliography on *Bemisia* of Middle Asia comprised of 59 articles, 13 of which contain different information on aphelinid wasps.

Until recently, the Turkmenian Institute of zoology was one of the centers of chalcid wasp studies in the former USSR (Trjapitzin & Sugonjaev 1989). Unfortunately, Turkmenian science has many problems, impeding further development. Currently, I am the only specialist on chalcid taxonomy for Turkmenistan and the Middle Asia region. Middle Asian chalcid fauna is very unique and numerous, but many species are unknown to science. For example, out of 30 collected species of parasitic wasps from the family Eupelmidae, over 1/3 are new to science. In the future, I would like to continue studying species of Encyrtidae and Aphelinidae. Therefore, I would like cooperative efforts from colleagues as well as support for chalcid studies.

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In 1999, I managed to considerably expand my collection of Hymenoptera, especially of Tetrastichinae and other Chalcidoidea in the steppe and foothill regions of the Kzassnodas Territory. I continue to study the following: the host-parasite relations of miners; parasitoids of Tortricidae, including *Cydia pomonella*; the role of natural populations of parasitoid complexes in the dynamics of leaf roller moths, and methods of increasing the effectiveness of these populations; and the possibility of cultivation and use of some species of tortricid.

Tidbits

Michael W. Gates, formerly of Riverside, California, completed his Ph.D. under Dr. John M. Heraty in October 2000. His dissertation is both a revision of the taxa of Rileyinae (Hymenoptera: Eurytomidae) on a worldwide level and a higher phylogenetic study of Eurytomidae using morphological and molecular datasets. As of the end of October, he has been working for Dr. Mike Schauff as a postdoctoral researcher on Eulophidae and Eurytomidae. Further, he is working to build a genetic repository of taxa of Eurytomidae, primarily from the Neotropical and Australasian regions, for future destructive morphological/molecular studies. Any extra eurytomids preserved in 70-95% ethanol from these regions would be greatly appreciated. Feel free to contact Mike via e-mail at: mgates@sel.barc.usda.gov or by sending a letter to the address below to discuss exchanges or gifts of chalcidoid taxa. — *Michael Gates, Systematic Entomology Laboratory, PSI, USDA-ARS, NHB 168, c/o National Museum Natural History, Washington, DC 20560-0168, USA*

A recent paper (Heraty & Gates) on diversity of Chalcidoidea in the Yucatan Peninsula in Mexico has been uploaded to the Web (http://cache.ucr.edu/~heraty/El_Eden/Maya_formatted.pdf).

This paper is included in the symposium volume: Lowland Maya Area: Three Millennia at the Human-Wildland Interface, with the symposium itself being held in January 2001 at the University of California, Riverside. In sampling the Chalcidoidea of Reserva Ecologia El Edén in Quintana Roo, Mexico, Active (sweeping) and passive (malaise and pan traps) insect techniques were used for a five month period in 1998. The Reserve consists of lowland, subtropical savanna, primary and secondary forest, and several lagoons. More than 192 species in 15 of 20 families of Chalcidoidea were discovered in a state that previously had only five species records. Comparisons are made between what is known about the species richness of Chalcidoidea from the Nearctic to the Neotro-

pical regions with reasons cited for apparent discrepancies. Methods for both understanding tropical diversity and capturing/comparing information from different sources are assessed.

Correction to **Chalcid Forum** 21:5 (1998) : Dr. Victor Fursov has indicated that the correct author of "Cynipoidea collection in Institute of Zoology, Kiev, Ukraine" is Dr. Djakonchuk Lyubov, Institute of Zoology, Ukrainian Academy of Science, Bogdan Khmelnytskyi Str. 15, Kiev, 252601, Ukraine.

Forum**Molecular systematics in Chalcidoidea: a brief review of gene choice implications**

Christopher Desjardins (Univ. of Maryland) and Michael Gates (USNM)

In both the Chalcidoidea and the Hymenoptera as a whole, tremendous morphological diversity makes robust phylogenetic analyses challenging due to problems with homology assessment. Since all characters in sequence data are theoretically restricted to four states (A, C, G, and T), which suggests that homology assessment should be much easier in a molecular versus a morphological study when examining deeply divergent or rapidly evolving groups. This issue, coupled with recent trends in research funding, has caused many researchers in Hymenoptera to explore molecular systematics in the past decade. In this review we will not attempt to summarize the results of or phylogenetic inferences made in the molecular studies concerning Chalcidoidea. Rather, emphasis will be placed on considerations for gene selection and their utility in these studies (Table 1). Additional information, when unavailable in the literature on Chalcidoidea, will be drawn from recent studies of Hymenoptera and Insecta in general. As uncovering the phylogeny of the Chalcidoidea is an enormous and tremendously difficult task, we hope that information herein will not only provide an inroad for those wishing to embark upon molecular studies, but also encourage discussion and cooperation among chalcid workers around the world.

Two major dichotomies exist when selecting a gene for study: nuclear versus mitochondrial, and a subset within each of these, ribosomal versus protein coding. Biologically, mitochondrial genes differ from nuclear in that they are maternally inherited and non-recombining, while nuclear genes are passed along by both sexes and undergo sexual recombination. Recent studies in the Chalcidoidea have focused primarily on nuclear ribosomal genes, as have most other studies involving the parasitic Hymenoptera (see Table 1). There have been limited number of protein coding gene studies conducted in the Hymenoptera, and these have mainly involved the cyto-

chrome oxidase genes (CO). However, a few other projects have looked at different protein coding genes (primarily Apoidea). Although most studies in the Chalcidoidea have involved nuclear genes (primarily 28S), many studies throughout the Hymenoptera have covered a range of both nuclear and mitochondrial genes. In the text to follow, an attempt will be made to outline both the positive and negative aspects of these gene types, or at least outline the current debate over them.

Ribosomal RNA (rRNA) from both the nucleus and the mitochondria are certainly the most popular genes being sequenced for phylogenetic studies today, not only within Hymenoptera but beyond. In Chalcidoidea, recent studies by Campbell *et al.* (2000), Gauthier *et al.* (2000), and Rasplus *et al.* (1998) all used portions of the 28S rRNA gene. Most work on mitochondrial rRNA utilized the 16S subunit (Derr *et al.* 1992a,b; Downton and Austin 1994, 1995, 1999) The popularity of these genes stems from the almost universal primers made from highly conserved stem regions. This obviates the need to spend time or money on primer development, and successful amplification from almost any organism (given proper preservation (Quicke *et al.* 1999b)) is nearly guaranteed. Upon transcription, rRNA folds characteristically to form unique secondary and tertiary structure based primarily upon nucleotide sequence and interactions. Secondary structure is characterized by stems (paired bases) and loops or bulges (unpaired bases). While these stem regions are structurally constrained and useful for examining deep divergences, the loop regions are freer to vary thus applicable for very recent divergences. Further, coding regions are separated by non-coding, internally transcribed spacers (ITS), thus are free from functional and structural constraints. Thus both the genes coding for ribosomes and spacer regions can be used over broad evolutionary time scales. These genes are also very abundant in the cells of organisms (tandemly repeated), enabling the gene to be successfully amplified from less than optimally preserved specimens. Nonetheless, rRNA genes are not problem free and ease of amplification should not be confused with ease of phylogenetic use.

One potential pitfall associated with rRNA is that of alignment. Stem regions are relatively simple to align due to their highly conserved nature, but point mutations and insertion-deletion events (indels) are much more common in the variable loop regions, making homology assessment in those regions difficult or even impossible for simple alignment programs to handle. Unfortunately, it is these difficult to align sections of the gene that most of the sequence variation occurs across taxa. Most studies initially use available alignment programs, but eventually resort to manual alignment, leaving homology assessment to the subjectivity of the author. Morrison and Ellis (1997) studied the effects of different types of alignments for a large 18S rRNA data set, and concluded that the phylogenetic hypotheses recovered were significantly dependent on the alignment method used, even in areas of high

support.

Many alignment options do exist, and secondary structure alignment is currently gaining popularity as extremely broad and detailed knowledge of the structure of rRNA genes has become generally available. By determining how the protein folds, bases in stems can be well aligned as can the positions of loops (although not the bases within those loops). However, Phillips *et al.* (2000) indicated that the assumptions made during homology assessment should reflect those made during phylogenetic analysis. If assumptions made during data set construction conflict with those made during tree construction, then the tree is not an accurate representation of the data. Secondary structure alignment brings us to this problem. Regardless of whether parsimony or maximum likelihood is used as the optimality criterion, both rely on independence of characters as a vital assumption. However, the premise of secondary structure alignment is that all of the characters are interdependent with one another, and it is that interdependence, which allows an accurate model of, the protein's folding to be generated. These conflicting assumptions might be avoided by using alignment/tree building programs that rely on the same assumptions (e.g. MALIGN (Wheeler and Gladstein 1994)), although this does not avoid the problem of potential interdependence in rRNA datasets. Maximum likelihood models are being developed to deal with interdependent data (e.g. Tillier and Collins 1995), and these methods may yet prove to be ideal for rRNA.

One other potential problem in rRNA homology assessment is slippage replication (Hancock 1995), in which mutation is based on fixation of indels instead of single point mutations, which most tree-building algorithms use. Unfortunately, slippage replication may create apparently homologous insertions in unrelated organisms independently, because the mechanisms of slippage are similar regardless of the region where it occurs. Slippage replication is most common in highly variable regions of rRNA where there is often sequence length variation, such as expansion segments. Vogler *et al.* (1997) studied the V4 expansion region (18S) in tiger beetles and found levels of slippage replication to be high, with a strong negative impact on phylogenetic reconstruction. This issue can be addressed using the sequence similarity program SIMPLE34 (Hancock and Armstrong 1994).

In contrast to ribosomal genes, protein-coding genes present more challenges in acquiring sequence data, as many of these regions lack effective primers. This problem is compounded by the lack of highly conserved regions, making primers taxon specific, especially for more rapidly evolving genes. Second, these genes often exist in low copy numbers in cells, making amplification from degenerate primers even more difficult. Most currently available primers are made from highly conserved genes, such as EF-1 α , where amplification is likely to be successful. These genes are useful for recovering both deep and recent phylogenetic divergences, because

nonsynonymous changes evolve very slowly while synonymous changes evolve rapidly, respectively. Although no recent studies of the Chalcidoidea utilize protein-coding genes, other taxa of Hymenoptera have examined. Danforth *et al.* (1999) used the nuclear EF-1 α to study the phylogeny of the bee genus *Halictus* (Apoidea: Halictidae), and in another study (Danforth 1999) used the mitochondrial COI gene to investigate *Lasioglossum* (Apoidea: Halictidae) phylogeny. Dowton and Austin (1994, 1999) also used mitochondrial CO genes in their study of the higher phylogeny of the Hymenoptera.

Unfortunately, they do not have characters that evolve at the proper rate to resolve phylogenies with a moderate divergence time, as may likely be the case in Chalcidoidea. Countless unstudied protein coding genes exist that evolve at more rapid rates, exacerbating the problem of primer construction and subsequent amplification. This is due both to sequence unavailability of closely related taxa and fewer areas in the gene conservative enough to amplify across a broad range of taxa. One of us is currently investigating the utility of two more rapidly evolving nuclear protein coding genes that have proven useful in Lepidoptera systematics, phosphoenolpyruvate carboxykinase (PEPCK) and dopa decarboxylase (DDC) (see Friedlander *et al.* 1996 for PEPCK; Friedlander *et al.* 1998, Fang *et al.* 1997 for DDC).

Although data acquisition can be difficult, protein-coding genes are fairly straightforward to align due to constrained evolution of codon triplets. Not only are first and second codon positions well conserved because of amino acid constraints, but indels and gaps in the alignment must appear in triplets, so that the proper reading frame is maintained. However, although these genes do not have the same interdependence problems of stems and loops in ribosomal genes, their mutation is often biased toward specific codons, and interdependence that does exist may be more difficult to model because of the sparse knowledge available on the structure and function of these infrequently used genes.

The differences between nuclear and mitochondrial genes, when applied to phylogenetics, are much less obvious than those between rRNA and protein coding genes. While mitochondrial sequence data gives a very accurate representation of the 'gene tree', this may conflict with the actual 'species tree' due to a process known as lineage sorting (Avice 1994). There seems to be little current consensus on the practical implications of lineage sorting, however, especially in studies dealing with levels of divergence deeper than intraspecific. In their study on gene selection, Brower and DeSalle (1994) state that "concern about gene tree versus species tree problems is overstated." They go on to say that lineage sorting cannot result in a well-supported, incorrect phylogeny. More likely, lineage sorting would further blur nodes that already contain little resolution. These areas are most likely to occur when a group undergoes extensive divergence in a short period of time. Unfortunately, this may be

just the case in the Chalcidoidea, and most studies done have showed fairly low support levels at many phylogenetic levels of interest. Ideally, mitochondrial and nuclear genes should be used together in a total evidence fashion to obtain the most accurate possible representation of organismal phylogenies.

Hopefully, this review has provided insight into gene selection for future studies and the utility of contemporary sequence data, or at least has shown that a restricted set of molecular data will not provide a simple answer to a difficult question. We would encourage chalcidologists both engaged in and looking toward molecular systematics to consider the issues that have been reviewed herein and initiate discussion with fellow chalcid workers. The task of elucidating phylogenetic hypotheses in Chalcidoidea is an enormous one, and only through communication and collaboration, such as promoted in *Chalcid Forum*, might we hope to truly resolve these issues.

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Gene/Region	Function	Properties	Utility	Potential Pitfalls	Sources
Nuclear - Ribosomal	Code for ribosomes which function in protein synthesis.	Multiple copies, variable sequence divergence within molecule, coding regions functionally constrained, concerted evolution.	Depending on region within molecule selected, useful for species to family level inference.	Alignment encumbered by postulated indel events. Aberrant copy might be amplified.	See below.
Divergent (D), domains	Region within the coding region.	Stems and loops, distinctive secondary and tertiary structure. Moderately to highly conserved.	These domains in 28S and 18S used at genus level and above.	See above.	Quicke <i>et al.</i> 1999a; Campbell <i>et al.</i> (1993, 2000); Rasplus <i>et al.</i> 1998.
Internal/External Transcribed Spacer (ITS, ETS)	Non-coding spacer between coding regions.	Highly variable since under no structural or functional constraint.	Useful for differentiating species or populations.	Quickly reach sequence saturation above genus level.	Campbell <i>et al.</i> 1993.
Nuclear - Protein Coding	Codes for a variety of proteins having various functions.	Usually single copy, functionally constrained and conservative, triplet coding, no indels.	Depending on region selected, can be useful at genus level and above.	3 rd codon position bias, synonymous substitutions, some 3 rd position bases preferred over others.	Brower & DeSalle 1994.
EF-1 α (Elongation Factor)	Codes for EF-1 α enzyme.	Few copies, highly conserved.	Useful at lower and higher levels (see potential pitfalls).	Synonymous vs. non-synonymous substitution differences in utility level.	Fang <i>et al.</i> 1997; Danforth <i>et al.</i> 1999;
DDC (dopa-decarboxylase)	Codes for DDC enzyme, which functions in converting dopa to dopamine (neurotransmitter).	Single copy (at least in Leps.), no internal repeats.	Useful at generic level and above.	Occasional (sometimes large) introns present, may be tricky to define primers.	Fang <i>et al.</i> 1997; Friedlander <i>et al.</i> 1994, 1998.
PEPCK (phosphoenolpyruvate carboxykinase)	Codes for PEPCK enzyme, which functions in the gluconeogenesis pathway (OAA \rightarrow PEP).	Single copy, moderately conserved.	Useful at generic level and above.	Occasional (sometimes large) introns present, may be tricky to define primers.	Friedlander <i>et al.</i> 1996.
Mitochondrial - Ribosomal (16S & 12S)	Codes for mitochondrial ribosomes which function in protein synthesis.	Clonally inherited, single copy, abundant, evolve faster than nuclear genome.	Useful from species to family (higher?) level, depending on specific region selected.	AT bias in insects, some variable-length regions.	Derr <i>et al.</i> 1992a,b; Dowton & Austin 1994, 1995, 1999; Machado <i>et al.</i> 1996.
Mitochondrial - Protein Coding	Codes for mitochondrial proteins	Conservative, triplet coding, no indels.	Useful at higher phylogenetic levels.	Similar to nuclear.	See below.
CO I-III (Cytochrome oxidase)	Codes for CO enzymes, which participate in electron transport system (ETS).	Stringent structural and functional constraints.	Useful at family level and above.	Similar to nuclear.	Danforth 1999; Dowton & Austin 1994, 1999.

Necrology

Oswald Peck
(1903—1999)

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Ozzie Peck was born on 27 April, 1903 in Bolton, England and at the age of 17 his family moved to a farm in Alberta. The acquired land proved to be practically untillable so Ozzie and his three brothers had one ambition in common—to get off the farm. Consequently, they pursued various other agricultural interests. Ozzie started his college career at Olds Agricultural College and later received a B. Sc. (1931) degree from the University of Alberta. His M.Sc. (1934) and Ph.D (1936) degrees were from MacDonald College (MacGill University) at Ste. Anne de Bellevue, Quebec.

He joined the Entomology Branch, Canada Department of Agriculture, Ottawa, in November, 1935, as an insect pest investigator and became a specialist in parasitic Hymenoptera, particularly the Chalcidoidea at the Canadian National Collection of Insects (CNC). He retired in 1969 with over 33 years of service. After retiring he was appointed as an Honorary Research Associate and continued his research for several more years. Ozzie's best known publication was his 1962 Catalog of the Nearctic Chalcidoidea, a 1,092 page work listing all references on species of the superfamily up to 1960. He was a very thorough worker. For example, for one nominal species, *Trichogramma minutum* Riley, Ozzie found about 625 references covering 20 pages. The other hymenopterists at the CNC delighted in finding even one reference that Ozzie had missed. There were very few. This work was done using index cards (well before the advent of personal computers). As every taxonomist knows, a comprehensive, well-done catalog is invaluable. A colleague, Stuart Walley, remembers a quote from an unknown source:

"Index learning turns no student pale

Yet hold the eel science by the tail."

Ozzie was a long-time member of the Entomological Society of Canada and the Entomological Society of America. He was also a Fellow of the latter Society, one of the few Canadians holding this distinction. In fact, in recent years there were only five living fellows, and now only two are left.

Ozzie was a very active person, a runner during university days and later a tennis player. At 75, he would take on the younger ones (50 years his junior) and most of the time he would beat them, much to their amazement. He was also involved with both the Boy Scouts and the Sea Scouts.

Ozzie and his wife Virginia (still living in Ottawa) were very enthusiastic gardeners and when he was not studying chalcids he was tending his large garden at home

or the one at his cottage on 17 acres near Ste. Agathe, Quebec. He was a Life Member of the Ottawa Horticultural Society.

He met Virginia Gardner, a home economics student, while studying at MacDonald College and they were married the day after Ozzie obtained his doctorate degree in October, 1936. They had three sons.

At 86 years old, Ozzie was the doyen at a memorable meeting of 17 chalcidologists at the house of Gary Gibson in 1989 that included Zdenek Boucek from England and Luis De Santis from Argentina.

Ozzie died at 95, the oldest Hymenopterist in Canada at the time.

Publications of Oswald Peck

compiled by John Huber

ECORC, Agriculture Canada, Onatrio,
Canada K1A 0C6, Canada)

- Peck, O. 1934. Some Ichneumonidae of Alberta: a review of the subfamily Joppinae. Unpublished M. Sc. thesis, McGill University.
- Peck, O. 1936. The male genitalia in the Hymenoptera (Insecta), especially the family Ichneumonidae. Unpublished Ph.D. thesis, McGill University.
- Peck, O. 1937a. The male genitalia in the Hymenoptera (Insecta), especially the family Ichneumonidae. I. Comparative morphology. Canadian Journal of Research, Section D 15: 221-252.
- Peck, O. 1937b. The male genitalia in the Hymenoptera (Insecta), especially the family Ichneumonidae. II. Taxonomy of the ichneumonid genera. Canadian Journal of Research, Section D 15: 253-274.
- Peck, O. 1937c. The males of *Urocerus albicornis* F. and *U. flavicornis* F. (Hymenoptera: Siricidae). The Canadian Entomologist 69: 275-276.
- Peck, O. and J.L. Bolton. 1946. Alfalfa seed production in northern Saskatchewan as affected by bees, with a report on means of increasing the populations of native bees. Scientific Agriculture 26(8): 388-418.
- Peck, O. 1963. A catalogue of the Nearctic Chalcidoidea (Insecta: Hymenoptera). The Canadian Entomologist Supplement 30. 1092 pp.
- Peck, O. 1964. Synopsis of the Nearctic Ichneumoninae Stenopneusticae with particular reference to the northeastern region (Hymenoptera). Part VIII. Addenda and corrigenda, host-parasite list and generic host index, index to ichneumonid names. Memoirs of the Entomological Society of Canada No. 35: 888-925.
- Peck, O., Z. Boucek, and A. Hoffer. 1964. Keys to the Chalcidoidea of Czechoslovakia (Insect: Hymenoptera). Memoirs of the Entomological Society of Canada No. 34. 120 pp.
- Peck, O. 1969. Chalcidoid (Hymenoptera) parasites of the alfalfa leaf-cutter bee, *Megachile rotundata*, in Canada. The Canadian Entomologist 101: 418-422.

- Peck, O. 1974a. Chalcidoid (Hymenoptera) parasites of the horn fly, *Haematobia irritans* (Diptera: Muscidae), in Alberta and elsewhere in Canada. *The Canadian Entomologist* 106: 473-477.
- Peck, O. 1974b. *Steffanolampus*, a new genus for *Perilampus salicetum* (Chalcidoidea) and its Nearctic distribution. *The Canadian Entomologist* 106:555-558.
- Peck, O. 1974b. Nearctic records of two European species of Pteromalidae (Hymenoptera: Chalcidoidea). *The Canadian Entomologist* 106: 623-625.
- Peck, O. 1985. The taxonomy of the Nearctic species of *Pediobius* (Hymenoptera: Eulophidae), especially Canadian and Alaskan forms. *The Canadian Entomologist* 117: 647-704.
- Atwood C.E. and Peck, O. 1943. Some native sawflies of the genus *Neodiprion* attacking pines in eastern Canada. *Canadian Journal of Research* 21: 109-144.
- Bolton, J.L. and Peck, O. 1946. Alfalfa seed production in northern Saskatchewan as affected by *Lygus* bugs, with a report on their control by burning. *Scientific Agriculture* 26(3): 130-137.

John L. "Jack" Beardsley

Emeritus Professor of Entomology John W. Beardsley passed away last Monday while working at the B.P. Bishop Museum. He was 74 years old. Dr. Beardsley was an internationally recognized authority in the areas of biological control and insect systematics, particularly with respect to the mealybugs and scale insects of major significance to agriculture in the State of Hawaii. During his career, he conducted extensive research on these insects as well as their natural enemies. He was recognized as an authority on Hawaiian insects as well as the mealybugs and scale insects of the world. During his extensive career, he authored over 150 scientific articles in refereed journals, book chapters, and reviews. He contributed over 500 published scientific notes on new immigrant insects, new host records and new island records. Dr. Beardsley served as Chair of the Department of Entomology from 1981-1991.

J. T. Wiebes (1931-1999)

The following information is excerpted from: Van Bruggen, A. C. and C. van Achterberg. 2000. In *Memoir Prof. Dr. J. T. Wiebes (1931-1999), evolutionary biologist and systematic entomologist*. *Zool. Med. Leiden* 74: 271-281.

Born on 13 September 1931 in Rotterdam, Jacobus Theodorus [Koos] Wiebes read biology at Leiden University where he obtained his Ph.D. in 1963 on studies of Indo-Australian fig wasps. He started working on spiders

(Lycosidae, Pisauridae) and beetles (Carabidae, Cetonidae, Helodidae), but he earned his scientific reputation as a specialist in fig wasps (Hymenoptera: Agaonidae, Torymidae), their parasitoids and intricate host relationships (1961-1994: 89 papers). He served for many years on the staff of the Rijksmuseum van Natuurlijke Historie, Leiden (1955-1970, initially as assistant, later as curator of Coleoptera and as assistant director since 1965), to return as director of the newly merged national zoology and geology museums (ad interim 1982-1984, director 1984-1989). In 1970 he was appointed to the chair of Systematic Zoology and Evolutionary Biology at Leiden University, where he worked successfully until returning to the museum. Wiebes initiated studies on the lepidopteran complex of *Yponomeuta* species and their host plants, studying speciation in a context of ecology, taxonomy and phylogeny. Most results in this field were published in conjunction with Dr W.M. Herrebut and various (mainly Ph.D.) students. Indeed, this research project attracted a host of students and also world-wide attention. Wiebes had a talent for organization and management so that he was frequently asked to serve on various committees mainly concerned with biology on an academic level. In 1978 he was elected a member of the Koninklijke Nederlandse Akademie van Wetenschappen, Amsterdam, where he later served on various councils. His influence on the organization of biology in the universities and research councils was indeed nationwide. Health problems forced him to take early retirement in 1989, but he insisted on completing publication of his work on the fig wasps. On 6 December 1999 he died in Leiderdorp leaving a fine reputation as an evolutionary biologist and a systematic entomologist.

Other Deaths

From Virendra Gupta we received notice of the following deaths (all from Aligarh, India):

Man Mohan Agarwal
D. Mashood Alam
S. Adam Shaffee

We have also learned of the following deaths:

Harry Anderson
Luis De Santis

Request for help

Chacidoidea of Yemen

From November 1990 until April 1994 and again since September 1997, I have been working as a biocontrol entomologist in the Republic of Yemen. During this time, I have reared many chalcidoid parasitoids from their hosts. In addition, I have collected many more specimens with Malaise and light traps. It has been difficult to get this material identified. I have received assistance from several colleagues, but 150 samples with several thousand specimens remain to be identified. They are mainly Eulophidae, Pteromalidae, and Eurytomidae. I would appreciate if anyone would be willing to look at some of this material. I am most interested in getting the reared specimens identified. Identified material can remain in the specialists' collections except some labelled material should be sent back to the Yemeni National Natural History Collection.—*Tony van Harten, Advisor for Biological Pest Control, General Department of Plant Protection, P.O. Box 26, Sana'a Republic of Yemen; Fax: (967)-1-228064/227972; E-mail: vanharten@y.net.ye.*

Recent Literature

Due to problems associated with databases, we cannot provide the literature information normally supplied by John Huber.

The following list of papers was submitted by V. N. Fursov, Institute of Zoology of Nation. Ukrain. Acad. Sc., Bogdan Khmel'nitskiy Str.15, Kiev, 252601, UKRAINE.

- Fursov, V. N. A new species of chalcidoid genus *Szelenyia* (Hym., Trichogrammatidae) from Spain. - Journal of Ukrainian Entomological Society, 1994 (1995), vol.2, N 1, pp.51-55.
- Fursov, V. N. Collecting Bruchid egg-parasitoids. - Chrysomela Newsletter, 1996, N 32, October, p.12
- Hirai, K., and V. N. Fursov. Description of *Trichogramma yawarae* Hirai et Fursov and redescription of *T. japonicum* Aschm. from Japan. Journal of Ukrainian Entomological Society, 1998, vol.4, N 3-4, pp. 35-40.
- Fursov, V. N. Problems of study and conservation of biodiversity of Hymenoptera Parasitica (Insecta). Journal "Vestnik Zoologii" (Kiev, Ukraine), Supplement, 1998, Vol.9, pp.178-182. (In Russian.)
- Fursov, V. N. Morphology of mesopleuro-sternal complex of thorax of Trichogrammatidae (Hymenoptera). Abstracts of V-th Congress of Ukrainian Entomology Society, 7-11.Sept.1998. - Kiev, 1998, pp.169-170. (In Russian.)
- Fursov, V. N., and B. Pintureau. Discovery of *Trichogramma cacoeciae* Marshal (Hymenoptera: Trichogrammatidae) new to England, at Chelsea Physic Garden, London. Bulletin of Irish Biogeographical Society (Dublin, Ireland), 1999, December, vol.22, N4, p.10-12.
- Fursov, V. N., and B. Pintureau. *Trichogramma cacoeciae* Marchal, a new species for the fauna of England. Journal "Vestnik Zoologii" (Kiev, Ukraine), 1999, N 1-2, p.34. (In English.)
- Kononova, S. V., and V. N. Fursov. A review of Palaearctic species of genus *Baeus* Haliday, 1833 (Scelionidae, Baeinae, Baeini) - egg-parasitoids of spiders (Arachnida). Zoologicheskii Zhurnal (Moscow), 1999, vol. 78, N 11, pp.1284-1291. (In Russian).
- Fursov, V. N. Egg-parasitoids (Hymenoptera) of aquatic beetles. Latissimus, Newsletter of Balfour-Browne Club, Scotland, UK, 2000, N 12, January, pp.16-17.
- Fursov, V. N. Review of chalcid wasps of the genus *Megaphragma* (Hymenoptera, Trichogrammatidae) - egg-parasitoids of thrips. Abstracts of Conference of Ukrainian Entomological Society, Nezhin, 19-23 September, 2000. - 2000. - p.132.
- Fursov, V. N. Discovery of four species of *Trichogramma* (Hymenoptera, Trichogrammatidae), new for the fauna of England. Journal "Vestnik Zoologii" (Kiev, Ukraine), 2000, Vo. 34, N 4-5, pp. 107-113. (In English.)

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Missing Persons

The last issue of **Chalcid Forum** sent to the following people were returned. If you know the correct address for these folks, please let us know.

Jean-Paul Aeschlimann (France)
Rose Broe (Australia)
Leopoldo E. Caltagirone (USA)
Andrew Davis (England)
Flavia Ejchel (Barsil)
Fernando Omar Cardoz Gamboa (Mexico)
David Johnson (USA)
Nick Mills (USA)
Hannah Nadel (Canada)
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Pedro Vargas-Piqueras (Spain)

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