General notes on changing and entering data for Chalcidoidea Database

ENTERING TAXONOMIC CHANGES

NOTE: In the MASTER table, the fields that constitute the Cited Name (Cited genus, Cited subgenus, Cited species, Cited subspecies) relate (via the "Taxon Code" field) directly to the name as used in publications referred to in the "Reference Code" field in the linked embedded tables (FAMTRIB, GENUS, SPECIES, TSTAT, HKNEW, HOSTS, DIST). For this reason, once entered, the contents of most fields that make up the Cited Name (Cited genus, Cited subgenus, Cited species, Cited subspecies) must NEVER change. These fields may only be changed if there is found to be an error in the original entry by the Database owner, eg. erroneous copying of spelling (by the database owner) from the original publication. The Cited author name may change for the same reason (e.g spelling Trjapitzin instead of Triapitsyn, Noort instead of van Noort). The year may be changed if there is evidence to show that the year of publication differs from that recorded in the Cited year field.

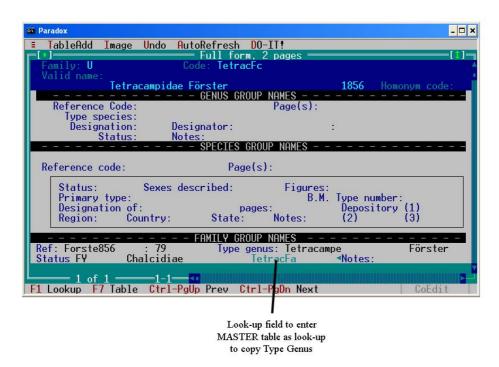
On the other hand, the Valid Name fields, can change to reflect changes in taxonomy.

<u>Unavailable names</u> (e.g. misspellings, nomina nuda) MUST NOT include a date of publication in the Cited Year field. A blank Cited Year field ALWAYS denotes an unavailable name in Chalcidoidea.

ENTERING NEW TAXONOMIC NAMES

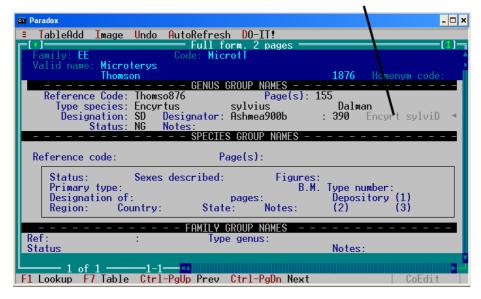
(New family group names, New genus group names, New species group names)

These are all pretty self explanatory, although two look up tables may need explanation. These are to be found in the FAMTRIB and GENUS tables are used to enter the Type Genus name and Type Species name respectively. To reduce the possibility of introducing a spelling error these names can be entered using the fields indicated below.



NOTE It can be seen above that the family group name and its author (both valid and cited) are both located in the "Author" field. This may seem illogical but it was initially done to save space on screen (and disk) because a MS-DOS window is limited in size and the font-size and format are set. It works very well and allowance has been made for this on the UCD web site [A family group name can always be recognized by the fact that the appropriate Valid genus/Valid species and Cited genus/Cited species fields are empty]. This also means that when the table is sorted on ValidGenus all the family group names appear to the front of MASTER which is convenient.

Look-up field to enter MASTER table as look-up to copy Type Species



HOMONYMS AND REPLACEMENT NAMES

Replacement names

Genus group names

a) Replaced valid genus group name

With MASTER table sorted by *Valid genus* go to the record with the "Valid genus" group name that is being replaced.

Move to the appropriate TSTAT table and enter the appropriate "reference code" in the *Reference* field and "page(s)" in the *Page*(s) field (of reference in which name is being replaced).

In Status field fill "JH" (for homonym)

Still in TSTAT table:

if genus group name is a junior homonym of a chalcidoid genus then go to *TaxonCode* and use as look up to insert the senior homonym genus, or,

if genus group name is a junior homonym of a non-chalcidoid name then enter genus group name and author in corresponding *genus* and *author* fields

Enter a comment in the *Notes* field using the format "[junior genus] [author], [year] is a junior homonym of [senior genus] [author], [year]: [journal] [volume]:[page] [(group)]."

With MASTER table still <u>sorted by *Valid genus*</u> [page up to move to Valid taxon name page] replace the *Valid genus*, *Valid author* and *Valid year* with the corresponding replacement name, author(s) and year. Clear *Homonym code* if necessary.

With MASTER table still <u>sorted by *Valid genus*</u> replace the *Valid genus* for all included species [including their synonyms, etc.] with the proposed replacement generic name. [The easiest way to move through the records is to put the cursor on the *Valid genus* field and <page down> whilst holding down the control key.] *Do not forget to make appropriate changes to brackets around the authors' names as required.*

With MASTER table still sorted by *Valid genus* move to the first record citing the newly proposed replacement name in the *Valid genus* field [the table will have automatically sorted the records as you move out of each record].

Move to the next record and press the "insert" key to insert a new (blank) record. Using "Control-D" (i.e. duplicate) duplicate the *Family* field, enter a new taxon code for the replacement name in *Taxon code* (using the normal rules), and enter the new replacement genus group name in *Valid genus*, the author(s) of the replacement name in *Valid author* and year of replacement in *Valid year*. Enter the replacement genus group name in the *Cited genus* field and the author(s) of the replacement name in the *Cited author* field and year in the *Cited year* field. [It may be necessary to enter **Cited subgenus** if required.]

Move to the GENUS table and enter the "reference code" in the *Reference code* field and "page(s)" in the *Page*(s) field.

Move to the *Status* field and enter "RN" (Replacement name).

Enter a comment in the *Notes* field using the format "Replacement name for [junior genus] [author], nec [author], [year]: [journal] [volume]:[page] [(group)]."

[NOTE: It may be that the authors of the replacement name are doing so unnecessarily because there are other names currently being treated as a synonym of the replaced name that could actually be used as a replacement name, therefore you will have to make the necessary adjustments in the above procedure in order to treat the oldest synonym as the valid name and the newly proposed replacement name of that name, etc. You will still need to complete the GENUS table and TSTAT table records as outlined above, but you will need to add an extra comment.]

b) Replaced invalid genus group name [unecessarly replaced]

This may happen if the so-called junior homonym has been already synonymised with a currently valid name.

With MASTER table sorted by *Cited genus* go to the cited genus group name that is being replaced.

Move to the appropriate TSTAT table and enter the appropriate "reference code" in the *Reference* field and "page(s)" in the *Page(s)* field (of reference in which name is being replaced).

In Status field fill "JH" (for homonym) Still in TSTAT table:

if genus group name is a junior homonym of a chalcidoid genus then go to *TaxonCode* and use as look up to insert the senior homonym genus, or,

if genus group name is a junior homonym of a non-chalcidoid name then enter genus group name and author in corresponding *genus* and *author* fields

Enter a comment in the *Notes* field using the format "[junior genus] [author], [year] is a junior homonym of [senior genus] [author], [year]: [journal] [volume]:[page] [(group)]."

With MASTER table still sorted by *Cited genus* move to next record and press the "insert" key to insert a new (blank) record. Using "Control-D" (i.e. duplicate) duplicate the *Family* field, enter a new taxon code for the replacement name in the *Taxon code* field (using the normal rules), and use "Control-D" to duplicate *Valid genus*, *Valid author*, *Valid year* and *Homonym code*. Enter the replacement genus group name in the *Cited genus* field and the author(s) of the replacement name in the *Cited author* field and year in the *Cited year* field.

Move to the GENUS table and enter the "reference code" in the *Reference code* field and "page(s)" in the *Page*(s) field.

Move to the *Status* field and enter "RN" (Replacement name).

Enter a comment in the *Notes* field using the format "Replacement name for [junior genus] [author], nec [author], [year]: [journal] [volume]:[page] [(group)]."

Species group names

a) Replaced valid species group name

With MASTER table sorted by *Valid genus* go to the record with the "Valid species" group name that is being replaced.

Move to the appropriate TSTAT table and enter the appropriate "reference code" in the *Reference* field and "page(s)" in the *Page(s)* field (of reference in which name is being replaced).

In Status field fill "JH" (for homonym)

or "CH" (for secondary homonym)

or "SH" (for junior homonym and synonym)

Still in TSTAT table:

go to *TaxonCode* and use as look up (MASTER table) to insert the senior homonym species

Enter a comment in the *Notes* field using the format "[genus] [junior species] [author], [year] is a junior primary/secondary homonym/homonym and synonym of [genus] [senior species] [author], [year]."

With MASTER table still <u>sorted by *Valid genus*</u> [page up to move to Valid taxon name page] replace *Valid genus* (if necessary), *Valid species*, *Valid author* and *Valid year* with the corresponding replacement Genus and species names, author(s) and year. Clear *Homonym code* if necessary.

With MASTER table still <u>sorted by *Valid genus*</u> repeat for all the Valid names of each record treated as a synonym of the **Junior** homonym. [The easiest way to move through the records is to put the cursor on the *Valid genus* field and <page down> whilst holding down the control key.]

With MASTER table still sorted by *Valid genus* move to the first record citing the newly proposed replacement name in the *Valid species* field [the table will have automatically sorted the records as you moved out of each record].

Move to the next record and press the "insert" key to insert a new (blank) record. Using "Control-D" (i.e. duplicate) duplicate the *Family* field, enter a new taxon code for the replacement name in *Taxon code* (using the normal rules), and enter the new genus group name in *Valid genus* (if necessary), the replacement species name in *Valid species*, the author(s) of the replacement name in *Valid author* and year of replacement in *Valid year*. Enter the replacement genus group name in the *Cited genus* field, the replacement species group name in the *Cited species* field and the author(s) of the replacement name in the *Cited author* field and year in the *Cited year* field. [It may be necessary to enter **Cited subgenus and Cited subpecies** if required.]

Move to the SPECIES table and enter the "reference code" in the *Reference code* field and "page(s)" in the *Page(s)* field.

Move to the *Status* field and enter "RN" (Replacement name).

Enter a comment in the *Notes* field using the format "Replacement name for [junior genus] [junior species] [junior author] [junior year] (add brackets around author and year if necessary), nec [author] [year] (add brackets around author and year if necessary), [journal] [volume]:[page]]."

[NOTE: It may be that the authors of the replacement name are doing so unnecessarily because there are other names currently being treated as a synonym of the replaced name that could actually be used as a replacement name, therefore you will have to make the necessary adjustments in the above procedure in order to treat the oldest synonym as the valid name and the newly proposed replacement name of that name, etc. You will still need to complete the SPECIES table and TSTAT table records as outlined above, but you will need to add an extra comment.]

b) Replaced invalid species group name [unecessarly replaced]

This may happen if the so-called junior homonym has been already synonymised with a currently valid name.

With MASTER table sorted by *Cited genus* go to the cited species group name that is being replaced.

Move to the appropriate TSTAT table and enter the appropriate "reference code" in the *Reference* field and "page(s)" in the *Page(s)* field (of reference in which name is being replaced).

In Status field fill "JH" (for homonym)

or "CH" (for secondary homonym) or "SH" (for junior homonym and synonym)

Still in TSTAT table:

go to *TaxonCode* and use as look up to insert the senior homonym species, Enter a comment in the *Notes* field using the format "[junior genus] [junior species] [junior author], [junior year] is a junior homonym of [senior genus] [senior species] [senior author], [senior year]: [journal] [volume]:[page]."

With MASTER table still sorted by *Cited genus* move to next record and press the "insert" key to insert a new (blank) record. Using "Control-D" (i.e. duplicate) duplicate the *Family* field, enter a new taxon code for the replacement name in the *Taxon code* field (using the normal rules), and use "Control-D" to duplicate *Valid genus*, *Valid species*, *Valid author*, *Valid year* and *Homonym code*. Enter the replacement name in the *Cited genus* and *Cited species* fields and the author(s) of the replacement name in the *Cited author* field and year in the *Cited year* field.

Move to the SPECIES table and enter the "reference code" in the *Reference code* field and "page(s)" in the *Page(s)* field.

Move to the *Status* field and enter "RN" (Replacement name).

Enter a comment in the *Notes* field using the format format "Replacement name for [junior genus] [junior species] [junior author] [junior year] (add brackets around author and year if necessary), nec [author] [year] (add brackets around author and year if necessary), [journal] [volume]:[page]]."

NEW COMBINATIONS

With master table indexed on Cited species in Table View

- 1. In Table View, use control-Z to search for Cited species name and move cursor to record that includes its original combination (CARE may be some homonyms)
- 2. Move cursor to Valid genus field
- 3. Re index table on Valid genus (Alt-S)
- 4. Toggle to Form View (F7).
- 5. Using Control Page Up, move to first record where Valid name is the same
- 6. Change Valid genus of old combination to genus name of new combination
- 7. Use Control Page Down to move to Valid genus field of next record and change to genus of new combination
- 8. Repeat until last record containing the old combination has been changed to the new combination
- 9. In Form View and with table still indexed on Valid genus move to Valid genus field of new generic combination.
- 10. Move to species name in new combination using either Page Down or change to Table View and scroll down until you reach the species name in the new combination.
- 11. If necessary toggle to Form View.
- 12. Insert new record.

- 13. Fill in family code (Control-D), the fill in both Valid name and Cited name using the new combination, author, year, etc. [It may be necessary to also include a subgeneric name if this is included by the author.]
- 14. Complete the TSTAT table with the Reference Code of the paper where the new combination is proposed, the pages, and "NC" (for New Combination) in the Status and fill in the code of the ORIGINAL COMBINATION in the Code field (can be done using the Look up table from the Code field) this will automatically fill up the full names of the original combination in the appropriate fields.

NOTES

- In the valid name only, do not forget to change the endings of the species epithet to agree with the gender of the generic name in the new combination.
- In the valid name only, do not forget to put brackets around the author's name if necessary.
- Check to ensure that a homonym has not been created by the new combination. If so put a letter "A", "B", etc. in the homonym field: leave blank for the oldest homonym, etc.
- Check to make sure that there has been no change to the family group in which the species is included by the change in combination (e.g. this could happen with a species that has been included in the type genus of a family group).

REVISED FAMILY GROUP PLACEMENTS

It can be important, when transferring any taxon, to check that the family group placement has not changed. On occasion also the family group placement of some genera or subfamilies can change for phylogenetic/taxonomic reasons. The family group placement can be changed very easily for a single taxon or for a number of taxa.

Single taxon.

Change family group placement using the Fgnames look-up table on the MASTER form.

Multiple taxa

If a family group or genus is to be included in a different family group then use the "ASK" function (F10/Ask/MASTER).

a) family group.

Move the cursor to the "Family" field and insert the 1-3 letter code for the previous family group placement then a comma then "Changeto XXX" where "XXX" is the 1-3 letter code for the new family group placement (enclose the family group codes in quotation marks). For instance, if Eriaphytinae is to treated as a synonym of Coccophaginae: "BE", changeto "BA".

b) genus group

Move the cursor to the "Valid genus" field and type in the genus name. Move the cursor to the "Family" field and insert "changeto XXX" where "XXX" is the 1-3 letter code for the new family group placement (enclose the family group code in quotation marks).

NEW SYNONYMIES

A) family synonymies

With MASTER table in FORM View and indexed (Alt-s) using Valid genus, locate family group name to be synonymized (Alt-z). Move to the "Valid author" field and change valid family and author and valid year to the appropriate family group name name, author and year. Still with the MASTER table indexed using Valid genus, locate other family group names (normally in synonymy with the same family group) that are regarded as synonyms of the family group name being placed in synonymy and repeat process. Add a new record to the appropriate TSTAT table(s) using similar process described under **New combinations**. Locate ALL taxa that have been included within the family group being placed in the new synonymy and change the code in the "Family" field in the MASTER table appropriately to reflect the new family placement (see notes under **Revised family group placements**).

B) generic synonymies

With MASTER table in Table View and indexed (Alt-s) using Cited genus, locate genus group name to be synonymized (Alt-z). Toggle to FORM view (F7) and move to the "Valid genus" field and change index (Alt-s) using Valid genus. Change Valid genus, Valid author and Valid year to the senior genus group name, author and year. Still with the MASTER table indexed using Valid genus, locate other records that include genus group names (normally in synonymy with the same genus group) that are regarded as synonyms of the genus group name being placed in synonymy and repeat process. Add a new record to the appropriate TSTAT table(s) quoting the reference proposing the new generic synonymy. Locate ALL taxa that have been included within the genus group being placed in the new synonymy and change Valid genus name to the appropriate name to reflect the new combination (where relevant add a new record to the appropriate TSTAT table(s) using similar process described under **New combinations**). Do not forget to make the appropriate changes to species names to reflect gender agreement and to review the use of brackets around the authors' names where there is a new generic combination.

NOTE. Where a genus includes several species is synonymised, it is often the case that the authority who proposes the synonymy makes no reference to the included species. These cannot be left "floating" so they must be moved into combination with the new genus. Normally in such cases no comment can be included in the TSTAT table.

C) species synonymies

With MASTER table in Table View and indexed (Alt-s) using Cited species, locate species group name to be synonymized (Alt-z). Toggle to FORM view (F7) and move to the "Valid genus" field. Index (Alt-s) on Valid genus. [If you toggle to Table View at this point, you will see how many records there are to change to reflect the new synonymy. Toggle back to form View.] Move to the

"Valid species" field and change Valid species, Valid author and Valid year to the senior species group name, author and year. [It may also be necessary to change Valid genus.] Still with the MASTER table indexed in Valid genus, locate the other records that include other combinations of the same species group name, misspellings and other species group names (normally in synonymy with the same species group) that are regarded as synonyms of the species group name being placed in synonymy and repeat process. Add a new record to the appropriate TSTAT table(s) quoting the reference proposing the new synonymy.

REMOVAL FROM SYNONYMY (E.G. STAT.REV.)

A) family group names

With MASTER table in FORM View and indexed (Alt-s) using Valid genus, locate family group name (in "Cited author" field) to be removed from synonymy (Alt-z). Move to "Valid author" field and change valid family and author and Valid year to the appropriate family group name name, author and year. Still with the MASTER table indexed using Valid genus, locate other family group names (normally in synonymy with the same family group) that are regarded as synonyms of the family group name being removed from synonymy and repeat process. Add a new record to the appropriate TSTAT table(s) using similar process described under **New combinations**. Locate ALL taxa that have been included within the family group being removed from synonymy and change the code in the "Family" field in the MASTER table appropriately to reflect the new family placement (see notes under **Revised family group placements**).

Do not forget that with the MASTER table indexed according to Valid genus, the valid family group names are arranged alphabetically in the Valid author field, but that any unavailable family group names are placed at the end of the group. It may be necessary to make changes to these unavailable names for some reason.

B) genus group names

With MASTER table in Table View and indexed (Alt-s) using Cited genus, locate generic name to be removed from synonymy (Alt-z) and toggle to Form View. Move to the Valid genus field and index (Alt-s) using Valid genus. Change Valid genus, Valid author and Valid year to the appropriate generic name, author and year. Still with the MASTER table indexed using Valid genus, locate other generic names (normally in synonymy with the same genus) that are regarded as synonyms of the generic name being removed from synonymy and repeat process. Locate ALL species that have been included within the genus to be removed from synonymy and if necessary change generic placement (using process described under **New combinations**). Add a new record to the appropriate TSTAT table(s) using process described under **New combinations**.

C) species group names

With MASTER table in Table View and indexed (Alt-s) using Cited species, locate species name to be removed from synonymy (Alt-z) and toggle to Form View. Move to the Valid genus field and index (Alt-s) using Valid genus. Change Valid species, Valid author and Valid year to the appropriate species name, author and year. Still with the MASTER table indexed using Valid genus, locate other combinations of species name, misspellings and other species names (normally in

synonymy with the same species) that are regarded as synonyms of the species being removed from synonymy and repeat process.

HKNEW TABLE (Key words)

Pretty straightforward entry. It is always necessary to include a comment in the NOTES field for Revisions, Reviews and Keys and mostly also a short statement relating to Biological control entries.

HOSTS TABLE

Comments on fields

<u>"Comment"</u> – this reflects whether or not the record is a primary one or secondary or the source of record if not from original publication.

or: primary (original) reference rv: secondary (review) reference

CP: information from CABIPEST abstracts

ZR: information from Zoological Record abstracts BA: information from Biological Abstract abstracts

"Lab record?" - indicates an "unnatural" association (Look-up field to Keywords):

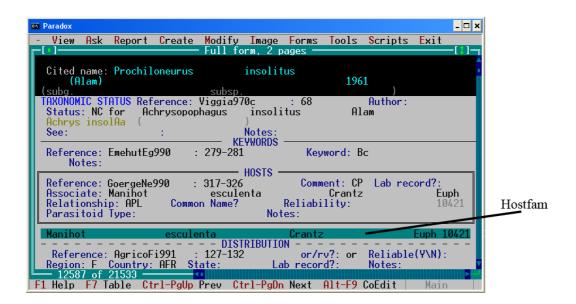
Lb: association in laboratory Bc: biocontrol association Gr: greenhouse association Sd: stored products association

"Associate"

This consists of five fields that gives the name of the taxon associated with the chalcidoid parasitoid ("Cited name" in the MASTER table).

After entering the appropriate Reference code, pages, etc. the five fields are filled in best by copying the record across from the hostfam table using Alt-H as follows:

- Complete "Reference", "pages", "comment" and "lab record?" ass appropriate
- Press the "Home" button
- Move to the HOSTFAM table (single record shown immediately below the embedded HOSTS table
- Using Alt-z locate generic name of associate
- Scroll down table until appropriate species is located
- Copy associate name across to HOSTS table suing Alt-h ("h" for host)



NOTE. The hosts records are automatically sorted (associate family first, then associate genus, etc.) when you leave the record

If an associate is not listed in the HOSTFAM table then a new record can be added as follows:

- open NEWHOST table
- Complete "Reference", "pages", "comment" and "lab record?" as appropriate
- Press the "Home" button
- Move to the HOSTFAM table (single record shown immediately below the embedded HOSTS table
- Using Alt-z locate generic name of associate [if not present then you will need to enter the generic name after inserting a new record]
- Page down and press Insert to enter a new record
- Control-D in the "Genus" field will copy the generic name from the record above
- Type in the species name in the species field
- Type in the author's name in the "Author field"
- Fill in the Associate's family name using either Control-D or the "Family" field as a Look-up field.
- Press Alt-n to copy across the new associate's name (A script will automatically add a "1" on to the Host number of the last associate) (if this NEWHOST table is not opened you will get an error message).

"Relationship"

This records the relationship between the chalcidoid parasitoid (cited in the MASTER table) and the associate.

Hyperparasitoid always cause problems. The appropriate entries are explained below"

Example

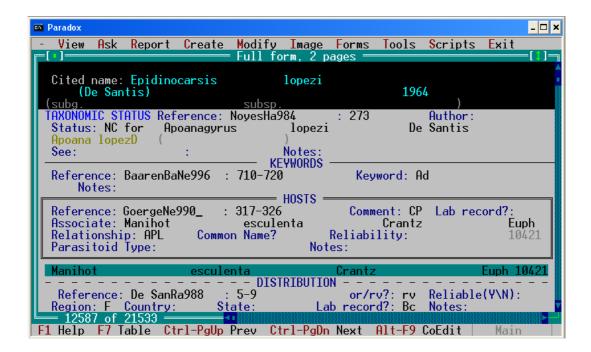
Prochiloneurus insolitus (chalcidoid hyperparasitoid) is a hyperparasitoid of Epidinocarsis lopezi (chalcidoid primary parasitoid) attacking Phenacoccus manihoti (coccid host) feeding on Manihot esculenta (host plant)

Or

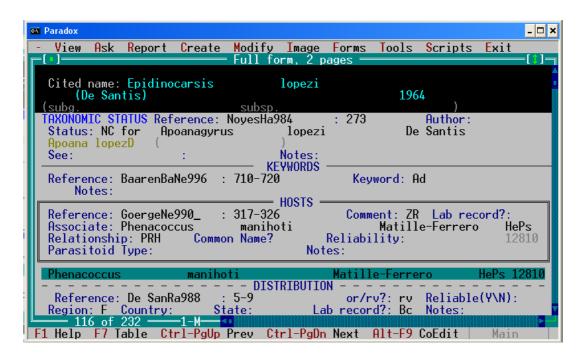
Epidinocarsis lopezi attacking Phenacoccus manihoti on Manihot esculenta is hyperparasitized by Prochiloneurus insolitus

Or

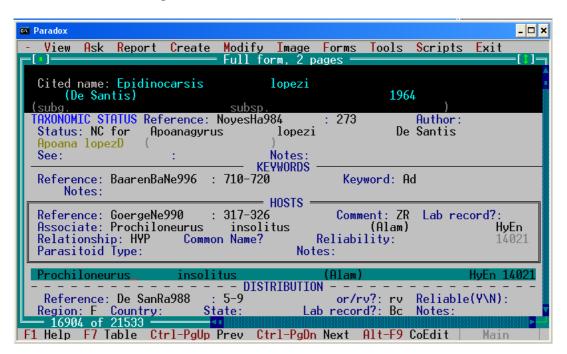
Prochiloneurus insolitus is a hyperparasitoid of Phenococcus manihoti on Manihot esculenta through/via Epidinocarsis lopezi



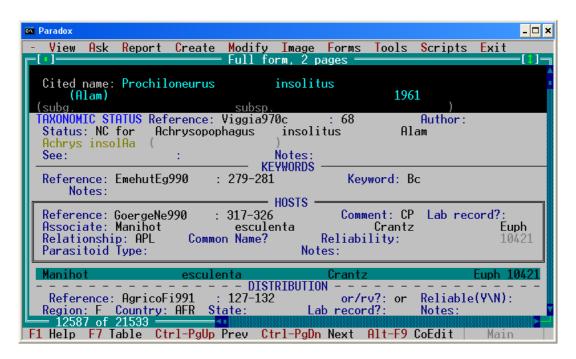
1. Put primary parasitoid (*Epidinocarsis lopezi*) in "master table" Copy host plant (*Manihot esculenta*) to "host table" Put APL in "relationship" field



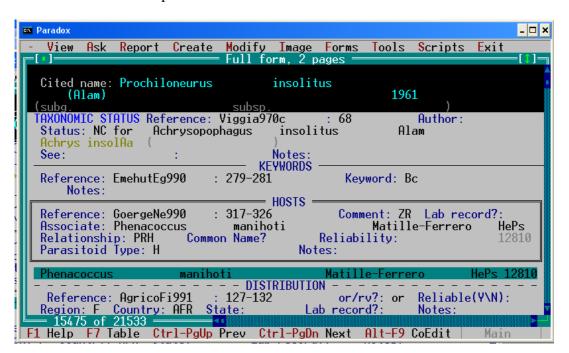
2. With primary parasitoid (*Epidinocarsis lopezi*) in "master table" Copy host (*Phenacoccus manihoti*) to "host table" Put PRH in "relationship" field



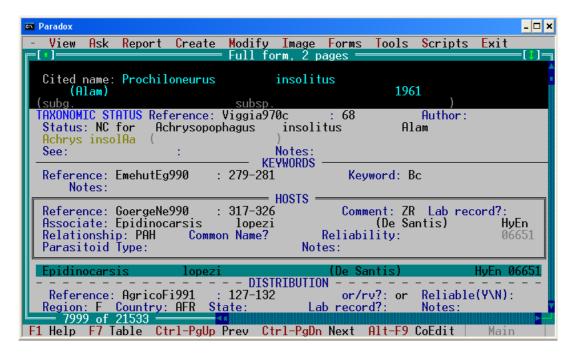
3. With primary parasitoid (*Epidinocarsis lopezi*) in "master table" Copy hyperparasitoid (*Prochiloneurus insolitus*) to "host table" Put HYP in "relationship" field



4. Move to hyperparasitoid (*Prochiloneurus insolitus*) in "master table" Copy host plant (*Manihot esculenta*) to "host table" Put APL in "relationship" field



5. With hyperparasitoid (*Prochiloneurus insolitus*) in "master table" Copy (primary) host (*Phenacoccus manihoti*) to "host table" Put PRH in "relationship" field Put "H" in "Parasitoid Type" field



6. With hyperparasitoid (Prochiloneurus insolitus) in "master table"

Copy (parasitoid) host (*Epidinocarsis lopezi*) to "host table"

Put PAH in "relationship" field

Put "H" in "Parasitoid Type" field.

[Also if the authors say that Prochiloneurus is a parasitoid of the pupae or larvae of Epidinocarsis then put "P" or "L" in Parasitoid Type field]

"Parasitoid Type"

Four fields with links to a look-up table (P-Type) that provides a two letter code reflecting the type of parasitoid.

"Reliability"

Two fields with links to a look-up table (Reliable) that provides a single number of letter code that reflects the reliability of the parasitoid or host identification or the record as a whole.

DIST TABLE

The Look-up Country table is designed in such a way that it is only possible to enter a country record by moving the cursor to the "Country" field, using the Look-up table and F2 to copy across and fill in the appropriate "Region", "Country" and "State" field. However, you can do the same by entering the Code number in the "Country" field of the DIST table, e.g. 169 for Italy, 422 for England.

Comments on Fields

<u>"Comment"</u> – this reflects whether or not the record is a primary one or secondary or the source of record if not from original publication.

or: primary (original) reference rv: secondary (review) reference

CP: information from CABIPEST abstracts

ZR: information from Zoological Record abstracts BA: information from Biological Abstract abstracts

"Lab record?" - indicates an "unnatural" association:

Lb: association in laboratory Bc: biocontrol association Gr: greenhouse association Sd: stored products association

REFS TABLE

Reference code

This is important since the whole database is reliant on the correct link between each component and the REFS table. Each reference code is unique. It is composed of the first six letters of the first author's family name (including spaces, hyphens and capitals) followed by the first two letters of each of the next two authors' names, flowed by the year (drop the millennium for years before 2000 but include the millennium for years from 2000 onwards.

Examples:

Noyes 1976 -> Noyes 976

Noyes2006 -> Noyes2006

Subba Rao 1976 -> Subba 976 (note space)

Hex-Bloggs 1980 -> Hex-Bl980

Mar N., 1998 _>Mar N998 (this form is quite common in Spanish speaking countries as the mother's maiden name is abbreviated.

Förster1856 -> Forste856 (not dropped umlaut)

Subba Rao, Maharashtra & Bloggs 1980 -> Subba MaB1980

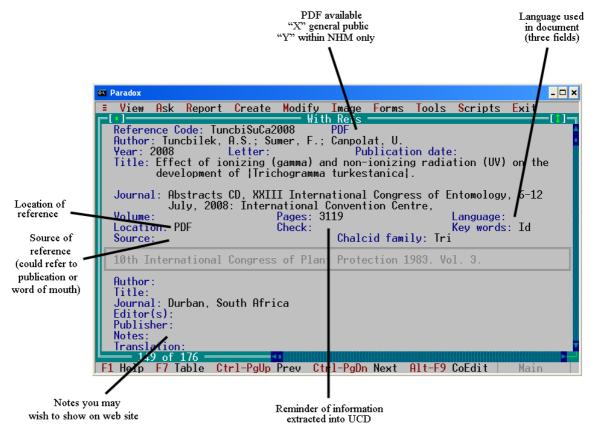
McAdams1925 -> McAdam925

Also for Dutch, Franch, German names including the equivalent to "of" whatever this part is put last, e.g. Jaques van Alphen becomes Alphen, J. van.

Examples

Jaques van Alphen 2003 – Alphen 2003 Peter van den Bosch 1950 – Bosch 950 However, some compound names of this type have the "of" equivalent with an upper case first letter (usually these are Italian or French names), e.g.

Alla Greca 2003 becomes Alla G2003



A few others insist that this part of their name is included with the family name, eg. Simon van Noort so this is written:

Simon van Noort 2006 -> van No2006

NOTE. It is especially important to remember that in Paradox the code is case sensitive, but in Access (and thus the web version) it is not. In Paradox Johans996 is different from Johans996 whilst in Access they are precisely the same.

NOTE. Reference codes always exclude accents and diacritic marks (this makes it easier to search for a given reference). For instance Förster, Gützmacher & Évërt 1964 will be ForsteGuEv964 and NOT FörsteGüÉv964.

Duplicate RefCode

If a record code is duplicated but the reference is not (in the case of an author(s) published more than once in a year then simply add a "b", "c", etc to the code and enter the same letter in the "letter" field.

Authors field:

Authors' names are ALWAYS separated by a semicolon (never by an amphisdand (&)).

Date of publication

The actual date of publication of the paper/book is added to the "Publication date" Field. This is a "date" field and has a specific format: date-mon-year, e.g. 29-Aug-2008. If you do not know the exact day within the month then use the last day of that month and enter a tilde (~) in the (unnamed) field to the right of the "Publication date" field. Similarly for unknown date in year then use last day of year and add an apostrophe (') in this field

- < denotes that publication date is known to be before this date
- > denotes that publication date is known to be after this date
- ~ denotes that publication date was sometime in month given
- ' denotes that publication date was sometime in year given
- # has been used for denote that publication date was sometime in month given

Language (3 fields)

The first field indicates the main language in which a publication is written and is signified by the first letter being upper case, e.g. Fr for French. The second and third fields indicate thee summary language(s) and are signified by the first letter being lower case, e.g. fr for French. Appears on the UCD.

Key words (3 fields)

Provide three selected key words that best describe the publication. Appears on the UCD.

Location

An "aide de memoire" that does not appear on the UCD. Indicates where the reference may be found:

PDF – as PDF on server.

R – Separate available in Chalcidoidea reprint boxes

HR – Separate available in Hymenoptera reprint boxes

BR – Separate available in Bound Hymenoptera reprints

EL – Entomology library, usually with call numbers

ZL, BL, GL,. Etc. various museum libraries, occasionally with call numbers

AP, JSN ZB – copy with Andrew Polaszek, etc.

Source

An "aide de memoire" that gives the source that originally provided the reference. It may be a person or a reference code or the database that provided it (CP for Cabipest and ZR for Zoological Record). Does not appear on the UCD.

Check

An important "aide de memoire". This prevents duplication of effort and provides information on what sort of information has been added to the UCD from a publication. It is important that something is added to this field whenever information is added to the UCD from a publication. I use the following codes:

- C All relevant information extracted from reference (Completed).
- T bare taxonomic information: new taxa, nomenclatural changes, keys; this also includes all information on distribution and hosts of all new taxa described, but NOT of previously described taxa.
- B References (Bibliography) at end of a paper checked against refs to ensure relevant papers have been included in REFS.
- D All information on distribution of taxa added to database.
- H All information on biology and hosts of all included taxa added to database.
- CP All relevant information added from the Abstract of the paper as appearing in Cabipest abstracts. Original reference should be examined eventually.
- ZR All relevant information added from the Abstract of the paper as appearing in Zoological Record abstracts. Original reference should be examined eventually.
- BA All relevant information added from the Abstract of the paper as appearing in Biological Abstracts abstracts. Original reference should be examined eventually.

Chalcid family

Three letter codes (Enc, Eul, Eur, etc.) denoting chalcidoid family referred to in the publication. An "aide de memoire" that does not appear in the UCD. Ptobably eventually completely meaningless if classification of Chalcidoidea changes dramatically!

Notes

This includes notes that can be useful. Careful – they will appear on the UCD!!

Translation

This includes notes on any translations into English that may be available, e.g. Entomological Review (gives year, volume and page numbers).

Adding in references from another computer

If you add in new references on another computer and want to add them in to the main database then add the references to a blank REFS table on the other computer. When they are ready to add use Tools/More/Add source table f:Refs *(if you use a memory stick "e" or "f"), target table REFS. Any records with a duplicate RefCode field will be put in a temporary table called "KeyViolations". Rename this table Temp (Tools/Rename/Table) so that you do not lose it if you turn off the computer. Check the Key Violations and delete any duplicates or change the RefCode for those that are not duplicate records. Make a note of those that you change/delete and go to f:Refext (on the memory stick) and delete the appropriate records or change the RefCode as required. When you are confident that you have added the new references into the main database successfully you can then empty the REFS and REFNEW tables on the subsidiary computer to prepare it for any new records to be added. I would suggest that you do not use the

TOOLS/MORE/EMPTY command since this is permanent and there is no come back. It would be safer to use the ASK command and put "delete" in the first field. Press F2 and you will get a table called "Deleted" which you can rename something like "Year" "Month" "Ref"/"Year" "Month" "Ext", e.g. 0901ref and 0901ext. These tables can be deleted at some point in the future when you are absolutely certain the records are not required anymore.

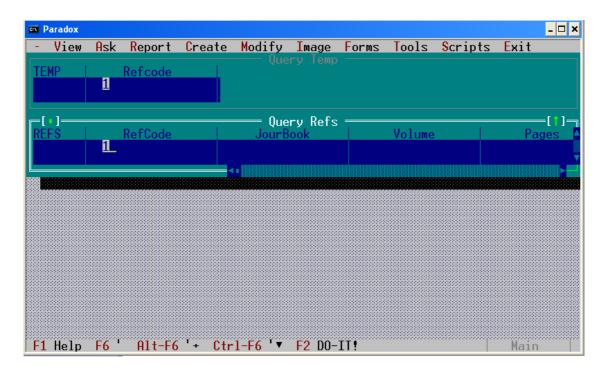
Checking data from entries by volunteers, etc.

Normally I allow volunteers to add to three tables (versions of HKNEW, HOSTS, DIST) only in a separate database that uses the most up-to-date version of the MASTER table. This is accessed by volunteers using one of the subsidiary forms (for instances HKSUE, HOSTSUE, DISTSUE for use by Susan Leigh) that I have built for the MASTER table. You will probably need a separate version for every volunteer that you use, but these can be copied across and altered/named accordingly so that each knows the form they should be using. You could copy the whole database across to a separate memory stick for each volunteer and thus it would also act as a backup of the database. itself.

From my experience it is ALWAYS necessary to check the entries of volunteers before adding them to the main database. This may take an hour every four weeks or so.

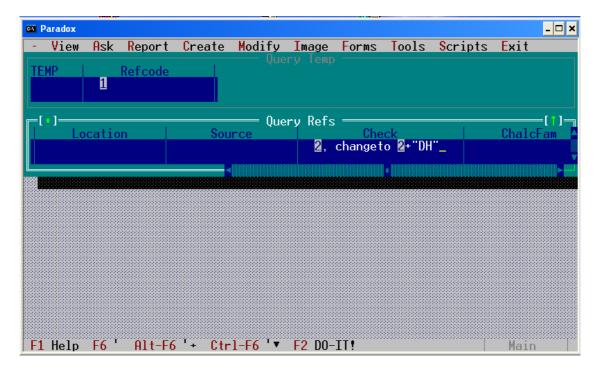
- 1. The "note" fields of all the tables should be checked for content, format and English. Fields where data can be entered can be located by putting the cursor on the "note" field and using ALT-Z and "@.." for the search ("@" is a wild card signifying one character and ".." is a wild card signifying any characters in a variable length string).
- 2. The Relationship fields and Host Family fields in the HOSTS table should be checked. To ensure that entries are correctly related. This is especially important for hyperparasitoids because everyone has difficulty with this. Also you want to ensure that non-phytophagous chalcidoids do not have "PLH" in the relationship field and vice versa, etc. You can scan for these problems fairly quickly, although it will be necessary to have some knowledge of chalcidoids and their biology, some of these may be unfamiliar. The best way to do this it to move the fields on the *Image*. To do this: F10/Image/Move and choose "Relation". Put the cursor on the field to right of "HosFam" (HosGenus) and click Enter/Return. This will move the Relation field (on the *image* only – temporary) to a position between HosFam and HosGenus. You should now index (Alt-S) on the HosFam field (it may be necessary to allow the computer to build and index the first time you do this). You can then quickly scan down the associates' families and see if there are any anomalies (in relation to HostFam or the HosGenus) that need checking, e.g. a plant genus name in the HosGenus field that has PRH next to it (REMEMBER, all animal families have the format Upper case/lower case/Upper case/lower case, e.g. HePs for Pseudococcidae; all non animal families are Uppercase/lower case/lower case, e.g. Poac for Poaceae). Check in the same way by indexing on the "Relation" field. You should be able to guess the chalcidoid name

- in the MASTER table from the TaxonCode, but you may need to refer to the master table just to be sure.
- 3. You may also like to scan down the distribution entries in the DIST table just to see if any obvious problems are present. Unfortunately is not possible to 100% certain about entries here unless you go back and check all entries by the volunteer. However, some erroneous entries may be pretty obvious.
- 4. Once you are sure that the entries in the volunteer's tables are acceptable then add them to the relevant tables in the master database. F10/Tools/More/Add, etc. Remember to put in the correct source table and target table names. The first few times that you do this it may be advisable to make a backup of the entire database in case you make a mistake.
- 5. Once you have added the volunteer's data to the main database return to the volunteer's data. Using ASK/HKSUE (or whatever) record all the references from which the data was abstracted using a check in the "Refcode" field. When the "answer" table appears rename the first table "TEMP" (you may have to overwrite and previously written "TEMP" table. Repeat the query (ASK) for each of the two other tables in turn and after each action add the resulting table to the TEMP table. You should then have run the query on the three tables used by the volunteer, then added the answers together into a single TEMP table. Next you need to restructure the TEMP table to remove any duplicated RefCode. Use F10/Restructure/Temp. Add an asterisk (*) to A15 in Field Type, i.e. A15* and press F2 (DO-IT!). This adds an index to the RefCode field and throws out any duplicate values (and puts them into a temporary table called KeyViolations).
- 6. Now you need to alter the "Check" field in the REFS table to indicate the information that has been extracted for the relevant publications by your volunteer:
 - a) Clear the work space (Alt-F8)
 - b) F10/ASK/Temp
 - c) F10/ASK/REFS
 - d) Move the cursor to RefCode in the TEMP ask table, press F5 and then "1" (not F1)
 - e) Move the cursor to the REFS table (using F4). Move to RefCode, press F5 and then "1". [This indicates that during the query only those records with matching RefsCodes will be queried.]



Still in the REFS ask table move the cursor to the "Check" field, press F5 and then "2" then "," then a space then "changeto" then press F5 and then "2" and then "+" ""DH"". It should look something like:

2, changeto 2+"DH" [with each 2 highlighted] (see below).



This ensures that if there is anything in the "Check" field from previous work(e.g. "TB") then the "DH" will be added to that rather than it get

- deleted by merely using "changeto ""DH"". If you want to add a space between previous codes and whatever you put in then add a space between the first quotation mark and the DH, i.e. ""DH"".
- f) When you are sure that you have this correct (make doubly sure that you have the proper examples in the Refcode field or you may end up changing all the references!) press F2 (DO-IT!). This will then change the "Check" field in the relevant REFS records accordingly. Just to check you should get a temporary table created called "Changed" that should have exactly the same number of records in it as your TEMP table. If there is a difference then you have problem.
- g) Once you are sure that this has all gone OK you can remove the data from the volunteer's tables using F10/ASK (delete) etc. (temporary) or F10/TOOLS/MORE/EMPTY (permanent, irreversible).

PROBLEMS

Losing links to Look-up tables

This may happen periodically for a number of reasons. To reconnect the Look-up table you must be in Edit mode (F9) **NOT** Coedit (Alt-F9).

- 1. Go into Edit mode
- 2. F10 to ValCheck.
- 3. Drop down menu choose "Define"
- 4. Move cursor to field for which you want to set check and press "Return" (= Enter) and follow instructions, usually it is as follows:
- 5. Go into Edit mode
- 6. F10 to ValCheck.
- 7. Drop down menu choose "Define"
- 8. Move cursor to field for which you want to set check and press "Return" (= Enter) and follow instructions, usually it is as follows:
- a. Table Look-up
- b. (Enter) name of table (to be used as Look-up)
- c. Make choice of number of fields to be copied across and whether it should be Help and Fill (normal requirement) or whatever
- d. Press "Return"

ERROR MESSAGES

Unexpected condition at . . . leaving paradox

Normally a glitch in the programme, in which case reopen Paradox and it should work OK.

If problem continues it may be a table has become corrupted. To find if this is the case open each table in turn (starting with Master table and then those linked to it in the data input form – FamTribe; Genus, Species, Tstat; HKnew; Hosts; Dist). Put cursor in first field of first record in "Table view" and scroll all the way down continuously to the end, or use "PageDown" key repeatedly. This may take a little while with a large table such as Hosts. If you get to the end then

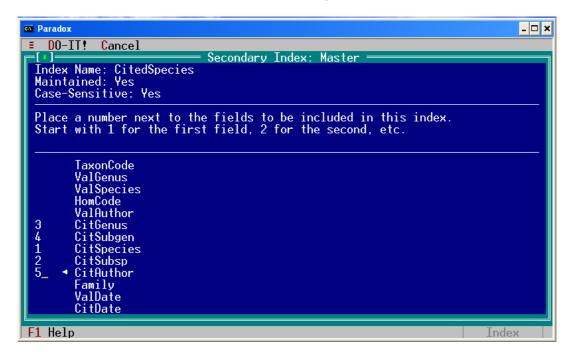
the table is OK. If you get thrown out of the table (by Unexpected Condition . . .) at the same point more than once then you have found the corrupted table. This does not happen often – perhaps once in two or three years!

To remedy a corrupted table, exit Paradox open the MSdos window, then go to the Paradox directory, (CD Pdox45, etc.), then to the TUtility subdirectory and type in "Tutility". Follow instructions for rebuilding the table. The rebuild may take several minutes. You may find that the number of records in the table you rebuild is increased by one or two.

NOTE:

If a table has a complex series of **indexes** (e.g. MASTER or HOSTS) it may be advisable to remove the indexes before rebuilding. [If you do not, the rebuild may get "stuck" in which case it might be necessary to rebuild at least some or all of the tables' forms (hours work).] If you do remove the indexes then it will be necessary to rebuild them (5 minutes per form) (see below).

- To remove a tables' indexes use Tools/Delete/Index/All.
- To rebuild an index use Modify/Index. (example below)



NOTE: If TUTILITY refuses to rebuild the table because of a broken "memo link" go back into paradox. Open the problem table. Use the "Modify" "Restructure" command. Change the Memo field to alphanumeric field and click on Do-It (Restructure). When this is done repeat the process but change the same field back from an alphanumeric field to a memo field. Repeat the process for "Rebuild" for this table in TUtility.