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Morphological study and classification of a group of genera of Lymantriidae, using the HENNIG program (Lepidoptera)

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Summary

A morphological study of 20 genera and 1 aberrant species of Afrotropical Lymantriidae based on external characters (a total of 56 characters with 200 character states) is presented. The HENNIG program was used for the classification of these genera. The very few trees generated by the program and the consistency among them will probably allow a suprageneric classification of the whole family to be determined, but the way the taxa would be described could be unconventional.

Introduction

The last catalogue on a world basis for the Lymantriidae, which is still the best reference for the family, was written by Bryk (1934). Unlike earlier works, for the first time a subfamily division was proposed : the Lymantriinae, the Anthelinae and the Pterothysaninae. However, the latter two subfamilies have since been recognised as separate families (Watson *et al.*, 1980). The Lymantriidae have therefore never had, and still have no family group division.

The only key to the genera ever produced on a world basis is that by Walker (1855). Many genera have since been transferred to other families and many new ones have been described so this key has become completely obsolete. The only keys now available are those for regional faunas, of which that by Collenette (1955) for the Afrotropical fauna is the most useful. However, this key has also become out of date, due to the description of new genera and splitting up of old ones. This is the present situation of the systematics of the Lymantriidae, a family with more than 2500 species, of which more than 1200 occur in the Afrotropical region, and which comprises more than 300 recognised genera.

Aim, collections and methodology

At first the aim was to construct a key to the genera based on the material at our disposal (the collections of the Musée Royal de l'Afrique-Centrale, Tervuren, and the Institut des Sciences naturelles de Belgique, Brussels) using a great variety of different characters, most of which were never used before. Starting progressively to analyse these characters it became clear that they showed a very high degree of incongruence. Having discussed this with a few colleagues they persuaded me to use the HENNIG program (Farris, 1988) to calculate the affinities between the taxa. In order to use this program all characters and their states have to be coded in a specific way. However, this coding and additional observations was so time-consuming that I had to restrict myself to twenty genera and one aberrant species of Afrotropical Lymantriidae.

Characters and their states

When starting to observe and code the characters and their states it became obvious that a satisfactory coding was going to be very difficult to achieve. Although many characters and their states can readily be described (for example, the number of hairs on top of pectinations of the antennae : one, two, three or more), there are others which need careful observation before a satisfying description or coding can be carried out. An example is the areole in the forewing (a small cell sometimes present above the distal part of the central cell). Former authors (e.g. Collenette, 1955) used as character states in their identification keys : areole absent, areole present. But the character state 'areole present' includes at least two states : in the Lymantriidae the areole can be formed by R2 touching stalk R3+4 and then diverging, or by a small vein joining R2 with stalk R3+4. These are two different states. Using the character state 'areole absent' is equally unsatisfactory : the absence of an areole can be due to the fact that R2 does not touch stalk R3+4, that there is no small vein joining R2 to R3+4 or even that R2 does not originate from the cell, but from the stalk R3+4 so that no areole can be formed. This demonstrates the difficulties encountered even in such an apparently easy exercise as describing and coding characters and their states.

Each character also had to be labeled as additive or nonadditive. If a character is additive the number of steps between the two states of the two taxa is taken into account by the program for calculating the dissimilarity of the two taxa (for example if a vein originates to the left, midway or to the right of a connecting vein, the taxa having the vein to the left and to the right are more different from each other than those same taxa in relation to the taxon having this vein midway). If the character is nonadditive then all the different states of a character between any two taxa is treated with equal weight.

For the taxa analysed we found the following characters to be appropriate (bold = structure to which the following characters belong (if bold is within the

double quotes there is only one character) ; number = number of the character ; a or n = additive or nonadditive character ; between double quotes = name of the character ; at the end in brackets = number of states of the character).

Pectination of antennae : 0 ,n,"Colour of hairs (5)" ; 1 ,a,"Hairs alongside, perpendicular (4)" ; 2 ,a,"Hairs alongside, parallel (3)" ; 3 ,a,"Hairs on top (9)" ; 4 ,a,"Scales (2)" ; 5 ,a,"Distance (3)" ; 6 ,a,"Number (4)" ; 7 ,n,"Inner lining hairs (3)".
Flagellum : 8 ,n,"Colour compared to frons (6)" ; 9 ,n,"Pectination aspect (3)".
Palpi : 10 ,n,"Direction of scales (3)" ; 11 ,n,"Colour compared to frons (5)" ; 12 ,n, "Length (7)".
13 ,n,"**Proboscis** (2)" ; 14 ,n,"**Frons** colour (2)" ; 16 ,n,"**Leg** scaling (5)" ; 16 ,a,"Length of **Femora** (2)".
Hind tibiae : 17 ,a,"Pairs of spurs (2)" ; 18 ,a,"Length of spurs on (1 p.sp.) (2)" ; 19 ,a,"Length 1st p. of spurs (2 p.sp.) (3)".
20 ,a,"Ventral spines on **hind tarsi** (2)" ; 21 ,a,"**Claw lobe** (3)" ; 22 ,a,"**Pronotum** collar (2)" ; 23 ,a,"**Notum** drawing (2)".
Wing : 24 ,a, "Texture (4)" ; 26 ,n,"Colour in general (7)" ; 26 ,n,"Postmedian fascia (2)" ; 27 ,n,"Vein colour (4)".
Forewing venation : 28 ,a,"Cell length (% of wing length) (5)" ; 29 ,a,"R1 direction (2)" ; 30 ,a,"Second areole (2)" ; 31 ,n,"R2 connection (6)" ; 32 ,a,"Basis of areole or distal part of cell (2)" ; 33 ,a,"Origin of R2 (4)" ; 34 ,n,"Origin of R4 (3)" ; 35 ,a,"Stalk R3+4 (3)" ; 36 ,a,"Origin of R5 (4)" ; 37 ,a,"Origin of M1 (4)" ; 38 ,n,"Discocellulars angle (4)" ; 39 ,a,"Distance between M1 and M2 (2)" ; 40 ,a,"Traces of median vein in cell (2)" ; 41 ,a,"M2-M3 distance (2)" ; 42 ,a,"Cu1a origin (4)" ; 43 ,n,"Cu1a direction (6)" ; 44 ,n,"Cu1b direction (3)" ; 45 ,a,"Cup at outer margin (2)".
Hindwing venation : 46 ,n,"Sc touching cell (4)" ; 47 ,a,"Rs and M1 stalk (5)" ; 48 ,n,"Discocellulars angle (3)" ; 49 ,a,"Discocellulars length (5)" ; 50 ,a,"M2 origin (2)" ; 51 ,a,"M3 origin (2)" ; 52 ,a,"Cu1a origin (4)" ; 53 ,n,"Direction of Cu1b (4)".
54 ,n,"**1st abdominal segment** (7)" ; 55 ,n,"**Tymbal** organ (3)".

With these characters Table 1 could be mapped, ready to be used by the HENNIG program.

Results with the HENNIG program

The big surprise when running the HENNIG program for the first time with the mh* ;bb* ; options was that only 3 trees were generated. When improving the coding and labeling for additivity or not, the number of trees even dropped to 2. This was quite unlike analyses made by a few colleagues working with other groups of invertebrates who had to cope with tens and even hundreds of different trees per data matrix. The reason for the few number of trees in this application soon became clear : unlike the matrices of my colleagues, mine comprised very many characters with many states, which apparently eased the construction of the trees by the program. Even comparing the trees raised

optimism (Fig. 1) : they differed only in three lines. Ancestor 25 (the ancestors are represented by the numbers inside the trees, in our case 21 to 39) groups *Creagra* and *Crorema* in one tree, and groups *Creagra* with the rest of the genera in the second tree. This seems very promising for future research, even if through the use of a great number of characters the options ie, ie* and ie- which find the trees of minimal length but are very time-consuming could not be used.

As the trees have a length of 394, it is very impractical to analyse them cladistically ; we performed it typologically by comparing the characters of the different genera of the subtrees in the data matrix. A first subtree groups the genera *Stilpnaroma*, *Leucoperina*, *Stracilla* and *Eala* in which few characters of the head, but many of those of legs and general wing aspect are in common ; unlike the following groups there is a great similarity in most characters of the hindwing venation. The second subtree groups *Anexotamos*, *Pirga*, *Cimola* and to a lesser degree *Cadurca*. In this, the characters of the antennae are also very dissimilar, but those of frons and palpi on the other hand are similar. Unlike the preceding subtree, a group of characters of the venation of forewing (M1, M2, Cu1a, Cu1b) is very concordant, but in the hindwing venation there is no character at all in common. The last subtree which can easily be analysed is the one grouping *Parapirga*, *Olapa* and *Croremopsis*. These genera have many characters of all kinds of structures in common, but for the first time, for example, the claws and the tymbal organs. The rest of the tree is more difficult to analyse because of the branchings leaving mostly one genus against the rest of the tree.

Table 1

Map of the characters and states ready for use with the HENNIG program

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States/char.     054392343633572252232322472452262433444222463245352244 73
Additive/not     naaaaaannnnnnnnnaaaaaaaannnaaanaanaaanaaaannanananaaaannn
Number of the    0         1         2         3         4         5
   character     012345678901234567890123456789012345678901234567890123 45
  0 Coll_croc    111213323321111411001211351151121312222111422123131121 51
  1 Olapa        141912313123321312102111301141131012224111431112131121 41
  2 Parapirga    141912210121321312202111341441141212224111431113231141?1
  3 Cropera      144171231312142131112311261141111212224111431134131141 02
  4 Pteredoa     111122332132432141212111151141151312223111312223221141 02
  5 Leptepilep   144171331112321312102111351131142312312111331123231131?1
  6 Marblepsis   141713211211511411031111331451121212223111163123231241 40
  7 Leucoperin   112613411132621512201311351142161412412211423135251132 51
  8 Stilpnarom   111213221322311312201111351441002312223211323133241132 22
  9 Stracilla    111312313121621312102311251131161012414112012315111415 0
 10 Eala         111113410125121512101311271121161012412112031135251142 00
 11 Pseudobazi   131513211612132131122311271341121212213211332133231131 53
 12 Crorema      141512211123421311022311162131121212023211221123241141 31
 13 Croremopsi   231912213123321311022111351131141212322111222113141131 61
 14 Pirga        341712211221211122201122411250220223222111443132231124?1
 15 Collenette   313813323321421411031111351141121212222111322123141131 71
 16 Cadurca      342713335320712010201111352131121213224211421125111131 22
 17 Cimola       411912332221211212101211421451121233124121442125312223 12
 18 Anexotamo    411413331221211122201233411350121123241111443141141114?2
 19 Ogoa         444171211422221112201211351151121223214111443113431221 22?
 20 Creagra      511?122111223223110???111511211112012331113521232311 31?1

Number of character states 200
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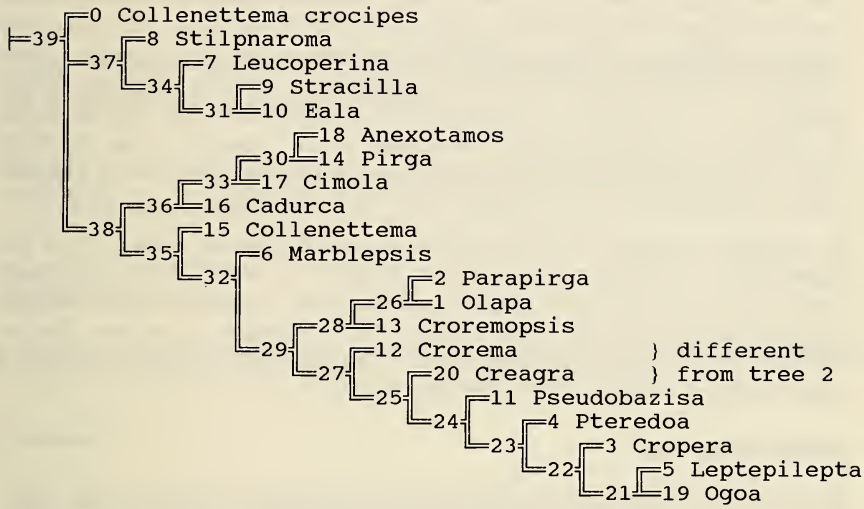
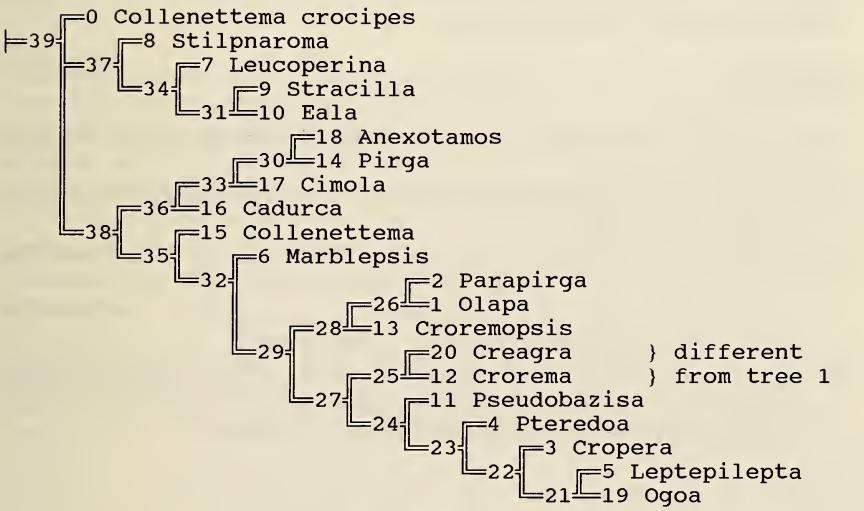


Tree 1



Tree 2

Fig. 1. Two trees produced by the HENNIG program for 20 genera and 1 aberrant species of Afrotropical Lymantriidae.

Conclusion

These very few observations give a clear indication that the results were in fact very similar to those before using the HENNIG program, but previously they were difficult to realise : a higher classification (say a grouping of these subtrees into tribes) would define these higher taxa using different sets of characters. For example, one taxon would be described with characters of the antennae, a second one with characters of the venation of the forewing and a third with characters of the abdomen and so on. This is very different from the usual way, but the idea gives one food for thought.

We can also conclude that this small scale morphological study gave us the opportunity to appreciate the practical qualities of the HENNIG program. The time lost in accurately coding the characters is largely retrieved at the stage of analysing the trees and finding back the relevant characters. We are confident that it will be of great help in constructing a classification on a larger scale and maybe at the family-group level.

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