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An attempt of distinguishing subgeneric taxa in the genus *Liochthonius* HAMMEN (*Acari, Oribatei, Brachychthoniidae*)

[With 2 tables and 18 text-figures]

To determine the affinity is the clue question of biological classification and the only legitimate is such a classification that is founded on the natural affinity of organisms that, in turn, reflexes processes of the evolution.

Since many years two currents of classification — phyletic and phenetic ones are developed by systematics. This is the arbitrary division only. Most frequently they are not applied in a pure form. The lack of fossils or enormous deficiency in paleontological knowledge of certain animal taxa make difficult or often practically impossible elaboration of a classification on phylogenetic grounds. Neontological studies as morphophysiological, anatomical, ecological, biogeographical analyses etc. enable often, it is true, a reconstruction of the past of a entity, an assessment of a certain set of characters — starting point i.e. determination of characters of a common ancestor. They make possible stemming out from this hipothetical ancestor individual phylogenetic lines on basis of which the natural classification will be built. Phyletic approach then, is characterized by the following sequence of operations: 1) a grouping of homologies, taxonomically significant are the similarities between homological characters. 2) an assessment of belonging to a common phylogenetic branch on the basis of commonly descending features. 3) a construction of classification. Proceeding in such a way may lead to errors.

Legitimacy of classification based on present day living animals may often be questioned with regard to observed phenomenon of parallel, mosaic evolution or convergence and phenomena of specific adaptations. Beside that,

an analysis of taxonomical characters, a choice of characters with a big taxonomical weight or characters that are not indices of relationship are often subjective, depend on personal qualifications of a student and current knowledge of an animal taxon in question. Whilst it is much easier to find taxonomical characters for diagnostic goals, it is more difficult to weigh these characters in such a way as to use them as indices of affinity in establishing entities of higher systematic categories. In any case, the phylogenetically founded classification is the only one basing on sound theoretical grounds and is in connection with a constant augmentation of information quantity following the increase of accuracy of comparing methods. Owing to this classification the systematics brings in an immense contribution to the study of evolutional processes, to biological theory.

On the other hand the phenetic classification bases excusively on the dergee of similarity and on the assumption that the maximum resemblance corresponds to the closest affinity, the assumption most commonly true after all. Thus, an undubitable advantage of the phenetic classification comes from a taking in consideration a large number of examined characters that carry much information. Moreover, by the equivalent treating of all, characters errors of subjectivism are avoided. Finally, it makes possible an employing of mathematical grouping methods and information arrangement by means of speed computers. The phenetic approach differs also from the phyletic one by sequence of operations carried. When the correlation of similarity of taxonomical characters is arrived at, the construction of classification begins and later it should be followed by phylogenetic interpretation, often neglected by taxonomists. There exist various techniques and means to determine similarity between taxa. The subdivision of the phenetic taxonomy into numerical and congregational taxonometry, the two main currents, may appear useful.

The numerical taxonometry assumes taxonomical equivalence of all characters. Any of taxonomical characters is equally valid, it is describe to have plenty of them. This controversial assumption is frequently considered to be simplifying since certain features solely separate OTUs (operational taxonomical unit, for example: individual, population, species or organism, taxon, unit). In the congregational taxonometry the informative value of any character is differentiated. This is the peculiar technique of phenetic classification which combines mathematical ordering and observations grouping methods and in some way recognizes "phylogenetic", "non numerical", unequal classifying value of a taxonomical character though this recognition has not been precised. This method does not assume a priori what are phylogenetic values of taxonomical characters but once the operation of their assembling is settled the assemblages of these characters may decide upon the final elaboration of classification and, their interpretation may assign the characters a considerable phylogenetic value. Making use of this method the characters differentiating and grouping OTUs are processed. Both numerical and congregational techni-

ques differ already at the first steep of proceeding that leads to creation of phenetic classification, at the stage of searching for some numerical dimension that would characterize the degree of resemblance or difference between OTUs. One of methods founded on congregational taxonometry is the taxonomical analysis worked out by SMIRNOV (1968). A principle that value of information is inversely proportional to a character frequence (constance) is the essential point of this method. In other words, the similarity of two OTUs is measured not only by the presence or absence of a given character but also by its frequency of occurence in other OTUs of the compared group.

Making use of SMIRNOV's taxonomical analysis an attempt of distinguishing subgeneric taxa in the genus *Liochthonius* (*Acari, Oribatei, Brachychthoniidae*) has been made. In this genus the dynamic speciation is under way and therefore it seemed to be heterogeneous and comprising a sufficient number of species (19 recorded from Poland) that could be subject to grouping, ascertaining the similarity between obtained groups and possibly to erecting taxa of subgeneric level.

For this purpose 37 morphological characters as body proportions or small elements on the notogaster and one ecological character have been chosen. The ventral side of body does not have features which would allow discrimination of species. Chaetotaxy of legs has not been analysed. The SMIRNOV's method permits operating bimodal characters only (with a positive and negative) and hence a few polimodal characters occurring in the investigated species had to be transformed into bimodal ones, in order to obtain a combination of optional 0's and 1's (Table I).

To calculate values of similarity between taxa the following formula has been employed (SMIRNOV 1968):

$$t_{xy} = \frac{s}{n} \frac{\Sigma}{f} \left(\frac{1}{B} \right) - 1,$$

where s = number of examined taxa, n = number of examined characters, f = number of coincidental characters (positive and negative ones), B = frequency of a character.

SMIRNOV introduces also an idea of taxonomical relation of the species to itself i.e. the index of intraspecific similarity:

$$t_{xx} = \frac{s}{n} \frac{\Sigma}{n} \left(\frac{1}{B} \right) - 1.$$

Naturally, values of this index are always the highest and constitute a point of reference for values of interspecific index of similarity on a particular column (Table II). Since particular values calculated according to the formula

Table I. Taxonomical characters of *Liochthonius* HAMMEN species in the bimodal system.

	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.	16.	17.	18.	19.	20.	21.	22.	23.	24.	25.	26.	27.	28.	29.	30.	31.	32.	33.	34.	35.	36.	37.	38.
L. alpestris	0	1	0	0	1	0	0	1	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1
L. ensifer	0	0	1	0	0	1	0	0	1	0	1	0	1	0	0	1	0	1	1	0	0	1	1	1	0	1	0	0	1	0	0	1	0	1	0	1	1	0
L. evansi	1	0	0	1	0	0	0	1	0	1	0	0	1	0	1	1	1	0	1	0	1	0	1	0	0	1	0	0	1	0	1	0	0	1	0	0	0	1
L. forsslundi	1	0	0	1	0	0	0	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	0	1
L. gisini	1	0	0	1	0	0	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	0	0	1	0	0	0	1	0	1	0	1	1	1	0	0	0	1
L. globuliferus	0	1	0	0	1	0	0	1	0	1	0	0	1	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	1	0
L. horridus	1	0	0	1	0	0	0	1	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	0
L. hystricinus	0	1	0	0	1	0	0	1	0	0	1	0	0	1	1	1	1	1	0	1	1	1	0	1	0	1	0	1	1	0	0	0	1	1	0	1	1	0
L. lapponicus	0	1	0	0	1	0	0	1	0	1	0	0	1	0	0	1	0	0	0	0	1	1	0	1	1	0	1	0	0	0	0	1	0	1	0	0	0	1
L. muscorum	0	0	1	0	0	1	0	1	0	0	1	1	0	0	0	0	0	1	1	0	1	1	0	1	0	0	1	0	0	1	0	1	0	1	0	0	0	0
L. occultus	0	1	0	0	1	0	0	1	0	1	0	1	0	1	0	0	1	1	0	0	0	1	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1
L. perpusillus	0	1	0	0	1	0	0	1	0	0	1	0	1	0	1	1	1	1	0	0	0	0	0	0	0	1	0	0	1	1	0	1	0	1	0	1	0	1
L. piluliferus	1	0	0	1	0	0	1	0	0	1	0	1	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	1	1	0	1
L. plumosus	0	1	0	1	0	0	1	0	0	1	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0	1	0	0	0	1	0	1	1	0	0	0	0	1
L. propinquus	1	0	0	1	0	0	0	1	0	1	0	1	0	1	0	1	0	0	1	0	1	0	1	1	1	1	1	0	1	0	0	1	0	0	0	0	0	0
L. sellnicki	0	0	1	0	0	1	0	1	0	1	0	1	0	0	0	0	0	1	1	0	1	1	1	1	1	1	0	1	0	0	1	0	0	0	0	0	0	0
L. simplex	0	1	0	1	0	0	1	0	0	1	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0
L. strenzkei	0	1	0	1	0	0	0	1	0	1	0	1	0	1	0	0	1	0	1	0	0	1	0	1	0	1	1	0	0	1	0	1	0	1	0	1	0	0
L. tuxeni	0	1	0	0	1	0	0	1	0	0	1	0	1	0	1	1	1	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0

	The characters chosen (positive side)	(negative side)
1.	Body length < 170 μm	bigger than 170 μm
2.	Body length 170–195 μm	body length different
3.	Body length > 195 μm	less than 195 μm
4.	Body width < 101.1 μm	more than 101.1 μm
5.	Body width 101.1–125 μm	body width different

6.	Body width > 125 μm	less than 125 μm
7.	Length of sensillus < 28 μm	more than 28 μm
8.	Length of sensillus 28–39 μm	length of sensillus different
9.	Length of sensillus > 39 μm	less then 39 μm
10.	Length of "ro" setae 10–20 μm	more than 20 μm
11.	Length of "ro" setae 20–30 μm	less than 20 μm
12.	Length of e_1 setae < 25 μm	more than 25 μm
13.	Length of e_1 setae 25–37 μm	length of e_1 setae different
14.	Length of e_1 setae > 37 μm	less than 37 μm
15.	Length r–b < 55.0 μm	more than 55.0 μm
16.	Value of $(r-b)/e_1$ index < 2.1	more than 2.1
17.	Tergit PY broadly rounded in posterior part	pointed or narrowing
18.	Propodosoma basis almost as large as hysterosoma	narrower than hysterosoma
19.	Propodosoma constricted before "ex" setae	not constricted
20.	Propodosoma surface covered with fields (except "int" fields)	no fields (except "int" fields)
21.	"Int" fields present on propodosoma	"int" fields absent
22.	Hysterosoma surface covered with fields	fields lacking
23.	Characteristical folds in the anterior of propodosoma	folds absent
24.	Chitinous lamellae joining "ex" setae on propodosoma	lamellae absent
25.	f_1 setae on hysterosoma are surrounded by bow-like, chitinous lamellae	lamellae absent
26.	f_1 setae on hysterosoma stick on characteristical prominens	prominens absent
27.	Sensillus head biforcated at its end	not biforcated
28.	Sensillus head round	different
29.	Broadly lancet-like setae	different
30.	Moderately lancet-like setae	different
31.	Very thin setae	different
32.	Setae edges smooth	different
33.	Setae on tergit NA thiner than those on tergits NM and PY	all setae evenly large
34.	„ro" setae distint from rostrum margin	setae at the end of rostrum
35.	„int" setae close together	"int" setae distant
36.	„ro" setae longer than e_1 ones	"ro" setae shorter than e_1 ones
37.	End of d_1 setae reach beyond bases of e_1 setae	do not
38.	Species preferring forests, especially coniferous ones	preferring other biotopes

t_{xx} are not comparable, the value of t_{xx} is being considered as 100 and the remaining values in the diagram are transformed according to the formula[1]:

$$\frac{2 \cdot t_{xx} \cdot 100}{t_1 xx + t_2 xx}.$$

The values obtained as a result of this process are also presented in the Table II.

The second step of phenetic classification is the same for both the numerical and congregational taxonomies. In this step methods of grouping like CZEKA-NOWSKI's square, methods of dendrtes or dendrograms are commonly used. Among them the most useful seems to be the method of dendrograms that links two first OTUs on the ground of the highest index of similarity i.e. smallest Euklides distance, while for any subsequent OTU its average index of similarity to all OTUs already inserted in the dendrogram is calculated (fig. 18). In the drawn dendrogram species of the genus *Liochthonius* HAMMEN are clustered in different ways into 4 separate groups. The grouping and consequently the classification received by SMIRNOV's method is the preliminary ordered picture of the information wanted. The obtained picture has to be evaluated. Once the analysis is completed and peculiarities of the groups estimated, there are three possibilities to choose: or this is a sufficient classification, or either it should be additionally perfected or the desire of recognition of it as a valid classification should be given up.

The group IV has nine common characters, none of them exclusive for this group. The most important of the characters (having the highest informative value) are the presence of plates on the hysterosome, presence of interlamellar plates, the body length above 195 μm.

The group III is also deprived of exclusive taxonomical characters. Of 11 common characters the most important are: the value of the index $\frac{r-b}{e_1} > 2.1$ the length of setae $e_1 < 25$ μm and length of rostral setae comprised between 10–20 μm.

The group II is characterized first of all by the following features: length of body 170–195 μm, body width 101–125 μm, presence of moderately lancet--like setae. The total number of common characters for this group is 9 but none of them is exclusive.

The group I has 12 common characters. One of them — the presence of broadly lancet-like setae is not encountered in other species of the genus *Liochthonius* HAMMEN. The other more important characters: body width < 101 μm, length of setae e_1 25–37 μm, value of the index $\frac{r-b}{e_1} < 2.1$, rostral setae distant from the rostrum edge.

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[1] The formula was originally proposed by Dr. E. BIESIADKA, unpublished.

Table II. Taxonomical relationship of species of the genus *Liochthonius* HAMMEN as calculated in the SMIRNOV's method (upper, right part of the diagram) and after transformation according to the formula of BIESIADKA (left, lower part of the diagram)

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	alpestris	+0.79 100	-0.19	-0.13	-0.30	-0.39	-0.01	-0.33	+0.03	+0.19	-0.03	+0.09	-0.15	+0.15	-0.23	-0.04	+0.05	+0.31	+0.25	-0.12
2	ensifer	-13.57	+2.01 100	-0.25	-0.22	-0.15	-0.36	-0.10	+0.55	-0.10	+0.32	-0.23	-0.18	-0.34	-0.10	-0.38	+0.48	-0.40	-0.25	-0.14
3	evansi	-13.69	-18.59	+0.68 100	+0.37	+0.31	+0.10	+0.13	-0.25	-0.15	-0.22	-0.25	-0.06	+0.07	+0.11	+0.07	-0.23	-0.07	-0.03	-0.25
4	forsslundi	-36.81	-15.44	+48.68	+0.84 100	+0.53	-0.21	+0.48	-0.10	-0.32	-0.21	-0.42	+0.09	-0.08	+0.30	-0.11	-0.29	-0.24	-0.09	-0.10
5	gisini	-44.83	-10.13	+38.04	+59.22	+0.95 100	-0.05	+0.76	-0.15	-0.41	-0.27	-0.40	-0.11	+0.08	+0.59	-0.08	-0.60	-0.22	-0.39	-0.06
6	globuliferus	-1.18	-24.66	+12.58	-24.00	-5.38	+0.91 100	-0.23	-0.24	+0.07	-0.22	+0.28	+0.16	+0.04	-0.03	+0.23	-0.34	-0.07	-0.14	+0.08
7	horridus	-37.93	-6.76	+15.95	+53.63	+80.00	-24.73	+0.95 100	-0.09	-0.46	-0.32	-0.21	-0.16	+0.03	+0.54	-0.13	-0.54	-0.17	-0.34	+0.13
8	hystricinus	+2.83	+32.93	-24.87	-9.22	-13.16	-21.43	-7.90	+1.33 100	+0.02	-0.22	-0.11	+0.05	-0.45	+0.01	-0.48	-0.06	-0.13	+0.15	+0.09
9	lapponicus	+26.39	-7.52	-22.56	-42.95	-51.25	+8.97	-57.50	+2.02	+0.65 100	-0.02	+0.31	+0.04	-0.19	-0.25	+0.15	+0.24	+0.14	+0.07	-0.04
10	muscorum	-2.42	+17.30	-18.56	-16.60	-20.45	-16.92	-24.24	-14.57	-1.71	+1.69 100	-0.12	+0.05	+0.03	-0.35	-0.06	+0.57	-0.17	+0.03	-0.01
11	occultus	+11.61	-16.61	-34.72	-52.50	-46.78	+33.53	-24.56	-10.53	+43.97	-9.79	+0.76 100	+0.05	+0.04	-0.24	+0.05	+0.01	+0.14	-0.03	+0.21
12	perpusillus	-22.22	-14.01	-9.68	+12.86	-14.57	+21.77	-21.19	+5.29	+6.61	+4.44	+7.57	+0.56 100	-0.42	+0.05	-0.08	-0.15	-0.10	-0.05	+0.37
13	piluliferus	+11.81	-18.08	+5.76	-6.18	+5.92	+3.01	+2.22	-29.22	-15.83	+1.74	+3.19	-36.36	+1.75 100	-0.28	+0.13	-0.38	+0.15	-0.02	-0.37
14	plumosus	-30.06	-7.27	+15.49	+37.97	+69.82	-3.64	+63.90	+0.97	-35.97	-28.81	-32.00	+7.69	-22.49	+0.74 100	-0.15	-0.55	-0.06	-0.24	+0.09
15	propinquus	-5.19	-27.54	+9.79	-13.84	-9.41	+27.71	-15.29	-46.15	+21.43	-4.92	+6.62	-12.21	+10.40	-20.13	+0.75 100	-0.04	+0.23	+0.05	-0.16
16	sellnicki	+3.60	+24.00	-17.23	-20.49	-40.82	-22.07	-36.73	-3.61	+18.18	+30.98	+0.73	-11.76	-20.32	-40.29	-2.92	+1.99 100	-0.05	+0.10	-0.23
17	simplex	+44.93	-30.77	-11.02	-33.57	-28.57	-9.33	-22.08	-13.54	+22.58	-14.91	+20.74	-17.39	+12.82	-9.02	+34.33	-3.07	+0.59 100	+0.15	-0.07
18	strenzkei	+30.49	-17.48	-3.92	-10.65	-43.33	-15.91	-37.78	+13.76	+9.33	+2.36	-3.73	-7.09	-1.54	-30.19	+6.25	+7.04	+20.83	+0.85 100	-0.13
19	tuxeni	-16.55	-10.49	-37.31	-13.33	-7.45	+10.19	+16.15	+9.04	-6.11	-0.85	+29.58	+60.65	-30.70	+12.86	-22.69	-17.35	-11.20	-17.22	+0.66 100

Any of the species group II, III or IV, does not meet requirements for an independent taxon. They are not divided by phenetic discontinuity, and above all, any of them is too heterogeneous. This indicates the fact that the resemblance among the individual groups is deeper than between the species (fig. 18).

Theoretically nothing impedes to create polythetic taxa for the major part of the complex of features characterizing a given group. However, assuming the stand-point that there should be a gap between the potential subgenera, an unnecessary dividing of taxon will be avoided in the present paper.

For a possible erecting of a subgeneric taxon solely the species group I is worth of more careful consideration. About $\frac{1}{3}$ of distinguished taxonomical characters occur in any species of this group. In the dendrogram this group is distinctly separated from the others (fig. 18). It is characterized by the scarciest similarity to other groups of species. At last, this group is separated from the rest by a distinct phenetic gap. This difference is made by the presence of broadly lancet-like setae, absent in other species of the genus *Liochthonius* HAMMEN. It happens rarely, however, that a single character suffices to establish subgeneric taxa.

We work however with groups of species that require many elements for their characteristics because each character may evolve in its proper way in any phyletic line. A type of setae like the mentioned appears, for example in *Brachychochthonius zelawaiensis* (SELLNICK) and *Brachychochthonius foliatus* (HAMMER), thus the species belonging to other genus. Maybe, morphological changes in related lines of subgenera of *Brachychochthonius* JACOT and *Liochthonius* HAMMEN occured parallel in such a way that analogical stages or evolutional steps appeared. These stages e.g. "broadly lancet-like setae" are more similar each other than successive stages of a phyletic line. Thus, the occurring of parallel evolution frequently coupled with fluctuating rate of changes (mosaic evolution) imposes a considerable difficulty on classification and often upsets the previous arrangements. Moreover, it is hard to found a taxon diagnosis on a character when the least suspicion arises that it could be convergent. The convergence is not an obstacle in constructing a natural classification because it rarely occurs among entire phenotypes, yet it is frequent amongst closely species and concerns singular characters and organs.

Thus, also for the group I there is not a sufficient reason of distinguishing it as a separate taxon. The dimension of the gap measured by the phenetic distance, though the gap apparently occurs, is so inconspicuous as to be easily questioned.

Hitherto natural, "phylogenetic" classification of the family *Brachychthoniidae* species bases on a number of suprapleural plates mainly and on the degree of advancement of the pleural plate Pl_2 with the tergit PY (NIEDBAŁA 1972). On this ground a sequence of genera evolution was established, the sequence in which the most primitive was found in *Eobrachychthonius* with

four free suprapleural plates and the pleural Pl_2 that is totally separated from
the tergit PY. In the course of this evolution the suprapleural plates fuse or
fuse with the tergit. As a result of this there are no free suprapleural plates,
while the pleural plate Pl_2 is, in fact, entirely fused with the tergit PY in the
most evolutionally advanced genus *Liochthonius* HAMMEN. The phylogenetically
youngest genus is very plastic and considerably differentiated and contains
the highest number of species in comparison with other genera of *Brachy-
chthoniidae* (NIEDBAŁA 1974).

In many species of the genus *Liochthonius* HAMMEN the suprapleural
plates and the pleural plate Pl_2 fuse to a various extent with the tergits NA,
NM, PY. Marks of a suprapleural plates fusing are visible quite often by the
tergite NA and NM. On this ground species of the genus *Liochthonius* HAMMEN
may be filed up in an evolutionary sequence at the beginning of which the
species with very distinct traces of suprapleural plates will be found and con-
cluded with species without such traces. In the species with traces of supra-
pleural plates the presence of this character is in correlation with the presence
of an incision or furrow that are a proof of phylogenetically older separation
of the pleural plate Pl_2 from the tergit PY (figs 1–17).

An examination of the obtained evolutionary sequence of species demon-
strates a continuous variability without any marked gap. The lack of discon-
tinuity renders it imposible to set species in order in separate groups and does
not allow the establishing of a subgeneric taxon. This is an example when
the evolutional continuity makes unfeasible the ultimate classification.

It must be pointed out that there is no regularity or correlation between
the sequence of species based on the fusion of suprapleural plates[1] and the
groups of species obtained as a result of the taxonomical analysis of Smirnov.
It is obvious since in the two methods of classifying different taxonomical
characters were processed. Phylogenetic classification was based on so called
high evolutional value characters, whereas the method of congregation taxo-
nometry was founded on a big number of characters, most probably equi-
valent phylogenetically though bearing different information (not necessary
phylogenetically significant).

It should be emphasized, apart from the precedent question, that phylo-
genetic or congregation approaches result in a similar notion as to classifi-
cation of the genus *Liochthonius* HAMMEN. Thus, this example confirms the
view that, as a rule, data of the congregation taxonometry reaffirm classifi-
cations obtained by the phylogenetic method. If the elaboration of the ma-
terial were stopped at the grouping of species in the dendrogram without an
additional interpretation, the erecting of 4 or at least 2 subgenera would have

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[1] Suprapleural plates are a typical example of taxonomical characters of high value
in the inductive operation — creating a natural system and of little use in deductive ope-
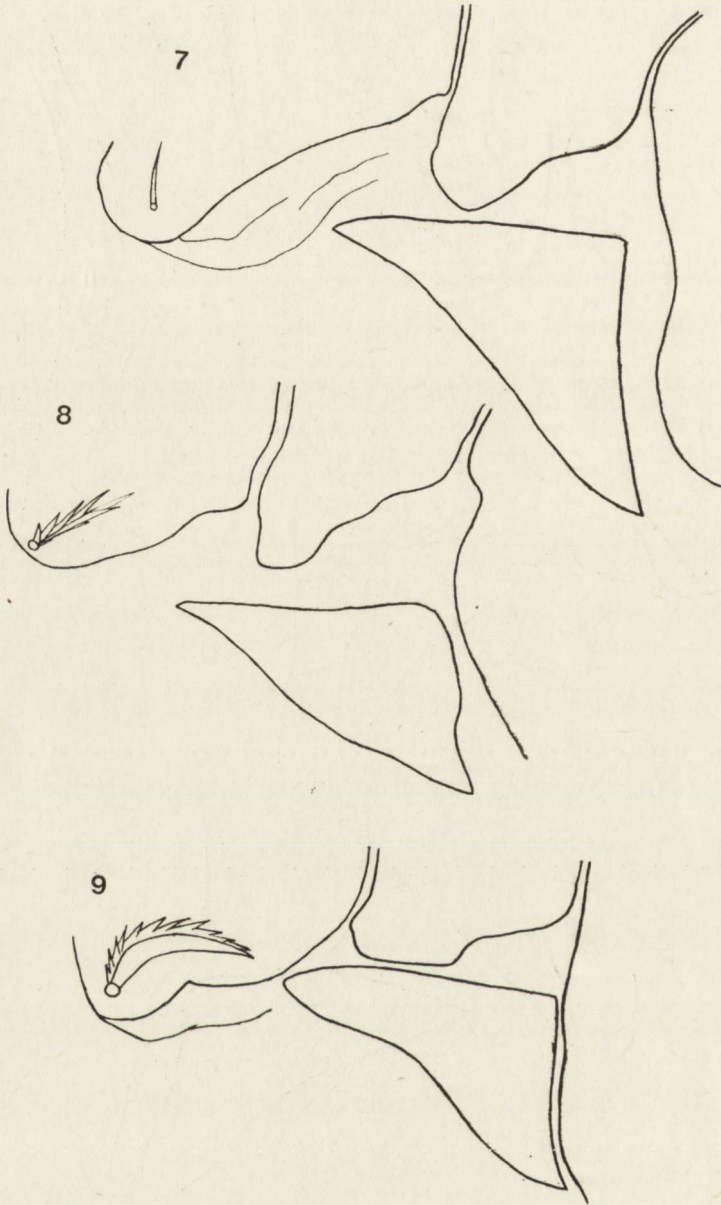ration — identification; they are hard to perceive.
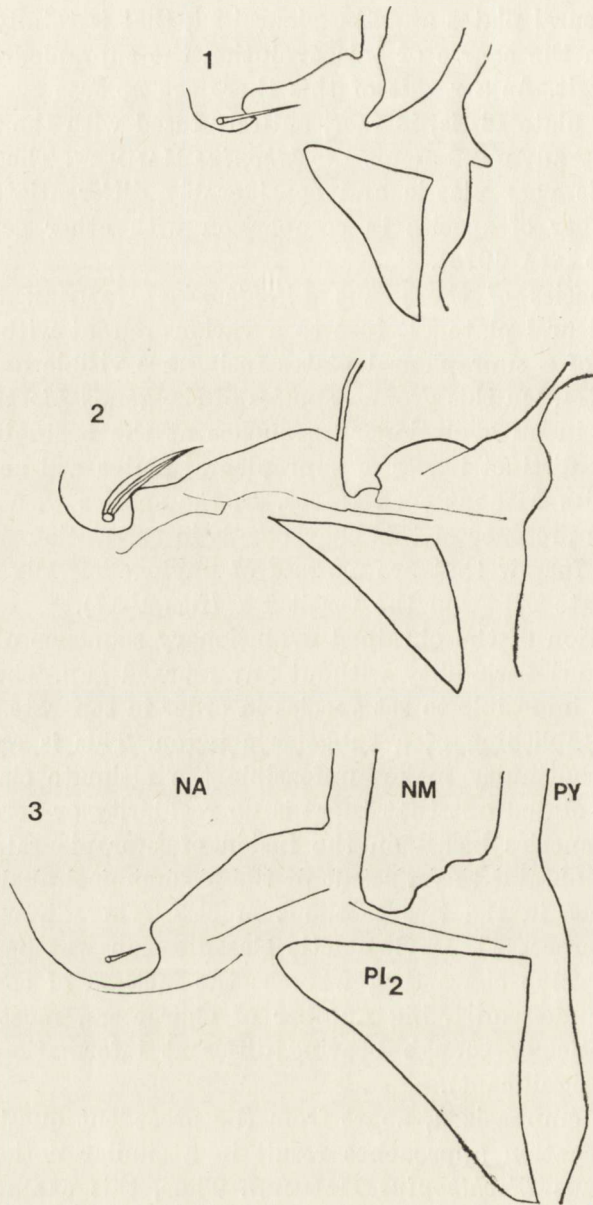
Figs. 1–3. Lateral side of: 1 — *Liochthonius ensifer* (STRENZKE), 2 — *L. intermedius* CHINONE, AOKI, 3 — *L. strenzkei* FORSSLUND.
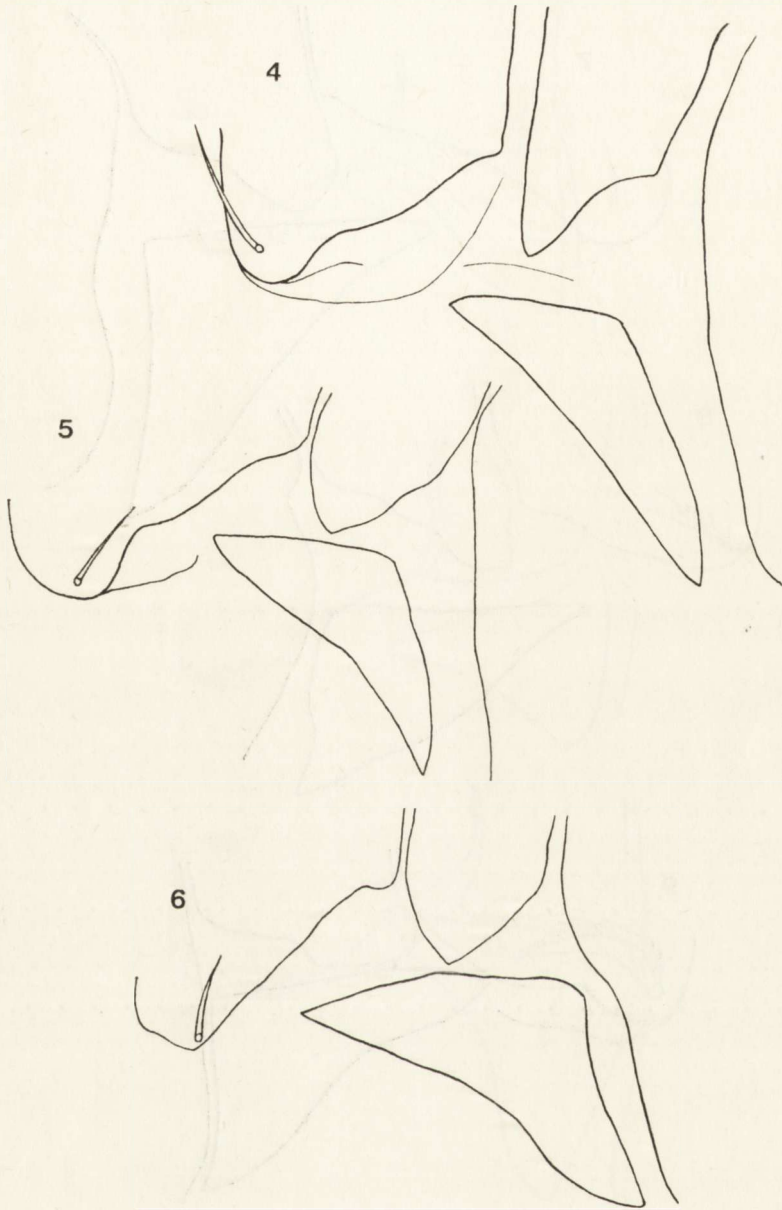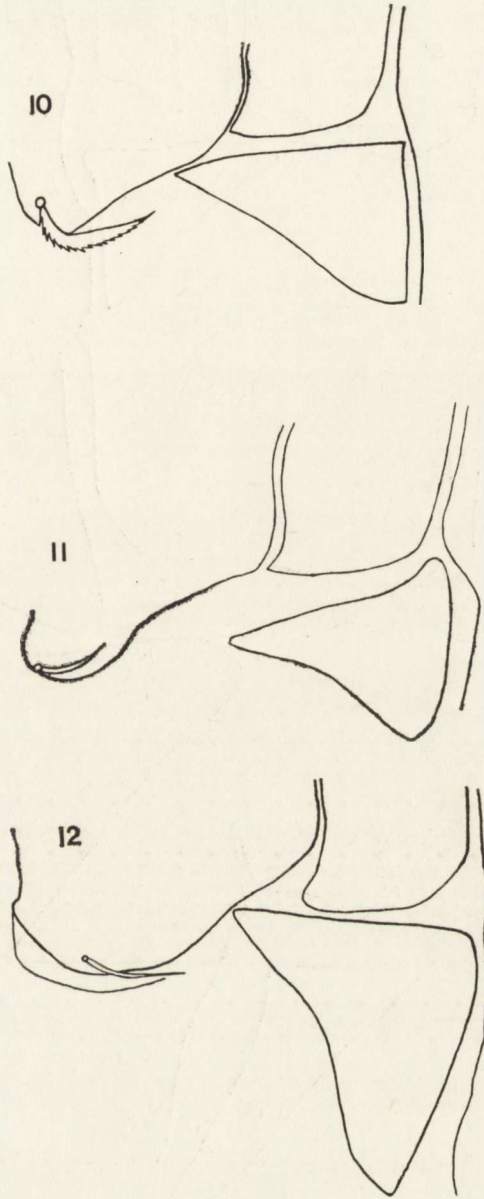
Figs. 4–6. Lateral side of: 4 — *Liochthonius perpusillus* (BERLESE), 5 — *L. tuxeni* (FORSSLUND)
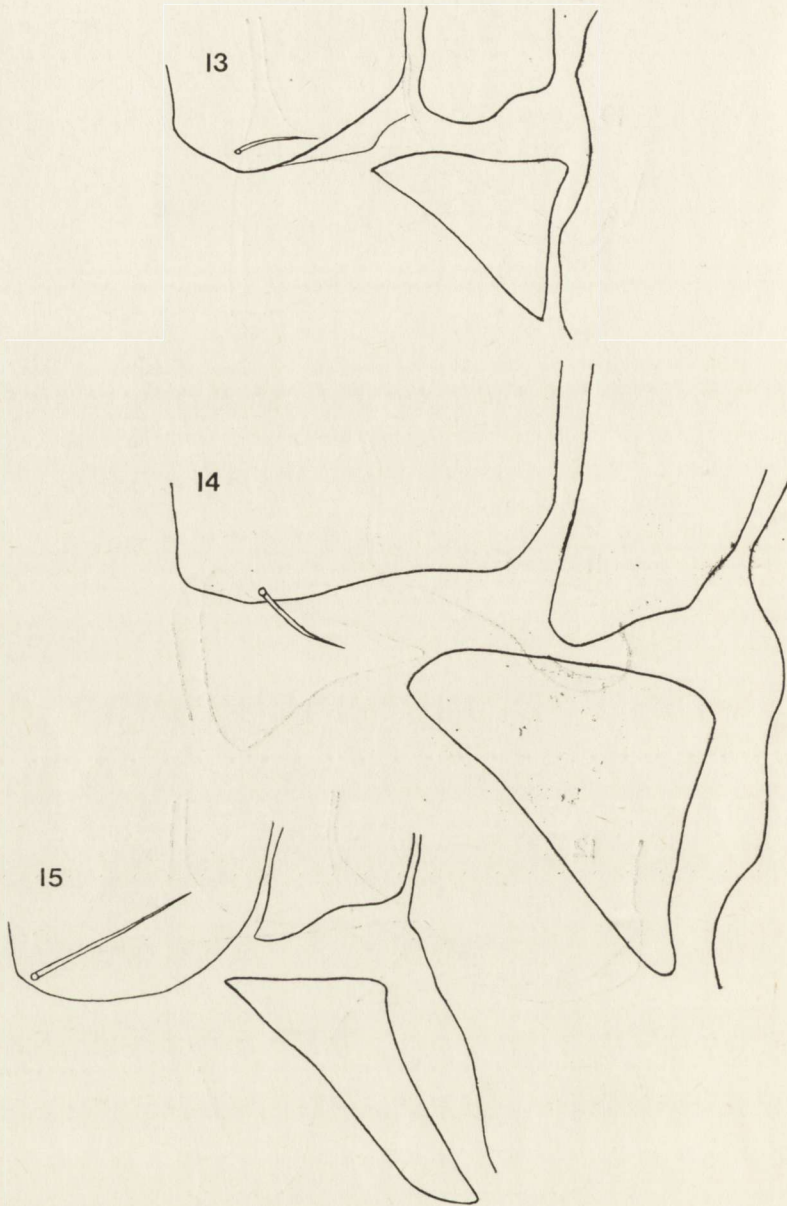6 — *L. alpestris* (FORSSLUND).

Figs. 7–9. Lateral side of: 7 — *Liochthonius sellnicki* (THOR), 8 — *L. plumosus* MAHUNKA, 9 — *L. horridus* (SELLNICK).

Figs. 10–12. Lateral side of: 10 – *Liochthonius forsslundi* MAHUNKA, 11 – *L. occultus* NIEDBAŁA, 12 – *L. lapponicus* (TRÄGÅRDH).

Figs. 13–15. Lateral side of: 13 — *Liochthonius propinquus* NIEDBAŁA, 14 — *L. muscorum* FORSSLUND, 15 — *L. hystricinus* (FORSSLUND).
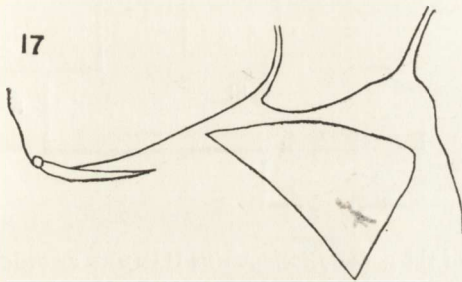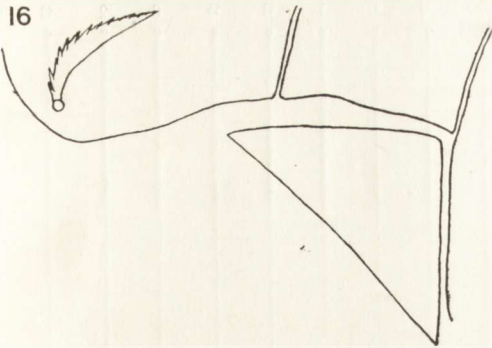
Fig. 16 and 17. Lateral side of: 16 — *Liochthonius gisini* (SCHWEIZER), 17 — *L. evansi* (FORSSLUND).

taken place, while the pure phylogenetical approach to the genus *Liochthonius* HAMMEN would not have been concluded with creation of the four groups. These groups do not entitle a researcher establish subgeneric taxa but undoubtedly the mathematically formed congregations came into existence owing to a well expressed divergence of taxonomical characters.

Of course, numbers and indices will not create a perfect system. Yet they have the superiority over feelings, experience and familiarity with an animal group that, if skilfully and honestly applied, may be opinions objectivizing factor, opinions being affected by various fluctuations of trends.

<div align="center">SUMMARY</div>

Both approaches being developed by the systematics: phylogenetical and phenetic have been discussed at the beginning of this paper. Their advantages and utility have been also considered. This has been followed by an attempt of distinguishing subgeneric taxa in the genus *Liochthonius* HAMMEN (*Acari, Oribatei, Brachychthoniidae*) making use of the SMIRNOV's taxonometric analysis. By the methods of dendrograms the four species groups have been created. After a further analysis and evaluation of their peculiarity the author came to a conclusion that none of them satisfies conditions of an independent sub-
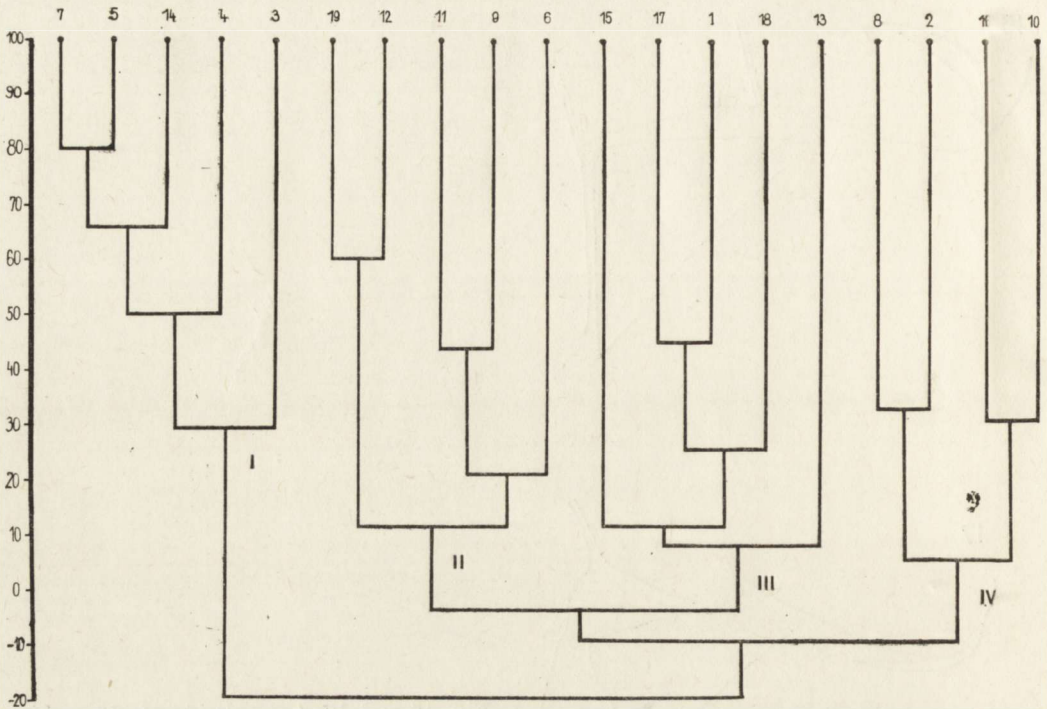
Fig. 18. Dendrogram of similarity of the species of the genus *Liochthonius* HAMMEN as ordered by SMIRNOV's method (names of species according to Tab. II.

generic taxon, the conclusion being also supported by the fact the similarity between particular species groups is deeper than between the species (fig. 18). The discovered one separating distance is also not a sufficient reason to establish a separate taxon because of suspicion that mosaic or parallel evolution or convergence took place.

Applying the natural, "phylogenetical" classification of the members of *Brachychthoniidae* that bases on a reduction of suprapleural plates and on progress of fusion of the pleural plate Pl_2 with the tergit PY, the author has aligned the species of the genus *Liochthonius* HAMMEN in an evolutionary sequence, in which no phenetic gap is observed. Thus, the idea that the similar view on the classification of members of the genus *Liochthonius* HAMMEN by both phenetic and phylogenetic approaches is gained, has been provided another proof.

An erecting of subgeneric taxa in *Liochthonius* HAMMEN would bear a mark of excessive splitting tendencies.

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STRESZCZENIA

[Tytuł: Próba wyróżnienia taksonów podrodzajowych w rodzaju *Liochthonius* Hammen (*Acari, Oribatei, Brachychthoniidae*)]

Autor na wstępie omówił rozwijane w systematyce dwa nurty klasyfikacji: filogenetyczną i fenetyczną. Scharakteryzował krótko ich zalety i użyteczność. Następnie, posługując się analizą taksonometryczną Smirnova poddał próbie wyróżnienia taksonów podrodzajowych w rodzaju *Liochthonius* Hammen (*Acari, Oribatei, Brachychthoniidae*). Metodą dendrogramów wyróżnił w rodzaju 4 grupy gatunków. Po dokonanej analizie i ocenie odrębności tych grup autor doszedł do wniosku, że żadna z nich nie spełnia warunków samodzielnego taksonu podrodzajowego, między innymi dlatego, że podobieństwo między poszczególnymi grupami gatunków jest większe niż między samymi gatunkami (rys. 18). Istniejąca jedyna luka fenotypowa, w postaci szeroko lancetowatych szczecin oddzielająca jedną z tych grup od pozostałych, także niedostatecznie uzasadnia wyróżnienia jej jako odrębnego taksonu, ze względu na podejrzenie zachodzenia ewolucji równoległej, mozaikowej lub konwergencji.

Stosując naturalną, „filogenetyczną" klasyfikację wewnątrz rodziny *Brachychthoniidae* opartą na redukcji płytek suprapleuralnych i stopniu zlewania się płytki pleuralnej Pl₂ z tergitem PY, autor uszeregował gatunki rodzaju *Liochthonius* Hammen w ciąg ewolucyjny, w którym nie zaznacza się jakakolwiek luka.

Autor udowodnił więc, że korzystając równocześnie z podejścia filogenetycznego i fenetycznego uzyskujemy podobny pogląd na klasyfikację w rodzaju *Liochthonius* Hammen. Utworzenie w tym rodzaju taksonów podrodzajowych nosiłoby piętno spliterskie.

РЕЗЮМЕ

[Заглавие: Проба выделения подродовых таксонов в роде *Liochthonius* HAMEN (*Acari, Oribatei, Brachychthoniidae*)]

Во вступлении автор обсуждает два направления классификации, развивающиеся в систематике: филогенетическое и численной фенетики. Кратко характеризует их достоинства и применение. Затем, пользуясь таксонометрическим анализизом Смирнова, предпринял попытку выделения подродовых таксонов в роде *Liochthonius* HAMEN (*Acari, Oribatei, Brachychthoniidae*). Выделил по методу дендрограмммов в данном роде 4 группы видов. Проанализирова ви оценив обособленность этэтих групп, автор пришел к выводу, что ни одна из них не отвечает критериям самосостоятельного подродового таксона по той причине, что сходство между группапами видов больше, чем между самими видами (рис. 18). Единственный имеющиийся фенотипический разрыв в виде широких ланцетовидных щетинок, отделяюющий одну из этих групп от остальных, также недостаточно обоснован для выделенения ее как самостоятельного таксона, так как можно предположить наличие параллельньной эволюции, мозаичной эволюции или конвергенции.

Применяя естественную „филогенетическую” классификацию внут рисемейсйства *Brachychthoniidae*, основанную на редуцировании суpraплевральных пластиинок и степени слияния плевральной пластинки Pl_2 с тергитом PY, автор распредеделил виды рода *Liochthonius* HAMEN в эволюционный ряд, в котором не выступаупает какой-либо разрыв.

Таким образом автор доказывает, что, применяя одновременно филогене нетический и фенетический подход, мы получаем сходную картину классификацкации в роде *Liochthonius* HAMEN. Создание подродовых таксонов в этом роде имемело бы характер ненужного раздробления.

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