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Body form of leeches (Hirudinida: Piscicolidae) parasitizing fishes[1]

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ABSTRACT. The body form of leeches, which becomes a modeling object, is a valid ectosomatic feature. It describes borders, in which, we can find internal organs of an individual. The range of realization of the body form, proposed for different groups of leeches, characterize their life spaces. These life spaces are distinct in term of position of body of leeches to the host and to the environment. Individuals originated from the Caspian Sea, Baikal Lake, and from fresh waters of Italy, Finland, Russia, Germany and Poland. Over 1200 individuals, belonging to 11 genera were measured. The measurements have been made according to the model of the leech body form.

Key words: Hirudinida, Piscicolidae, body form, phylogeny

Introduction

Systemic mathematical modeling, first time in history of animal systematic was used by Raup [1–3], who described spirally coiled shells of fossils. The same method of mathematic modeling was used by Epshtein [4–6] and Bielecki and Epshtein [7,8], however, in this case the objects of modeling was the body form of leeches.

Leeches have different body shapes, that can be easily formalized, and because of that it became an object of mathematical modeling. This mathematical model describes the borders of space, in which, the topographic differences of internal organs derive. Range of realization, proposed for different groups of leeches, characterizes the life forms, that are dissociates by the way of position of leech body due to the substrate and the host.

During the last 50 years in the systematic of leeches parasitizing fishes (Piscicolidae Johnston, 1865), there were numbers of change, mainly because of research carried out by Epsthein [4–6,9,10], Bielecki [11–14], Siddall and Buresson [15], Utevsky and Trontelj [16]. Despite of that, the body form of leeches has never been used for phylogenetic speculations that utilized programs for phylogenetic analysis. The mathematic model of leech body form proposed by Bielecki and Epshtein [7,8] closed the gap described above.

Till now, the body form of leeches has been represented only as a tree clustering algorithm to interpret its similarity [9,11–14,17]. Though, the body form is an important ectosomatic character, and in lower taxa has even more important character with phylogenetic meaning.

Materials and methods

The specimens for research derived from waters around the Antarctica, Caspian Sea, Baikal and from an inland waters of Italy, Finland, Russia, Germany and Poland. The leeches of species *Acipenserobdella pawlowskii*, *Baicalobdella cottidarum*, *B. torquata*, *Caspiobdella caspica*, *Codonobdella truncata*, *Beringbdella rectangulata*, *Truliobdella capitis* and *Limnotrachelobdella sinensis* were gifts from others researchers: Prof. V.M. Epshtein, Prof. B. Sket, Dr S. Utevsky and Dr A. Utevsky. Over 1200 of leeches, belonging to 11 genera: *Acipenserobdella* Epshtein, 1969; *Baikalobdella* Dogiel et Bogolepova, 1957; *Caspiobdella* Epshtein, 1966; *Cystobranchus* Diesing, 1859; *Codonobdella* Gru-

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be, 1873; *Italobdella* Bielecki, 1993; *Piscicola* De Blainville, 1818; *Pawlowskiella* Bielecki, 1997, were measured. There were also the leeches from 3 genera that belonged to the outgroups of *Beringbdella* (Levinsen, 1882), *Truliobdella* Brinkmann, 1947 and *Limnotrachelobdella* Epshtein, 1968.

The measurements were accomplished due to the postulate of the leech body form model [7,8,11,13,14] (Fig. 1).

The model presents the leech body on a plane, as two ellipses that represent suckers, and trapeziums situated between them (anterior body part – trachelosome – 2 trapeziums; posterior body part – urosome – 4 trapeziums). Transverse sections through the trachelosome and urosome are considered as two ellipses.

The model is constructed according to the following parameters:

Parameters describing the form of the anterior sucker: C_1 = horizontal diameter; $C^1{}_1$ = vertical diameter; R_1 = length of anterior part of sucker; and M_1 = length of posterior part of sucker. Parameters describing the form of the trachelosome: d_1 = width at sucker junction; d_2 = width at outline narrowing; d_3 = width at border with urosome; D_1 = largest width of trachelosome; N_1 = largest height of trachelosome; S_1 = height of first trapezium; S_2 = height of second trapezium; and $L_1 = (S_1 + S_2)$ = length of trachelosome.

Parameters describing the form of the urosome: width at places of outline distortion (bases of consecutive trapeziums); d_4 = base of first trapezium; d_5 = base of second trapezium; d_6 = base of third trapezium; d_7 = base of fourth trapezium (width at sucker junction); D_2 = largest width of urosome; N_2 = largest height of urosome; $L_2 = (S_3 + S_4 + S_5 + S_6)$ = urosome length (height of consecutive trapeziums); S_3 = height of first trapezium; S_4 = height of second trapezium; S_5 = height of third trapezium; S_6 = height of fourth trapezium; K_1 = distance from d_3 to D_2; and K_2 = distance from D_2 to d_7.

Parameters describing the form of the posterior sucker: $C^1{}_2$ = horizontal diameter; C_2 = vertical diameter; M_2 = length of anterior part of sucker; and R_2 = length of posterior part of sucker.

The 32 body proportion indices (invariants) are:

1. Index describing L/D_2 = relative body length.

Indices describing anterior sucker: 2. $C^1{}_1/d_1$ = ratio of horizontal diameter of sucker to trachelosome width at sucker junction; 3. $C^1{}_1/D_1$ = ratio of horizontal diameter of sucker to greatest width of trachelosome; 4. R_1/M_1 = ratio of dorsal part of

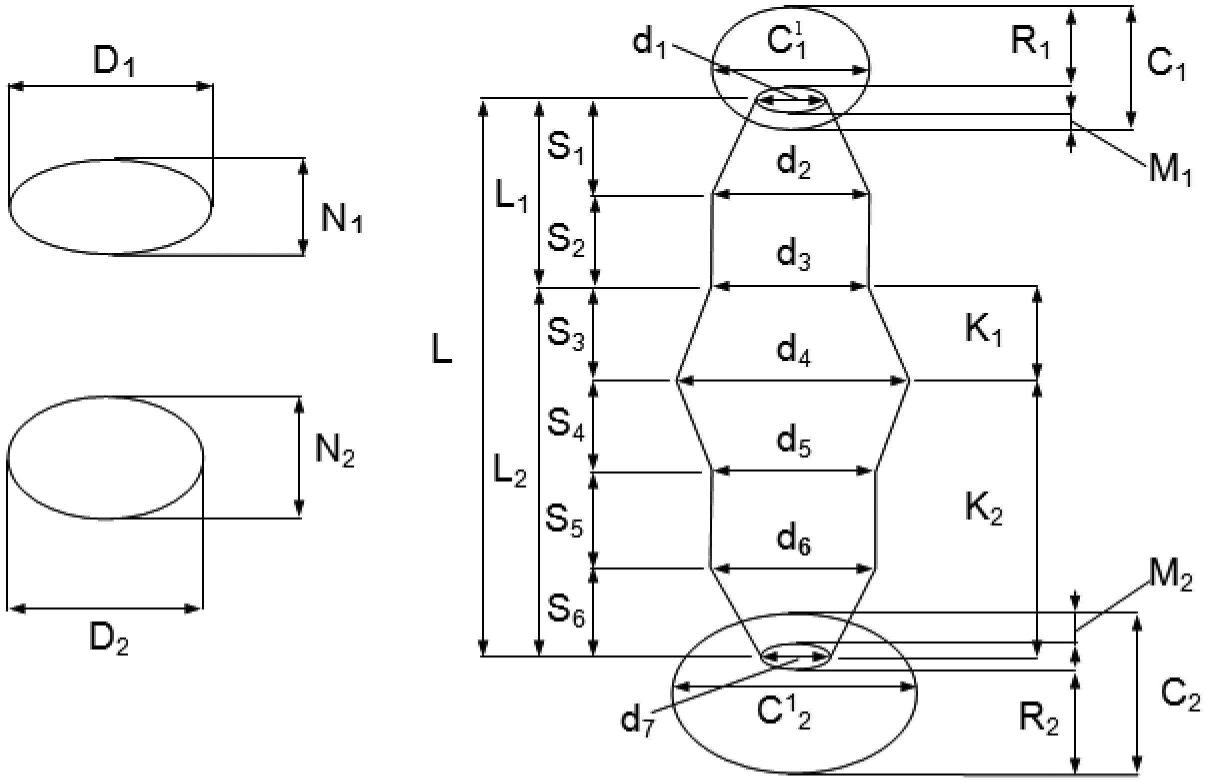

Fig. 1. Model of the leech body form

sucker to its ventral part; and 5. C^1_1/C_1 = ratio of horizontal diameter of sucker to its vertical diameter.

Indices describing trachelosome: 6. L_1/D_1 = ratio of trachelosome length to its greatest width; 7. D_1/N_1 = ratio of greatest trachelosome width to its greatest height; 8. S_1/S_2 = index describing position of greatest width of trachelosome; 9. L_1/L = ratio of trachelosome length to body length; and 10. N_1/L_1 = ratio of greatest height of trachelosome to trachelosome length.

Indices describing urosome: 11. L_2/D_2 = ratio of urosome length to its greatest breadth; 12. D_2/N_2 = ratio of greatest urosome width to its greatest height; 13. K_1/K_2 = ratio describing position of greatest width of urosome; and 14. N_2/L_2 = ratio of greatest height of urosome to its length.

Indices describing the posterior sucker: 15. C^1_2/d_7 = ratio of horizontal diameter of sucker to urosome width at sucker junction; 16. C^1_2/D_2 = ratio of horizontal diameter of sucker to greatest body height; 17. R_2/M_2 = ratio of dorsal part of sucker to its ventral part; and 18. C^1_2/C_2 = ratio of horizontal diameter of sucker to its vertical diameter.

Indices describing relations between the urosome and trachelosome: 19. L_2/L_1 = ratio of urosome length to trachelosome length; 20. L_2/L = ratio of urosome length to body length; 21. D_2/D_1 = ratio of greatest width of urosome to greatest width of trachelosome; and 22. N_2/N_1 = ratio of greatest height of urosome to greatest height of trachelosome;.

Index describing proportions of the suckers: 23. C^1_2/C^1_1 = ratio of horizontal diameter of posterior sucker to horizontal diameter of anterior sucker; 24. C^1_1/C_2 = ratio of horizontal diameter of sucker to vertical diameter of posterior sucker; 25. C^1_2/C_1 = ratio of horizontal diameter of posterior sucker to vertical diameter of anterior sucker; 26. C_2/C_1 = vertical diameter of posterior sucker to vertical diameter of anterior sucker; and 27. $(C_2\text{-}R_2\text{-}M_2)/(C_1\text{-}R_1\text{-}M_1)$ = attachment of posterior sucker to attachment of anterior sucker.

Other indexes: 28. C_2/N_2 = vertical diameter of posterior sucker to ratio of greatest height of urosome; 29. C_1/N_1 = vertical diameter of anterior sucker to ratio of greatest height of trachelosome; 30. $C_2/(C_2\text{-}R_2\text{-}M_2)$ = vertical diameter of posterior sucker to its attachment; 31. $C_1/(C_1\text{-}R_1\text{-}M_1)$ = vertical diameter of anterior sucker to its attachment; and 32. d_7/d_1 = base of fourth trapezium to width at sucker junction.

The matrix used in analyses based on 32 indexes, where (0) means plesiomorphy and (1), (2) and (3) are ranks of apomorphy (Table 1):

1. C^1_1/d_1 – (0) 0.00–1.62; (1) 1.71–1.95; (2) 2.12–2.95; (3) 3.00–3.24

2. R_1/M_1 – (0) 0.00–1.94; (1) 2.00–2.92; (2) 3.63–4.76; (3) 10.00

3. C^2_1/C_1 – (0) 0.00–125; (1) 1.97–3.71; (2) 1.31–1.50; (3) 1.52–1.86

4. S_1/S_2 – (0) 0.68–1.02; (1) 1.04–1.81; (2) 2.44–2.67

5. K_1/K_2 – (0) 0.18–0.37; (1) 0.38–0.41; (2) 0.42–0.89; (3) 1.08–1.14

6. C^2_1/d_7 – (0) 0.89–1.49; (1) 1.55–2.48; (2) 3.05–3.46

7. R_2/M_2 – (0) 1.05–1.50; (1) 1.57–2.17; (2) 2.22–3.97; (3) 5.42

8. C^2_1/C_2 – (0) 0.66–0.96; (1) 0.97–1.00; (2) 1.01–1.25

9. L_2/L_1 – (0) 1.47–2.01; (1) 2.02–2.96; (2) 3.10–4.41

10. N_2/N_1 – (0) 1.02–1.40; (1) 1.45–2.01; (2) 2.00–2.51

11. C^2_1/C^1_1 – (0) 0.00–1.29; (1) 1.99–3.57; (2) 1.41–1.68; (3) 1.70–1.89

12. L_1/L – (0) 0.18–0.24; (1) 0.25–0.41; (2) 1.81

13. L_2/L – (0) 0.59–0.69; (1) 0.70–0.83; (2) 1.81

14. C_2/C_1 – (0) 0.00–0.94; (1) 1.50–3.04; (2) 1.08–1.49

15. C_1/N_1 – (0) 0.00–1.36; (1) 1.40–1.99; (2) 2.00–3.93; (3) 5.03

16. C_2/N_2 – (0) 0.43–1.35; (1) 1.36–2.08; (2) 2.19–2.36; (3) 4.61–5.12

17. $C_2/(C_2\text{-}R_2\text{-}M_2)$ – (0) 1.49–3.81; (1) 13.92–26.36; (2) 4.19–5.95; (3) 6.00–9.84

18. $C_1/(C_1\text{-}R_1\text{-}M_1)$ – (0) 0.00–3.96; (1) 4.00–8.02; (2) 10.38–15.50

19. d_7/d_1 – (0) 0.60–1.99; (1) 2.00–3.20; (2) 23.21

20. $(C_2\text{-}R_2\text{-}M_2)/(C_1\text{-}R_1\text{-}M_1)$ – (0) 0.00–1.39; (1) 1.40–1.97; (2) 2.06–2.80; (3) 3.05–4.98

21. L/D_2 – (0) 1.55–5.28; (1) 5.34–9.59; (2) 10.90–19.46; (3) 23.20–27.80

22. C^1_1/C_1 – (0) 0.00–0.97; (1) 1.00–1.37; (2) 1.41–1.98

23. L_1/D_1 – (0) 0.88–2.67; (1) 10.14–15.00; (2) 2.82–3.55; (3) 3.64–9.38

24. D_1/N_1 – (0) 0.68–0.99; (1) 2.13–3.14; (2) 1.00–1.79

25. L_2/D_2 – (0) 0.97–3.94; (1) 4.01–9.46; (2) 10.11–18.50; (3) 22.24

26. D_2/N_2 – (0) 0.83–0.88; (1) 0.91–4.32; (2) 12.86

27. C^2_1/D_2 – (0) 0.06–0.90; (1) 1.01–1.84; (2) 2.29–2.33

Table 1. Matrix of indexes used in parsimony analysis

Species/Index number	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
A. pawlowskii (Sket, 1968)	1	3	3	2	0	1	2	2	2	0	3	1	2	1	2	3	3	1	0	0	1	1	3	1	1	1	1	1	0	1	2	0
A. volgensis (Zykoff, 1903)	1	2	2	0	0	0	1	1	2	1	2	1	1	2	0	0	2	1	0	2	1	0	0	2	1	1	0	0	1	0	1	2
B. cottidarum Dogiel et Bogolepova, 1957	0	1	0	0	1	0	1	0	0	0	2	1	0	0	2	2	0	0	0	0	1	1	3	2	1	1	0	0	1	2	0	1
B. torquata Grube, 1871	0	0	0	0	0	0	1	1	1	2	3	1	0	2	1	0	2	0	1	0	0	0	0	2	0	1	0	1	1	0	0	0
C. caspica (Selensky, 1915)	0	1	3	0	2	0	1	2	1	1	2	1	0	2	0	0	2	0	0	0	1	0	3	2	1	1	0	0	1	0	1	2
C. fadejewi (Epshtein, 1961)	1	2	2	1	1	1	1	1	2	0	2	1	1	2	1	1	2	1	0	2	2	2	3	2	1	1	1	0	1	2	2	1
C. mammilatus Malm, 1863	2	0	1	0	0	1	0	2	2	2	3	1	1	1	2	1	2	1	1	1	1	1	0	1	1	1	1	1	1	0	1	0
C. truncata Grube, 1873	1	0	0	0	2	0	0	2	2	2	0	0	1	2	1	0	0	0	0	1	1	1	2	2	1	1	0	1	1	0	2	2
I. epshteini Bielecki, 1997	3	0	2	1	0	2	0	2	2	0	0	0	1	2	1	1	2	2	0	2	1	2	0	2	1	1	1	1	1	2	1	2
I. ciosi Bielecki, 1993	0	2	2	0	3	0	0	1	2	2	2	0	1	2	0	0	0	1	0	3	1	0	0	2	1	1	0	1	1	0	0	1
P. annae Bielecki, 1997	2	2	3	0	1	1	2	1	1	1	3	1	1	1	1	1	2	1	1	2	2	2	3	2	2	1	1	1	0	2	2	1
P. borowieci Bielecki, 1997	2	1	3	0	0	1	1	1	1	0	3	1	1	1	1	1	2	1	1	1	2	2	3	0	2	1	1	0	0	1	2	0
P. brylinskae Bielecki, 2001	1	1	3	1	2	1	0	1	0	1	2	1	0	1	1	1	3	1	0	0	1	1	2	2	1	1	1	0	0	2	1	1
P. elishebae Bielecki, 1997	1	1	0	0	0	0	2	0	1	1	2	1	1	2	2	2	3	1	0	1	1	1	2	1	1	1	1	0	1	2	0	1
P. fasciata Kollar, 1842	3	0	3	0	0	1	0	2	2	1	3	0	1	1	1	2	2	1	1	2	1	1	2	2	1	1	1	0	1	2	2	0
P. geometra (Linneaus, 1761)	1	1	2	1	3	1	2	0	0	1	3	2	2	1	2	2	3	1	0	2	0	2	0	2	2	1	1	1	2	1	0	0
P. kusznierzi Bielecki, 1997	3	1	0	0	1	0	1	0	1	1	0	1	0	2	2	1	0	1	1	0	3	2	3	2	2	1	1	0	0	1	1	2
P. margaritae Bielecki, 1997	2	1	2	0	1	1	2	0	1	1	2	1	1	2	1	1	3	1	1	2	1	1	3	2	1	1	1	0	1	2	2	1
P. niewiadomskae Bielecki, 1997	1	0	3	0	2	0	1	0	1	2	3	1	0	1	1	0	2	0	1	1	2	1	3	2	1	1	1	1	0	2	2	0
P. pojmanskae Bielecki, 1994	0	0	2	1	0	0	1	2	2	1	3	0	1	2	2	1	2	0	0	0	1	0	0	1	1	1	1	0	1	2	0	1
P. pomorskii Bielecki, 1997	2	0	0	0	0	2	0	0	1	0	2	1	1	1	1	2	2	2	0	1	2	2	3	2	2	1	1	0	1	1	2	1
P. respirans Troschel, 1850	0	1	2	1	2	1	1	0	2	0	3	0	1	1	2	2	3	1	0	2	0	1	0	1	0	1	1	0	1	2	0	1
P. wiktori Bielecki, 1997	2	0	2	0	1	0	1	0	1	2	3	1	1	2	2	1	2	0	2	1	2	1	1	2	2	1	1	1	0	1	0	0
P. witkowskii Bielecki, 1997	1	1	3	1	1	0	1	2	2	1	2	0	1	2	1	0	3	1	1	0	1	1	2	2	1	1	1	0	1	2	2	1
P. sp. nov. 1	2	1	3	0	2	1	2	1	2	1	2	0	1	1	3	3	3	1	0	2	2	2	3	1	2	1	1	0	0	1	2	1
P. sp. nov. 2	2	2	2	1	1	1	3	1	2	1	2	0	1	1	2	1	3	1	1	1	3	2	3	2	2	0	2	0	0	1	2	1
P. stenosa Bielecki, 1997	2	2	3	1	0	1	1	1	2	0	3	0	1	1	1	2	2	1	0	2	3	2	3	0	3	1	2	0	0	1	1	0
**B. rectangulata* (Levinsen, 1882)	0	1	1	2	2	2	0	2	1	1	1	1	0	1	1	1	1	2	0	1	0	0	0	1	0	1	1	0	0	0	1	0
**T. capitis* Brinkmann, 1948	0	0	0	1	0	0	0	0	0	1	0	1	0	0	2	1	1	1	0	0	0	0	0	1	0	1	0	1	1	0	0	0
**L. sinensis* (Blanchard, 1896)	0	1	1	0	2	0	1	2	0	0	1	1	0	1	0	0	0	0	1	2	0	0	2	0	1	1	0	1	1	0	1	0

Explanations: indexes states list in Material and methods. The asterisks (*) indicate the species included to outgroup

28. D_2/D_1 – (0) 1.14–1.70; (1) 1.71–2.65; (2) 11.25
29. N_1/L_1 – (0) 0.08–0.19; (1) 0.20–0.75; (2) 1.81
30. N_2/L_2 – (0) 0.16–0.41; (1) 0.02–0.08; (2) 0.10–0.16
31. C^1_1/C_1 – (0) 0.00–0.88; (1) 1.00–1.33; (2) 0.91–0.99
32.C^1_1/C_2 – (0) 0.00–0.56; (1) 0.57–0.68; (2) 0.71–1.16

Parsimony analyses were performed using PAUP* 4.06b10 program for Windows, for IBM PC (Swofford 2000) utilizing the heuristic search option. The analyses used 100 replicates of random taxon addition and tree-bisection-reconnection branch swapping. All characters were equally weighted. Thirty one characters were parsimony-informative, and one character was parsimony-uninformative. *B. rectangulata*, *T. capitis* and *L. sinensis* were treated as the outgroup.

The most parsimonious trees were edited in Mesquite 2.6 program for Windows.

Results

Parsimony analysis of 30 species and 32 characters of Hirudinida concerning body form of leeches resulted in seven most parsimonious trees (length=333; CI=0.2252; HI=0.7748; RI=0.4545; CI excluding uninformative character=0.2229; HI excluding uninformative character=0.7771; and Rescaled consistency index=0.1024). One of the seven most parsimonious trees is shown on Fig. 2.

Outgroup contained two marine species *Beringbdella rectangulata* and *Trulliobdella capitis*. It included also one freshwater species – *Limnotrachelobdella sinensis*. *Baicalobdella torquata* occurred to be sister to *Trulliobdella capitis*.

Parsimony analysis shows many non-monophyletic groups, in which we found body forms from different genera: *Acipenserobdella volgensis* and *Italobdella ciosi*, *Cystobranchus mammilatus* and *Piscicola pojmanskae*, *Baicalobdella cottidarum* and *Piscicola elishebae*, *Pawlowskiella stenosa* and *Acipenserobdella pawlowskii* (Sket, 1968) [syn. *Cystobranchus pawlowskii* Sket, 1968; *Piscicola pawlowskii* (Sket, 1968)].

Species from *Italobdella* genus also turn out to be non-monophyletic: *I. ciosi* aggregate with *A. volgensis*, however *I. epshteini* appeared to be sister to the clad that contained *C. mammilatus* and *P. pojmanskae*.

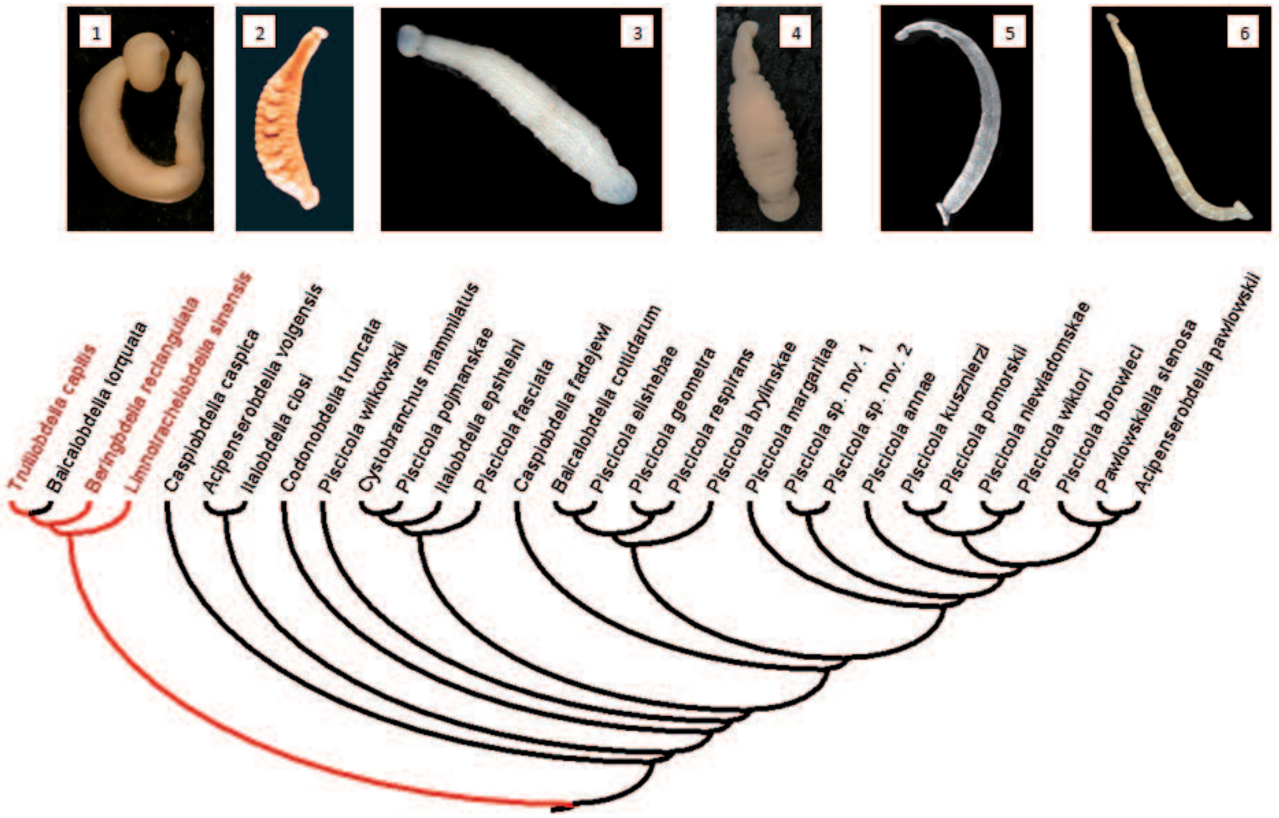

Fig. 2. One of the most parsimonious trees for 30 species of Hirudinida based on 32 characters of the leech body form. Species marked on red are included to outgroup.
1. *Beringbdella rectangulata*, 2. *Acipenserobdella volgensis*, 3. *Italobdella epshteini*, 4. *Piscicola respirans*, 5. *Piscicola annae*, 6. *Piscicola borowieci*

What is more interesting, species from *Acipenserobdella*, *Baicalobdella* and *Caspiobdella* genera were placed in different locations of the tree. Moreover, *Codonobdella truncata*, *Caspiobdella torquata* and *Caspiobdella fadejewi* made individual clades.

According to body form, genus *Piscicola* turn out to be non-monophyletic, but the major part of representatives of this genus realized sister similarity of body form, for example: *Piscicola geometra* and *P. respirans*, *P.* sp. nov. 1 and *P.* sp. nov. 2, *P. kusznierzi* and *P. pomorskii*, *P. niewiadomskae* and *P. wiktori*. *P. fasciata* turn out to be sister to the grouping that include *C. mammilatus*, *P. pojmanskae* and *I. epshteini*. While, *P. borowieci* was sister to clad created by *P. stenosa* and *A. pawlowskii*. Some species from *Piscicola* genus, like *P. witkowskii*, *P. margaritae* and *P. annae*, constituted different clades, that are not sister to any others members of their genus.

Discussion

Till now body form, as a parameter only, was not used in phylogenetic deliberations. Most often we can find phylogenetic trees based on morphological data [15,18] or connecting morphological and molecular data [16,19]. Mathematic model proposed by Bielecki and Epshtein [7,8], which characterized the body form of leeches, closed specific space and frame it clearly in ways of morphological data.

Body form is realized in a mosaic way in all groups of Hirudinida, which can be told even before the phylogenetic analysis. That is why, acquired results are not a suprise, especially when we consider the fact, that some Platybdellinae (*T. capitis*) body forms are closed to species from the Glossiphoniidae family. Whereas, some of Glossiphoniidae have body form like Piscicolidae (*Hemiclepsis marginata*), and most of Erpobdellidae had body form characteristic for Hirudinidae.

Utevsky and Trontelj [16] using molecular and morphological data characterized Platybdellinae as a sister group to Piscicolinae. This contradicts the traditional position of Platybdellinae from the beginning of piscicolid classification [9,20]. Nevertheless, a study based only on body form, classified two of species belonging to Platybdellinae (*B. rectangulata* and *T. capitis*) as truly sister group to Piscicolinae.

The clad witch *B. cottidarum* and species from Piscicola genus should be taken into careful consideration. It is important to see, that *B. cottidarum* belongs to trib Piscicolini, Johnston, 1865, which embody Palearctic genus *Piscicola*. What is more interesting, the similarity of Baicalian Piscicolids to the genus *Piscicola* could be a result of convergence of reproductive organs [10]. Moreover, *C. mammilatus*, *Piscicola* spp. and *Baicalobdella* are characterized by copulation area located posterior to male gonopore. It is one of the reasons, why some scientists think about transferring genus *Baicalobdella* to genus *Piscicola* [16].

P. borowieci, *P. stenosa* and *A. pawlowskii* created a separate clad. It looks strange, but when we carefully take under consideration indexes connected with suckers – posterior and anterior (C^{2}_{1}/C_{2}, C^{2}_{1}/C^{1}_{1}, C^{1}_{1}/C_{2}), ratio of greatest height of trachelosome to trachelosome length (N_{1}/L_{1}), ratio of greatest height of urosome to its length (N_{2}/L_{2}) and ratio of trachelosome length to body length (L_{1}/L), it occurs that differences between indexes are almost invisible (SD from 0.008 to 0.04). Likewise looks the situation in clad made by *C. mammilatus*, *P. pojmanskae*, *P. fasciata* and *I. epshteini*. In this case, the ratio of greatest height of urosome to its length (N_{2}/L_{2}), ratio of urosome length to body length (L_{2}/L) and ratio of trachelosome length to body length (L_{1}/L) is also very small (SD from 0.02 to 0.03). However, if we want to conclude, with a higher level of assurance, about their common origin or close affinity, we should complete our analysis using morphological, anatomical, behavioral and molecular data.

The genus *Piscicola* is distributed in the Holarctic. Evidently, this genus is the most ancient representative of freshwater Piscolidae. In ancient lakes from Baikal to Aral Sea a series of *Limnotrachelobdella* species are present. It can be concluded that contemporary fish leeches of Baikal are the result of divergence from a general ancestor, who was connected with *Limnotrachelobdella* by the common origin; thus, the similarity of Baicalian *Piscicolidae* with *Piscicola* is a result of convergence.

On the territory of East Europe in waters deriving from the Tethys Sea the Caspian fauna had developed, which includes the piscicolid genera *Caspiobdella* and others, sharply different from previous one due to the construction of the reproductive system.

The fourth element of the piscicolid fauna of Holarctic is *Cystobranchus mammilatus*, that invaded continental waters in the time of quaternary transgression of the Arctic Ocean. Some continental waters are referred to species of the marine subfamily Platybdellinae (lakes Chilika and Tanganyika; North America) [10].

The outgroup includes two species of marine piscicolids: *B. rectangulata* and *T. capitis* as well as, one freshwater relict species *L. sinensis*. It can be concluded, that leeches parasitizing fishes originally descended from freshwater, afterwards moved to sea-waters in Devonian and do not exist in freshwaters till Cretaceous. From that moment leeches started to colonized freshwaters several times, independently in different regions and in Eurasia and North America [4,16]. In clad with the outgroup there is also *B. torquata* as species sister to *T. capitis*. Either of this species have got relatively wide – as for piscicolids – flattened body, more of theirs body form is parallel to species from Glossiphoniidae family. Likewise flattened body has also *L. sinensis*, which is sister to the rest of species in this clad. It can testify about its original, neolimnic origin (neolimnic fauna – evolved from marine ancestors in Mesosoic and Tertiary) [10].

Phylogenetic deduction about relations among Piscicolidae, only with data from body form of leeches, is for sure a preliminary deduction. However, it shows a mosaic mode of realization the body form in this group of animals.

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