



New Contributions to the Diversity of Hypotrichous Ciliates: Description of a New Genus and Two New Species (Protozoa, Ciliophora)

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OPEN ACCESS

Edited by:

Weiwei Liu, South China Sea Institute of Oceanology, Chinese Academy of Sciences, China

Reviewed by:

Shahed Uddin Ahmed Shazib, Smith College, United States Jiamei Jiang, Shanghai Ocean University, China

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Specialty section:

This article was submitted to Aquatic Microbiology, a section of the journal Frontiers in Microbiology

Received: 20 May 2021 Accepted: 07 July 2021 Published: 05 August 2021

Citation:

Ma J, Zhang T, Song W and Shao C (2021) New Contributions to the Diversity of Hypotrichous Ciliates: Description of a New Genus and Two New Species (Protozoa, Ciliophora). Front. Microbiol. 12:712269. doi: 10.3389/fmicb.2021.712269 Ciliated protists (ciliates) are extremely diverse and play important ecological roles in almost all kinds of habitats. In this study, two new hypotrichs, Wilbertophrya sinica n. g. and n. sp. and Bakuella xianensis n. sp., from China are investigated. Wilbertophrya n. g. can be separated from related genera mainly by the combination of lacking a buccal cirrus, pretransverse cirri, and caudal cirri, while possessing frontoterminal cirri. Analyses based on morphological and molecular data confirm the validity of the species, W. sinica n. sp., which is characterized as follows: body 50-115 μ m \times 15-35 μ m in vivo; midventral complex comprises four or five cirral pairs only and terminates above mid-body; three frontal, two frontoterminal cirri, and two to four transverse cirri; about 15 macronuclear nodules; colorless cortical granules sparsely distributed. Another new species, B. xianensis n. sp., was isolated from a freshwater wetland and is defined as follows: body 115–150 μ m × 40–65 μ m *in vivo*; about 70 macronuclear nodules; darkbrownish cortical granules in groups; midventral complex comprises 8-12 cirral pairs forming a row that terminates posteriorly in mid-body region and two or three short midventral rows that are continuous with the row of midventral pairs; three frontal, four to six frontoterminal, and three to five fine transverse cirri; three bipolar dorsal kineties. Phylogenetic analyses based on small subunit ribosomal DNA (SSU rDNA) sequence data suggest that the new genus Wilbertophrya n. g. belongs to an isolated clade, which might represent an undescribed taxon at the family level, whereas B. xianensis n. sp. groups with several congeners and members of other related genera are within the core urostylids.

Keywords: Bakuella xianensis n. sp., molecular phylogeny, morphology, Wilbertophrya sinica n. g., n. sp.

INTRODUCTION

Hypotrich ciliates are a large, ubiquitous group that play key roles in many ecosystem processes and as model organisms in a wide range of biological studies (Berger, 1999, 2011; Song and Shao, 2017; Chen et al., 2019, 2020; Kim and Min, 2019; Kim et al., 2019; Li et al., 2019; Wang et al., 2019; Gao et al., 2020; Sheng et al., 2020). New hypotrich taxa are continuously being discovered, supporting

the notion posited by Foissner et al. (2008) that over 80% of ciliate diversity is still undescribed (Bharti et al., 2019; Hu et al., 2019; Kaur et al., 2019; Moon et al., 2019; Dong et al., 2020; Park et al., 2020; Xu et al., 2020).

Urostylids are one of the most speciose and best-known groups within the subclass Hypotrichia Stein, 1859. Nevertheless, their evolutionary relationships and genus- or family-level definitions remain problematic as recognized in several recent reports (Berger, 2006; Lu et al., 2018, 2020; Luo et al., 2018, 2019; Jung and Berger, 2019; Wang et al., 2021a; Zhang et al., 2020).

Here, we document two hypotrichs from inland China: a novel form that represents a new genus and a new species (*Wilbertophrya sinica* n. g., n. sp.) found in a puddle in a forest in Tibet and a freshwater species, *Bakuella xianensis* n. sp., isolated from a wetland in the Qinling Mountains area near Xi'an. Both species were characterized based on morphological observations of specimens *in vivo* and following silver staining. In addition, their molecular phylogeny was analyzed based on small subunit ribosomal DNA (SSU rDNA) sequence data.

MATERIALS AND METHODS

Sampling, Cultivation, and Morphological Studies

Wilbertophrya sinica n. g., n. sp. was collected on April 22, 2017, from a small puddle in a forest in Bomi County, Linzhi (29°39'N; 94°21'E), Tibet, where the altitude is about 3,000 m above sea level (**Figures 1A,C**).

Bakuella xianensis n. sp. was collected on May 25, 2019, from a well-vegetated freshwater pond located in Chanba National Wetland Park, Xi'an (34°31′N; 109°01′E), near the junction of the River Ba and River Wei (**Figures 1A,B**).

Uni-protistan cultures were established in Petri dishes containing rice grains to support the growth of bacteria, which served as a food source for the ciliates. The species was accurately identified based on its morphology *in vivo*. Moreover, no other urostylids morphotypes were present in the protargol preparation. We assure the accuracy of that identification for molecular studies, even though we were unable to establish clonal cultures.

Ciliate cells were observed *in vivo* using bright field and differential interference contrast microscopy. The protargol silver staining method according to Wilbert (1975) was used to reveal the infraciliature. Counts and measurements of stained specimens were performed at a magnification of \times 1,000. Drawings of stained specimens were performed at \times 1,250 magnification with the aid of a camera lucida. Terminology is mainly according to Berger (2006), and the systematic classification follows Lynn (2008).

DNA Extraction, PCR Amplification, and Sequencing

Single cells of each species were isolated from cultures, washed several times with distilled water using a micropipette in order to remove potential contamination, and then transferred to 1.5-ml microfuge tubes with a minimum volume of water. Genomic DNA extraction was performed with the DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany) according to the modified manufacturer's protocol (1/4 of suggested volume for each solution) (Chen et al., 2019; Lu et al., 2020). PCR amplification of the SSU rDNA was performed using Q5 Hot Start high fidelity DNA polymerase (NEB, Ipswich, MA, United States) to minimize the possibility of amplification errors. One cycle of initial denaturation at 98°C for 30 s, followed by 18 cycles of amplification (98°C, 10 s; 69-51°C touchdown, 30 s; 72°C, 1 min), and another 18 cycles (98°C, 10 s; 51°C, 30 s; 72°C, 1 min), with a final extension of 72°C for 5 min. Sequencing of PCR products was performed bidirectionally on an ABI 3700 sequencer using two PCR primers 18S-F (5'-AAC CTG GTT GAT CCT GCC AGT-3') and 18S-R (5'-TGA TCC TTC TGC AGG TTC ACC TAC-3') (Medlin et al., 1988).

Phylogenetic Analyses and Sequence Comparison With Related Species

In order to perform phylogenetic analyses, the SSU rDNA sequences of W. sinica n. g., n. sp. and B. xianensis n. sp. were aligned with other related sequences downloaded from the National Center for Biotechnology Information (NCBI) Database (accession numbers shown in Figure 2) on the GUIDANCE2 server¹ with default parameters (Sela et al., 2015). Representative species of the subclass Euplotia Jankowski, 1979, were selected as the outgroup. The aligned sequences were manually edited using the program BioEdit 7.2.5 (Hall, 1999), resulting in a final alignment with 1,772 sites. Both maximum likelihood (ML) and Bayesian inference (BI) analyses were performed on the final alignment. The ML analysis was performed with 1,000 rapid bootstrap replicates using RAxML-HPC2 on XSEDE v8.2.12 (Stamatakis, 2014) on CIPRES Science Gateway with the GTRGAMMA model (Miller et al., 2010). The BI analysis was computed by MrBayes on XSEDE 3.2.6 (Ronquist et al., 2012) on CIPRES Science Gateway with the GTR + I + G model selected by MrModeltest 2.2 (Nylander, 2004). Markov chain Monte Carlo (MCMC) simulations were run for 10,000,000 generations with sampling every 100 generations. The first 10,000 trees were discarded as burn-in. Seaview v.4.3.3 (Gouy et al., 2010) and MEGA v.6 (Tamura et al., 2011) were used to visualize the tree topologies.

The SSU rDNA sequences were aligned and manually modified (trimming ends and removing identical nucleotides) with BioEdit 7.0.5.2 (Hall, 1999).

RESULTS

ZooBank registration.

Present work: urn:lsid:zoobank.org:pub:C0BE1314-C4 93-430C-9903-8E1758A1F983 Subclass Hypotrichia Stein, 1859

Order Urostylida Jankowski, 1979 Genus *Wilbertophrya* n. g.

¹http://guidance.tau.ac.il/



FIGURE 1 | Sample sites. (A) The map of China from the MAP WORLD [www.tianditu.gov.cn, drawing review number: GS (2019) 1708] showing the location of the sampling sites. (B) Wetland at Chanba National Wetland Park, Xi'an, where *Bakuella xianensis* n. sp. was collected. (C) Forest in Bomi County, Linzhi, Tibet, where *Wilbertophrya sinica* n. sp. was collected.

Description of Wilbertophrya n.g.

ZooBank registration.

Wilbertophrya n. g.: urn:lsid:zoobank.org:act:61BC94E 2-17BA-48D8-9219-921267C0919B

Diagnosis: Urostylid with a continuous adoral zone; three clearly differentiated frontal cirri; midventral complex composed only of cirral pairs arranged in a zigzag pattern; frontoterminal and transverse cirri present; buccal, pretransverse, and caudal cirri absent; one marginal row on each side, the anterior end of the left marginal row not curved rightward; three dorsal kineties.

Type species: W. sinica n. sp.

Dedication: This new genus is named after the eminent ciliatologist Prof. Norbert Wilbert, University of Bonn, Germany, in recognition of his life-long contributions to the taxonomy of ciliates. Feminine gender.

Description of Wilbertophrya sinica n. sp.

ZooBank registration.

| Wilbertophrya | sinica | n. | sp.: |
|--------------------------|---------------|--------------|------|
| urn:lsid:zoobank.org:act | F2D0E277-FB7A | A-493F-90AC- | |
| 8D9875AC347F | | | |

Diagnosis: Body 50–115 μ m × 15–35 μ m *in vivo*, elliptical in outline; 13–19 macronuclear nodules; contractile vacuole located ahead of mid-body; cortical granules colorless, about 1 μ m

across, irregularly distributed; about 15–18 adoral membranelles; four or five midventral pairs in anterior half of cell; three frontal, two frontoterminal, and two to four transverse cirri; the left marginal row is composed of 13–21 cirri, and right marginal row is composed of 14–25 cirri; three bipolar dorsal kineties; freshwater habitat.

Type material: One protargol-stained slide (No. MJY2017042201-3) with the holotype specimen (**Figure 3I**) circled in ink and two paratype slides (No. MJY2017042201-1, 2) were deposited in the Laboratory of Protozoological Biodiversity and Evolution in Wetland, Shaanxi Normal University, China.

Type locality: Puddle in a forest in Bomi County, Linzhi (29°39'N; 94°21'E), Tibet, China.

Etymology: The species-group name *sinica* recalls that this species was first discovered in China.

Description (Figures 3A–N and Table 1).

Body size 50–115 μ m × 15–35 μ m *in vivo*. Cell outline variable, generally elliptical to elongate-elliptical, right cell margin slightly concave, left margin slightly convex; usually widest in front of mid-body; dorsoventrally flattened; slightly flexible but non-contractile (**Figures 3A, B, G**). Nuclear apparatus composed of about 15 ellipsoidal nodules and one to four, on average two, micronuclei up to 2 μ m in diameter (**Figures 3F, L**). Contractile vacuole about 7 μ m in diameter, located slightly ahead of mid-body near left body margin,



expected substitutions per site.

contracting at intervals of about 7 s (Figures 3A, B). Cortical granules colorless, globular, about 1 μ m across, irregularly distributed (Figures 3C, H, arrows). Cytoplasm colorless or grayish, often containing numerous densely packed lipid droplets (Figures 3A, G). Locomotion by moderately fast crawling on the bottom of Petri dish, occasionally jerking back and forth; when suspended in water, cells often swim continuously in circles.

Infraciliature as shown in **Figures 3D–F,I–K,M,N**. The adoral zone is composed of 15–18 membranelles, occupying about 1/4-1/3 of body length (**Table 1**). In living cells, cilia of distal membranelles about 12 μ m in length, and those of proximal membranelles are about 6 μ m long. The distal end of the adoral zone extends only slightly onto right body margin forming a question mark shape as in other urostylids. Paroral longer than endoral, both generally straight and optically intersect at their upper region (**Figures 3D, E**). Three slightly enlarged frontal cirri about 8 μ m in length, rightmost one located behind the distal end of the adoral zone (**Figure 3D**, pink area,

Figure 3E, double arrowheads). Two frontoterminal cirri behind the distal end of the adoral zone (**Figure 3E**, arrowheads); buccal cirrus lacking (**Figures 3D**, **E**); two to four slightly enlarged transverse cirri, up to 12 μ m long *in vivo*. Pretransverse cirri absent. Midventral complex composed of four or five pairs of cirri, terminating ahead of mid-body (**Figure 3E**, arrows). Left and right marginal rows composed of 13–21 and 14–25 cirri, respectively, with the anterior end of the left marginal rows not curved rightward (**Figure 3E**).

Three dorsal kineties arranged in typical *Gonostomum* pattern, with bristles about $3 \mu m$ in length (Figures 3F,J).

Description of Bakuella xianensis n. sp.

ZooBank registration.

Bakuella xianensis n. sp.: urn:lsid:zoobank.org:act:7C3FA85 3-C973-402B-824D-21F5337CB63E

Diagnosis: Body 115–150 μ m \times 40–65 μ m in vivo, elliptical in outline; about 70 macronuclear nodules; contractile vacuole



located ahead of mid-body; dark-brownish cortical granules arranged in groups, about 0.7 μ m across; about 23–33 adoral membranelles; midventral complex composed of 8–12 cirral pairs, terminating at about mid-body; two or three short ventral rows continuous with midventral pairs; three frontal, four to six frontoterminal, and three to five fine transverse cirri; one right and one left marginal rows with 24–38 and 22–33 cirri, respectively; three bipolar dorsal kineties; freshwater habitat.

Type material: One protargol-stained slide (No. MJY2019052501-1) with the holotype specimen (**Figure 4B**) circled in ink and two paratype slides (No. MJY2019052501-2, 3, 4) were deposited in the Laboratory of Protozoological

Biodiversity and Evolution in Wetland, Shaanxi Normal University, China.

Type locality: A freshwater pond in Chanba National Wetland Park, Xi'an (34°31'N; 109°01'E), China.

Etymology: The species-group name *xianensis* recalls that this species was first discovered in Xi'an, China.

Description (Figures 4A-M and Table 1).

Body about 115–150 μ m × 40–65 μ m *in vivo*, outline elongate-elliptical with both ends slightly narrow, length-to-width ratio approximately 3:1, flexible and dorsoventrally flattened (**Figures 4A,G–I** and **Table 1**). One contractile vacuole, about 15 μ m across, positioned slightly in front of mid-body near left margin (**Figures 4A,I**, arrow).

TABLE 1 | Morphometric data of *Wilbertophrya sinica* n. g., n. sp. (*Ws*, upper line) and *Bakuella xianensis* n. sp. (*Bx*, lower line).

| Characters | Species | ΗТ | Min | Max | Mean | Med | SD | cv | n |
|---|---------|-----|-----|-----|-------|-----|------|------|----|
| Body, length in μ m | Ws | 118 | 69 | 118 | 91.1 | 90 | 13.9 | 15.3 | 20 |
| | Bx | 103 | 84 | 129 | 109.6 | 110 | 13.8 | 12.6 | 18 |
| Body, width in μ m | Ws | 38 | 14 | 38 | 22.1 | 20 | 6.7 | 30.1 | 20 |
| | Bx | 50 | 29 | 58 | 47.1 | 48 | 8.5 | 18.0 | 18 |
| AZM, length in μ m | Ws | 31 | 16 | 31 | 25.1 | 26 | 4.8 | 19.1 | 20 |
| | Bx | 42 | 31 | 50 | 40.7 | 41 | 4.8 | 11.7 | 18 |
| Adoral membranelles, number | Ws | 17 | 15 | 18 | 16.7 | 17 | 0.9 | 5.6 | 20 |
| | Bx | 25 | 23 | 33 | 28.4 | 29 | 2.8 | 9.9 | 18 |
| Frontal cirri, number | Ws | 3 | 3 | 3 | 3.0 | 3 | 0 | 0 | 20 |
| | Bx | 3 | 3 | 3 | 3.0 | 3 | 0 | 0 | 18 |
| Buccal cirri, number | Bx | 1 | 1 | 1 | 1.0 | 1 | 0 | 0 | 18 |
| Frontoterminal cirri, number | Ws | 2 | 2 | 2 | 2.0 | 2 | 0 | 0 | 20 |
| | Bx | 5 | 4 | 6 | 4.8 | 5 | 0.8 | 16.8 | 17 |
| Number of cirral pairs in midventral complex | Ws | 4 | 4 | 5 | 4.4 | 4 | 0.5 | 11.5 | 15 |
| | Bx | 9 | 8 | 12 | 10.9 | 11 | 1.3 | 12.1 | 17 |
| Cirri in ventral row 1, number | Bx | 3 | 2 | З | 2.1 | 2 | 0.3 | 16.1 | 16 |
| Cirri in ventral row 2, number | Bx | 4 | З | 5 | 3.7 | 4 | 0.6 | 16.3 | 16 |
| Cirri in ventral row 3, number | Bx | - | 4 | 5 | 4.8 | 5 | 0.5 | 10.5 | 4 |
| Transverse cirri, number | Ws | 3 | 2 | 4 | 3.0 | З | 0.5 | 15.3 | 20 |
| | Bx | 4 | З | 5 | 4.3 | 4 | 0.6 | 13.7 | 17 |
| Pretransverse cirri, number | Bx | 1 | 1 | 1 | 1.0 | 1 | 0 | 0 | 12 |
| Left marginal cirri, number | Ws | 15 | 13 | 21 | 16.0 | 15 | 2.1 | 13.3 | 20 |
| | Bx | 23 | 22 | 33 | 26.9 | 27 | 3.6 | 13.3 | 17 |
| Right marginal cirri, number | Ws | 17 | 14 | 25 | 18.1 | 18 | 2.4 | 13.3 | 20 |
| | Bx | 28 | 24 | 38 | 31.8 | 32 | 3.6 | 11.2 | 17 |
| Dorsal kineties, number | Ws | 3 | З | З | 3.0 | З | 0 | 0 | 20 |
| | Bx | 3 | З | З | 3.0 | З | 0 | 0 | 18 |
| Macronuclear nodules, number | Ws | 16 | 13 | 19 | 15.2 | 15 | 1.3 | 8.6 | 20 |
| | Bx | 66 | 50 | 106 | 69.6 | 65 | 16.7 | 24.0 | 17 |

All data are based on protargol-stained specimens.

AZM, adoral zone of membranelles; CV, coefficient of variation in %; DK, dorsal kineties; HT, holotype specimen; Max, maximum; Mean, arithmetic mean; Med, median; Min, minimum; N, number of cells measured; SD, standard deviation; –, data unavailable.

Pellicle thin and soft, with globular, dark-brownish cortical granules (about 0.7 μ m across) in densely arranged groups on both ventral and dorsal sides, rendering cells slightly brownish at lower magnifications (**Figures 4E, F, J**). Cytoplasm colorless to grayish, usually packed with numerous small lipid droplets (about 3 μ m across) and several large food vacuoles (about 8 μ m across) containing ingested diatoms, bacteria, and/or ciliates. About 70 ellipsoidal macronuclear nodules scattered in cytoplasm (**Figures 4C,M** and **Table 1**). Locomotion by continuous, slow, to moderately fast, crawling on substrate.

Infraciliature as shown in **Figures 4B–D,K–M**. The adoral zone is about 40 μ m long, occupying about 1/3 of body length, and composed of about 28 membranelles on average (**Table 1**). Endoral and paroral prominent *in vivo*, that is, long and curved, optically intersecting at the paroral's mid-region. Most somatic cirri are relatively fine with cilia about 10–15 μ m long. Constantly

three relatively stout frontal cirri (FC, Figure 4D), apically positioned. Invariably one buccal cirrus, about level of endoral's mid-region (Figure 4B, arrow). Four to six fine frontoterminal cirri (Figure 4B, arrowheads). Three to five transverse cirri form roughly V-shaped (Figures 4B,L), protruding beyond rear end of body. Cilia of which is 13-15 µm long. Of the 18 examined specimens, 12 had one pretransverse cirrus, while the remainder lacked the cirrus. Midventral complex terminates at about posterior 1/4 of body length, composed of about 8-12 cirral pairs forming a zigzag row that extends to about mid-region of the cell, and two, sometimes three, short ventral rows that are continuous with a row of midventral pairs (Figures 4B, D, VR and arrows, inset). One right and one left marginal rows composed of 24-38 and 22-33 cirri, respectively (Table 1); the right marginal row commences slightly ahead of level of buccal cirrus, always with two pairs of basal bodies ahead of its anterior end (Figures 4C,M, arrows). Three bipolar dorsal kineties arranged in typical *Gonostomum* pattern (Figures 4C,M).

Phylogeny Based on Small Subunit Ribosomal DNA Sequence Data

The SSU rDNA sequences of *Wilbertophrya sinica* n. sp. and *Bakuella xianensis* n. sp. were deposited to GenBank with accession numbers, length, and guanine–cytosine (GC) content as follows: MT809485, 1,762 bp, 45.40% and MT819382, 1,770 bp, 44.18%, respectively. *W. sinica* and nine morphologically related isolates generated a nucleotide matrix with 204 unmatched sites (**Figure 5A**), while *B. xianensis* and five related taxa formed the table with 57 unmatched sites (**Figure 5B**).

Phylogenetic trees inferred from the SSU rDNA sequences using ML and BI had similar topologies; therefore, only the ML tree is shown with nodal support from both methods (Figure 2). W. sinica n. sp. clustered with Anteholosticha monilata (KJ958488) with high support (87% ML, 1.00 BI), which together grouped with four sequences of Extraholosticha sylvatica (MG603613, MG603614, KJ958490, and MN160327) with full support (Figure 2). This group was sister to the clade composed of Eschaneustyla lugeri (KY874005) and Holostichides heterotypicus (KY231187). Consequently, a comparison was made among these seven and two other morphologically similar species of W. sinica n. sp., namely, Adumbratosticha tetracirrata (KJ958491) and Caudikeronopsis marina (KR612270) (Figure 5A). The sequence differences between W. sinica n. sp. and these nine "related" taxa are as follows: 15 bp for A. monilata, 16–33 bp for the four sequences of *E. sylvatica*, 63 bp for *E. lugeri*, 67 bp for H. heterotypicus, 84 bp for A. tetracirrata, and 126 bp for C. marina.

Bakuella xianensis n. sp. clustered with Bakuella incheonensis (KR024011), and two sequences of Bakuella subtropica (KC631826 and KY874001) and Anteholosticha paramanca (KF806443) with moderate-to-strong support (90% ML, 1.00 BI), which together formed a clade with two species of Anteholosticha. Two other Bakuella species (Bakuella litoralis and Bakuella granulifera) belong to other groups, i.e., B. litoralis KR024010 + the Neobakuella–Apobakuella–Diaxonella complex and B. granulifera + Urostyla + Neobakuella. Hence, all known



FIGURE 4 | Morphology of *Bakuella xianensis* n. sp. from life (**A**, **E**–**J**) and after protargol staining (**B**–**D**,**K**–**M**). (**A**) Ventral view of a representative specimen. (**B**,**C**) Ventral (**B**) and dorsal (**C**) views of the holotype specimen to show the infraciliature and nuclear apparatus. In (**B**), arrow marks the buccal cirrus, arrowheads show the frontoterminal cirri, and double arrowheads mark a short ventral row (in green box). In (**C**), arrows indicate the basal body pairs ahead of the right marginal row. (**D**) Ventral view to show details of buccal field and midventral complex; inset (**a**,**b**) shows two different arrangements of ventral rows (VR, arrows). (**E**,**F**,**J**) Detail of distribution of cortical granules in irregular longitudinal rows on ventral (**E**) and dorsal (**F**,**J**) sides. (**G**–**I**) Ventral views to show different body shapes due to flexibility of cells. Arrow indicates the contractile vacuole. (**K**) Ventral view to show details of buccal field and midventral complex, arrows show the frontoterminal cirri, and arrowheads indicate the midventral rows. (**L**,**M**) Ventral (**L**) and dorsal (**M**) views of the same specimen showing infraciliature and nuclear apparatus. Arrows indicate the basal body pairs ahead of right marginal row. AZM, adoral zone of membranelles; BC, buccal cirrus; CV, contractile vacuoles; E, endoral; FC, frontal cirri; FTC, frontoterminal cirri; LMR, left marginal row; Ma, macronuclear nodules; **M**VP, midventral pairs; P, paroral; PTVC, pretransverse ventral cirri; RMR, right marginal row; TC, transverse cirri; VR, ventral row; 1–3, dorsal kineties. Scale bars: (**A–C,G,H**) = 60 μm, (**E,F**) = 7 μm.

congeners in *Bakuella* belong to three separate (but neighboring) branches within the core-urostylid lineage (**Figure 2**).

DISCUSSION

Systematic Position of *Wilbertophrya* n. g. and Comparison With Related Taxa

The possession of three clearly differentiated frontal cirri and a midventral complex composed of midventral pairs only places *Wilbertophrya* n. g. unequivocally in the family Holostichidae (*sensu* Berger, 2006). Based on the following combination of features, that is, single left and right marginal rows, a continuous adoral zone, presence of frontoterminal cirri, clearly differentiated frontal cirri, and midventral cirral pairs arranged in a zigzag pattern, five genera in the family Holostichidae should be compared with *Wilbertophrya* n. g., namely, *Anteholosticha* Berger, 2003; *Arcuseries* Huang et al., 2014; *Afrothrix* Foissner, 1999; *Acuholosticha* Li et al., 2017; and *Holosticha* Wrzesniowski, 1877 (Berger, 2003; Huang et al., 2014; Li et al., 2017). All five of these genera differ from *Wilbertophrya* n. g. in having a buccal cirrus and pretransverse cirri, whereas both these structures are lacking in the new genus (Berger, 2006; Huang et al., 2014; Li et al., 2017). Furthermore, *Acuholosticha* possesses caudal cirri, whereas these are absent in *Wilbertophrya* n. g. (Berger, 2006; **Figure 6; Table 2**). The

| Α | | | | | | | |
|--|--|---|--|--|--|--|--|
| position | 22 24 25 25 29 29 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20 | $\begin{array}{c} 102\\ 107\\ 110\\ 1110\\ 1115\\ 1119\\ 1150\\ 150\\ 151\\ 151\\ 152\end{array}$ | 154 164 165 168 174 180 182 197 197 201 | 210 211 268 271 336 331 336 337 372 403 | 409 411 412 413 416 419 423 434 433 433 | 442 450 453 453 453 551 551 551 551 553 563 | 564 565 565 567 571 571 581 591 591 |
| Wilbertophrya sinica n. sp. MT809485 Anteholosticha monilata KJ958488 | A A A - C T G T T G | TTTAGGTCGT | - ATCAGTATT T | CGTAAAAATT | T - TTTACAAG | A T T G T A A G G G G C · · · · C · A · · · | GCGGTCGAAG |
| Extraholosticha sylvatica 1 MG603614 Extraholosticha sylvatica 2 MG603613 Extraholosticha sylvatica 3 KJ958490 | · · · · · T · · · · · · · · · · · · · · | | | G | · · · · · · · · · · · · · · · · · · · | | |
| Extraholosticha sylvatica 4 MN160327 Eschaneustyla lugeri KY874005 | T TTCAA | | GTA | | · · · · · · · · · · · · · · · · · · · | C C | |
| Holosticha heterotypicus KY231187 Adumbratosticha tetracirrata KJ958491 Caudikeronopsis marina KR612270 | $\begin{array}{c} \mathbf{I} \cdot \cdot \cdot = \mathbf{I} \cdot \mathbf{A} \mathbf{C} \mathbf{A} \mathbf{A} \\ \cdot \cdot \cdot = \cdot \mathbf{C} \cdot \cdot \mathbf{A} \mathbf{A} \\ \cdot \mathbf{C} \mathbf{G} \mathbf{C} \mathbf{T} \cdot \cdot \mathbf{C} \mathbf{A} \mathbf{A} \end{array}$ | $\begin{array}{c} \mathbf{C} \\ $ | - G . GG GCC | . A | $C - AC \cdot T \cdot T \cdot T \cdot CCG \cdot GGTG \cdot C$ | $\begin{array}{c} \mathbf{C} \mathbf{A} \\ \mathbf{C} \mathbf{A} \\ \mathbf{A} \\ \mathbf{C} \\ \mathbf{C} \\ \mathbf{C} \\ \mathbf{G} \\ \mathbf{C} \\ \mathbf{G} \\ \mathbf{C} \\ \mathbf{C} \\ \mathbf{G} \\ \mathbf{C} \\$ | . GCC.GTT CGTTA |
| position | 595 597 598 598 599 602 603 603 624 624 | 628 634 634 636 637 637 637 637 637 637 637 637 637 | 735 742 742 743 743 744 755 763 763 763 771 | 802 816 834 835 906 916 917 | 918 920 925 925 926 927 928 929 | 933 947 947 963 965 968 968 970 1063 1082 | 1131 1132 1133 1134 1134 1134 1254 1259 1260 1261 |
| <i>Wilbertophrya sinica</i> n. sp. MT809485 Anteholosticha monilata KJ958488 | CTGCCTCCTC | CCACGGCGCC AT | T T C T T A A A A C G | TGAAAAAGGA | C GGTAGTCTA | C A A C C T T T A G T T T | T TG C A A A C A G |
| Extraholosticha sylvatica 1 MG603614 Extraholosticha sylvatica 2 MG603613 | | T A T A | | ••••• | | · · · · · · · · · T · · · | |
| Extraholosticha sylvatica 3 KJ958490 Extraholosticha sylvatica 4 MN160327 | | T A T A | | | ACGTACTCT | | C |
| Eschaneustyla lugeri KY874005 Holosticha heterotypicus KY231187 | GCTA. GA.TTG.TA. | TATA TATA | CGG CGA.G | T | | . GCT . GCT | GCGGT GCGGT |
| Adumbratosticha tetracirrata KJ958491 Caudikeronopsis marina KR612270 | GGC.T.TA.T GCT.T | TACGTA.TTA TACGTA.T.G | . A G T G A T C T T | •••••••••••••••••••••••••••••••••••••• | | . G.TTC.AT . GACAT.C | C.ATG.C.GA .A.TGGC.GA |
| position | 1262 1264 1266 1266 1266 1268 1271 1273 1274 1275 1275 | 1277 1278 1279 1279 1304 1305 1305 1305 1305 1305 1305 1305 1305 | 1405 1412 1413 1413 1413 1413 1422 1457 1457 1457 | 1472 1472 1502 1502 1510 1510 1511 1512 1513 | 150/ 1591 1595 1596 1596 1598 1598 1599 1600 1601 | 1604 1606 1608 1610 1611 1612 1613 1613 1613 1613 1617 1618 | 1620 |
| Wilbertophrya sinica n. sp. MT809485 Anteholosticha monilata K.1958488 | TGTACTTACT | TCCTTTTTCTC | GAACA - CTAA | AGGACCCCT' | GCGCTCGGT | C CTCCTGATTG | Α |
| Extraholosticha sylvatica 1 MG603614 Extraholosticha sylvatica 2 MG603613 | CCATG . CCATG . | · . G | | | T | | • |
| Extraholosticha sylvatica 3 KJ958490 Extraholosticha sylvatica 4 MN160327 | CCATG . CCATGA | · . G | | | | T A G | • |
| Eschaneustyla lugeri KY874005 Holosticha heterotypicus KY231187 | . CAG CTGA . CAG CTGA | $C_{T,C}$ | A.G | | | A T C | : |
| Adumbratosticha tetracirrata KJ958491 Caudikeronopsis marina KR612270 | •••••••••••••••••••••••••••••••••••••• | · T . C T CTTCC C - AT | ACG.T-A.A ACG.TAGCO | AATTGTT. G CAATTTC | . AGATCT.A. . T T.TC | TGC. T . TCTACTGCC. | Ġ |
| В | | | | | | | |
| position | 34 90 1121 1149 1168 1168 1182 1182 1182 | 190 191 388 392 395 395 541 543 | 544 5578 575 575 575 575 575 575 575 575 57 | 604 664 716 961 962 968 985 1214 1266 | 1267 1270 1301 1302 1302 1408 1472 1498 1498 | 1590 11594 11595 11598 11602 11610 | |
| Bakuella xianensis n. sp. MT819382 | CTTTCTGACA TCACTCACTC | AGTGACCAAA | TCGTCGTTCA | GAAGTAATTC TCCAAT T | AGCA - CGTAA | ACGTTCC | |
| Bakuella subtropica KC631826 | | | A1 | · · · · · · · · · C . | G | | |
| Bakuella incheonensis KR024011 Bakuella subtropica KY874001 | ••••• | | | · · · · · · · · · · · · | · · · · · · · · · · · · · · · · · · · | | |
| Bakuella litoralis KR024010 | C | G | •••••••••••••••••••••••••••••••••••••• | $\mathbf{T} \cdot \cdot \cdot \mathbf{GC} \cdot \mathbf{T}$ | · A · · · · · · · · (| G T.C. T | |
| FIGURE 5 (A) Comparison of sm related species (for GenBank acce | nall subunit ribosor ession numbers, se | mal DNA (SSU rDN ee Figure 2). (B) C | A) sequences sho omparison of SSL | wing the unmatch J rDNA sequences | ed nucleotides be showing the unm | etween <i>Wilbertophry</i> a | a <i>sinica</i> n. sp. and between <i>Bakuella</i> |

xianensis n. sp. and related species (for GenBank accession numbers, see Figure 2). Nucleotide positions are given at the tradeletions are compensated by introducing alignment gaps (-). Matched sites are represented by dots (.).

validity of the new genus is also supported by the molecular data (Figure 5A).

Eight other morphologically similar genera are compared with *Wilbertophrya* n. g., namely, *Adumbratosticha* Li et al., 2017; *Caudikeronopsis* Li et al., 2017; *Extraholosticha* Li et al., 2017; *Limnoholosticha* Li et al., 2017; *Multiholosticha* Li et al., 2017; *Periholosticha* Hemberger, 1985; *Psammomitra* Borror, 1972; and *Uroleptus* Ehrenberg, 1831 (Figure 6; Table 2). *Wilbertophrya* n. g. can be separated from each of these by the following combination of characters: (1) presence of frontoterminal cirri; (2) absence of pretransverse, caudal, and buccal cirri; (3) adoral zone of membranelles continuous; and (4) three complete dorsal kineties (Figure 6; Table 2).

The systematic position of *Wilbertophrya* n. g. remains unclear considering that the family assignment though morphological information supports its possible assignment to the family Holostichidae. The SSU rDNA tree reveals that *Wilbertophrya* groups with seven representatives of four genera: *Anteholosticha*, *Extraholosticha*, *Eschaneustyla*, and *Holostichides* (**Figure 2**). It is most closely related to *A. monilata* (KJ958488), the identification of which needs to be verified since there is another sequence with the same name but which occupies a different position in the tree (**Figure 2**, double arrowheads). Previous molecular phylogenetic analyses suggest that the genus *Anteholosticha* is not monophyletic and that most of its nominal species belong to the Urostylidae + Pseudokeronopsidae + Pseudourostylidae complex, which is the sister group of the clade that includes *Wilbertophrya* (**Figure 2**; Shao et al., 2011; Li et al., 2017; Luo et al., 2018; Xu et al., 2020).

In the SSU rDNA tree (Figure 2), the new genus clusters with several representatives of the genus Extraholosticha followed by E. lugeri + H. heterotypicus. This large clade is separated from other sequences at a deep level, suggesting that it might represent an undefined group at about family level. In terms of its morphology, however, the genus Wilbertophrya should be assigned to the family Holostichidae (see above). But as revealed in previous studies, the Holostichidae complex molecular (e.g., Holostichidae + Urostylidae + Pseudokeronopsidae) is a so-called melting pot of taxa, the evolutionary relationships of which cannot be resolved using phylogenetic analyses of single-gene sequence data (Bernhard et al., 2001; Yi and Song, 2011; Zhao et al., 2015; Luo et al., 2018; Jung and Berger, 2019; Paiva, 2020; Wang et al., 2021b;



FIGURE 6 | Comparison of infraciliature patterns of genera related to *Wilbertophrya* n. g. Arrows indicate the gap in the adoral zone of membranelles; arrowheads show the presence of a buccal cirrus. (A1,A2) Ventral (A1) and dorsal (A2) views of *Wilbertophrya* n. g.; double arrowheads in (A) indicate the frontoterminal cirri, while in (C), they mark the curved anterior end of left marginal row. (B) *Anteholosticha*. (C) *Holosticha*. (D) *Periholosticha*. (E) *Afrothrix*. (F) *Arcuseries*. (G1,G2) ventral (G1) and dorsal (G2) views of *Psammomitra*. (H) *Acuholosticha*. (I) *Extraholosticha*. (J) *Adumbratosticha*. (K) *Caudiholosticha*. (L) *Multiholosticha*. (M) *Caudikeronopsis*. (N) *Limnoholosticha*. Ma, macronuclear nodules. Question mark in (L) indicates presence/absence of frontoterminal questionable. Question mark in (N) indicates presence/absence of frontoterminal and pretransverse ventral cirri not known.

TABLE 2 | Morphological comparison of Wilbertophrya n. g. with similar genera.

| CharacterGenera | Buccal cirrus | Pretransverse ventral cirri | Caudal cirri | Adoral zone of membranelles | Number of dorsal kineties | Frontoterminal cirri | Other structures | Data source |
|----------------------------|------------------|--------------------------------|-----------------|-----------------------------|---------------------------------|----------------------|---|-----------------------|
| Acuholosticha | Present | Present or absent | Present | Continuous | 2–4 | Present | | Li et al., 2017 |
| Adumbratosticha | Present | Present or absent | Present | Continuous | More than 3 | Present | | Li et al., 2017 |
| Afrothrix | Present | Present | Absent | Bipartite | 2–3 | Present | | Berger, 2006 |
| Anteholosticha | Present | Present or absent | Absent | Continuous | 3–6 | Present | | Berger, 2006 |
| Arcuseries | Present | Present | Absent | Continuous | 3 | Present | | Huang et al., 2014 |
| Caudikeronopsis | Present | Present | Present | Continuous | More than 3 | Present | | Li et al., 2017 |
| Extraholosticha | Present | Present | Present | Continuous | More than 3 | Present | A short cirral row formed by anlage I | Li et al., 2017 |
| Holosticha | Present | Present | Absent | Bipartite | More than 3 | Present | Rear membranelles of proximal portion slightly to distinctly wider than remaining; anterior end of left marginal row distinctly curved rightward; number of transverse cirri equal to or only slightly lower than number of midventral pairs | Berger, 2006 |
| Limnoholosticha | Present | NA | Present | Continuous | NA | NA | | Li et al., 2017 |
| Multiholosticha | Present | Present | Present | Continuous | 6 | NA | | Li et al., 2017 |
| Periholosticha | Absent | NA | Present | Bipartite | 3 or 2 | Present or absent | | Berger, 2006 |
| Psammomitra | Present | NA | Absent | Continuous | 4 | Present | Body tripartite in head, trunk, and tail | Berger, 2006 |
| Uroleptus | Present | Absent | Present | Continuous | 5 | Present | | Li et al., 2017 |
| <i>Wilbertophrya</i> n. g. | Absent | Absent | Absent | Continuous | 3 | Present | | Present work |

NA, not available.

Xu et al., 2020). Similarly, it is difficult to place *Wilbertophrya* n. g. into any known family based on SSU rDNA sequence data. Since ontogenetic information is unavailable for the new genus, we suggest that *Wilbertophrya* n. g. should be regarded as

incertae sedis within the order Urostylida pending the availability of further data.

Wilbertophrya n. g. is a monotypic genus, and thus, the type species, *W. sinica* n. sp., can be separated from its most "similar"

TABLE 3 | Morphological comparison of *Bakuella xianensis* n. sp. with closely related species.

| Character Species | Body length <i>in vivo</i> (μm) | AZM, no. | Buccal cirri, no. | Frontoterminal cirri, no. | Midventral pairs, no. | Midventral rows, no. | Midventral complex, length | Transverse cirri, no. | Cirri in LMR, no. | Cirri in RMR, no. | Cortical granules | Data source |
|---|------------------------------------|-------------|----------------------|---------------------------------|-----------------------|--|--|--------------------------|----------------------|----------------------|--|-----------------------|
| Bakuella agamalievi | 100–150 | 26–37 | 1 | 4–7 | 9–18 | 3–6 | Terminates bout 67% down length of body | 4–7 | 30–40 | 34–47 | 0.8 μm across; colorless or slightly greenish | Berger, 2006 |
| Bakuella crenata | About 210 | 28–30 | 3 or 4 | 7–9 (data from illustration) | About 5 | 10–12 | Terminates slightly ahead of transverse cirri | 7–9 | 36–40 | 40–50 | NA | Berger, 2006 |
| Bakuella edaphoni | 190–300 | 34–45 | 5–9 | 2–5 | 5–14 | 5–10 with more than 3 cirri and 1–6 with 3 cirri | Terminating close to transverse cirrus | 6–11 | 44–56 | 43–55 | Absent | Berger, 2006 |
| Bakuella granulifera | 270–400 | 44–62 | 7–10 | 3–5 | 12–23 | 3–5 | Terminates at right transverse cirrus | 9–15 | 54–77 | 54–76 | 1.3– 1.5 μm × 0.8– 1.0 μm; brilliant citrine | Berger, 2006 |
| Bakuella incheonensis | 70–105 | 21–25 | 1 | 3 or 4 | 7–10 | 1 or 2 | Terminates bout 62% down length of body | 4 or 5 | 20–28 | 25–32 | 0.7 μm across; yellowish | Jo et al., 2015 |
| Bakuella marina | About 200 | 28–51 | 2–5 | 5–11 | 4–12 | 4–8 | Extends almost to transverse cirral row | 5–11 | 23–56 | 34–63 | NA | Berger, 2006 |
| Bakuella nilgiri | About 158 | 42–54 | 4–8 | 2-4 | 18–23 | 2–10 | Extends to near transverse cirri | 6–11 | 38–56 | 49–65 | About 0.7 μm across; colorless | Kumar et al., 2010 |
| Bakuella pampinaria oligocirrata | 80–150 | 22–34 | 2–5 | 1–7 | 3–7 | 3–5 | Terminates very close to right transverse cirrus | 3–7 | 24–42 | 25–42 | About 1.0 μm × 0.7 μm; citrine to yellowish | Berger, 2006 |
| Bakuella pampinaria pampinaria | 90–180 | 22–39 | 3–6 | 5–8 | 6–13 | 2–6 | Terminates very close to right transverse cirrus | 2–5 | 24–47 | 23–51 | 1.5– 2.0 μm × 1.0– 1.5 μm; yellowish | Berger, 2006 |
| Bakuella subtropica | 100–150 | 25–44 | 1 | 4–12 | 9–23 | 1 or 2 | Terminates bout 80% down length of body | 3–6 | 30–54 | 28–64 | 1–2 μm across; yellow-brownish to yellow-greenish | Chen et al., 2013 |
| <i>Bakuella xianensis</i> n. sp. | 115–150 | 23–33 | 1 | 4–6 | 8–12 | 2 or 3 | Terminates bout 75% down length of body | 3–5 | 22–33 | 24–38 | about 0.7 μm cross; dark-brownish | Present work |

AZM, adoral zone of membranelles; LMR, left marginal row; NA, not available; RMR, right marginal rows.

morphospecies, that is, members of the genera Adumbratosticha, Periholosticha, Afrothrix, and Acuholosticha (see Figure 6) by the same combination of features that define the genus, i.e., the absence of the buccal cirrus and pretransverse cirri, and the presence of sparsely distributed cortical granules and the conspicuously short midventral rows (Berger, 2003; Li et al., 2017; Shao et al., 2020). The validity of *W. sinica* n. sp. as a distinct species is also firmly supported by the molecular data, which demonstrates its considerable difference from other taxa (Figure 5A).

Systematic Position of *Bakuella xianensis* n. sp. and Comparison With Congeners

The well-defined genus *Bakuella* can be recognized by its midventral complex comprising pairs of cirri arranged in a zigzag pattern and several obliquely oriented fragment-like ventral rows (Borror and Wicklow, 1983; Berger, 2006; Song and Shao, 2017; Shao et al., 2020). To date, 12 nominal species have been reported (**Table 3**), three of which have a single buccal cirrus and more than two frontoterminal cirri, and so should be compared with *B. xianensis* n. sp., namely, *Bakuella agamalievi* Borror and Wicklow, 1983; *B. subtropica* Chen et al., 2013; and *B. incheonensis* Jo et al., 2015.

Bakuella xianensis n. sp. can be distinguished from *B. subtropica*, a brackish water form originally found in a subtropical area in China (estuary of the Pearl River, Chen et al., 2013; **Figures 7A, B**) by (1) the size of the cortical granules (about 0.7 μ m in diameter vs. 1–2 μ m in diameter); (2) its habitat (freshwater vs. brackish water in mangrove wetlands); (3) having fewer cirral pairs in the

midventral complex (8–12 vs. 9–23); and (4) having fewer left (22–33 vs. 30–54) and right (24–38 vs. 28–64) marginal cirri (Chen et al., 2013).

Bakuella xianensis n. sp. differs from *B. agamalievi*, a marine form originally found in the Caspian Sea (Agamaliev, 1972; **Figures 7C, D**) and redescribed by Song et al. (2002) as having dark-brownish (vs. colorless or slightly greenish) cortical granules, fewer ventral rows in the midventral complex (two or three vs. three to six), fewer cirri in both right (24–38 vs. 40–47) marginal rows, and in its freshwater (vs. marine) habitat (Agamaliev, 1972; Song et al., 2002; Berger, 2006).

Bakuella xianensis n. sp. differs from *B. incheonensis* (Figures 7E, F) by its larger body size (115–150 μ m × 40–65 μ m vs. 70–105 μ m × 20–40 μ m *in vivo*), the color and arrangement of cortical granules (dark-brownish vs. yellowish), and its freshwater (vs. marine) habitat (Figures 4E, F, J, 7E, F). In addition, the cortical granules in *B. incheonensis* appear to be large, conspicuous, and possibly ellipsoid in shape (Figure 7F, arrows, not mentioned in original report), whereas those in *B. xianensis* n. sp. are small, globular, and inconspicuous (Figures 4E, F, J; Jo et al., 2015).

Including *B. xianensis* n. sp., SSU rDNA sequence data are available for only six species of *Bakuella*. These are grouped into three neighboring clades in the SSU rDNA tree (**Figure 2**). *B. xianensis* n. sp. is placed within the core clade of the genus. It is noteworthy, however, that some *Bakuella* sequences group with non-bakuellid genera, e.g., nominal isolates of genera such as *Urostyla*, *Diaxonella*, and *Anteholosticha*, with high support. This is consistent with previous reports (Chen et al., 2010, 2013) and indicates that none of the families Bakuellidae, Urostylidae, and Holostichidae is monophyletic; and the systematics of each requires further investigation.





DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/ supplementary material.

AUTHOR CONTRIBUTIONS

JM carried out the live observation and protargol impregnation. TZ was responsible for DNA amplification and sequencing, and the molecular phylogenetic analyses. JM, TZ, and CS performed the manuscript draft. CS and WS performed the manuscript review and editing. All authors helped to revise the manuscript, and read and approved the final manuscript.

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FUNDING

This work was supported by the National Natural Science Foundation of China (project numbers 32070428 and 32030015) and the China Postdoctoral Science Foundation (No. 2021M692010).

ACKNOWLEDGMENTS

The authors would like to express their sincere thanks to Alan Warren (NHM) for his helpful critiques in enhancing the language of this manuscript. Many thanks are given to Yurui Wang (OUC) for her help with phylogenetic analyses.

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