

Weighted parsimony phylogeny of the family Characidae (Teleostei: Characiformes)

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Abstract

The family Characidae, including more than 1000 species, lacks a phylogenetic diagnosis, with many of its genera currently considered as *incertae sedis*. The aims of the present study are to propose a phylogenetic diagnosis and to assess higher-level relationships of and within Characidae. In this regard, 360 morphological characters are studied for 160 species of Characidae and related families. Phylogenetic analyses under implied weighting and self-weighted optimization are presented, exploring a broad range of parameters. The analysis under self-weighted optimization is innovative for this size of matrices. Familial status of Serrasalminae is supported, and Acestrorhynchidae and Cynodontidae are included in a monophyletic Characidae. *Engraulisoma taeniatum* is transferred from Characidae to Gasteropelecidae. Thus constituted, the monophyly of Characidae is supported by seven synapomorphies. A new subfamily, Heterocharacinae, is proposed, and the subfamilies Aphyocharacinae, Aphyoditeinae, Characinae, Gymnocharacinae, and Stevardiinae are redefined. The Glandulocaudinae are included in Stevardiinae together with remaining members of “clade A” (*sensu* Malabarba and Weitzman, 2003. *Comun. Mus. Ciénc. Tecnol. PUCRS, Sér. Zool.* 16, 67–151.) and the genera *Aulixidens* and *Nantis*. Most *incertae sedis* genera are assigned, at least tentatively, to a phylogenetically diagnosed clade.

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The family Characidae is the fourth most diverse family of fishes, and the most diverse among Neotropical fishes, with more than 1000 species distributed from the southern USA to northern Patagonia (Argentina); many fishes of this family are commonly known as tetras. This family lacks a phylogenetic diagnosis and its classification is subject to constant changes. Much characid systematics was delineated in a series of seminal papers by Eigenmann (1912, 1915, 1917, 1918, 1921, 1927), and Eigenmann and Myers (1929), in which most genera were defined with combinations of alternative states of 17 characters. This classical systematics was followed by most subsequent authors (e.g. Greenwood et al., 1966; Géry, 1977), until Rosen (1972) and especially Weitzman and Fink (1983) highlighted the importance of a classification reflecting the phylogeny of the family. Several papers have dealt with the phylogeny of some genera and subfamilies of Characidae (e.g.

Machado-Allison, 1983; Weitzman and Fink, 1985; Reis, 1989; Malabarba, 1998a; Weitzman and Menezes, 1998). There have also been studies of the phylogeny and relationships of the family (Uj, 1990; Lucena, 1993; Buckup, 1998; Calcagnotto et al., 2005). Lucena (1993) analysed a matrix of 129 characters for 66 characid species; although he obtained a rather poor resolution and did not explicitly diagnose the family, his study forms the principal basis for the present one.

Lima et al. (2003) restricted the subfamilies of Characidae to those having some evidence of monophyly, leaving 88 genera as *incertae sedis*. Malabarba and Weitzman (2003) hypothesized the monophyly of a clade referred as “clade A” which, as redefined by Weitzman et al. (2005), includes 20 *incertae sedis* genera and the subfamilies Glandulocaudinae and Stevardiinae. Later, four new *incertae sedis* genera were described (*Myxiops* Zanata and Akama, 2004; *Nantis* Mirande et al., 2004, 2006; *Bryconadenos* Weitzman et al., 2005; *Dectobrycon* Zarske and Géry, 2006), and the monotypic *incertae sedis* genus *Carlasyanax* was synonymy-

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mized with *Astyanax* (Ruiz-C. and Román-Valencia, 2006). Thus, 92 of the 170 genera of Characidae are currently considered as *incertae sedis*. After more than 35 years since the first phylogenetically based contribution to classification of the family (Rosen, 1972), a systematic arrangement more than 90 years old (Eigenmann, 1917) is still used for most characids.

Most Characidae are morphologically rather conservative, and important sources of variation are related to diet and miniaturization events, which often result in highly homoplastic characters (Weitzman and Fink, 1983; Lucena, 1993); thus, a weighting scheme taking into account such homoplasy during parsimony analysis is especially desirable. The criterion of weighting against homoplasy has been variously defended (e.g. Farris, 1969, 1983; Goloboff, 1993, 1995, 1997; Ramírez, 2003; Aguilera and Mirande, 2005; Goloboff et al., 2008). Also, as demonstrated by Goloboff et al. (2008), the implied weighting method (IW) (Goloboff, 1993) usually increases the support and stability relative to the commonly used equal weighting scheme. Miniaturization events have been proposed to have occurred several times within Characiformes (Weitzman and Fink, 1983; Buckup, 1993; Bührnheim et al., 2008); this kind of evolutionary process is commonly correlated with the reduction of several features, such as the lateral-line system and infraorbital bones (Weitzman and Fink, 1983; Buckup, 1993; Bührnheim et al., 2008). Self-weighted optimization (SL) (Goloboff, 1997), a weighting scheme which considers these kind of characters, in particular, with more transformations in one direction than in others, is used here in addition to IW.

The objectives here are to propose a phylogenetic diagnosis and to assess higher-level relationships of and within Characidae that can serve as a framework for future studies, providing also a tentative subfamilial classification. This paper also provides an example of weighted parsimony analysis of a relatively large morphological matrix, under IW and SL, delineating a protocol for future analyses of matrices of this size and complexity.

Materials and methods

Taxon sampling

Selection of species was intended to sample most of the morphological and taxonomic diversity within Characidae, directing relatively more attention to *incertae sedis* genera (*sensu* Lima et al., 2003) than to members of evidently monophyletic groups. However, some representatives of most subfamilies (Cardoso, 2003a,b; Lima, 2003a,c; Lima and Zanata, 2003; Lucena and Menezes, 2003; Malabarba, 2003; Moreira, 2003; Reis, 2003a,b; Weitzman et al., 2005; Bührnheim, 2006;

Quevedo, 2006) were included in order to test their monophyly in a familial context and to evaluate their relationships within the family. Taxon sampling includes members of all recognized subfamilies except the monotypic Clupeacharacinae (Lima, 2003b). As most genera lack phylogenetic diagnoses, and some are even explicitly considered paraphyletic [e.g. *Astyanax* (from Eigenmann, 1917; to Abilhoa and Duboc, 2007)], terminal taxa in this analysis are species.

The data set consists of 160 species, 137 from the ingroup and 23 forming the outgroup. The analyses were rooted in *Puntius tetrazona* (Bleeker) as a representative of Cypriniformes, considered the sister order of [Characiformes (Siluriformes + Gymnotiformes)] (Fink and Fink, 1981, 1996); coding of the root, however, is intended to represent the ancestral character states in Cypriniformes, and it was modified from observations in this species when morphological information on supposedly “basal” Cypriniformes was available (Howes, 1978, 1979, 1980; Vari, 1979; Fink and Fink, 1981, 1996). Other taxa from the outgroup are representatives of the characiform African superfamily Citharinoidei [considered as sister group of remaining Characiformes (Vari, 1979; Buckup, 1998)], the Neotropical families Acestrorhynchidae, Anostomidae, Crenuchidae, Curimatidae, Cynodontidae, Erythrinidae, Gasteropelecidae, Hemiodontidae, Lebiasinidae, Parodontidae, Prochilodontidae, and Serrasalminidae, and the trans-Atlantic family Alestidae. The ingroup comprises members of (in parentheses, number of species included) the subfamilies Agoniatinae (1), Aphyocharacinae (3), Bryconinae (4), Characinae (10), Cheirodontinae (6), Glandulocaudinae (1), Iguanodectinae (2), Paragoniatiinae (4), Rhoadsiinae (2), Stethaprioninae (2), Stevardiinae (4), Tetragonopterinae (1), *incertae sedis* within Clade A (19), and *incertae sedis* not included in Clade A (77) (Cardoso, 2003a,b; Lima, 2003a,c; Lima and Zanata, 2003; Lucena and Menezes, 2003; Malabarba, 2003; Moreira, 2003; Reis, 2003a,b; Weitzman et al., 2005; Bührnheim, 2006; Quevedo, 2006).

Specimens were cleared and stained (C&S) following Taylor and Van Dyke (1985). Osteological nomenclature follows Weitzman (1962), with modifications from Zanata and Vari (2005). See Supporting Information for a complete list of C&S specimens examined.

Character sampling

Sampling of characters was intended to capture as much morphological variation as possible. Most entries were directly observed by the author, although data from the literature were used to complete ranges of meristic characters and to assess probable intraspecific variation; thus, characters for which published information was in conflict with that observed herein were coded as polymorphic. Only *Brycon meeki* was coded

exclusively from the literature, by using the detailed osteological description of Weitzman (1962).

Most characters are osteological, but several involving variations in other structures such as muscles or nervous system are also included. The 360 characters are from (number of characters in parentheses) neurocranium (54), infraorbital series (17), laterosensory system (22), upper jaw (12), lower jaw (11), teeth (32), suspensorium (28), branchial skeleton (41), Weberian apparatus (5), vertebrae (7), pectoral girdle and fins (26), pelvic girdle and fins (9), dorsal fin and pterygiophores (19), anal fin and pterygiophores (12), caudal fin and hypural system (10), bony hooks on fins (7), scales (12), muscles (12), and miscellaneous characters (24). Most characters are binary; additive characters were coded as binary to accelerate searches under SL. The data matrix was constructed in Mesquite (Maddison and Maddison, 2008). The list of characters, with some comments on the new characters analysed herein, is provided in Appendix 1; detailed discussions of the taxonomic and character-evolution implications of this analysis will be published elsewhere. The data matrix is provided as Appendix 2.

Methodological overview

Differentially weighted phylogenies have been published, in some way, since the early years of systematics. Classical taxonomists gave different “weights” to different features, considering them as defining groups at different taxonomic ranks or not defining them at all. In the cladistic era, the use of equal weighting in phylogenetic analyses was, apparently, just a management shortcut with the basic methodology and tools available at the time; this assertion is supported by the fact that a method to weight characters (according to their homoplasy) was available only 3 years after Hennig (1950) was translated from German to Spanish and English (Hennig, 1966; Farris, 1969). Goloboff (1993, 1997) refined methods to weight characters according to their homoplasy; IW weights characters as a whole (Goloboff, 1993), whereas SL was designed to weight transformations between character states. SL frequently produces asymmetrically weighted character–state transformations, according to the number of transformations between each character–state (Goloboff, 1997). The SL method was originally implemented in the beta program SLF-WT (Goloboff, 1996), and only recently included in TNT (Goloboff et al., 2003b, 2008); its implementation in TNT permits faster searches and parallel analyses, and makes the method more stable and flexible. Both kinds of weighting methods have a K -value that determines how strong the analyses will weight against homoplasy. Under IW, lower (stronger) values approximate a clique. Under SL, lower (stronger) values tend to prevent reversals, explaining most homoplasy as

parallelisms. With higher (weaker) K -values the two methods approximate equal weighting. There are not, however, well-justified criteria to choose some particular value of K , and this decision is probably matrix-dependent (Goloboff, 1993). Analyses under SL are not common in the literature, but some were published using the implementation in SLF-WT (e.g. Molineri, 2006).

Cladistic methods

The basic idea in these analyses is to explore, as broadly as possible, different parameters (different K -values) of both IW and SL, subsequently restricting the results to a strict consensus of most-parsimonious trees obtained under a range of parameters, which represents a balance between stability and resolution, in a kind of sensitivity analysis (Wheeler et al., 1995; Whiting et al., 1997; Prendini, 2000; Giribet, 2003). The strategy used here, however, differs from most published stability analyses in the use of a strict consensus among trees obtained from a range of parameters, instead of choosing one particular set of parameters. Thus, results are comparatively less resolved but remain more cautious.

As stated by Goloboff (1993), due to the concave/convex shape of the curve of K versus fit/distortion at regular intervals, higher values of K tend to produce more similar results; weighting strength (and usually also the resultant trees) are more similar between, for example, $K = 6$ and 7, than between $K = 1$ and 2. As a result, a measure of stability of trees obtained under regularly distributed K -values is artificially biased towards higher values. In order to perform this analysis, then, it is important to set K -values for each weighting scheme that permit appropriate comparisons between hypotheses. The basic strategy, applicable to both analyses, is to divide in regular intervals the values of fit/distortion produced by the most-parsimonious trees obtained under different K -values. The K -values for which most-parsimonious trees divide the range of fit/distortion in regular intervals will be considered as a better sample of possible values. This can be done using the weighting formulae of each kind of analysis to calculate these intervals on an “average” character. The main parameter considered in both kinds of analyses is the degree of homoplasy of each character, so that an “average” character is here considered to be a character with an “average” number of steps (for simplicity, on most-parsimonious trees under equal weights).

Under IW, the fit (F) of a character is calculated as:

$$F = K/(S + K)$$

where S = number of homoplastic steps. Note that if a character has no homoplasy, $F = 1$, and if it has the same number of homoplastic steps as the value of K

used, $F = 0.5$. In the latter case, two “average” characters will have, together, the same weight as a perfectly hierarchical one; in other words, an “average” character will have 50% of the weight of a perfectly hierarchical one. This ($K = S$) is the lower (stronger) value of K used here under IW; so a perfectly hierarchic character will never have more weight than two characters with an average number of steps. The values of K used in the analysis under IW were those that assign to an “average” character fits of 50, 54, 58, 62, 66, 70, 74, 78, 82, 86 and 90% of the fit of a perfectly hierarchic one. Searches under every K -value were performed by using the parsimony ratchet (Nixon, 1999), sectorial searches, tree fusing, and tree drifting (Goloboff, 1999). Searches were carried out under each K -value until the best fit was obtained three times, with “xmult: hits3”, giving a relatively high degree of confidence of having found optimal trees. These analyses produce 11 groups of trees obtained at each K -value. TNT scripts for these calculations and searches are provided as Supporting Information.

The K -values under SL are calculated in an analogous way. The formulae used by TNT (Goloboff et al., 2003b) for the calculation of the distortion (D) of each character are as follows:

$$\text{if } S_{ij} = 0 \rightarrow D = 0$$

$$\text{if } S_{ij} = 1 \rightarrow D = 1$$

$$\text{if } S_{ij} \geq 2 \rightarrow D = 2 + [K * (S_{ij} - 2) / K + S_{ij} - 2]$$

where S_{ij} = number of steps from state i to state j of a given character. The lowest (stronger) limit of K was calculated in a way similar to that for IW; this value is the one that assigns to a parallel state transformation of an “average” character (as under IW) with all its transformations in the same direction, a 50% of the distortion that such transformation would add if it were in a different direction (e.g. a reversion). This limit implies that an event of parallelism on each of two “average” characters would never have more weight than a reversion in one of them. The values of K used in the analysis under SL were those that apply to a new parallel character–state transformation 50, 54, 58, 62, 66, 70, 74, 78, 82, 86, and 90% of the weight that it would have if it were a reversion. As these values are ratios between distortions, calculations of K -values are rather complicated; then, values of K were calculated heuristically with a simple TNT script (always for an “average” character, not for the whole matrix, which currently would be too time-consuming). Optimizations under SL are comparatively rather time-consuming; time of searches increases with the size and complexity

of the matrices and with the number of states and polymorphisms in multistate characters (Goloboff, 1997). The analysed matrix was then “adapted” to this kind of analysis, by re-coding the additive (ordered) characters as binary and considering all polymorphisms as missing data. Both solutions affect, at least potentially, the results under SL and should be avoided if possible. In this particular case, analyses without these strategies are much more time-consuming and the results apparently not so different (at least under the K -values tested). Exploratory searches showed that (as predicted by Goloboff, 1997) SPR had a better performance (in terms of time and optimality) than TBR; initial searches were then performed with SPR and a complete round of TBR was only done at the end of each run. Among the “new technologies” implemented in TNT, sectorial searches (Goloboff, 1999) proved to be too time-consuming and were not used here; conversely, parsimony ratchet (Nixon, 1999), tree drifting, and especially tree fusing (Goloboff, 1999) were very effective in searches. A particular case of ratchet (Nixon, 1999) that only inactivates characters, swaps to completion in the perturbation phase, and fuses trees in every round, was implemented as a TNT script. Analyses under SL were performed both on a personal computer (2.66 GHz) using most-parsimonious trees under IW as starting points, and on a cluster of ten computers (3 GHz) from Wagner trees (Farris, 1970). Results of these analyses (after comparing trees obtained in both searches) are 11 groups of trees (one from each K -value of SL). Both parallelized and non-parallelized searches were performed with TNT scripts.

Trees obtained in each K -value, under both IW and SL, were reduced to a strict consensus; the result of these searches are 22 trees (one—the strict consensus—resulting from each K -value of the two weighting schemes).

The main criterion used here to evaluate reliability of trees and to select among most-parsimonious trees under different parameters is their stability (Giribet, 2003); a tree is considered more stable if nodes are (as an average) less parameter-dependent. That is, after analysing the data set under all the selected range of parameters (under IW and SL), the most stable trees are those that share a higher number of nodes with the remaining trees; according to this reasoning, globally more stable hypotheses will be topologically more similar to remaining ones than unstable hypotheses. Measurements used to compare trees are the distortion coefficient (Farris, 1989), which compares the retention indices of each tree on every source tree, and SPR distance (Goloboff, 2008), which calculates the minimum number of SPR movements required to transform each tree in every source tree. Trees preferred under these methods will not necessarily be the same, and its convergence could be judged as a measure of confidence of results. This comparison is a kind of sensitivity

analysis (Wheeler et al., 1995; Prendini, 2000; Giribet, 2003), but the present analysis is neither used to choose particular parameters nor to calculate a majority consensus (as most published sensitivity analyses). Here, sensitivity analysis is used as a meta-criterion to select a group of hypotheses to condense on a strict consensus, considered to represent the most stable solutions under different parameters. This criterion has, over the selection of particular parameters of analysis (e.g. equal weighting or some particular value of K), the advantages of considering a broad range of parameters, and the selection of trees maximizing stability; it also represents an intermediate solution between considering a consensus of all obtained trees (which would produce very robust hypotheses, but with low informativeness) and selecting particular conditions of analysis (which would produce better resolved solutions, but with lower robustness). Support was estimated through Bremer and relative Bremer support indices (Bremer, 1994; Goloboff and Farris, 2001), and symmetric resampling expressed as GC values (Goloboff et al., 2003a). Support of each node of the final hypothesis is provided in Appendix 3.

Results

Character analysis

Most characters are osteological (324 characters, 90%), although some characters of musculature, coloration, and the reproductive system are included. From the 360 characters, 135 were not previously used in phylogenies of the family, while the remainder were described in a series of papers and unpublished theses (Eigenmann, 1917; Fink and Fink, 1981, 1996; Machado-Allison, 1983; Uj, 1990; Lucena, 1993, 1998; Vari, 1995; Buckup, 1998; Lucena and Menezes, 1998; Malabarba, 1998a,b; Weitzman and Menezes, 1998; Toledo-Piza, 2000; Vari and Harold, 2001; Moreira, 2002; Bertaco, 2003; Cardoso, 2003a; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Bührnheim, 2006; Lima, 2006; Quevedo, 2006).

Phylogenetic analysis

The analysis under IW took several minutes, while that under SL was completed in 15 h on the ten-computer cluster, and several days on the single PC. As a broad range of parameters were explored, a strict consensus from all the most-parsimonious trees obtained has a relatively low resolution (76 of 158 possible nodes; agreement subtree with 59 of 160 species).

According to the stability analysis the most stable tree is the strict consensus obtained at the 7th value of K under IW ($= 12.9$). The four most stable consensus are

those obtained from the 4th to 7th values of K under IW analysis ($K = 7.4$ – 12.9); two trees were obtained under each of these four values of K , which ranges from 2125 to 2135 steps. The consensus of these eight trees has 137 from the 158 possible nodes (Figs 1–3), and it is the final hypothesis proposed here, as a balance between robustness and resolution. The most stable tree under SL is that obtained at the 9th value of K . A consensus from the trees obtained at this value of K , and three contiguous values (for comparability with IW analysis), is presented on Fig. 4. As can be seen, the analysis under SL resulted in a less resolved tree (116 of 158 possible nodes). A table of results is presented in Appendix 4. Also, an equally weighted analysis was performed for comparison purposes; it produced 8256 most-parsimonious trees of 2101 steps; this consensus tree shares most of the highly supported clades with the differentially weighted analyses, although some strange results are obtained, such as the non-monophyly of *Jupiaba*. A strict consensus of these trees is presented as Supporting Information.

Analyses under IW were less parameter-dependent, and therefore the final hypothesis was obtained from this weighting method. The biological significance of such relatively better performance of IW, however, is difficult to interpret (if possible). There are many documented cases of miniaturization in species of Characiformes (Weitzman and Fink, 1983; Buckup, 1993; Bührnheim et al., 2008) correlated with similar morphological changes, such as reductions in the lateral line system and infraorbital bones; these changes were hypothesized to have occurred as parallelisms in one direction (reductions) much more frequently than in the inverse one (acquirements). According to such reasoning, this data set would probably fit better in an SL weighting scheme; however, as mentioned, in this case the IW method performed better, at least considering stability as a criterion to evaluate trees. It is notable, however, that most of the highly stable nodes under IW are also supported under SL; 76 from the 83 nodes present in most-parsimonious trees over all the explored range of IW parameters are also present in the entire range under SL.

Proposed classification of Characoidea

This classification is mainly based on the proposed phylogeny but some genera not included are tentatively assigned to a subfamily or family based on the literature or some presumably derived character–state shared with members of this group (these taxa are listed with question marks). Some proposed groups are new and some have a different composition relative to previous studies. A conservative criterion to the creation of new categories is used; several groups are redefined as more inclusive, containing basal taxa of the clade in which

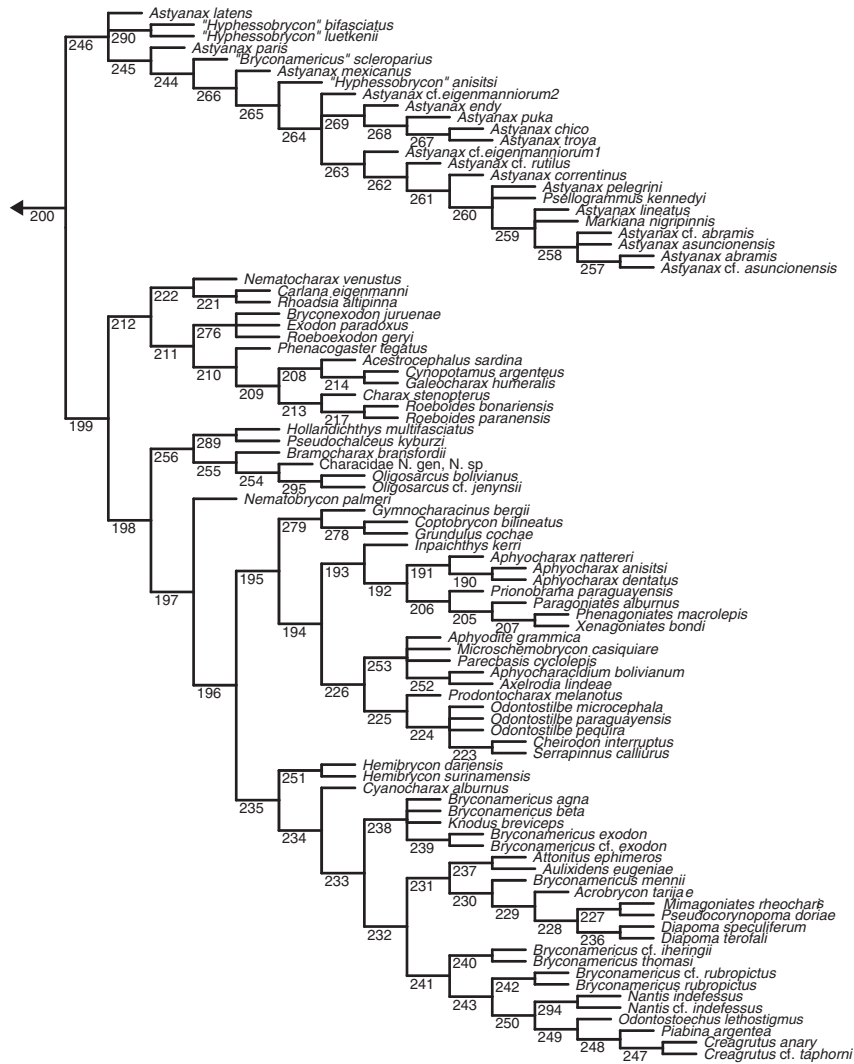


Fig. 2. Final hypothesis under IW. Part 2: "distal" characids. Number of nodes corresponds to Appendix 3.

Bryconinae (*Brycon*, *Chilobrycon*, *Henocheilus*, *Lignobrycon*?, and *Triportheus*)

Iguanodectinae (*Iguanodectes* and *Piabucus*)

Bryconops clade (*Bryconops*)

Heterocharacinae n. subf. (*Gnathocharax*?, *Heterocharax*, *Hoplocharax*, and *Lonchogenys*)

Jupiaba clade (*Jupiaba*)

Tetragonopterinae (*Tetragonopterus*)

Stethaprioninae n. def. (*Brachychalcinus*, *Gymnoorymbus*, *Orthospinus*, *Poptella*, *Stethaprion* and *Stichonodon*)

Hemigrammus clade (*Bario*, *Deuterodon*, *Hasemania*, *Hemigrammus*, *Hyphessobrycon*, *Moenkhausia*, *Myxiops*?, *Paracheiroidon*, *Petitella*?, *Pristella*, *Probolodus*, and *Thayeria*)

Astyanax clade (*Astyanacinus*?, *Astyanax*, some "*Bryconamericus*", *Ctenobrycon*?, some "*Hyphessobrycon*", *Markiana*, and *Psellogrammus*)

Rhoadsiinae (*Carlana*, *Nematocharax*?, *Parastremma*, and *Rhoadsia*)

Characinae n. def. (*Acanthocharax*, *Acestrocephalus*, *Bryconexodon*?, *Charax*, *Cynopotamus*, *Exodon*?, *Galeocharax*, *Phenacogaster*, *Priocharax*?, *Roeboexodon*?, and *Roeboides*)

Bramocharax clade (*Bramocharax*, *Hollandichthys*?, *Oligosarcus*, *Pseudochalceus*?, and an undescribed new genus).

Nematobrycon clade (*Nematobrycon*)

Gymnocharacinae n. def. (*Coptobrycon*, *Grundulus*, and *Gymnocharacinus*)

Aphyocharacinae n. def. (*Aphyocharax*, *Inpaichthys*, *Leptagoniates*?, *Paragoniates*, *Phenagoniates*, *Prionobrama*, *Rachoviscus*?, and *Xenagoniates*)

Aphyoditeinae n. def. (*Aphyocharacidium*, *Aphyodite*, *Axelrodia*, *Leptobrycon*?, *Microchemobrycon*, *Oxybrycon*?, *Parecbasis*, and *Tyttobrycon*?)

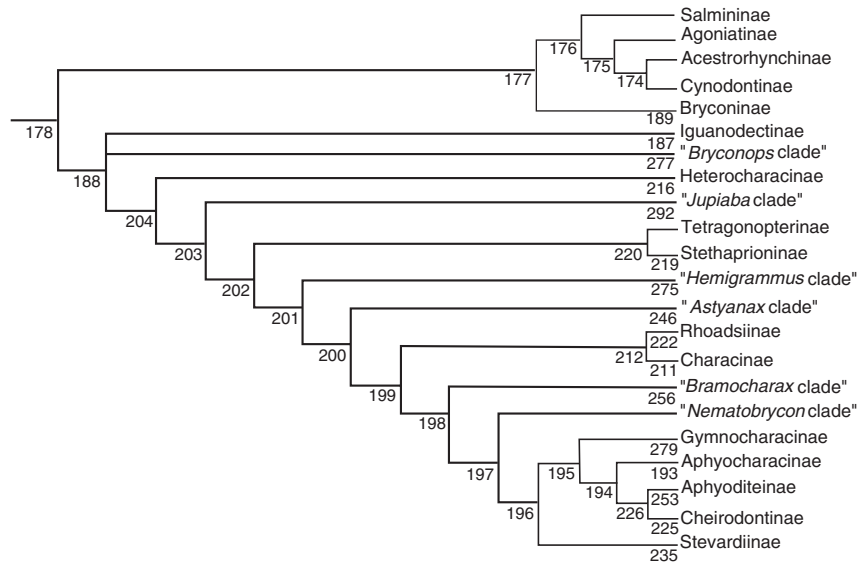


Fig. 3. Summary of relationships between subfamilies and presumably monophyletic clades, as proposed here. Number of nodes corresponds to Appendix 3.

Cheirodontinae (*Acinocheiroidon*, *Aphyocheiroidon*, *Cheiroidon*, *Cheiroidontops*, *Compsura*, *Heterocheiroidon*, *Kolpotocheiroidon*, *Macropsobrycon*, †*Megacheiroidon*, *Nanocheiroidon*, *Odontostilbe*, *Prodontocharax*, *Pseudocheiroidon*, *Saccoderma*, *Serrapinnus*, and *Spintherobolus*)

Stevardiinae n. def. (*Acrobrycon*, *Argopleura*, *Attonittus*, *Aulixidens*, *Boehlkea*?, *Bryconacidnus*?, *Bryconadenos*?, *Bryconamericus*, *Caiapobrycon*?, *Ceratobranchia*?, *Chrysobrycon*, *Corynopoma*, *Creagrutus*, *Cyanocharax*, *Diapoma*, *Gephyrocharax*, *Glandulocauda*, *Hemibrycon*, *Hypobrycon*?, *Hysteronotus*, *Iotabrycon*, *Knodus*, *Landonia*, *Microgenys*?, *Mimagoniates*, *Monotocheiroidon*?, *Nantis*, *Odontostoechus*, *Othonocheiroidus*?, *Phenacobrycon*, *Piabarchus*?, *Piabina*, *Planaltina*, *Pseudocorynopoma*, *Pterobrycon*, *Ptychocharax*, *Rhinobrycon*?, *Rhinopetitia*?, *Scopaeocharax*, *Tyttocharax*, and *Xenurobrycon*)

Taxonomic implications

The superfamily Characoidea was proposed by Buckup (1998) as containing the families Gasteropelecidae and Characidae [excluding Acestrorhynchidae and Cynodontidae, and including Serrasalminae (*sensu* Jégu, 2003)]. However, no gasteropelecids were included in his phylogeny, and the position of this family remained uncertain. A new definition of this superfamily is proposed here, including four families: Alestidae, Characidae, Gasteropelecidae, and Serrasalminae; in this new classification the superfamilies Alestoidea (including only the Alestidae) and Cynodontoidea [including the (sub)families Acestrorhynchidae(nae) and Cynodontidae(nae)], as proposed by Buckup (1998), are unjustified. Relationships between these families are not completely

resolved, with the Gasteropelecidae as sister group of the remaining three families of this clade, which form a tricotomy; in the analysis under SL, Alestidae plus Serrasalminae form the sister group of Characidae. The Gasteropelecidae, as proposed here, includes *Engraulisoma taeniatum*, which is removed from Characidae, along with the hatchetfishes (genera *Carnegiella*, *Gasteropelecus*, and *Thoracocharax*); the relationships between *E. taeniatum* and the hatchetfishes is stable through all the parameters explored, with relatively high support. *Clupeacharax anchoveoides* is the only member of the characid subfamily Clupeacharacinae according to most authors (e.g. Géry, 1977; Lima, 2003b); this species shares seven synapomorphies with *Engraulisoma*, according to Castro (1984), of which three are diagnostic of Gasteropelecidae, as defined here. *Clupeacharax anchoveoides* is thus here removed from Characidae and included in the Gasteropelecidae, at least tentatively.

The composition of the family Characidae varies slightly across different classifications (e.g. Greenwood et al., 1966; Géry, 1977; Reis et al., 2003). The last revisions (Buckup, 1998; Lucena and Menezes, 1998; Menezes, 2003) exclude Acestrorhynchidae and Cynodontidae from the Characidae; the definition proposed here again includes these two clades (as subfamilies Acestrorhynchinae and Cynodontinae) in Characidae. Conversely, the subfamily Serrasalminae is excluded from Characidae (as family Serrasalminae, in agreement with Géry, 1977).

The synapomorphies of Characidae, as recognized here are as follows: slender orbitosphenoid distant from parasphenoid (ch. 37, st. 0); rhinosphenoid present (ch. 47, st. 1); more than 40 vertebrae (ch. 227, st. 1); more than 24 branched anal-fin rays (ch. 288, st. 1); anterior-

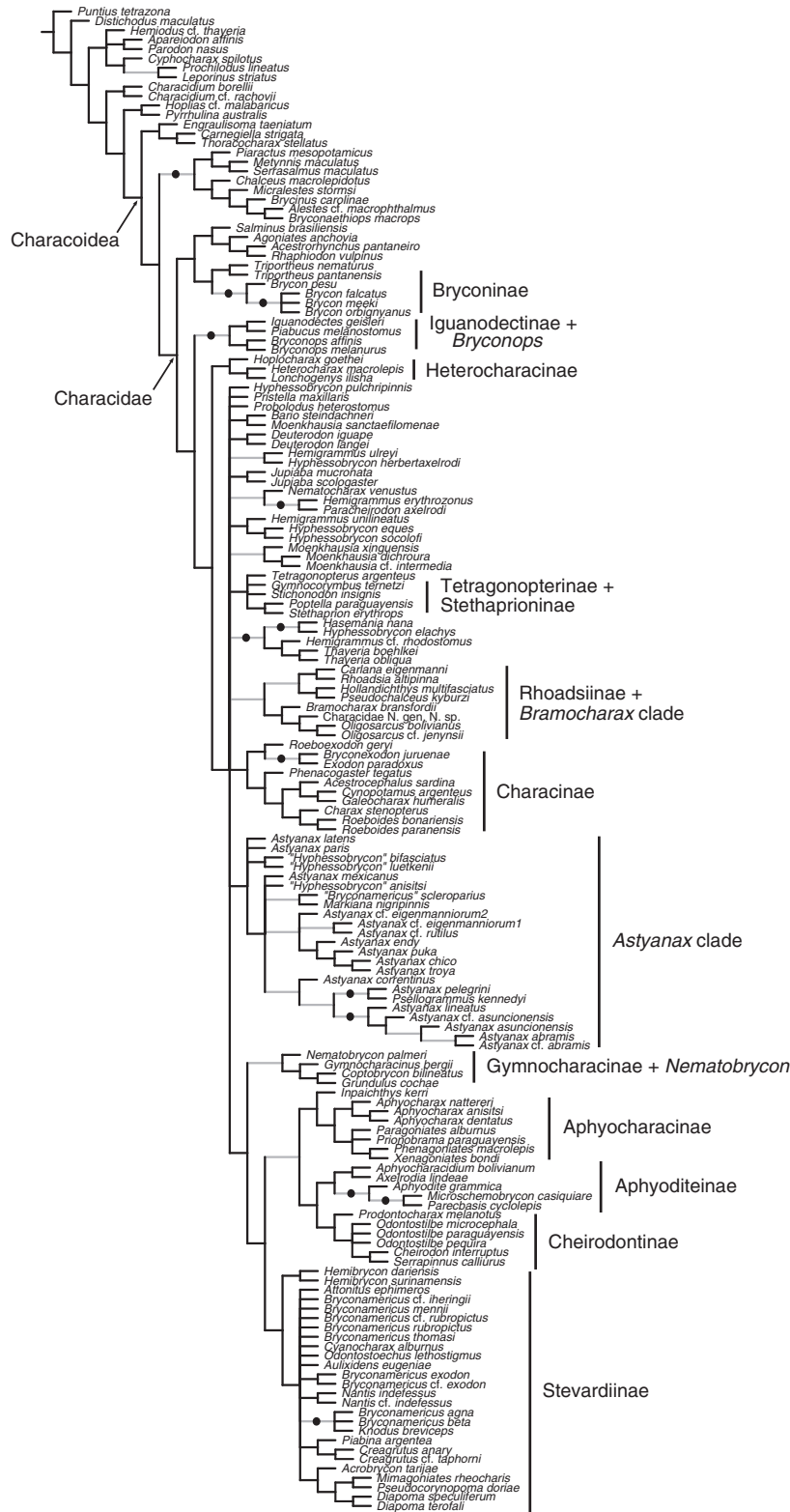


Fig. 4. Phylogenetic hypothesis under SL. Grey branches were not obtained in the final hypothesis under IW; from these branches, those marked with a black dot are compatible with the final hypothesis, showing a resolution for polytomies under IW. Clades congruent with the final hypothesis are indicated.

ormost procurent caudal-fin rays fused in vertical plates (ch. 304, st. 2); radii of scales confluent in focus (ch. 318, st. 0); tendon from A1 section of *adductor mandibulae* partially attached to the quadrate (ch. 329; st. 0). The only unreversed and uncontradicted synapomorphy of Characidae, according to this analysis, is the fusion of the anteriormost procurent caudal-fin rays in medial bony plates, parallel to the remaining rays (ch. 304); the remaining synapomorphies have different degrees of homoplasy (see Appendix 1).

The subfamilial classification proposed in the present paper is concordant with the revisions of Géry (1977) and Reis et al. (2003). A group of “basal” Characidae was recognized based on the presence of a supraorbital bone by several authors (e.g. Malabarba and Weitzman, 2003). This paraphyletic group of subfamilies is obtained in the present analysis, as the sister group of a monophyletic clade of characids lacking a supraorbital, as hypothesized by Malabarba and Weitzman (2003). This “basal” group of characids includes *Bryconops* and the subfamilies Agoniatinae, Acestrorhynchinae, Salmininae, Cynodontinae, Bryconinae, Heterocharacinae, and Iguanodectinae. The subfamilies Agoniatinae, Bryconinae, Acestrorhynchinae, and Cynodontinae were recognized as subfamilies by Géry (1977), although the latter two were subsequently considered as separate families (Lucena and Menezes, 1998). Salmininae was recognized as a tribe (Salminini) of Bryconinae by Géry (1977) and its single genus *Salminus* was classified as *incertae sedis* within Characidae by Lima et al. (2003). The new subfamily Heterocharacinae (type genus: *Heterocharax*) is proposed here, as comprising three genera (tentatively four) included in Characinae by Géry (1977) and Lucena and Menezes (1998); the genus *Bryconops* would deserve subfamilial status under most IW analyses including the hypothesis herein proposed, whereas it appears as the sister group of Iguanodectinae under SL. The Heterocharacinae (with a variably present supraorbital) is the sister group of the characids without supraorbital in all the analyses.

The “distal” characids, lacking an ossified supraorbital, form a monophyletic group obtained under all the explored parameters. Internal relationships of this highly diverse group of species are rather variable between different analyses; this clade includes most species considered as *incertae sedis* within Characidae by Lima et al. (2003), along with several subfamilies long recognized as natural groups, some of them redefined to include a slightly different set of species. The most basal clade according to the classification proposed here comprises species of *Jupiaba*; although the monophyly of *Jupiaba* has general consensus (Zanata, 1997), the relationships of this genus remain obscure, and its position is unstable through different analyses. The subfamily Tetragonopterinae included most characids in the classification of Géry (1977) and was further

restricted to its type genus *Tetragonopterus* by Reis (2003b) *Tetragonopterus*, in this analysis, is the sister group of Stethaprioniinae. The subfamily Stethaprioniinae as defined here includes the genus *Gymnocorymbus*, in addition to those genera proposed by Reis (1989) for this clade; it is notable that Reis (1989) considered *Gymnocorymbus* as closely related to the Stethaprioniinae and used it as outgroup of his analysis.

The presence and composition of the *Hemigrammus* clade varies across different analyses; however, this group is present in the globally more stable hypotheses. This diverse assemblage includes some specious genera, such as the true *Hemigrammus* and *Hyphessobrycon*, related to (or included in) the probably monophyletic “rosy tetra clade” of Weitzman and Palmer (1997), and the true *Moenkhausia*, along with some less diverse and morphologically more divergent genera, such as *Deuterodon*, *Probolodus*, and *Thayeria*. The single synapomorphy of this clade is a dorsal bony process in the rhinosphenoid, separating the anteriorly orientated ophthalmic nerves; this character is rather homoplastic, and the validity and composition of this clade should be further tested.

The *Astyanax* clade includes (along with all included species of *Astyanax*) *Markiana*, *Psellogrammus*, probably *Ctenobrycon* (not included in the analysis), and some “*Bryconamericus*” and “*Hyphessobrycon*”. Most ichthyologists agree that *Astyanax* is not monophyletic, but according to this analysis this highly diverse genus could be diagnosed as monophyletic with relatively few changes in its composition; specific studies on this point are currently underway by the author. No subfamilial status is assigned to this group because under some parameters it appears as related to *Tetragonopterus*, and the subfamily Tetragonopterinae would have preference. The subfamily Rhoadsiinae was long recognized to include the genera *Carlana*, *Parastremma*, and *Rhoadsia*; the genus *Nematocharax* is included in the Rhoadsiinae in the final hypothesis but its presence is variable across different analyses. The Characinae are redefined as excluding the heterocharacins, and putatively including the lepidophagous genera *Bryconexodon*, *Exodon*, and *Roebioxodon*. The miniature genus *Priocharax* (not included in the analysis) was included in Characinae as the sister group of remaining members of this subfamily (plus Heterocharacinae) by Lucena (1998); as Characinae (*sensu* Lucena, 1998) is herein split, the position of *Priocharax* should be further re-evaluated. The *Bramocharax* clade includes the geographically divergent genera *Bramocharax* and *Oligosarcus* plus an undescribed new genus and species, along with a clade formed by *Hollandichthys* and *Pseudochalceus*; although each of these clades is well supported, this clade as a whole is rather unstable; also, under some conditions the three former genera are included in the *Astyanax* clade.

A close relationship of the geographically divergent and odd looking genera *Coptobrycon*, *Grundulus*, and

Gymnocharacinus has never previously been proposed; however, the subfamily Gymnocharacinae (resurrected and redefined to include these three genera) is well supported and stable in all the analyses performed. The subfamily Aphyocharacinae is redefined to include, along with *Aphyocharax*, most members of the Paragoniinae of Géry (1972, 1977) and *Inpaichthys*, as sister group of the remaining members of the subfamily. The subfamily Aphyoditeinae as redefined here is a subgroup of the “Aphyoditeina” of Géry (1965, 1973, 1977), with the exclusion of *Oligobrycon* (*incertae sedis*), *Atopomesus* (*incertae sedis*), *Paracheirodon* (*Hemigrammus* clade), *Prodontocharax* (Cheirodontinae), *Brittanichthys* (*incertae sedis*), *Macropsobrycon* (Cheirodontinae), and *Thrissobrycon* (*incertae sedis*). The subfamily Cheirodontinae is probably the best studied among characids; this study corroborates the phylogeny of Malabarba (1998a).

Members of the “clade A” of Malabarba and Weitzman (2003) are included, according to this analysis, in the redefined subfamily Stevardiinae. This clade contains the Glandulocaudinae (*sensu* Weitzman et al., 2005), which forms a monophyletic lineage within Stevardiinae and does not deserve subfamilial status according to this hypothesis. Additionally, the genera *Aulixidens* and *Nantis* are included in Stevardiinae.

Most of the genera previously considered as *incertae sedis* within Characidae are included, at least tentatively, in some subfamily or presumably monophyletic group. However, we still lack clear evidence relating the genera *Astyanacinus* Eigenmann, *Atopomesus* Myers, *Bryconella* Géry, *Brittanichthys* Géry, *Dectobrycon* Zarske and Géry, *Genycharax* Eigenmann, *Gymnotichthys* Fernández-Yépez, *Mixobrycon* Eigenmann, *Oligobrycon* Eigenmann, *Parapristella* Géry, *Psalidodon* Eigenmann, *Schultzites* Géry, *Scissor* Günther, *Serrabrycon* Vari, *Stygichthys* Brittan and Böhlke, *Thrissobrycon* Böhlke, and *Tucanoichthys* Géry and Römer to any clade found here, and they are still considered as *incertae sedis* within Characidae. Although several genera appear as non-monophyletic in this analysis, taxon sampling is considered as insufficient to propose taxonomic changes at the generic level, leaving these matter to subsequent studies.

Availability of phylogenetic information

Several ichthyologists have summarized what is known about the morphology and phylogeny of Characidae, through important contributions (e.g. Eigenmann, 1917; Weitzman, 1962; Géry, 1977; Lucena, 1993, 1998; Malabarba, 1998a). However, published information is just the tip of the iceberg, and numerous unpublished theses (see References) also contain much useful data that would significantly contribute to characid phylogeny. This paper is far from providing a conclusive phylogeny of the family, but instead it intends to be a starting point for future

studies, encouraging colleagues to discuss in common terms and conciliate a phylogeny of the family from different contributions.

Conclusions

This analysis tries to consider all available evidence, from the construction of the data set (considering observations of previous authors) to the searches themselves (considering also the degree of homoplasy as useful information in the tree reconstruction). A protocol (which should be adjusted to particular cases) is proposed to analyse medium to large morphological matrices under IW and SL.

This analysis constitutes the most comprehensive phylogeny of the family Characidae, and tentative phylogenetic diagnoses and a classification in subfamilies and presumably monophyletic clades of Characidae are provided. The classification proposed is, in many respects, highly concordant with previous ones (e.g. Géry, 1977; Reis et al., 2003). Only *Engraulisoma taeniatum* and, tentatively, *Clupeacharax anchoveoides* are removed from Characidae, together with the Serrasalmidae, while Acestrorhynchinae and Cynodontinae are reincorporated within it. The subfamilies Aphyocharacinae, Aphyoditeinae, Bryconinae, Characinae, Gymnocharacinae, Salmininae, Stevardiinae, and Stethaprioninae are resurrected and/or redefined, the new subfamily Heterocharacinae is proposed, and the presumably monophyletic *Astyanax*, *Bramocharax*, *Bryconops*, *Hemigrammus*, *Jupiaba*, and *Nematobrycon* clades are proposed. Thus, 75 of 92 *incertae sedis* genera within Characidae are classified, at least tentatively, within some presumably monophyletic clade.

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References

- Abilhoa, V., Duboc, L.F., 2007. A new species of the freshwater fish genus *Astyanax* (Ostariophysi: Characidae) from the rio Iguacu basin, southeastern Brazil. *Zootaxa* 1587, 43–52.
- Aguilera, G., Mirande, J.M., 2005. A new species of *Jenynsia* (Cyprinodontiformes: Anablepidae) from northwestern Argentina and its phylogenetic relationships. *Zootaxa* 1096, 29–39.
- Benine, R.C., 2004. Análise filogenética do gênero *Moenkhausia* Eigenmann, 1903 (Characiformes: Characidae) com uma revisão dos táxons do alto rio Paraná. Master thesis, Universidade Estadual Paulista, Botucatu, São Paulo.
- Bertaco, V.A., 2003. Taxonomia e filogenia do gênero *Hollandichthys* Eigenmann, 1909 (Teleostei: Characidae) do sul e sudeste do Brasil. Master thesis, Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, Brazil.
- Bremer, K., 1994. Branch support and tree stability. *Cladistics* 10, 295–304.
- Buckup, P.A., 1993. Phylogenetic interrelationships and reductive evolution in Neotropical Characidiine fishes (Characiformes, Ostariophysi). *Cladistics* 9, 305–341.
- Buckup, P.A., 1998. Relationships of the Characidiinae and phylogeny of characiform fishes (Teleostei, Ostariophysi). In: Malabarba, L., Reis, R., Vari, R., Lucena, Z.M.S., Lucena, C. (Eds.), *Phylogeny and Classification of Neotropical Fishes*. EDIPUCRS, Porto Alegre, Brazil, pp. 123–143.
- Bührnheim, C.M., 2006. Sistemática de *Odontostilbe* Cope, 1870 com a proposição de uma nova tribo Odontostilbini e redefinição dos gêneros *incertae sedis* de Cheirodontinae (Ostariophysi: Characiformes: Characidae). PhD thesis, Pontifícia Universidade Católica de Rio Grande do Sul, Porto Alegre, Brazil.
- Burns, J.R., Weitzman, S.H., 1996. Novel gill-derived gland in the male swordtail characin, *Corynopoma riisei* (Teleostei: Characidae: Glandulocaudinae). *Copeia* 1996, 627–633.
- Bushmann, P.J., Burns, J.R., Weitzman, S.H., 2002. Gill-derived glands in glandulocaudine fishes (Teleostei: Characidae: Glandulocaudinae). *J. Morph.* 253, 187–195.
- Bührnheim, C.M., Carvalho, T.P., Malabarba, L.R., Weitzman, S.H., 2008. A new genus and species of characid fish from the Amazon basin – the recognition of a relictual lineage of characid fishes (Ostariophysi: Cheirodontinae: Cheirodontini). *Neotrop. Ichthyol.* 6, 663–678.
- Burns, J.R., Weitzman, S.H., 1996. Novel gill-derived gland in the male swordtail characin, *Corynopoma riisei* (Teleostei: Characidae: Glandulocaudinae). *Copeia* 1996, 627–633.
- Bushmann, P.J., Burns, J.R., Weitzman, S.H., 2002. Gill-derived glands in glandulocaudine fishes (Teleostei: Characidae: Glandulocaudinae). *J. Morph.* 253, 187–195.
- Calcagnotto, D., Schaefer, S.A., DeSalle, R., 2005. Relationships among characiform fishes inferred from analysis of nuclear and mitochondrial gene sequences. *Mol. Phylogenet. Evol.* 36, 135–153.
- Cardoso, A., 2003a. Sistemática e filogenia da subfamília Rhoadsiinae (Teleostei: Characiformes: Characidae). Master thesis, Pontifícia Universidade Católica de Rio Grande do Sul, Porto Alegre, Brazil.
- Cardoso, A., 2003b. Rhoadsiinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 213–214.
- Castro, R.M.C., 1984. Osteologia e relações filogenéticas de *Engraulisoma taeniatum* Castro, 1981 (Ostariophysi, Characiformes, Characidae). Master thesis. Universidade de São Paulo, Brazil.
- Eigenmann, C.H., 1912. The freshwater fishes of British Guiana, including a study of the ecological grouping of species and the relation of the fauna of the plateau to that of the lowlands. *Mem. Carnegie Mus.* 5, 1–578.
- Eigenmann, C.H., 1915. The Cheirodontinae, a subfamily of minute characid fishes of South America. *Mem. Carnegie Mus.* 7, 61–90.
- Eigenmann, C.H., 1917. The American Characidae. *Mem. Mus. Comp. Zool.* 43, 1–102.
- Eigenmann, C.H., 1918. The American Characidae. *Mem. Mus. Comp. Zool.* 43, 103–208.
- Eigenmann, C.H., 1921. The American Characidae. *Mem. Mus. Comp. Zool.* 43, 209–310.
- Eigenmann, C.H., 1927. The American Characidae. *Mem. Mus. Comp. Zool.* 43, 311–428.
- Eigenmann, C.H., Myers, G.S., 1929. The American Characidae. *Mem. Mus. Comp. Zool.* 43, 429–558.
- Farris, J.S., 1969. A successive approximations approach to character weighting. *Syst. Zool.* 18, 374–385.
- Farris, J.S., 1970. Methods for computer Wagner trees. *Syst. Zool.* 19, 83–92.
- Farris, J.S., 1983. The logical basis of phylogenetic analysis. In: Platnick, N.I., Funk, V.A. (Eds.), *Advances in Cladistics II*. Columbia University Press, New York, pp. 7–36.
- Farris, J.S., 1989. The retention index and the rescaled consistency index. *Cladistics* 5, 417–419.
- Fink, S.V., Fink, W.L., 1981. Interrelationships of the ostariophysan fishes (Teleostei). *Zool. J. Linn. Soc.* 72, 297–353.
- Fink, S.V., Fink, W.L., 1996. Interrelationships of the ostariophysan fishes (Teleostei). In: Stiassny, M.L.J., Parenti, L.R., Johnson, G.D. (Eds.), *Interrelationships of Fishes*. Academic Press, San Diego, CA, pp. 209–249.
- Fink, W.L., Weitzman, S.H., 1974. The so-called cheirodontin fishes of Central America with descriptions of two new species (Pisces: Characidae). *Smith. Contr. Zool.* 172, 1–46.
- Franz-Odenaal, T.A., Hall, B.K., 2006. Skeletal elements within teleost eyes and a discussion on their homology. *J. Morphol.* 267, 1326–1337.
- Géry, J., 1965. A new genus from Brazil – *Brittanichthys*, a new, sexually-dimorphic characid genus with peculiar caudal ornament, from the Rio Negro, Brazil, with a discussion of certain cheirodontin genera and description of two new species, *B. axelrodi* and *B. myersi*. *Trop. Fish Hobbyist* 13, 13–24, 61–69.
- Géry, J., 1972. Poissons Characoïdes des Guyanes. I. Généralités. *Zool. Verhandelingen*, 122, 1–250.
- Géry, J., 1973. New and little-known Aphyoditeina (Pisces, Characoïdei) from the Amazon basin. *Stud. Neotrop. Fauna* 8, 81–137.
- Géry, J., 1977. *Characoids of the World*. TFH Publications, Neptune City, NJ.
- Giribet, G., 2003. Stability on phylogenetic formulations and its relationship with nodal support. *Syst. Biol.* 52, 554–564.
- Goloboff, P.A., 1993. Estimating character weights during tree search. *Cladistics* 9, 83–91.
- Goloboff, P.A., 1995. Parsimony and weighting: a reply to Turner and Zandee. *Cladistics* 11, 91–114.
- Goloboff, P.A., 1996. SLF-WT, ver. 0.80. A prototype program implementing character state reconstructions under non-linear functions of the state changes. Software available from the author.
- Goloboff, P.A., 1997. Self-weighted optimization: tree searches and character state reconstructions under implied transformation costs. *Cladistics* 13, 225–245.
- Goloboff, P.A., 1999. Analyzing large data sets in reasonable times: solutions for composite optima. *Cladistics* 15, 415–428.
- Goloboff, P.A., 2008. Calculating SPR distances between trees. *Cladistics* 24, 591–597.
- Goloboff, P.A., Farris, J.S., 2001. Methods for quick consensus estimation. *Cladistics* 17, S26–S34.
- Goloboff, P.A., Farris, J.S., Källersjö, M., Oxelman, B., Ramírez, M.J., Szumik, C.A., 2003a. Improvements to resampling measures of group support. *Cladistics* 19, 324–332.

- Goloboff, P.A., Farris, J.S., Nixon, K., 2003b. TNT: Tree Analysis Using New Technology. Version 1.1, Software and documentation available from the authors and at <http://www.zmuc.dk/public/phylogeny>.
- Goloboff, P.A., Farris, J.S., Nixon, K.C., 2008. TNT, a free program for phylogenetic analysis. *Cladistics* 24, 774–786.
- Goloboff, P.A., Carpenter, J.M., Arias, J.S., Miranda Esquivel, D.R., 2008. Weighting against homoplasy improves phylogenetic analysis of morphological data sets. *Cladistics* 24, 758–773.
- Greenwood, P.H., Rosen, D.E., Weitzman, S.H., Myers, G.S., 1966. Phyletic studies of teleostean fishes, with a provisional classification of living forms. *Bull. Am. Mus. Nat. Hist.* 131, 339–456.
- Hennig, W., 1950. Grundzüge einer Theorie der phylogenetischen Systematik. Deutscher Zentralverlag, Berlin.
- Hennig, W., 1966. *Phylogenetic Systematics*. University of Illinois, Urbana, Illinois.
- Howes, G.J., 1976. The cranial musculature and taxonomy of characoid fishes of the tribes Cynodontini and Characini. *Bull. Brit. Mus. Nat. Hist. (Zool.)* 29, 203–248.
- Howes, G.J., 1978. The anatomy and relationships of the cyprinid fish *Luciobrama macrocephalus* (Lacepède). *Bull. Brit. Mus. Nat. Hist. (Zool.)* 34, 1–64.
- Howes, G.J., 1979. Notes on the anatomy of *Macrochirichthys macrochirus* (Valenciennes), 1844, with comments on the Cultrinae (Pisces, Cyprinidae). *Bull. Brit. Mus. Nat. Hist. (Zool.)* 36, 147–200.
- Howes, G.J., 1980. The anatomy, phylogeny and classification of Bariliinae cyprinid fishes. *Bull. Brit. Mus. Nat. Hist. (Zool.)* 37, 129–198.
- Jégu, M., 2003. Serrasalminae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 182–196.
- Lima, F.C.T., 2003a. Bryconinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 174–181.
- Lima, F.C.T., 2003b. Clupeacharacinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, 171 p.
- Lima, R.S., 2003c. Aphyocharacinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 197–199.
- Lima, F.C.T., 2006. Revisão taxonômica e relações filogenéticas do gênero *Salminus* (Teleostei: Ostariophysi: Characiformes: Characidae). PhD thesis. Universidade de São Paulo, São Paulo, Brazil.
- Lima, F.C.T., Zanata, A., 2003. Agoniatinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, 170 p.
- Lima, F.C.T., Malabarba, L.R., Buckup, P.A., Pezzi da Silva, J.F., Vari, R.P., Harold, A., Benine, R., Oyakawa, O.T., Pavanelli, C.S., Menezes, N.A., Lucena, C.A.S., Malabarba, M.C.S.L., Lucena, Z.M.S., Reis, R.E., Langeani, F., Cassati, L., Bertaco, V.A., Moreira, C., Lucinda, P.H.F., 2003. Characidae, genera incertae sedis. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 106–169.
- Lucena, C.A.S., 1993. Estudo filogenético da família Characidae com uma discussão dos grupos naturais propostos (Teleostei, Ostariophysi, Characiformes). PhD thesis. Universidade de São Paulo, Brazil.
- Lucena, C.A.S., 1998. Relações filogenéticas e definição do gênero *Roeboides* Günther (Ostariophysi: Characiformes: Characidae). *Comun. Mus. Ciênc. Tecnol. PUCRS, Sér. Zool.* 11, 19–59.
- Lucena, C.A.S., Lucena, Z.M.S., 2002. Redefinição do gênero *Deuterodon* Eigenmann (Ostariophysi: Characiformes: Characidae). *Comun. Mus. Ciênc. Tecnol. PUCRS, Sér. Zool.* 15, 113–135.
- Lucena, C.A.S., Menezes, N.A., 1998. A phylogenetic analysis of *Roestes* Günther and *Gilbertolus* Eigenmann, with a hypothesis of the relationships of the Cynodontidae and Acestrorhynchidae (Teleostei: Ostariophysi: Characiformes). In: Malabarba, L., Reis, R., Vari, R., Lucena, Z.M.S., Lucena, C. (Eds.), *Phylogeny and Classification of Neotropical Fishes*. EDIPUCRS, Porto Alegre, Brazil, pp. 261–277.
- Lucena, C.A.S., Menezes, N.A., 2003. Characinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 200–208.
- Machado-Allison, A., 1983. Estudios sobre la subfamilia Serrasalminae (Teleostei-Characidae). Parte II. Discusión sobre la condición monofilética de la subfamilia. *Acta Biol. Venez.* 11, 145–196.
- Maddison, W.P., Maddison, D.R., 2008. Mesquite: A Modular System for Evolutionary Analysis. Version 2.5, <http://mesquiteproject.org>.
- Malabarba, L.R., 1998a. Monophyly of the Cheirodontinae, characters and major clades (Ostariophysi, Characidae). In: Malabarba, L., Reis, R., Vari, R., Lucena, Z.M.S., Lucena, C. (Eds.), *Phylogeny and Classification of Neotropical Fishes*. EDIPUCRS, Porto Alegre, Brazil, pp. 193–234.
- Malabarba, L.R., 1998b. Phylogeny of fossil Characiformes and paleobiogeography of the Tremembé Formation, São Paulo, Brazil. In: Malabarba, L., Reis, R., Vari, R., Lucena, Z.M.S., Lucena, C. (Eds.), *Phylogeny and Classification of Neotropical Fishes*. EDIPUCRS, Porto Alegre, Brazil, pp. 69–84.
- Malabarba, L.R., 2003. Cheirodontinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 215–221.
- Malabarba, L.R., Weitzman, S.H., 2003. Description of a new genus with six species from southern Brazil, Uruguay and Argentina, with a discussion of a putative characid clade (Teleostei: Characiformes: Characidae). *Comun. Mus. Ciênc. Tecnol. PUCRS, Sér. Zool.* 16, 67–151.
- Menezes, N.A., 2003. Family Acestrorhynchidae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 231–233.
- Miranda, J.M., Aguilera, G., Azpelicueta, M.M., 2004. A new genus and species of small characid (Ostariophysi, Characidae) from the upper río Bermejo basin, northwestern Argentina. *Rev. Suisse Zool.* 111, 715–728.
- Miranda, J.M., Aguilera, G., Azpelicueta, M.M., 2006. Nomenclatural note on the genus *Nans* (Ostariophysi, Characidae). *Rev. Suisse Zool.* 113, 305.
- Molineri, C., 2006. Phylogeny of the mayfly family Leptohephidae (Insecta: Ephemeroptera) in South America. *Syst. Entomol.* 31, 711–728.
- Moreira, C.R., 2002. Relações filogenéticas em Iguanodectinae (Teleostei; Characiformes; Characidae). Master thesis, Universidade de São Paulo, Brazil.
- Moreira, C.R., 2003. Iguanodectinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater Fishes of South and Central America*. EDIPUCRS, Porto Alegre, Brazil, pp. 172–173.
- Murray, A.M., Stewart, K.M., 2002. Phylogenetic relationships of the African genera *Alestes* and *Brycinus* (Teleostei, Characiformes, Alestidae). *Can. J. Zool.* 80, 1887–1899.
- Nixon, K.C., 1999. The parsimony ratchet, a new method for rapid parsimony analysis. *Cladistics* 15, 407–414.
- Prendini, L., 2000. Phylogeny and classification of the superfamily Scorpionoidea Latreille 1802 (Chelicerata, Scorpiones): an exemplar approach. *Cladistics* 16, 1–78.
- Quevedo, R., 2006. Estudo taxonômico e filogenético da subfamilia Paragoniatinae Géry (Characiformes: Characidae). PhD thesis. Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil.
- Ramírez, M.J., 2003. The spider subfamily Amaurobioidinae (Araneae, Anyphaenidae): a phylogenetic revision at the generic level. *Bull. Amer. Mus. Nat. Hist.* 277, 1–262.
- Reis, R.E., 1989. Systematic revision of the Neotropical characid subfamily Stethaproninae (Pisces, Characiformes). *Comun. Mus. Ciênc. Tecnol. PUCRS, Sér. Zool.* 2, 3–86.
- Reis, R.E., 2003a. Subfamily Stethaproninae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), *Check List of the Freshwater*

- Fishes of South and Central America. EDIPUCRS, Porto Alegre, Brazil, pp. 209–211.
- Reis, R.E., 2003b. Subfamily Tetragonopterinae. In: Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr (Eds.), Check List of the Freshwater Fishes of South and Central America. EDIPUCRS, Porto Alegre, Brazil, 212 p.
- Reis, R.E., Kullander, S.O., Ferraris, C.J. Jr. 2003. Check List of the Freshwater Fishes of South and Central America. EDIPUCRS, Porto Alegre, Brazil.
- Roberts, T.R., 1969. Osteology and relationships of characid fishes particularly of the genera *Hepsetus*, *Salminus*, *Hoplias*, *Ctenolucius* and *Acestrorhynchus*. Proc. Calif. Acad. Sci. 36, 391–500.
- Roberts, T.R., 1974. Osteology and classification of the Neotropical fishes of the families Hemiodontidae (including Anodontidae) and Parodontidae. Bull. Mus. Comp. Zool. 146, 411–472.
- Rosen, D.E., 1972. Origin of the characid fish genus *Bramocharax* and a description of a second, more primitive, species in Guatemala. Amer. Mus. Novitates 2500, 1–21.
- Ruiz-C., R.I., Román-Valencia, C., 2006. Osteología de *Astyanax aurocaudatus* Eigenmann, 1913 (Pisces, Characidae), con notas sobre la validez de *Carlastyanax* Géry, 1972. Anim. Biodivers. Conserv. 29.1, 49–64.
- Serra, J.P., 2003. Análise filogenética e revisão taxonômica de Hasemania Ellis, 1911 (Characiformes, Characidae). Master thesis. Universidade Estadual Paulista, São José do Rio Preto, São Paulo, Brazil.
- Serra, J.P., Langeani, F., 2006. Redescricao e osteologia de *Bryconamericus exodon* Eigenmann, 1907 (Ostariophysi, Characiformes, Characidae). Biota Neotrop. 6, 1–14.
- Starks, E.C., 1930. The primary shoulder girdle of the bony fishes. Stanford Univ. Pub. Univ. Ser. Biol. Sci. 6, 149–239.
- Taylor, W.R., Van Dyke, G.C., 1985. Revised procedures for staining and clearing small fishes and other vertebrates for bone and cartilage study. Cybium 9, 107–119.
- Toledo-Piza, M., 2000. The Neotropical fish subfamily Cynodontinae (Teleostei: Ostariophysi: Characiformes): a phylogenetic study and a revision of *Cynodon* and *Rhaphiodon*. Amer. Mus. Novitates 3286, 1–88.
- Toledo-Piza, M., 2003. Family Cynodontidae. In: Reis, R.E., Kullander, S.O., Ferraris Jr., C.J., (Eds.), Check List of the Freshwater Fishes of South and Central America. EDIPUCRS, Porto Alegre, Brazil, p. 234.
- Toledo-Piza, M., 2007. Phylogenetic relationships among *Acestrorhynchus* species (Ostariophysi: Characiformes: Acestrorhynchidae). Zool. J. Linn. Soc. 151, 691–757.
- Uj, A., 1990. Étude comparative de l'ostéologie crânienne des poissons de la famille des Characidae et son importance phylogénétique. PhD thesis. Faculté des Sciences, Université de Genève, Switzerland.
- Vari, R.P., 1979. Anatomy, relationships and classification of the families Citharinidae y Distichodontidae (Pisces, Characoidea). Bull. Brit. Mus. Nat. Hist. (Zool.) 36, 261–344.
- Vari, R.P., 1983. Phylogenetic relationships of the families Curimatidae, Prochilodontidae, Anostomidae, and Chilodontidae (Pisces: Characiformes). Smith. Contr. Zool. 378, 1–60.
- Vari, R.P., 1995. The Neotropical fish family Ctenoluciidae (Teleostei: Ostariophysi: Characiformes): supra and infrafamilial phylogenetic relationships, with a revisionary study. Smith. Contr. Zool. 564, 1–97.
- Vari, R.P., Harold, A.S., 2001. Phylogenetic study of the Neotropical fish genera *Creagrutus* Günther and *Piabina* Reinhardt (Teleostei: Ostariophysi: Characiformes), with a revision of the cis-Andean species. Smith. Contr. Zool. 613, 1–239.
- Weitzman, S.H., 1962. The osteology of *Brycon meeki*, a generalized characid fish, with an osteological definition of the family. Stanford Icht. Bull. 8, 3–77.
- Weitzman, S.H., Fink, W.L., 1983. Relationships of the neon tetras, a group of South American freshwater fishes (Teleostei: Characidae), with comments on the phylogeny of New World characiforms. Bull. Mus. Comp. Zool. 150, 339–395.
- Weitzman, S.H., Fink, W.L., 1985. Xenobryconin phylogeny and putative pheromone pumps in Glandulocaudinae fishes (Teleostei: Characidae). Smith. Contr. Zool. 421, 1–119.
- Weitzman, S.H., Menezes, N.A., 1998. Relationships of the tribes and genera of the Glandulocaudinae (Ostariophysi, Characiformes, Characidae) with the description of a new genus, *Chysobrycon*. In: Malabarba, L., Reis, R., Vari, R., Lucena, Z.M.S., Lucena, C. (Eds.), Phylogeny and Classification of Neotropical fishes. EDIPUCRS, Porto Alegre, Brazil, pp. 171–192.
- Weitzman, S.H., Palmer, L., 1997. A new species of *Hyphessobrycon* (Teleostei: Characidae) from the Neblina region of Venezuela and Brazil, with comments on the putative 'rosy tetra clade'. Ichthyol. Explor. Freshw. 7, 209–242.
- Weitzman, S.H., Menezes, N.A., Evers, H.-G., Burns, J.R., 2005. Putative relationships among inseminating and externally fertilizing characids, with a description of a new genus and species of Brazilian inseminating fish bearing an anal-fin gland in males (Characiformes: Characidae). Neotrop. Ichthyol. 3, 329–360.
- Wheeler, W.C., Gatesy, J., DeSalle, R., 1995. Elision: a method for accommodating multiple molecular sequence alignments with alignment-ambiguous sites. Mol. Phylogenet. Evol. 4, 1–9.
- Whiting, M.F., Carpenter, J.M., Wheeler, Q.D., Wheeler, W.C., 1997. The Strepsiptera problem: phylogeny of the holometabolous insect orders inferred from 18S and 28S ribosomal DNA sequences and morphology. Syst. Biol. 46, 1–68.
- Winterbottom, R., 1974. A descriptive synonymy of the striated muscles of the Teleostei. Proc. Acad. Nat. Sci. Phila. 125, 225–317.
- Zanata, A.M., 1997. *Jupiaba*, um novo gênero de Tetragonopterinae com osso pélvico em forma de espinho (Characidae, Characiformes). Iheringia Sér. Zool. 83, 99–136.
- Zanata, A.M., Akama, A., 2004. *Myxiops aphos*, new characid genus and species (Characiformes: Characidae) from the rio Lençóis, Bahia, Brazil. Neotrop. Ichthyol. 2, 45–54.
- Zanata, A.M., Vari, R.P., 2005. The family Alestidae (Ostariophysi, Characiformes): a phylogenetic analysis of a trans-Atlantic clade. Zool. J. Linn. Soc. 145, 1–144.
- Zarske, A., Géry, J., 2006. Beschreibung einer neuen Salmmler-Gattung und zweier neuer Arten (Teleostei: Characiformes: Characidae) aus Peru und Brasilien. Zool. Abhand. (Dresden) 55, 31–49.

Supporting Information

Additional supporting information may be found in the online version of this article.

Appendix S1. List of examined C&S specimens.

Appendix S2. List of autapomorphies.

Appendix S3. TNT script for IW searches (aaa.run).

Appendix S4. TNT script for IW searches (aab.run).

Appendix S5. TNT script for SL searches (aas.run).

Appendix S6. TNT script for SL searches (kswap.run).

Appendix S7. Consensus tree obtained under equal weighting.

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Appendix 1

List of characters including number of steps, and consistency and retention indices of each character in the final hypothesis herein proposed. Characters included in previous papers are cited even in cases in which state definitions are not exactly the same. Number of steps and indices are from most-parsimonious trees with K -value = 12.9, under IW. Characters not previously used are described briefly.

1. Posterior laminar expansion of epiphyseal bar: (0) absent; (1) present (Lucena, 1993, 1998) (4 steps, CI = 25, RI = 25).
2. Ventral longitudinal ridges of basioccipital: (0) not reaching posterior border of basioccipital; (1) reaching posterior border of cranium (3 steps, CI = 33, RI = 93). The ventral area of prootic bears two parallel ridges articulating with the parasphenoid, which are variably extended under the basioccipital; in some species these ridges are absent or restricted to the anterior area of the basioccipital, while in others they are extended posteriorly, reaching the posterior margin of this bone.
3. Ventral projection of lagenar capsule: (0) not projected ventrally to horizontal through articulation between basioccipital and parasphenoid; (1) projected ventrally to this articulation (Uj, 1990; Zanata and Vari, 2005) (8 steps, CI = 12, RI = 77).
4. Epioccipital bridge over posttemporal fossa: (0) absent; (1) present (Bührnheim, 2006) (not informative).
5. Form of epioccipital bridge: (0) cylindrical or vertically expanded in transverse section; (1) depressed (1 step, CI = 100, RI = 100). The epioccipital bridge crosses longitudinally the posttemporal fossa; this anterior projection of the epioccipital is cylindrical in most species, while it is depressed in cross-section, in other taxa.
6. Anterior articulation of epioccipital bridge: (0) with parietal and pterotic; (1) only with parietal (Weitzman and Fink, 1983) (2 steps, CI = 50, RI = 0).
7. Epioccipital spine, posteriorly orientated: (0) present; (1) absent (Lucena, 1993, 1998) (5 steps, CI = 20, RI = 56).
8. Ventromedial opening of posttemporal fossa: (0) absent; (1) present (Uj, 1990; Lucena, 1993; Buckup, 1998; Toledo-Piza, 2000; Vari and Harold, 2001; Benine, 2004; Zanata and Vari, 2005; Lima, 2006) (7 steps, CI = 14, RI = 60).
9. Position of ventromedial opening of posttemporal fossa: (0) between epioccipital and exoccipital; (1) bordered entirely by epioccipital (Vari and Harold, 2001; Zanata and Vari, 2005) (3 steps, CI = 33, RI = 67).
10. Length of sphenotic spine: (0) not extended ventrally to articulation between sphenotic and hyomandibular; (1) projected ventrally to articulation between sphenotic and hyomandibular (Bertaco, 2003) (10 steps, CI = 10, RI = 84).
11. Position of sphenotic spine relative to hyomandibular: (0) aligned with anterior margin of hyomandibular; (1) displaced anteriorly relative to anterior margin of hyomandibular (6 steps, CI = 17, RI = 55).
12. Position of sphenotic spine relative to orbit: (0) bordering orbit posteriorly, aligned with anterior border of fourth and fifth infraorbitals; (1) conspicuously posterior to orbital margin (7 steps, CI = 14, RI = 45).
13. Temporal fossa: (0) well developed; (1) absent or much reduced (Vari and Harold, 2001; Lima, 2006) (4 steps, CI = 25, RI = 40).
14. Form of anterior process of lateral ethmoid: (0) broad in ventral view, contacting proximal region of vomer in its entire length; (1) slender, leaving a space with vomer (Moreira, 2002) (6 steps, CI = 17, RI = 71).
15. Lateral opening between ventral diverging lamellae of mesethmoid and anterior process of lateral ethmoid: (0) broad; (1) small and ovate, partially occluded by diverging lamellae of mesethmoid and anterior process of lateral ethmoid (Lucena, 1993) (4 steps, CI = 25, RI = 40).
16. Dorsal margin of lateral ethmoids: (0) aligned; (1) situated obliquely in dorsal view, converging in an anteriorly directed angle (5 steps, CI = 20, RI = 91). The lateral ethmoids dorsal margins are dorsally visible for transparency of the frontals and mesethmoid; in most species the dorsal margins of lateral ethmoids are aligned, while in others their medial regions are anteriorly directed converging in an angle. The latter configuration of the lateral ethmoids would permit an anterior displacement of the olfactory capsules of the brain and the anterior myodome.
17. Articulation between medial region of lateral ethmoid and frontal or mesethmoid: (0) absent; (1) extensive articulation of entire lateral ethmoid dorsal margin (2 steps, CI = 50, RI = 88). In most examined species only the lateral region of the lateral ethmoid dorsal

margin articulates firmly with the frontals, while the median region is relatively distant from the frontals and mesethmoid. In a small group of species also the median region of the lateral ethmoid dorsal margin is articulating with the frontals and mesethmoid.

18. Subtemporal fossa: (0) medially extended to middle exoccipital; (1) restricted to pterotic (4 steps, CI = 25, RI = 73). The subtemporal fossa is medially limited by the intercalar; in most species the intercalar is situated just in the articulation between the pterotic and exoccipital, and the subtemporal fossa is restricted to the pterotic. In some species, instead, the intercalar is situated entirely under the exoccipital, and the subtemporal fossa is partially contained in the ventral surface of this bone.

19. Ascending process on postero-dorsal angle of exoccipital, directed to neural complex of Weberian apparatus: (0) absent; (1) present (Uj, 1990) (not informative).

20. Anterior extension of frontal: (0) reaching posterior margin of nasal opening; (1) extended between nasals, reaching middle length of nasal opening (2 steps, CI = 50, RI = 50).

21. Contact between frontals anteriorly to frontal fontanel: (0) absent; (1) present (Vari and Harold, 2001; Moreira, 2002; Serra, 2003; Benine, 2004; Zanata and Vari, 2005) (22 steps, CI = 5, RI = 54).

22. Frontal fontanel: (0) present; (1) totally occluded by frontals (Lucena, 1993; Buckup, 1998; Malabarba, 1998b; Serra, 2003; Zanata and Vari, 2005; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 44).

23. Relative size of frontal and parietal fontanels: (0) length of frontal fontanel up to 2/3 length of parietal fontanel; (1) length of frontal fontanel 3/4 or more than length of parietal fontanel (13 steps, CI = 8, RI = 71).

24. Dilator fossa on lateral surface of frontal, where dilator operculi muscle attaches: (0) absent, dilator operculi inserts ventrally to frontal; (1) present (Lucena, 1993; Buckup, 1998) (2 steps, CI = 50, RI = 67).

25. Anterior end of mesethmoid: (0) trifurcate, with processes directed to depressions on premaxillae; (1) not trifurcate, with a triangular anterior spine and articular processes reduced or absent (Uj, 1990; Lucena, 1993; Buckup, 1998) (3 steps, CI = 33, RI = 67).

26. Ventral projection of mesethmoid spine, forming a keel between premaxillae: (0) absent; (1) present (Vari and Harold, 2001) (2 steps, CI = 50, RI = 67).

27. Form of mesethmoid spine: (0) slender in dorsal view, developed between premaxillae; (1) broad in dorsal view and relatively short, with premaxillae articulating each other anteriorly to mesethmoid (Bührnheim, 2006) (4 steps, CI = 25, RI = 79).

28. Posterior region of mesethmoid spine: (0) relatively slender; (1) as broad as lateral wings of mesethmoid (1 step, CI = 100, RI = 100).

29. Lateral wings of mesethmoid: (0) present; (1) absent (Uj, 1990; Lucena, 1993; Buckup, 1998; Bührnheim, 2006) (2 steps, CI = 50, RI = 90).

30. Ventral diverging lamellae of mesethmoid: (0) absent; (1) present (Lucena, 1993; Buckup, 1998; Toledo-Piza, 2000; Zanata and Vari, 2005) (2 steps, CI = 50, RI = 94).

31. Anterior convergence of ventral diverging lamellae with nasal septum of mesethmoid: (0) absent, or confluent near anterior end of nasal septum; (1) confluent at posterior end of nasal septum (11 steps, CI = 9, RI = 58). Ventral divergent lamellae of the mesethmoid are independent each other in most species, reaching separately the region articulating with the vomer, or they are confluent at the anterior end of the nasal septum. In a group of species, these lamellae are confluent with the posterior region of the nasal septum of mesethmoid, which forms the single vertical bony wall between the nasal capsules.

32. Nasal septum of mesethmoid: (0) a single longitudinal lamella; (1) two parallel lamellae apparently formed, in part, by ventral diverging lamellae (1 step, CI = 100, RI = 100). In most species the nasal septum of mesethmoid is a single medial lamella, visible dorsally by transparency of the dorsal roof of this bone. In a small group of species, there are two closely disposed parallel lamellae forming this septum.

33. Nasal: (0) present; (1) absent (Zanata and Vari, 2005) (2 steps, CI = 50, RI = 0).

34. Bony lamellae bordering sensory canal of nasal: (0) absent or more slender than tubular region; (1) wider, in some point, than tubular region (Lucena, 1993; Vari, 1995; Moreira, 2002; Lima, 2006; Toledo-Piza, 2007) (5 steps, CI = 20, RI = 33).

35. Synchondral articulation between lateral ethmoid and antero-dorsal border of orbitosphenoid: (0) present; (1) absent, with orbitosphenoid distant from lateral ethmoid (5 steps, CI = 20, RI = 64). The dorsal margin of the orbitosphenoid articulates with the orbital lamella of the frontal, and extends anteriorly in a variable length among the examined species; in most species this margin does not reach the posterior surface of the lateral ethmoid, while in others it articulates synchondrally with the lateral ethmoid.

36. Lateral bony covering of olfactory nerve: (0) absent; (1) covered by a posterior expansion of lateral ethmoid; (2) covered by an anterior tubular projection of orbitosphenoid; (3) covered lateral and inferiorly by orbitosphenoid and lateral ethmoid, which are not forming a canal (Uj, 1990; Zanata and Vari, 2005) (3 steps, CI = 100, RI = 100).

37. Form of orbitosphenoid: (0) slender and relatively small, separated from parasphenoid; (1) massive, almost reaching parasphenoid ventrally (Uj, 1990; Lucena, 1998; Toledo-Piza, 2000; Benine, 2004; Bührnheim, 2006) (9 steps, CI = 11, RI = 71).

38. Distance between cartilage anterior to orbitosphenoid and lateral ethmoids: (0) contacting, or almost contacting lateral ethmoids; (1) distant from lateral ethmoids (11 steps, CI = 9, RI = 71). An arched cartilage projected anteriorly from the dorsal margins of the orbitosphenoid surrounds anteriorly the olfactory lobe of the brain. The distance between this cartilage and the lateral ethmoids gives an idea of the position of the olfactory lobe relative to the remaining structures of the cranium. In most species these cartilages are contacting, or almost contacting the lateral ethmoids, while in others are distant, as evident dorsally by transparency of the frontal and mesethmoid.

39. Opening between orbitosphenoid, pterosphenoid, and frontal: (0) present, rounded or ovate; (1) absent (Machado-Allison, 1983) (3 steps, CI = 33, RI = 94).

40. Anterior paired projections of parasphenoid: (0) absent; (1) present (Benine, 2004) (6 steps, CI = 17, RI = 72).

41. Parietal fontanel: (0) present in adults; (1) completely occluded by parietals (Lucena, 1993; Buckup, 1998; Zanata and Vari, 2005; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 38).

42. Trigemino-facialis foramen: (0) broad, dorsally limited by sphenotic; (1) narrow, as a cleft almost completely limited by prootic and pterosphenoid (1 step, CI = 100, RI = 100). In characids the trigemino-facialis foramen is situated at the anterior surface of prootic, forming part of the posterior wall of the orbit. In most examined species this foramen is broadly triangular, with its upper margin limited by the prootic and sphenotic; in a small group of species it is reduced to a narrow cleft limited almost completely by the pterosphenoid and prootic.

43. Large foramen on pterosphenoid: (0) absent, only small foramina; (1) present, well developed (1 step, CI = 100, RI = 100). The lateral surface of the pterosphenoid is usually pierced only by small foramina for the entrance of nerves or blood vessels to the neurocranium; in a small group of species there is a large ovoid foramen situated in the middle of this bone, which is not apparently pierced by vessels or nerves.

44. Small foramen near posterior margin of pterosphenoid: (0) absent, or not pierced by nerves; (1) present, pierced by a branch of supraorbital nerve (2 steps, CI = 50, RI = 95). The supraorbital nerve in most species enters into the braincase through the trigemino-facialis foramen, which is limited by the sphenotic, pterosphenoid and prootic; in a group of species the postero-dorsal region of the pterosphenoid is apparently pierced by a branch of the supraorbital nerve, while the remaining ones enters the braincase through the trigemino-facialis foramen.

45. Process of pterotic where fibers from epaxial musculature attaches: (0) absent or ventrally projected from tube for horizontal semicircular canal; (1) dorsally projected from tube for semicircular canal (7 steps, CI = 14, RI = 57). In most species the epaxial musculature attaches anteriorly in the pterotic tube for the horizontal

semicircular canal or in a descendant process from this tube; in some species, instead, there is a dorsal projection of the pterotic where these fibers attach.

46. Relative length of pterotic spine: (0) posteriorly projected from attachment site of hyomandibular ligament; (1) extended only to attachment region of hyomandibular ligament (3 steps, CI = 33, RI = 94). The posterior region of the hyomandibular have a short ligament attached to a variably developed ventral projection of the pterotic. In most species this projection is not posteriorly projected from the attachment site of such ligament, while in others it is extended conspicuously more posteriorly than the attachment site of the hyomandibular ligament.

47. Rhinosphenoid: (0) absent or not ossified; (1) present, ossified (Uj, 1990; Lucena, 1993; Buckup, 1998; Malabarba, 1998b; Toledo-Piza, 2000; Bertaco, 2003; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Bührnheim, 2006; Lima, 2006; Quevedo, 2006; Toledo-Piza, 2007) (16 steps, CI = 6, RI = 66).

48. Dorsal expansion of rhinosphenoid: (0) absent; (1) present, forming a bony wall between olfactory nerves (Serra, 2003; Benine, 2004) (7 steps, CI = 14, RI = 87).

49. Posterior extension of rhinosphenoid cartilage: (0) projected near vertical through middle length of orbitosphenoid; (1) extended only to vertical through region of articulation between orbitosphenoid and pterosphenoid (2 steps, CI = 50, RI = 0). The rhinosphenoid cartilage is projected posteriorly from the rhinosphenoid, just dorsal to the parasphenoid; in most species it extends posteriorly only to middle length of the orbitosphenoid while in others is comparatively more developed, reaching the articulation region between the orbitosphenoid and pterosphenoid.

50. Ventral border of rhinosphenoid: (0) separated from parasphenoid; (1) almost contacting parasphenoid (2 steps, CI = 50, RI = 75).

51. Anterior border of supraoccipital: (0) completely behind vertical through posterior border of the orbit; (1) anterior to vertical through posterior border of the orbit (3 steps, CI = 33, RI = 60).

52. Length of supraoccipital spine: (0) projected dorsal to entire neural complex of Weberian apparatus; (1) projected dorsal to approximately middle length of neural complex (Machado-Allison, 1983; Malabarba, 1998b; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Quevedo, 2006) (4 steps, CI = 25, RI = 70).

53. Length of supraoccipital spine: (0) projected dorsal to, at least, middle length of neural complex of Weberian apparatus; (1) projected just to anterior axis of neural complex (Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Quevedo, 2006) (17 steps, CI = 6, RI = 77).

54. Dorsal ridges on vomer orientated to diverging ventral lamellae of mesethmoid: (0) absent; (1) present (5 steps, CI = 20, RI = 33). In most species there is a single medial vertical lamella in the vomer, articulating the mesethmoidal nasal septum, while in others there are two additional lamellae articulating or directed to the ventral diverging lamellae of the mesethmoid.

55. Antorbital: (0) present; (1) absent or fused with first infraorbital (Lucena, 1993; Vari, 1995; Buckup, 1998; Zanata and Vari, 2005) (3 steps, CI = 33, RI = 0).

56. Position of antorbital relative to lateral ethmoid: (0) antorbital entirely anterior to lateral ethmoid; (1) antorbital overlapping lateral ethmoid in lateral view (Toledo-Piza, 2000) (4 steps, CI = 25, RI = 50).

57. Anterior end of antorbital and first infraorbital: (0) anterior margin of antorbital either aligned or anterior than first infraorbital; (1) first infraorbital anteriorly projected relative to antorbital (Zanata and Vari, 2005) (3 steps, CI = 33, RI = 87).

58. Bony lamellae bordering laterosensory canal of first infraorbital: (0) present; (1) absent on first infraorbital but present on remaining infraorbitals (Zanata and Vari, 2005) (1 step, CI = 100, RI = 100).

59. Expansion of first infraorbital lateral to maxilla: (0) covering less than middle length of maxilla; (1) covering laterally most of maxillary length (Toledo-Piza, 2007) (5 steps, CI = 20, RI = 33).

60. Overlapping of first infraorbital by anterior margin of second infraorbital: (0) absent; (1) present (2 steps, CI = 50, RI = 67).

61. Overlapping of maxilla by second infraorbital: (0) absent; (1) present (Lucena and Menezes, 1998) (7 steps, CI = 14, RI = 60).

62. Articulation between second and third infraorbitals: (0) vertical; (1) antero-ventrally oblique; (2) postero-ventrally oblique (10 steps, CI = 20, RI = 86).

63. Anterior region of third infraorbital: (0) not much expanded relative to posterior region of second infraorbital; (1) abruptly expanded relative to posterior region of second infraorbital (2 steps, CI = 50, RI = 50).

64. Ventral covering of third infraorbital: (0) reaching horizontal arm of preopercle; (1) not reaching horizontal arm of preopercle, at least anteriorly (Eigenmann, 1917; Machado-Allison, 1983; Uj, 1990; Bührnheim, 2006) (29 steps, CI = 3, RI = 61).

65. Posterior extension of third infraorbital: (0) covering angle of preopercle; (1) relatively reduced, with angle of preopercle covered partially by fourth infraorbital (Moreira, 2002) (4 steps, CI = 25, RI = 0).

66. Fourth infraorbital: (0) present, well developed; (1) absent, fused with fifth infraorbital, or reduced and bordered posteriorly by third and fifth infraorbitals (Lucena, 1993, 1998; Vari, 1995; Bertaco, 2003; Zanata and Vari, 2005; Quevedo, 2006; Toledo-Piza, 2007) (13 steps, CI = 8, RI = 40).

67. Form of fourth infraorbital: (0) approximately squared or more developed longitudinally than dorsoventrally; (1) longer dorsoventrally than longitudinally (Serra, 2003; Benine, 2004; Bührnheim, 2006) (18 steps, CI = 6, RI = 70).

68. Posterior dorsoventral expansion of fourth infraorbital: (0) absent; (1) fourth infraorbital expanded between fifth infraorbital and preopercle (Toledo-Piza, 2007) (3 steps, CI = 33, RI = 67).

69. Lateral covering of *dilator fossa* by sixth infraorbital: (0) almost complete, at least in its ventral border; (1) leaving a conspicuous naked area in anterior region of dilator fossa (Uj, 1990; Serra, 2003; Toledo-Piza, 2007) (15 steps, CI = 7, RI = 79).

70. Supraorbital: (0) present; (1) absent (Uj, 1990; Lucena, 1993; Buckup, 1998; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Quevedo, 2006; Toledo-Piza, 2007) (5 steps, CI = 20, RI = 88).

71. Contact between supraorbital and sixth infraorbital: (0) absent; (1) present (Machado-Allison, 1983; Uj, 1990; Lucena, 1993; Malabarba, 1998b; Moreira, 2002; Zanata and Vari, 2005; Lima, 2006) (5 steps, CI = 20, RI = 69).

72. Laterosensory canal in antorbital: (0) absent; (1) present (Uj, 1990; Malabarba, 1998b; Moreira, 2002; Serra, 2003; Benine, 2004) (4 steps, CI = 25, RI = 25).

73. Laterosensory canal of first infraorbital: (0) projected dorsally from main body of first infraorbital; (1) absent or not projected dorsally (Lucena, 1993; Malabarba, 1998b) (3 steps, CI = 33, RI = 71).

74. Branching of laterosensory canals of fourth or fifth infraorbitals: (0) reduced or absent; (1) present, conspicuous (Benine, 2004; Lima, 2006; Toledo-Piza, 2007) (13 steps, CI = 8, RI = 52).

75. Direction of posterior branch of laterosensory canal of fourth or fifth infraorbital: (0) to a pore on preopercle near hyomandibular condyle; (1) to a pore conspicuously ventral to hyomandibular condyle (2 steps, CI = 50, RI = 0). In most species, a branching of the laterosensory system is orientated from the fourth or fifth infraorbital to a pore situated in the preopercle, close to its articulation with the opercle; in some examined species, instead, this canal is more ventrally orientated, opening in a pore of the preopercle situated conspicuously ventral to its articulation with the opercle.

76. Laterosensory canal of sixth infraorbital: (0) not branched; (1) branched (Moreira, 2002; Zanata and Vari, 2005; Bührnheim, 2006; Toledo-Piza, 2007) (16 steps, CI = 6, RI = 50).

77. Position of opening on neurocranium for laterosensory canal from sixth infraorbital: (0) between frontal and pterotic; (1) in frontal (Vari and Harold, 2001; Moreira, 2002; Zanata and Vari, 2005; Toledo-Piza, 2007) (9 steps, CI = 11, RI = 50).

78. Relative position of opening in neurocranium receiving sixth infraorbital laterosensory canal: (0) lateral or slightly anterior to sphenotic tube for vertical semicircular canal; (1) conspicuously anterior to sphenotic tube for vertical semicircular canal (1 step, CI = 100, RI = 100).

79. Extension of laterosensory canal of dentary: (0) piercing almost entire length of dentary; (1) reduced or absent (7 steps, CI = 14, RI = 14).

80. Pores of laterosensory canal of lower jaw: (0) six or less; (1) seven or more (8 steps, CI = 33, RI = 75).

81. Lateral covering of vertical canal of preopercle: (0) by musculature and/or infraorbitals; (1) absent, canal situated posteriorly to musculature and infraorbitals (Uj, 1990; Zanata and Vari, 2005) (8 steps, CI = 12, RI = 73).

82. Dorsal end of laterosensory canal of preopercle: (0) not overlapping anterodorsal projection of opercle; (1) overlapping, in lateral view, anterodorsal corner of opercle (Buckup, 1998; Zanata and Vari, 2005) (16 steps, CI = 50, RI = 90).

83. Anterior region of laterosensory canal of frontal: (0) contained completely by frontal to its anterior opening; (1) open in a chamber limited dorsally by frontal, and ventrally by lateral ethmoid (3 steps, CI = 33, RI = 92). The laterosensory canal of the frontal is narrow and contained completely by the frontal in most members from the outgroup, while in most characids it opens anteriorly in a chamber limited ventrally by the lateral ethmoid, and it is not continuous to the nasal laterosensory canal.

84. Epiphyseal branch of frontoparietal laterosensory canal: (0) present; (1) absent (3 steps, CI = 33, RI = 91). The laterosensory canal of the frontal usually have a medially orientated branching just dorsal to the epiphyseal bar, which opens in a pore situated just lateral to the cranial fontanel. In a group of species, instead, this branching and the corresponding opening are completely lacking.

85. Epiphyseal laterosensory canals: (0) both aligned with epiphyseal bar; (1) orientated obliquely, opening posteriorly to epiphyseal bar (2 steps, CI = 50, RI = 50). In most species the epiphyseal branch of the laterosensory system is aligned with the epiphyseal bar, while in some species this branch runs obliquely and opens in a pore situated conspicuously posterior than the epiphyseal bar.

86. Opening of epiphyseal laterosensory canals: (0) at margin of cranial fontanel; (1) canals extended dorsomedially by soft tissue, opening over the cranial fontanel (3 steps, CI = 33, RI = 50).

87. Laterosensory canal on sphenotic: (0) absent; (1) present (Buckup, 1993) (1 step, CI = 100, RI = 100).

88. Posterior branch of posttemporal laterosensory canal: (0) present; (1) absent (Toledo-Piza, 2007) (5 steps, CI = 20, RI = 84).

89. Curvature of lateral line: (0) approximately straight; (1) curve in abdominal region (Eigenmann, 1917) (3 steps, CI = 33, RI = 78).

90. Curvature of lateral line: (0) straight or not much curved, with posterior region orientated to middle caudal-fin rays; (1) much curved and ventrally situated, with posterior region running by ventral half of caudal peduncle and orientated to inferior lobe of caudal fin (Eigenmann, 1917; Benine, 2004; Zanata and Vari, 2005) (4 steps, CI = 25, RI = 50).

91. Lateral line: (0) complete; (1) interrupted (Eigenmann, 1917; Vari, 1995; Malabarba, 1998a; Weitzman and Menezes, 1998; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Bührnheim, 2006; Quevedo, 2006) (20 steps, CI = 5, RI = 57).

92. Canal of lateral line on caudal-fin membrane: (0) absent; (1) present (Malabarba, 1998b; Zanata and Vari, 2005; Lima, 2006; Bührnheim, 2006) (19 steps, CI = 5, RI = 70).

93. Length of caudal-fin canal of lateral line: (0) reaching only half of caudal-fin length; (1) almost reaching posterior margin of caudal fin (Bührnheim, 2006; Lima, 2006) (6 steps, CI = 17, RI = 67).

94. Anterior end of ascending process of maxilla: (0) with a conspicuous notch; (1) pointed or rounded (Lucena, 1993; Zanata and Vari, 2005) (2 steps, CI = 50, RI = 90).

95. Ventral margin of toothed region of maxilla: (0) roughly straight; (1) strongly concave (1 step, CI = 100, RI = 100).

96. Margins of toothed region of maxilla: (0) roughly parallel; (1) dorsally divergent (Lucena and Lucena, 2002) (7 steps, CI = 14, RI = 54).

97. Expansion of lamellar portion of maxilla just posterior to toothed region: (0) absent or not pronounced; (1) much pronounced (4 steps, CI = 25, RI = 57).

98. Tubules for passage of blood vessels on lamellar portion of maxilla: (0) a single tubule, parallel to dorsal margin of maxilla; (1) with an anterior branch, parallel to anterior margin of maxilla, reaching one third of its length; (2) anastomosed tubules (Zanata and Vari, 2005) (5 steps, CI = 40, RI = 91).

99. Length of maxilla relative to infraorbitals: (0) not reaching second infraorbital; (1) extended to second infraorbital (Buckup, 1998; Malabarba, 1998a; Bertaco, 2003; Zanata and Vari, 2005; Bührnheim, 2006; Quevedo, 2006) (2 steps, CI = 50, RI = 86).

100. Length of maxilla relative to dentary: (0) maxilla reaching posterior end of Meckelian cartilage; (1) maxilla not reaching posterior end of Meckelian cartilage (4 steps, CI = 25, RI = 84).

101. Ontogenetic lengthening of maxilla: (0) absent; (1) present (1 step, CI = 100, RI = 100).

102. Dorsal projection of maxilla lateral to second infraorbital: (0) absent; (1) present when mouth is closed, covering lateral surface of second supraorbital (1 step, CI = 100, RI = 100).

103. Interdigitations between premaxillae: (0) present; (1) absent (Lucena, 1993; Zanata and Vari, 2005) (5 steps, CI = 20, RI = 64).

104. Length of ascending process of premaxilla: (0) reaching at least one-third of nasal length; (1) reaching just anterior end of nasal (Lucena, 1993) (21 steps, CI = 5, RI = 69).

105. Alignment of ascending process of premaxilla: (0) aligned with medial margin of nasal; (1) medially displaced, separated from nasal (2 steps, CI = 50, RI = 86). The premaxillary ascending process is usually limited medially by the anterior process of the mesethmoid, and laterally by the nasal; in some species, the anterior process of the mesethmoid is comparatively narrower and the premaxillary ascending process is consequently displaced medially, resulting separated from the nasal.

106. Form of posterolateral portion of premaxilla: (0) with a notch; (1) with a pedicle expanded laterally to maxilla (Lucena, 1993; Zanata and Vari, 2005) (1 step, CI = 100, RI = 100).

107. Lateral ridge of anguloarticular: (0) absent; (1) present (Bührnheim, 2006) (6 steps, CI = 17, RI = 55).

108. Horizontal process of anguloarticular: (0) covered laterally by dentary only at anterior end; (1) covered extensively by dentary, which reaches posterior border of Meckelian cartilage (7 steps, CI = 14, RI = 80). The anguloarticular has two discernible regions, the anterodorsal and the horizontal processes. The horizontal process contains the support for the posterior end of Meckelian cartilage and is laterally overlapped by the dentary in different degrees. In most species the dentary is not extensively overlapping the horizontal process of the anguloarticular, not reaching the posterior end of Meckelian cartilage, while in others it covers laterally almost the entire horizontal process of the anguloarticular, including the area that overlaps the posterior end of the Meckelian cartilage.

109. Ventral margin of horizontal process of anguloarticular: (0) posteroventrally oblique to laterosensory canal of dentary in medial view; (1) perpendicular to laterosensory canal of dentary (9 steps, CI = 11, RI = 82). A tendon from the Aw section of the *adductor mandibulae* muscle inserts just anteroventrally to the margin of the anguloarticular (Winterbottom, 1974; Howes, 1976); in this region, the anguloarticular of some species has a conspicuous notch delimiting the attachment site for this tendon, and the ventral margin is situated transversal to the longitudinally orientated laterosensory canal of the dentary.

110. Dorsal position of coronomeckelian: (0) mainly lateral to Meckelian cartilage; (1) mainly dorsal to Meckelian cartilage (Serra, 2003) (15 steps, CI = 7, RI = 78).

111. Interdigitations between dentaries: (0) absent; (1) present (Uj, 1990; Lucena, 1993; Buckup, 1998; Malabarba, 1998a; Zanata and Vari, 2005; Lima, 2006) (1 step, CI = 100, RI = 100).

112. Form of interdigitations between dentaries: (0) simple bony lamellae; (1) undulate lamellae (Zanata and Vari, 2005) (2 steps, CI = 50, RI = 67).

113. Form and dentition of anterior end of dentary: (0) toothed and not depressed anteriorly; (1) edentulous and much depressed anteriorly (Roberts, 1974) (1 step, CI = 100, RI = 100).

114. Anteroventral notch of dentary: (0) absent; (1) present (Lucena, 1993; Buckup, 1998) (1 step, CI = 100, RI = 100).

115. Medial process of dentary bordering Meckelian cartilage dorsal and medially: (0) absent; (1) present (Moreira, 2002) (1 step, CI = 100, RI = 100).

116. Bony lamella covering dentary foramen laterally: (0) absent; (1) present (1 step, CI = 100, RI = 100). The dentary foramen is situated just anterior and dorsally to the anterior end of the Meckelian cartilage in most examined species, and serves as passage for nerves and blood vessels; this foramen is externally visible in most examined species, while it is laterally covered by a bony lamella in some members of the subfamily Characinae.

117. Longitudinal ridge covering laterosensory pores of dentary: (0) absent; (1) present (1 step, CI = 100, RI = 100). In most species the laterosensory canal of the dentary has three or more pores, which are laterally visible; in some characins these pores are covered by a longitudinal bony ridge that borders dorsally the laterosensory canal of the dentary, projecting ventrally to a position that covers laterally such pores.

118. Morphology of premaxillary, maxillary, and dentary teeth: (0) all teeth conical, caniniform or mamiliform; (1) some teeth multicuspitate or molariform (Fink and Fink, 1981; Uj, 1990; Lucena, 1993, 1998; Buckup, 1998) (7 steps, CI = 14, RI = 60).

119. Premaxillary, maxillary, and dentary teeth: (0) absent, or pedunculate only in some of these bones; (1) pedunculate and uniformly shaped (Malabarba, 1998a; Bührnheim, 2006) (16 steps, CI = 50, RI = 90).

120. Mamiliform teeth outside the mouth: (0) absent; (1) present (Lucena, 1993) (3 steps, CI = 34, RI = 60).

121. A pair of conical teeth in premaxilla with smaller teeth in middle: (0) absent; (1) present (Lucena, 1993) (4 steps, CI = 25, RI = 57).

122. Number of premaxillary rows of teeth: (0) one; (1) two or three (Eigenmann, 1917; Machado-Allison, 1983; Lucena, 1993; Buckup, 1998; Malabarba, 1998a; Moreira, 2002; Bertaco, 2003; Zanata and Vari, 2005; Lima, 2006; Bührnheim, 2006; Quevedo, 2006) (11 steps, CI = 9, RI = 64).

123. Number of premaxillary rows of teeth: (0) one or two; (1) three (Eigenmann, 1917; Machado-Allison, 1983; Lucena, 1993; Buckup, 1998; Malabarba, 1998a; Moreira, 2002; Bertaco, 2003; Zanata and Vari, 2005; Lima, 2006; Bührnheim, 2006; Quevedo, 2006) (4 steps, CI = 25, RI = 67).

124. Alignment of teeth from first premaxillary row: (0) aligned; (1) not aligned, with one or two teeth situated anteriorly to remaining ones (1 step, CI = 100, RI = 100).

125. Cusps of teeth from first premaxillary row: (0) one to three cusps; (1) five or more cusps (Benine, 2004) (11 steps, CI = 9, RI = 41).

126. Teeth from second premaxillary row: (0) molariform; (1) with aligned or curvedly disposed cusps; (2) with curvedly disposed cusps plus an anterior cusp (Zanata and Vari, 2005) (2 steps, CI = 100, RI = 100). This character is treated as unordered.

127. Alignment of cusps of medial teeth from second premaxillary row: (0) forming a semicircle anteriorly concave in ventral view; (1) forming a shallow arch or aligned in ventral view (Zanata and Vari, 2005) (7 steps, CI = 14, RI = 60).

128. Form of teeth from posterior premaxillary row: (0) with cusps forming an anteriorly orientated arch; (1) with aligned cusps, without an anterior concavity (Moreira, 2002) (6 steps, CI = 17, RI = 74).

129. Number of teeth on second premaxillary row: (0) four or less; (1) five or more (Eigenmann, 1917; Bertaco, 2003; Malabarba and Weitzman, 2003; Benine, 2004; Zanata and Vari, 2005; Bührnheim, 2006) (13 steps, CI = 8, RI = 60).
130. Number of teeth on second premaxillary row: (0) seven or less; (1) eight or more (Bührnheim, 2006) (8 steps, CI = 12, RI = 42).
131. Polymorphism of teeth from posterior premaxillary row: (0) absent; (1) present, with two medial teeth somewhat larger and usually separated from remaining ones by a gap (2 steps, CI = 50, RI = 83). In most species the teeth of the second premaxillary row are gradually decreasing from the medial one, and there are not conspicuous gaps between them; in some species, the two medial teeth are much larger and separated by a conspicuous gap from the third.
132. Number of replacement teeth rows on premaxilla: (0) one; (1) two or more (2 steps, CI = 50, RI = 50). Most species have one row of replacement premaxillary teeth, which become functional whether simultaneously or not; parodontids and hemiodontids have simultaneously, instead, several rows of replacement premaxillary teeth.
133. Fossa for second row of premaxillary replacement teeth: (0) absent; (1) present (4 steps, CI = 25, RI = 67). Teeth of the second premaxillary row usually have a completely extraosseous development, developing in the soft connective tissue just posterior to the premaxilla. In a small group of species, such teeth are formed into shallow cavities or fossae situated in the posterior surface of the premaxilla.
134. Maxillary teeth: (0) absent; (1) present (Lucena, 1993; Moreira, 2002; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Bührnheim, 2006; Lima, 2006) (15 steps, CI = 7, RI = 46).
135. Number of maxillary teeth: (0) only one, or absent; (1) two or more (Lucena, 1993; Weitzman and Menezes, 1998; Malabarba, 1998b; Vari and Harold, 2001; Benine, 2004; Bührnheim, 2006) (16 steps, CI = 6, RI = 67).
136. Number of maxillary teeth: (0) up to three; (1) four or more (Lucena, 1993; Weitzman and Menezes, 1998; Malabarba, 1998b; Vari and Harold, 2001; Benine, 2004; Bührnheim, 2006) (18 steps, CI = 6, RI = 72).
137. Extension of maxillary teeth: (0) not reaching half maxillary lamella; (1) reaching almost entire maxillary lamella (Eigenmann, 1917; Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003; Quevedo, 2006) (11 steps, CI = 9, RI = 73).
138. Number of cusps of anterior maxillary teeth: (0) conical, a single cusp; (1) three or more cusps (Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Bührnheim, 2006; Quevedo, 2006) (11 steps, CI = 9, RI = 63).
139. Number of cusps of anterior maxillary teeth: (0) up to three; (1) five or more cusps (Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Bührnheim, 2006; Quevedo, 2006) (17 steps, CI = 6, RI = 57).
140. Ontogenetic growth of conical teeth on maxilla: (0) absent; (1) present (Fink and Weitzman, 1974) (1 step, CI = 100, RI = 100).
141. Orientation of anterior dentary teeth: (0) orientated dorsal or anterodorsally; (1) orientated anteriorly, almost parallel to main axis of dentary (2 steps, CI = 50, RI = 50).
142. Size and number of anterior dentary teeth: (0) four or five relatively broad teeth in front of dentary; (1) eight or more small and slender teeth in front of dentary (4 steps, CI = 25, RI = 57).
143. Second row of dentary teeth: (0) present; (1) absent (Uj, 1990; Lucena, 1993; Backup, 1998; Malabarba, 1998b; Moreira, 2002; Serra, 2003; Lima, 2006) (11 steps, CI = 9, RI = 62).
144. Symphyseal dentary teeth: (0) absent; (1) present (Uj, 1990; Lucena, 1993; Malabarba, 1998b; Serra, 2003; Zanata and Vari, 2005; Lima, 2006) (3 steps, CI = 33, RI = 83).
145. Articulation between dentary teeth: (0) absent; (1) present, with processes and fossae (Machado-Allison, 1983) (1 step, CI = 100, RI = 100).
146. Position of dentary anterior teeth: (0) in margin of dentary; (1) internally displaced, with dentary forming an anterior ridge (not informative).
147. Separation between posterior dentary teeth: (0) less than width of these teeth; (1) more than width of these teeth (4 steps, CI = 25, RI = 57).
148. Heterogeneity of dentary teeth: (0) absent, teeth gradually decreasing; (1) anterior teeth larger, with five or more cusps, and posterior teeth conical (Eigenmann, 1917; Serra, 2003; Zanata and Vari, 2005; Bührnheim, 2006) (13 steps, CI = 8, RI = 45).
149. Foramen on articular condyle of quadrate: (0) absent; (1) present (Lucena, 1993) (10 steps, CI = 10, RI = 50).
150. Form of quadrate: (0) with ventral portion longer than anterodorsal one; (1) with anterodorsal portion equal or longer than ventral one (Lucena, 1993; Lucena and Menezes, 1998; Moreira, 2002; Bertaco, 2003; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Quevedo, 2006) (7 steps, CI = 14, RI = 65).
151. Posterior extension of ventral process of quadrate: (0) reaching vertical through posterior margin of symplectic; (1) not reaching this margin (27 steps, CI = 4, RI = 62). The quadrate has a ventral process articulating laterally with the horizontal arm of the preopercle. In some species this process is extended equal or more posteriorly than the symplectic, while in others it does not reach the posterior end of the symplectic.
152. Longitudinal ridge in quadrate bordering ventrally and, in some measure, laterally the *adductor mandibulae* muscle: (0) absent; (1) present (Moreira, 2002) (16 steps, CI = 50, RI = 90).
153. Articulation between quadrate and anguloarticular: (0) anterior or at vertical through lateral ethmoid; (1) posterior to lateral ethmoid (Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003; Zanata and Vari, 2005; Quevedo, 2006) (3 steps, CI = 33, RI = 71).
154. Articulation between quadrate and anguloarticular: (0) anterior or at vertical through middle eye; (1) posterior to middle of eye (Lucena, 1993; Bertaco, 2003; Serra, 2003) (8 steps, CI = 12, RI = 68).
155. Articulation between ventral margin of metapterygoid and posterodorsal margin of quadrate: (0) absent; (1) present (Lucena, 1993; Moreira, 2002; Bertaco, 2003; Serra, 2003) (11 steps, CI = 9, RI = 44).
156. Form of ectopterygoid: (0) elongated; (1) triangular, much broadened anteriorly; (2) approximately square (not informative).
157. Form of anterior tip of ectopterygoid: (0) broad, articulating extensively with palatine and connected to neurocranium by ligaments; (1) slender, articulating only to lateral margin of palatine, and lacking ligaments to neurocranium (Zanata and Vari, 2005) (5 steps, CI = 20, RI = 56).
158. Dorsal process of ectopterygoid orientated to lateral ethmoid: (0) absent; (1) present (1 step, CI = 100, RI = 100).
159. Ectopterygoid teeth row: (0) absent; (1) present (Lucena, 1993; Vari, 1995; Backup, 1998; Moreira, 2002; Benine, 2004; Bührnheim, 2006; Lima, 2006; Quevedo, 2006; Toledo-Piza, 2007) (7 steps, CI = 14, RI = 33).
160. Patch of ectopterygoid teeth: (0) absent; (1) present (Lucena and Menezes, 1998; Toledo-Piza, 2000; Toledo-Piza, 2008) (2 steps, CI = 50, RI = 0).
161. Position of longitudinal cartilage dorsal to ectopterygoid: (0) limited medially by endopterygoid; (1) displaced laterally, separated from medial margin of endopterygoid (5 steps, CI = 20, RI = 64). A longitudinal cartilage is situated just dorsal to the ectopterygoid; in most species this cartilage runs along the articulation of this bone with the endopterygoid, while in others it is relatively displaced laterally, not contacting the endopterygoid.
162. Contact between ectopterygoid and anterodorsal region of quadrate: (0) present; (1) absent (Vari and Harold, 2001; Moreira, 2002; Serra, 2003; Benine, 2004) (9 steps, CI = 11, RI = 70).
163. Anterior extension of interopercle: (0) surpassing horizontal arm of preopercle; (1) not surpassing horizontal arm of preopercle (6 steps, CI = 17, RI = 67). The horizontal arm of the preopercle is articulating dorsally with the interopercle. In most species the anterior end of the interopercle is situated more anteriorly than the preopercle, while in others the preopercle reaches a more anterior position.

164. Posterior expansion of interopercle: (0) absent; (1) present, abrupt (6 steps, CI = 17, RI = 55). The interopercle is gradually deeper to its posterior margin; in most species this deepening is gradual and its posterior margin does not overlap the opercle, while in others the posterior region of the interopercle is much deeper, overlapping laterally the anteroventral margin of the opercle.

165. Endopterygoid teeth: (0) absent; (1) present (Uj, 1990; Lucena, 1993, 1998; Vari, 1995; Buckup, 1998; Lucena and Menezes, 1998; Toledo-Piza, 2000, 2007; Moreira, 2002; Bührnheim, 2006) (1 step, CI = 100, RI = 100).

166. Anterodorsal lobe of metapterygoid orientated to endopterygoid: (0) absent, or reduced and orientated dorsally; (1) present, conspicuous and orientated anteriorly (Malabarba, 1998b) (1 step, CI = 100, RI = 100).

167. Form of metapterygoid-quadrata fenestra: (0) rounded or ovate, anteriorly limited by anterodorsal region of quadrata; (1) anteriorly collapsed by convergence of metapterygoid and ventral region of quadrata (1 step, CI = 100, RI = 100).

168. Foramen in posterior region of metapterygoid: (0) absent; (1) present, contained by metapterygoid or limited partially by a cartilage; (2) an incomplete arch, limited posteriorly by hyomandibular (Lucena, 1993; Vari and Harold, 2001; Moreira, 2002; Serra, 2003; Benine, 2004; Lima, 2006; Quevedo, 2006) (6 steps, CI = 33, RI = 88).

169. Posteriorly directed radial striae from articular region of opercle: (0) absent; (1) present (2 steps, CI = 50, RI = 67). The opercle has a medial longitudinal ridge where the *adductor operculi* attaches; in some species there are, additionally, several ridges orientated radially from the articular region of the opercle, which apparently are not associated with muscles.

170. Length of medial bony ridge of opercle: (0) 60% or more than opercular length; (1) less than half opercular length (15 steps, CI = 7, RI = 39).

171. Ethmopalatine cartilage: (0) absent or reduced in size; (1) present, conspicuous (Fink and Fink, 1981) (15 steps, CI = 7, RI = 58).

172. Relative length of palatine: (0) approximately half length of ectopterygoid, or less; (1) longer than half length of ectopterygoid (Moreira, 2002) (16 steps, CI = 6, RI = 78).

173. Palatine foramen: (0) absent or reduced in size; (1) present, very conspicuous (Serra and Langeani, 2006) (2 steps, CI = 50, RI = 50).

174. Form of posteroventral corner of proopercle: (0) acute; (1) rounded (Lucena, 1993) (1 step, CI = 100, RI = 100).

175. Suprapreopercle: (0) fused to preopercle; (1) autogenous, separated from preopercle (Uj, 1990; Lucena, 1993; Buckup, 1998; Benine, 2004) (7 steps, CI = 14, RI = 40).

176. Bony lamellae bordering laterosensory canal of suprapreopercle: (0) absent; (1) present (2 steps, CI = 50, RI = 67).

177. Anterior projection of anterior ceratohyal, articulating laterally with hypohyals: (0) absent or much reduced; (1) present, reaching half length of hypohyals (Uj, 1990) (1 step, CI = 100, RI = 100).

178. Hyoid artery: (0) contained completely within anterior ceratohyal in its passage from posterior ceratohyal to hypohyals; (1) emerging from anterior ceratohyal near its articulation with posterior ceratohyal (Buckup, 1998; Benine, 2004; Zanata and Vari, 2005) (1 step, CI = 100, RI = 100).

179. Posterior margin of anterior ceratohyal: (0) smooth, without notches; (1) with notches for articulation of branchiostegal rays (Lucena, 1998; Bührnheim, 2006) (7 steps, CI = 14, RI = 78).

180. Notches in posterior margin of anterior ceratohyal: (0) absent, or two, corresponding with anterior two branchiostegal rays; (1) with a third notch, for third branchiostegal ray. (1 step, CI = 100, RI = 100). The anterior ceratohyal usually has two notches for the articulation of the two medial branchiostegal rays; in some cheirodontins, there is a third notch in the region where the third branchiostegal ray attaches.

181. Articulation between ceratohyals: (0) synchondral, without bony interdigitations; (1) with bony interdigitations between anterior and

posterior ceratohyals (Vari, 1995; Lima, 2006) (3 steps, CI = 33, RI = 50).

182. First basibranchial: (0) absent or much reduced, not articulating anteriorly with basihyal; (1) developed, articulating anteriorly with basihyal (2 steps, CI = 50, RI = 83).

183. Contact between first and second basibranchials: (0) absent; (1) present, through dorsal bony lamellae (10 steps, CI = 10, RI = 50).

184. Bony lamellae dorsal to second and third basibranchials: (0) absent; (1) present. (Toledo-Piza, 2007) (18 steps, CI = 6, RI = 29).

185. Bony lamella dorsal to fourth basibranchial: (0) present; (1) absent (Lucena, 1993; Vari and Harold, 2001; Moreira, 2002; Benine, 2004; Bührnheim, 2006; Lima, 2006; Toledo-Piza, 2007) (16 steps, CI = 6, RI = 69).

186. Fourth basibranchial: (0) completely cartilaginous; (1) ossified (1 step, CI = 100, RI = 100). The fourth basibranchial is cartilaginous in most examined species, although it is usually limited dorsally by a bony lamella which is apparently a serial homologous of the edentulous basihyal plate considered in the character 189. In several species, instead, the main body of the fourth basibranchial is ossified.

187. Teeth on lamella dorsal to fourth basibranchial: (0) absent; (1) present (Lucena and Menezes, 1998; Toledo-Piza, 2007) (2 steps, CI = 50, RI = 0).

188. Cartilages anterior to basihyal: (0) one block of cartilage, or two, but anterior one much reduced; (1) two well developed blocks of cartilage (Vari, 1995) (20 steps, CI = 5, RI = 30).

189. Edentulous basihyal plate: (0) absent; (1) present (Vari, 1983; Zanata and Vari, 2005; Lima, 2006) (8 steps, CI = 12, RI = 71).

190. Anterior development of basihyal: (0) broadly surpassing anterior margin of hypohyals; (1) reduced, slightly surpassing this margin (2 steps, CI = 50, RI = 71). The basihyal is usually the most anterior element of the hyoid arch; in some species, instead, this bone is greatly reduced, and the basihyals are the most anteriorly situated elements of the hyoid arch.

191. Anterior expansion of basihyal: (0) slender, with anterior margin much reduced relative to its length; (1) expanded, with anterior margin with approximately two thirds of its length (Serra, 2003) (7 steps, CI = 14, RI = 25).

192. Rows of gill rakers on first ceratobranchial: (0) one; (1) two (Lucena, 1993, 1998; Serra, 2003; Bührnheim, 2006; Toledo-Piza, 2007) (18 steps, CI = 6, RI = 58).

193. Rows of gill rakers on second ceratobranchial: (0) one; (1) two (Lucena, 1998; Serra, 2003; Toledo-Piza, 2007) (22 steps, CI = 5, RI = 65).

194. Rows of gill rakers on third and fourth ceratobranchials: (0) one; (1) two (Toledo-Piza, 2007) (not informative).

195. Number of gill rakers on first ceratobranchial: (0) 16 or more; (1) 15 or less (Malabarba, 1998b; Serra, 2003; Bührnheim, 2006) (15 steps, CI = 7, RI = 44).

196. Number of gill rakers on first ceratobranchial: (0) 11 or more; (1) ten or less (Malabarba, 1998b; Serra, 2003; Bührnheim, 2006) (28 steps, CI = 4, RI = 39).

197. Form of first ceratobranchial gill rakers: (0) pointed, not anteroposteriorly compressed; (1) laminary, much compressed, perpendicular to ceratobranchial; (2) short, broad and strongly denticulated (Uj, 1990; Lucena, 1993; Lucena and Menezes, 1998; Toledo-Piza, 2000, 2007) (2 steps, CI = 100, RI = 100).

198. Form of first ceratobranchial anterior gill rakers: (0) not fused; (1) with fused bases, forming plates extensively articulated with ceratobranchial (1 step, CI = 100, RI = 100).

199. Lateral base of gill rakers: (0) slender; (1) broad and laminar, at least in anteriormost gill rakers (5 steps, CI = 20, RI = 69). The gill rakers have two bases articulating them with the corresponding bone. In most species both bases of the first ceratobranchial gill rakers are slender and pointed, while in others the lateral base is laminary.

200. Form and ossification degree of first ceratobranchial gill rakers: (0) laminar, not ossified distal region; (1) rather strong, completely ossified distal region (6 steps, CI = 17, RI = 67).

201. Denticles on gill rakers: (0) present; (1) absent (Malabarba, 1998b; Serra, 2003; Bührnheim, 2006) (10 steps, CI = 10, RI = 61).
202. Distribution of denticles on gill rakers: (0) restricted to margins, or absent; (1) on entire surface of gill rakers (19 steps, CI = 5, RI = 53). In most species the gill-rakers denticles are aligned on their anterior and posterior margins, while in some species these denticles are spread over all their surface.
203. Rows of gill rakers on first epibranchial: (0) one; (1) two (Lucena, 1998) (2 steps, CI = 50, RI = 50).
204. Form of fifth ceratobranchial dentigerous plate: (0) rounded, with a posterior notch; (1) elongated, without posterior notch (Vari and Harold, 2001; Moreira, 2002) (7 steps, CI = 14, RI = 45).
205. Teeth on fifth ceratobranchial: (0) present; (1) absent (Vari, 1983) (1 step, CI = 100, RI = 100).
206. Teeth on third pharyngobranchial: (0) present; (1) absent (Lucena, 1998; Vari and Harold, 2001; Moreira, 2002; Serra, 2003; Bührnheim, 2006) (7 steps, CI = 14, RI = 40).
207. Teeth on fourth pharyngobranchial: (0) present; (1) absent (Buckup, 1998) (1 step, CI = 100, RI = 100).
208. Teeth on fifth pharyngobranchial: (0) present; (1) absent (Vari, 1983) (1 step, CI = 100, RI = 100).
209. Contact between fourth and fifth pharyngobranchial dentigerous plates: (0) absent; (1) present (Vari, 1983; Uj, 1990; Buckup, 1998) (1 step, CI = 100, RI = 100).
210. Interhyal: (0) present; (1) absent (2 steps, CI = 50, RI = 0).
211. Length of interhyal: (0) shorter than one third of symplectic length; (1) equal or longer than one half of symplectic length (4 steps, CI = 25, RI = 67). The interhyal is a rather columnar bone articulating the posterior ceratohyal with the suspensorium, which is present in almost all examined species. In most species this bone is reduced, being much shorter than the symplectic, while in others, the interhyal is relatively longer.
212. Number of branchiostegal rays: (0) three; (1) four or five (Vari, 1995; Lucena, 1998; Lucena and Menezes, 1998; Toledo-Piza, 2000; Zanata and Vari, 2005; Lima, 2006) (5 steps, CI = 20, RI = 0).
213. Number of branchiostegal rays: (0) three or four; (1) five (Vari, 1995; Lucena, 1998; Toledo-Piza, 2000, 2007; Zanata and Vari, 2005; Lima, 2006) (5 steps, CI = 20, RI = 0).
214. Anterior end of branchiostegal rays: (0) broadened near their articulation with ceratohyals; (1) slender in this region (Benine, 2004) (3 steps, CI = 33, RI = 78).
215. Attachment of first branchiostegal ray: (0) in proximal third of anterior ceratohyal; (1) in middle of anterior ceratohyal, or posteriorly to this point (1 step, CI = 100, RI = 100).
216. Distance between attachment site of first and second branchiostegal rays: (0) equal or shorter than distance between second and third ones; (1) longer than distance between second and third branchiostegal rays (1 step, CI = 100, RI = 100).
217. Number of branchiostegal rays attached to posterior ceratohyal: (0) one; (1) two (Vari, 1995; Lucena, 1998; Lucena and Menezes, 1998; Toledo-Piza, 2000, 2007) (1 step, CI = 100, RI = 100).
218. Form and articulation of neural pedicle of third vertebra: (0) well developed pedicle, articulating synchondrally with neural complex; (1) much reduced, without an articular surface with neural complex (1 step, CI = 100, RI = 100). In the examined outgroups and basal characids, the neural complex of the Weberian apparatus is synchondrally articulated with the neural pedicles of the third and fourth vertebrae; in a diverse group of characids, the neural pedicle of the third vertebra is much reduced and the neural complex is articulated almost exclusively with the pedicle of the fourth vertebra.
219. Development of transverse process of third vertebra neural arch: (0) not reaching anterior margin of tripus; (1) well developed, surpassing anterior margin of tripus (Vari, 1995; Zanata and Vari, 2005) (14 steps, CI = 7, RI = 24).
220. Ascending process of neural pedicle of third vertebra: (0) absent; (1) present, reaching or not neural complex (Uj, 1990; Lucena, 1993) (3 steps, CI = 33, RI = 83).
221. Dorsal development of dorsal process of third vertebra neural pedicle: (0) not extensively overlapping neural complex; (1) conspicuously overlapping neural complex (Uj, 1990; Lucena, 1993; Buckup, 1998) (2 steps, CI = 50, RI = 96).
222. Neural arch and vertebral centrum of fourth vertebra: (0) not fused, autogenous fourth neural arch; (1) fused each other (Buckup, 1998) (1 step, CI = 100, RI = 100).
223. Anteriorly directed spine at base of first rib: (0) absent; (1) present (Lucena, 1993) (3 steps, CI = 33, RI = 60).
224. Laminary bony ridge on dorsal margin of abdominal ribs: (0) absent; (1) present (Benine, 2004) (3 steps, CI = 33, RI = 33).
225. Abdominal ribs on anterior caudal vertebrae: (0) absent; (1) present, associated to first and occasionally second caudal vertebrae (1 step, CI = 100, RI = 100). Pleural ribs are associated only with abdominal and transitional vertebrae in most species, while in the examined serrasalmids, the posterior ribs are associated with vertebrae having a complete haemal spine, which characterizes caudal vertebrae.
226. Proportion of precaudal and caudal vertebrae: (0) two or more precaudal than caudal vertebrae; (1) equal or more caudal than precaudal vertebrae (Lucena, 1993; Moreira, 2002) (7 steps, CI = 14, RI = 67).
227. Number of vertebrae: (0) 40 or less; (1) 41 or more (9 steps, CI = 11, RI = 50).
228. Number of “type I” transitional vertebrae, with haemal processes but without haemal spine: (0) four or more; (1) three or less (Uj, 1990; Zanata and Vari, 2005) (8 steps, CI = 12, RI = 71).
229. Presence of “type II” transitional vertebrae, with haemal canal but without haemal spine: (0) present, in variable number; (1) absent (19 steps, CI = 5, RI = 56). Two kinds of transitional vertebrae are recognized here, both lacking a haemal spine; the “type I” vertebrae have haemal processes but not necessarily a closed haemal canal, while the “type II” have also a closed haemal canal. The presence of vertebrae with a developed haemal canal but lacking a haemal spine is coded in this character.
230. Margin of first pectoral ray in adult specimens: (0) not serrated; (1) conspicuously serrated (Bertaco, 2003) (3 steps, CI = 33, RI = 60).
231. Base of second pectoral ray: (0) expanded, partially overlapping base of first pectoral ray, in medial view; (1) reduced, similar to that of posterior rays (Zanata and Vari, 2005) (10 steps, CI = 10, RI = 69).
232. Anterior margin of cleithrum: (0) slightly sinuous; (1) with an anterior angle expanding laterally attachment site for *sternohyoideus* muscle (Uj, 1990; Lucena, 1998; Toledo-Piza, 2007) (3 steps, CI = 33, RI = 60).
233. Form of posterior margin of cleithrum: (0) convex or slightly sinuous just dorsal to pectoral-fin insertion; (1) with a notch just anterior to pectoral-fin insertion (Uj, 1990; Lucena, 1993, 1998; Buckup, 1998; Moreira, 2002; Toledo-Piza, 2007) (3 steps, CI = 33, RI = 50).
234. Posterior margin of cleithrum: (0) without a concavity ventral to first postcleithrum; (1) with a concavity (Benine, 2004) (20 steps, CI = 5, RI = 74).
235. Posterior margin of cleithrum: (0) with a concavity not pronounced or lacking; (1) a markedly concave margin, almost forming a straight angle (Benine, 2004) (10 steps, CI = 10, RI = 31).
236. Medial laminar expansion at dorsal tip of cleithrum: (0) absent; (1) present (Malabarba, 1998b) (1 step, CI = 100, RI = 100).
237. Dorsal development of cleithrum: (0) much extended dorsally to mesocoracoid; (1) mesocoracoid almost reaching dorsal tip of cleithrum (Lucena and Menezes, 1998; Malabarba, 1998b; Toledo-Piza, 2007) (2 steps, CI = 50, RI = 50).
238. Development of medial lamella of coracoid: (0) not expanded; (1) expanded as a keel (Malabarba, 1998b; Moreira, 2002) (6 steps, CI = 17, RI = 29).
239. Bony ridge of coracoid between base of mesocoracoid and ventral margin of interosseous space: (0) absent; (1) present (3 steps, CI = 33, RI = 94). A laterally orientated longitudinal ridge of the surface of the coracoid between the interosseous space (*sensu* Starks,

1930) and the mesocoracoid was observed in some outgroups and basal characids, while it is absent in most distal characids.

240. Anterior extension of coracoid ventral lamella: (0) reaching cleithrum; (1) not reaching cleithrum (Uj, 1990; Lucena, 1993; Buckup, 1998) (not informative).

241. Ventral extension of coracoid lamella: (0) reaching ventral margin of cleithrum; (1) not reaching ventral margin of cleithrum, which is ventrally projected in relation to coracoid (2 steps, CI = 50, RI = 67). In most species the coracoid lamella is extended ventrally to the articulation between the contralateral cleithra; in some species, instead, the coracoid lamella is not reaching the ventral margin of the articulation between the cleithra, which result the most ventral bones of the pectoral girdle.

242. Anterior limit of interosseous space: (0) formed by dorsal margin of coracoid medial lamella and dorsal margin of cleithrum; (1) formed by dorsal margin of coracoid medial lamella and an oblique bony ridge just ventral to dorsal margin of cleithrum (2 steps, CI = 50, RI = 86). In most species the interosseous space is completely delimited by the coracoid medial lamella and the dorsal margin of the cleithrum. In some species from the outgroup, the anterior margin of the interosseous space is not limited by these structures, but by an oblique bony ridge in the medial surface of the cleithrum; in such cases, the anterior margin of the interosseous space appears to be “open”, given that it is not delimited by the same structures that form the remaining margins.

243. Coracoid foramen: (0) absent or reduced to a small pore; (1) well developed (Lucena, 1993; Malabarba, 1998b; Bertaco, 2003; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 62).

244. Process of scapula forming anterior border of scapular foramen: (0) present; (1) absent (Lucena, 1993; Vari and Harold, 2001; Zanata and Vari, 2005) (10 steps, CI = 10, RI = 31).

245. Articulation between a descendent process of mesocoracoid and dorsal margin of scapula: (0) absent or reduced; (1) present, with conspicuous articular margins (Vari and Harold, 2001) (4 steps, CI = 25, RI = 40).

246. Ventral articulation of mesocoracoid: (0) anteriorly with coracoid and posteriorly with scapula; (1) only with coracoid (not informative). The mesocoracoid is usually articulated ventrally with the coracoid and the scapula; in *Prionobrama paraguayensis*, among the examined species, the mesocoracoid articulates only with the scapula.

247. First postcleithrum: (0) present; (1) absent (Vari and Harold, 2001; Zanata and Vari, 2005; Quevedo, 2006) (2 steps, CI = 50, RI = 80).

248. Second postcleithrum: (0) present; (1) absent (Lucena, 1993; Vari, 1995; Buckup, 1998; Lucena and Menezes, 1998; Malabarba, 1998b; Toledo-Piza, 2000; Moreira, 2002; Zanata and Vari, 2005; Quevedo, 2006) (5 steps, CI = 20, RI = 43).

249. Third postcleithrum: (0) present; (1) absent (Lucena, 1993; Vari, 1995; Buckup, 1998; Lucena and Menezes, 1998; Malabarba, 1998b; Toledo-Piza, 2000; Zanata and Vari, 2005; Quevedo, 2006; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 38).

250. Form of third postcleithrum: (0) slender, without associated lamella; (1) with a posterior lamella (Bertaco, 2003; Cardoso, 2003a; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Quevedo, 2006; Toledo-Piza, 2007) (10 steps, CI = 10, RI = 78).

251. Dorsal development of third postcleithrum: (0) well projected dorsal to posterior region of scapula; (1) not projected dorsally to posterior region of scapula (3 steps, CI = 33, RI = 50).

252. Position of ventral end of posttemporal: (0) anterior to lateral margin of epioccipital; (1) lateral or posterior to epioccipital (Benine, 2004; Bührnheim, 2006) (10 steps, CI = 10, RI = 44).

253. Position of ventral end of posttemporal: (0) overlapping laterally, or anterior to lateral margin of epioccipital; (1) posterior to epioccipital (Benine, 2004; Bührnheim, 2006) (12 steps, CI = 8, RI = 61).

254. Ventral exit of supracleithrum laterosensory canal: (0) medial, laterally covered by a continuous posterior lamella of supracleithrum;

(1) posterior, just ventral to lamella of supracleithrum (Serra, 2003) (4 steps, CI = 25, RI = 92).

255. Fusion between posttemporal and supracleithrum: (0) absent; (1) present (Castro, 1984) (1 step, CI = 100, RI = 100).

256. First pelvic-fin ray: (0) not branched; (1) branched (Bertaco, 2003) (not informative).

257. Relative length of males first pelvic-fin ray: (0) not projected; (1) projected from remaining rays (Malabarba, 1998a; Bührnheim, 2006) (2 steps, CI = 50, RI = 67).

258. Number of branched pelvic-fin rays: (0) six or less; (1) seven or more (Lucena, 1993; Buckup, 1998; Malabarba, 1998a; Moreira, 2002; Bertaco, 2003; Benine, 2004; Zanata and Vari, 2005; Quevedo, 2006) (18 steps, CI = 6, RI = 48).

259. Number of branched pelvic-fin rays: (0) seven or less; (1) eight or more (Lucena, 1993; Buckup, 1998; Moreira, 2002; Bertaco, 2003; Zanata and Vari, 2005; Quevedo, 2006) (4 steps, CI = 25, RI = 70).

260. Pelvic bone: (0) not bifurcated anteriorly; (1) bifurcated, with a conspicuous notch (Uj, 1990; Buckup, 1998; Moreira, 2002; Zanata and Vari, 2005) (2 steps, CI = 50, RI = 50).

261. Articulation between contralateral pelvic bones: (0) through ligaments; (1) with bony interdigitations between ischiatic processes (Castro, 1984; Uj, 1990) (3 steps, CI = 33, RI = 33).

262. Anterior extension of pelvic-bone principal axis: (0) not projected anterior to lateral lamellae; (1) projected anterior to lateral lamellae of pelvic bone (Malabarba, 1998b; Zanata and Vari, 2005; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 38).

263. Anterior tip of pelvic bone: (0) rounded and limited by a small cartilage; (1) pointed and lacking an associated cartilage, frequently projected outside body wall (Zanata, 1997) (1 step, CI = 100, RI = 100).

264. Broadened axes of pelvic bone: (0) two anteriorly divergent axes; (1) a single axis (2 steps, CI = 50, RI = 92). In most species there is a single cylindrical longitudinal axis in the pelvic bone and associated lateral lamellae; in some members of the outgroup there is an additional anteriorly divergent axis which is formed by the broadened surface of the medial lamella of the pelvic bone.

265. Relative position of dorsal-fin anterior insertion: (0) anterior or at vertical through pelvic-fin origin; (1) posterior to vertical through pelvic-fin origin (Malabarba, 1998b) (12 steps, CI = 8, RI = 59).

266. Dorsal-fin rays articulated with first dorsal pterygiophore: (0) two; (1) three or four (Lucena, 1998; Serra, 2003; Zanata and Vari, 2005) (17 steps, CI = 6, RI = 77).

267. Anteriorly directed spine formed by first dorsal-fin ray: (0) absent; (1) present (Reis, 1989) (1 step, CI = 100, RI = 100).

268. Dorsal fin of adult males: (0) not extended posteriorly; (1) with anterior rays extended posteriorly to a position close to adipose fin (Bertaco, 2003; Cardoso, 2003a) (4 steps, CI = 25, RI = 40).

269. Length of last unbranched dorsal-fin ray in adult males: (0) not projected; (1) projected as a filament (Malabarba, 1998a; Bührnheim, 2006) (2 steps, CI = 50, RI = 50).

270. Number of branched dorsal-fin rays: (0) eight or less; (1) nine or more (Machado-Allison, 1983; Bertaco, 2003; Malabarba and Weitzman, 2003; Benine, 2004; Quevedo, 2006) (10 steps, CI = 10, RI = 71).

271. Relative length of anterior dorsal-fin rays: (0) not reaching tip of posterior rays when adpressed; (1) reaching tip of posterior rays when adpressed (5 steps, CI = 20, RI = 60). In most species the anterior rays of the dorsal fin are relatively longer than the posterior ones, reaching a more posterior position when these rays are adpressed; in some members of the outgroup the posterior dorsal-fin rays are comparatively longer and the adpressed anterior rays do not reach the tip of the posterior ones.

272. Number of dorsal-fin rays on last pterygiophore: (0) one; (1) two, adnates (Lucena, 1993; Buckup, 1998; Moreira, 2002; Zanata and Vari, 2005) (5 steps, CI = 20, RI = 73).

273. Myorhabdoi: (0) absent; (1) present (Toledo-Piza, 2000) (2 steps, CI = 50, RI = 50).

274. Position of anteriormost epineurals: (0) lateral to fourth or fifth vertebra; (1) from cranium or posttemporal fossa (Lucena and Menezes, 1998; Moreira, 2002; Zanata and Vari, 2005; Toledo-Piza, 2007) (7 steps, CI = 14, RI = 40).
275. Predorsal spine formed by first dorsal pterygiophore: (0) absent; (1) present (Machado-Allison, 1983) (1 step, CI = 100, RI = 100).
276. Number of dorsal pterygiophores: (0) nine; (1) 10 or more (Lucena, 1993; Bertaco, 2003; Zanata and Vari, 2005) (10 steps, CI = 10, RI = 75).
277. Number of dorsal pterygiophores: (0) 10 or less; (1) 11 or more (Lucena, 1993; Bertaco, 2003; Zanata and Vari, 2005) (10 steps, CI = 10, RI = 36).
278. Number of dorsal pterygiophores: (0) 11 or less; (1) 12 or more (Lucena, 1993; Bertaco, 2003; Zanata and Vari, 2005) (5 steps, CI = 20, RI = 33).
279. Supraneural anterior to neural spine of fourth vertebra: (0) absent or much reduced; (1) present, vertically elongated (Lucena, 1993; Buckup, 1998; Moreira, 2002; Serra, 2003; Benine, 2004; Zanata and Vari, 2005; Lima, 2006; Quevedo, 2006; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 68).
280. Number of supraneurals: (0) four or less; (1) five or more (Moreira, 2002; Serra, 2003; Benine, 2004) (14 steps, CI = 7, RI = 66).
281. Number of supraneurals: (0) seven or less; (1) eight or more (Moreira, 2002; Serra, 2003; Lima, 2006; Quevedo, 2006) (12 steps, CI = 8, RI = 56).
282. Bony lamellae associated to supraneurals: (0) absent or reduced; (1) wider than main axis of supraneurals (Moreira, 2002; Serra, 2003; Benine, 2004; Lima, 2006) (19 steps, CI = 5, RI = 70).
283. Position of last supraneural: (0) two or less vertebrae in front of first dorsal pterygiophore; (1) more than two vertebrae in front (6 steps, CI = 17, RI = 29). In most species, the last supraneural is just anterior to the first dorsal-fin pterygiophore; in some species, instead, the most posterior supraneural is situated two or three vertebrae anterior to the first dorsal-fin pterygiophore.
284. Anal-fin position: (0) posterior or almost posterior to vertical line through last dorsal-fin ray; (1) ventral to dorsal fin (Eigenmann, 1917) (7 steps, CI = 14, RI = 68).
285. Number of unbranched anal-fin rays: (0) three or less; (1) four or more (Zanata and Vari, 2005; Lima, 2006) (6 steps, CI = 17, RI = 77).
286. Number of branched anal-fin rays: (0) 10 or less; (1) 11 or more (Uj, 1990; Lucena, 1993; Buckup, 1998; Serra, 2003; Benine, 2004; Lima, 2006) (2 steps, CI = 50, RI = 92).
287. Number of branched anal-fin rays: (0) 17 or less; (1) 18 or more (Lucena, 1993; Weitzman and Menezes, 1998; Moreira, 2002; Serra, 2003; Benine, 2004; Lima, 2006) (8 steps, CI = 12, RI = 76).
288. Number of branched anal-fin rays: (0) 24 or less; (1) 25 or more (Malabarba, 1998b; Moreira, 2002; Serra, 2003; Benine, 2004) (18 steps, CI = 6, RI = 69).
289. Number of branched anal-fin rays: (0) 34 or less; (1) 35 or more (Lucena, 1993; Buckup, 1998; Malabarba, 1998b; Moreira, 2002; Serra, 2003; Benine, 2004; Quevedo, 2006) (12 steps, CI = 8, RI = 69).
290. Form and length of anterior anal-fin rays: (0) similar to posterior ones; (1) longer and compressed laterally (Bürrnheim, 2006) (2 steps, CI = 50, RI = 0).
291. Number of rays on last anal pterygiophore: (0) two, adnates; (1) one (2 steps, CI = 50, RI = 0).
292. Anterior notch on first anal pterygiophore: (0) absent; (1) present (2 steps, CI = 50, RI = 50). The first anal pterygiophore is anteriorly margined by a bony lamella; in most species this lamella is entire, while it is anteriorly notched in the parodontids and *Markiananigripinnis*.
293. Number of anal pterygiophores anterior to first haemal spine: (0) three or less; (1) four or more (Lucena, 1998) (4 steps, CI = 25, RI = 50).
294. Proximal and medial anal pterygiophores: (0) fused on anterior five pterygiophores; (1) fused in most pterygiophores; (2) medial pterygiophores absent or completely fused with proximal ones (Benine, 2004; Zanata and Vari, 2005) (10 steps, CI = 20, RI = 69).
295. Lateral lamellae on anterior anal pterygiophores: (0) absent; (1) present (Zanata and Vari, 2005) (2 steps, CI = 50, RI = 94).
296. Number of epurals: (0) one; (1) two or three (Lucena, 1993; Buckup, 1998; Vari and Harold, 2001; Moreira, 2002; Benine, 2004; Toledo-Piza, 2007) (6 steps, CI = 17, RI = 17).
297. Number of epurals: (0) one or two; (1) three (Lucena, 1993; Buckup, 1998; Malabarba, 1998b; Moreira, 2002; Zanata and Vari, 2005; Toledo-Piza, 2007) (3 steps, CI = 33, RI = 78).
298. Fusion of second hypural to last compound centrum: (0) absent; (1) present (Uj, 1990) (6 steps, CI = 17, RI = 50).
299. Fusion between first and second hypurals: (0) absent; (1) present (Uj, 1990; Lucena, 1993; Buckup, 1998) (3 steps, CI = 33, RI = 0).
300. Posterior margin of third hypural: (0) equal or more slender than posterior margin of fourth hypural; (1) deeper than posterior margin of fourth hypural (4 steps, CI = 25, RI = 62).
301. Ventral procurrent caudal-fin rays of adult males: (0) slender; (1) laminar (Malabarba, 1998a; Bürrnheim, 2006) (2 steps, CI = 50, RI = 50).
302. Number of ventral procurrent caudal-fin rays: (0) 11 or less; (1) 12 or more (Malabarba, 1998a; Bertaco, 2003; Bürrnheim, 2006) (5 steps, CI = 20, RI = 50).
303. Ventral procurrent caudal-fin rays of adult males: (0) not projected from peduncle musculature and skin; (1) projected ventrally from peduncle musculature and skin (Malabarba, 1998a; Bürrnheim, 2006) (3 steps, CI = 33, RI = 33).
304. Anterior ventral procurrent caudal-fin rays: (0) paired, only distally fused; (1) with longitudinal stays; (2) fused in laminar medial bones (Roberts, 1969; Lucena, 1993; Vari, 1995; Buckup, 1998; Murray and Stewart, 2002; Zanata and Vari, 2005) (2 steps, CI = 100, RI = 100).
305. Uroneurals: (0) one pair; (1) two pairs (Uj, 1990; Lucena, 1993; Buckup, 1998; Moreira, 2002; Zanata and Vari, 2005; Lima, 2006) (13 steps, CI = 8, RI = 74).
306. Bony hooks on fins: (0) absent; (1) present in adult males (Malabarba, 1998b; Bertaco, 2003; Serra, 2003; Lima, 2006) (19 steps, CI = 5, RI = 60).
307. Bony hooks on anal and pelvic fins of adult males: (0) present in both fins; (1) on anal fin only; (2) on pelvic fin only (Malabarba, 1998b) (14 steps, CI = 14, RI = 14).
308. Bony hooks on pectoral, dorsal and caudal fins of adult males: (0) absent; (1) present on dorsal, and occasionally on pectoral and caudal fins; (2) present only on pectoral fins; (3) present only on caudal fin (Malabarba, 1998a; Bertaco, 2003; Bürrnheim, 2006) (14 steps, CI = 21, RI = 15).
309. Bony hooks on base of pelvic-fin rays of adult males: (0) absent, or reduced in number; (1) as numerous as in segmented portion of rays (7 steps, CI = 14, RI = 73). In most species having bony hooks on pelvic fin, these hooks are mostly distributed on the segmented portion of the rays, being absent or much reduced in number in the basal, unsegmented, region. In some species, instead, the bony hooks are densely distributed from the base of the pelvic-fin rays.
310. Bony hooks on last pelvic-fin ray of adult males: (0) absent or reduced in number; (1) as numerous as in other rays (7 steps, CI = 14, RI = 74). In most species having pelvic-fin bony hooks, these are distributed by all the rays excepting the first, unbranched, and the last branched rays. In some species some or both these rays have also bony hooks; these cases are considered in this character and the following one.
311. Bony hooks on first pelvic-fin ray of adult males: (0) absent; (1) present (6 steps, CI = 17, RI = 38).
312. Position of anal-fin bony hooks of adult males: (0) paired; (1) medial, orientated posteriorly; (2) assymmetrically disposed, disordered (Reis, 1989; Malabarba, 1998a; Bürrnheim, 2006) (5 steps, CI = 40, RI = 40).
313. Ctenii or spines on scales: (0) absent; (1) with ctenii on posterior margin of scales; (2) with conspicuous spines on surface of posterior field of scales (Eigenmann, 1917; Lucena, 1993) (3 steps, CI = 67, RI = 67).

314. Anterior margin of scales: (0) uniformly curved or slightly undulated; (1) with conspicuous undulations (Lucena, 1993) (2 steps, CI = 50, RI = 0).

315. Circuli on posterior field of scales: (0) present; (1) absent (Lucena, 1993; Buckup, 1998; Zanata and Vari, 2005) (10 steps, CI = 10, RI = 73).

316. Radii on scales: (0) absent or reduced in number; (1) present and numerous on most scales (9 steps, CI = 33, RI = 83).

317. Radii orientated to anterior field of scales: (0) present; (1) only a longitudinal groove with not defined margins; (2) absent (Zanata and Vari, 2005) (5 steps, CI = 40, RI = 84).

318. Radii of scales: (0) not converging at focus; (1) converging at focus (8 steps, CI = 12, RI = 68). The radii usually are rather parallel, not converging each other at the focus, while in some species the radii are converging at the focus of the scales.

319. Semicircular grooves on posterior field of scales: (0) absent; (1) present (not informative).

320. Scales on supraoccipital spine: (0) not covering supraoccipital spine; (1) completely covering supraoccipital spine (Lucena, 1993; Vari, 1995; Buckup, 1998; Zanata and Vari, 2005; Lima, 2006; Toledo-Piza, 2007) (7 steps, CI = 14, RI = 40).

321. Predorsal scales: (0) covering entire predorsal region; (1) leaving a naked area anterior to dorsal fin (Eigenmann, 1917; Machado-Allison, 1983; Benine, 2004) (7 steps, CI = 14, RI = 33).

322. Ventral serrae: (0) absent; (1) present (Machado-Allison, 1983) (1 step, CI = 100, RI = 100).

323. Scales covering anal-fin base: (0) one or two rows of scales covering anal-fin base; (1) several rows covering basal third of anal fin (Eigenmann, 1917; Serra, 2003; Benine, 2004) (10 steps, CI = 10, RI = 50).

324. Scales covering caudal-fin lobes: (0) covering only their base; (1) covering one third of their length (Eigenmann, 1917; Malabarba, 1998b; Serra, 2003; Benine, 2004) (11 steps, CI = 9, RI = 52).

325. *Adductor mandibulae* tendon inserted on dentary: (0) absent; (1) present (1 step, CI = 100, RI = 100). Usually the A2 and A3 sections of the *adductor mandibulae* are forming anteriorly a strong tendon which is ventrally divided in two small tendons; these tendons are attached to the coronomeckelian and the dentary respectively. The ventral division of this tendon is absent in some members from the outgroup.

326. Insertion of *adductor mandibulae* tendon on dentary: (0) ventral to posterior half of Meckelian cartilage; (1) ventral to middle or anterior half of Meckelian cartilage (11 steps, CI = 9, RI = 72). The attachment site in the dentary of the *adductor mandibulae* tendon ventral division has a longitudinally variable position among the examined species. In most species it is attached in a position ventral to posterior half of Meckelian cartilage, while in others it is inserted more anteriorly.

327. Insertion of *adductor mandibulae* tendon on dentary: (0) ventral to Meckelian cartilage; (1) anterior to Meckelian cartilage (Zanata and Vari, 2005) (4 steps, CI = 25, RI = 62).

328. Posterior attachment of section A1 from *adductor mandibulae*: (0) principally attached to vertical arm of preopercle; (1) restricted or almost restricted to horizontal arm of preopercle (Uj, 1990; Lucena, 1993) (9 steps, CI = 11, RI = 47).

329. Medial tendon from section A1 of *adductor mandibulae*: (0) on quadrate, near its articulation with preopercle; (1) on preopercle, posteriorly to quadrate (3 steps, CI = 33, RI = 80). The medial surface of the *adductor mandibulae* A1 section is dorsally limited by a tendon, which usually inserts near the articulation between the quadrate and the preopercle. In some species, instead, this tendon runs laterally to this region and is attached to the preopercle, posteriorly to the quadrate.

330. Anterior insertion of section A1 from *adductor mandibulae*: (0) on maxilla; (1) on coronoid process of dentary (Howes, 1979; Vari, 1979) (1 step, CI = 100, RI = 100).

331. Contact between dorsal margin of *adductor mandibulae* and ventral margin of *dilator operculi*: (0) absent; (1) present (Lucena, 1993) (11 steps, CI = 9, RI = 41).

332. Anterior extension of *adductor arcus palatini*: (0) covering most of endopterygoid dorsal surface; (1) covering only half of endopterygoid (Lucena, 1993) (9 steps, CI = 11, RI = 47).

333. Posterior region of *levator arcus palatini*: (0) limited laterally by *adductor mandibulae* and medially by *adductor arcus palatini*; (1) limited lateral and medially by different sections of *adductor mandibulae* (Lucena, 1993) (6 steps, CI = 17, RI = 69).

334. Origin of *dilator operculi*: (0) dorsal to posterior margin of eye; (1) completely posterior to vertical line through posterior margin of eye (1 step, CI = 100, RI = 100).

335. Pseudotympanum limited by first pleural rib, *lateralis superficialis*, second pleural rib, *obliquus inferioris* and *obliquus superioris*: (0) absent; (1) present (Machado-Allison, 1983; Malabarba, 1998a; Zanata and Vari, 2005; Bührnheim, 2006) (6 steps, CI = 17, RI = 71).

336. Insertion of pterotic aponeurosis: (0) on pterotic spine or lateral surface of horizontal semicircular canal; (1) on a lobe situated dorsally to horizontal semicircular canal; (2) on pterotic or sphenotic, much dorsal to horizontal semicircular canal (Weitzman and Fink, 1983) (4 steps, CI = 50, RI = 50).

337. Humeral spot: (0) absent or vertically elongated; (1) horizontally ovate (Vari and Harold, 2001) (6 steps, CI = 17, RI = 38).

338. Second humeral spot: (0) absent or diffuse; (1) present as a conspicuous vertical bar (3 steps, CI = 33, RI = 0).

339. Dark conspicuous spot on dorsal fin: (0) absent; (1) present (Weitzman and Palmer, 1997; Malabarba, 1998a; Benine, 2004; Bührnheim, 2006) (1 step, CI = 100, RI = 100).

340. Horizontal line of chromatophores just dorsal to anal-fin base: (0) absent; (1) present (Malabarba, 1998b) (2 steps, CI = 50, RI = 67).

341. Color of caudal-fin lobes: (0) symmetrically hyaline, yellowish, reddish or violaceous; (1) ventral lobe orange or reddish, and dorsal lobe hyaline; (2) ventral lobe dark brown or black and dorsal lobe hyaline; (3) both lobes dark brown or black (Benine, 2004) (5 steps, CI = 60, RI = 60).

342. Diffuse spots on flanks of juveniles: (0) absent; (1) present (Machado-Allison, 1983) (1 step, CI = 100, RI = 100).

343. A little spot on each scale of flanks: (0) absent; (1) present (1 step, CI = 100, RI = 100).

344. Dark spot covering the entire depth of caudal peduncle: (0) absent; (1) present (Benine, 2004) (no informative).

345. Ventral confluence of gill membranes: (0) confluent anteriorly, not covering the isthmus; (1) confluent posteriorly, covering the isthmus but not attached to it; (2) confluent each other and with the isthmus (Moreira, 2002) (5 steps, CI = 40, RI = 57).

346. Sclerotic bones: (0) a single bone anteroventrally open; (1) two bones separated by cartilages (11 steps, CI = 9, RI = 74). Most species from the outgroup have two sclerotic bones, separated by cartilages situated dorsal and ventrally in the eye; this situation would be generalized for teleosts (Franz-Odenaal and Hall, 2006). In several characids these bones are fused each other at the dorsal surface of the eye, resulting in a single bone with a cartilage only in the ventral margin of the eye.

347. Nostrils: (0) rounded, divided by a skin fold; (1) two separate nostrils at each side of snout (3 steps, CI = 33, RI = 50). In most characiforms, the nostrils are a rounded opening divided by a flap of skin; in a group of species, instead, there are two separated nostrils on each side of the snout.

348. Gill-derived gland on males: (0) absent; (1) present (Burns and Weitzman, 1996; Bushmann et al., 2002) (4 steps, CI = 25, RI = 82).

349. Glandular fold on ventral lobe of caudal fin: (0) absent; (1) present (Eigenmann, 1917; Weitzman and Menezes, 1998) (1 step, CI = 100, RI = 100).

350. Adipose fin: (0) present; (1) absent (Eigenmann, 1917; Vari, 1995; Malabarba, 1998a; Bertaco, 2003; Serra, 2003; Quevedo, 2006) (5 steps, CI = 20, RI = 43).

351. Constriction on posterior chamber of gas bladder: (0) absent; (1) present (Vari, 1977) (1 step, CI = 100, RI = 100).

352. Papillae on tongue: (0) not aligned; (1) forming longitudinal rows anteriorly (1 step, CI = 100, RI = 100). The dorsal surface of primary tongue has variably distributed papillae. In most species these papillae are disorderly spread, not forming an aligned pattern; in a group of species, instead, the anterior papillae are aligned forming four to six easily visible rows.

353. Insemination: (0) absent; (1) present (Malabarba, 1998a; Weitzman and Menezes, 1998; Bührnheim, 2006; Quevedo, 2006) (2 steps, CI = 50, RI = 83).

354. Type of spermatozoa: (0) aquasperm; (1) introsperm (Malabarba, 1998a; Weitzman and Menezes, 1998; Bührnheim, 2006; Quevedo, 2006) (2 steps, CI = 50, RI = 80).

355. Sperm storage area on testes: (0) absent; (1) present (Weitzman and Menezes, 1998; Quevedo, 2006) (2 steps, CI = 50, RI = 80).

356. Number of 2n chromosomes: (0) 36 to 40; (1) 46 or more (2 steps, CI = 50, RI = 50).

357. Number of 2n chromosomes: (0) 48 or less; (1) 50 or more (4 steps, CI = 25, RI = 40).

358. Number of 2n chromosomes: (0) 50 or less; (1) 52 or more (12 steps, CI = 8, RI = 62).

359. Number of 2n chromosomes: (0) 52 or less; (1) 54 or more (3 steps, CI = 33, RI = 78).

360. Number of 2n chromosomes: (0) 56 or less; (1) 58 or more (1 step, CI = 100, RI = 100).

Appendix 2

Data set. The order of taxa follows the classification proposed here. Quotation marks indicates that a new generic assignment should be made for the referred species, according to the present analysis; however, such a generic change should be further evaluated in specific studies. Polymorphisms are denoted as z = [0 1], y = [0 2] and x = [1 2].

OUTGROUP									
Cypriniformes—Cyprinidae									
<i>Puntius tetrazona</i>									
--0----0-z	0010-00?0z	zz-1----1-	--00-31110	100?000?-	0---101000	---1-----0	0----0000-	-100--00z0	
?0-----0z1	0-11--0-0?	0-000-0---	-----	---0000---	-----00	-010---000	?00000z001	--011-0-00	
?00100??1	01111100-0	101101??0	000-00-000	-00000z000	1000000000	-100-0z00-	-10--00111	0-00010001	
01000000-z	z100000000	0000100100	000000----	--00z10101	00000--z?0	01z0000000	0000210-0z	00--?1zzz0	
Distichodontidae									
<i>Distichodus maculatus</i>									
010100110z	0011-00100	z0-10---10	--00131110	000?000?-	0110001000	-000001000	00100-----	0000000000	
00-1---0zz	0-01-000?0	0-00000--0	0100-----?	--00000--0	0100000000	0zz0000010	?000z00000	1101100000	
0111100111	0111000000	1011000010	010000000z	-00000z00?	1001000010	010000000-	??0-00111	0-00010001	
0101011111	1100100000	0000110011	000000----	--1000--00	00010--1?0	0110000000	0000010?00	0?????????	
Parodontidae									
<i>Apareiodon affinis</i>									
-101000110	1010-10101	11-10---10	--00111110	1000000-0-	0110001000	-?00001000	1010000000	11000-0000	
00-1010001	0011-00001	0-100001-0	0-0-----	-1-1100110	-----00	0010000000	0011000200	1101000000	
0001100?11	01110010-0	101?0??010	00000000?0	-100001001	0001100010	0000000001	0000000100	?000010001	
11000110z1	0100000000	0100110101	000010----	--00010101	00000--??1	0110000000	0000110?00	00??11110	
<i>Parodon nasus</i>									
-101000110	1010-10101	11-10---10	--00111110	1000000-0-	0110001000	-?00000000	1010000000	11000-0000	
00-1010001	0011000001	0-100001-0	0-0-----	-1-1100110	-----00	0010000000	0010000200	1101?00000	
0001100011	01110010-0	1011010010	0100000000	-100000001	0001100010	0000000001	0000000100	0000010001	
11000110z1	z100000000	0100110101	000010----	--00010101	00000--??1	0110000000	0000110?00	0????11110	
Hemiodontidae									
<i>Hemiodus cf. thayeria</i>									
0101001110	0011-00100	0011100010	--00100010	0000001100	0110001000	0000100000	0011110000	1100000010	
00-100z001	0011000001	0-00000100	000-----	-1-1110110	--00----00	1010000000	0000000200	0101000010	
0011100011	0111000000	1011000010	0100000011	1100001000	0001000010	0100000001	0100000110	0000000001	
1100010011	1000000000	0000111011	000010----	--00010000	00000--??1	0110000000	2000010?00	00??11110	
Anostomidae									
<i>Leporinus striatus</i>									
01010010-0	0010-00101	0011100010	0001001?10	0000000---	011-001000	-?01001000	001101000-	1100000000	
00-1---001	0011000---	0-00000-00	0-0-----	-0-0000--0	001-00-000	0100000000	?0-z0-0000	?101000010	
0001100?11	0111100010	1011011000	00000-0000	-100000000	00010000?0	0101000001	01000001z0	0000010001	
1100011001	0100000000	0000111101	000010----	--00010100	0000?--1?1	0010000000	00002?1?00	00??11110	
Curimatidae									
<i>Cyphocharax spilotos</i>									
0111001110	0010-00100	00110---10	--00101110	0000000-0-	0110001000	-000z01000	001z000000	?000000000	
00-1---001	0011000001	0-00000---	-----	---0000---	--1---?00	1000000000	0001000001	1101000010	
0001100?11	1111??00-0	1011111100	0100000000	-100000100	0001000010	0100000001	0100000110	0000010001	
1100011011	0100000000	0000111101	000010----	--0000--00	00000--1?1	00?0000000	00002?0?00	0????11110	
Prochilodontidae									
<i>Prochilodus lineatus</i>									
01010010-1	001--00100	00110---10	--00101110	0000000-0-	0100001000	-?01001000	1011010000	1100000000	
00-1---?0-	0011000000	0-00000---	-----	---0000---	--1-----00	0100000000	00-100-010	1101000010	
0001100011	0111000010	1011111100	0100000000	-100001000	0000000010	0100000001	0110000110	?000010001	
11000110z1	0100000000	0000111101	000010----	--00010101	00000--?01	0010000000	0000210?00	0000?11110	

Appendix 2
(Continued)

Crenuchidae									
<i>Characidium borellii</i>									
-101001100	--10-00100	11--0---10	-?00100010	0000001100	0110001000	-?0100-0-0	001-00-000	0000--1000	
00-1---011	0011000001	0-00000100	000-----	-0-0000--0	001-000010	0010000010	0001000201	0101000000	
0111000011	01111100-0	1010000010	0110000000	-100000001	00011000-0	0100100001	0100000110	0000010001	
0000010001	0000000000	0002110101	0000012000	0-00112000	00000--??1	1111000000	0000011?00	0? ??? 11000	
<i>Characidium rachovii</i>									
-101001100	--10-00-00	11--0---10	-?00100010	0000001100	0110001000	0?01-0---0	001----000	0-00--11--	
10-1?-011	001?00000z	0-00000100	000-----	-0-0000--0	001-000010	1010000010	00?1000201	0101000000	
0111000011	01111100-0	1010000010	010000000z	-100000101	00010000-0	0100100001	0100000110	0000010001	
0000011101	0000000000	0002110101	00000? ????	??00112000	00000--??1	1111100000	0000011?00	00? ?? 11000	
Erythrinidae									
<i>Hoplias cf. malabaricus</i>									
-101?010--	--10-00100	11-0100000	0-01101010	100-000?-	01101---00	10000000-1	---000-000	1000000000	
00-1000-10	0010000000	1000000000	0-0-----	-001111000	0000000001	-011-00011	0010000?00	00010-0000	
1111100-11	-11100?011	0111000010	1110--0000	-10000z000	-0000000-1	1-0110000?	0110000100	0100000001	
0000011101	0000000000	0002100000	000000----	--00010101	00001000?1	101-000000	0000010?01	0000?00000	
Lebiasinidae									
<i>Pyrrhulina australis</i>									
-100--10-0	0010-00100	11-0100010	--01101110	1000000-0-	0110001000	01001010-1	-010001000	1-000-0-00	
10-1000010	0011000001	1000000000	0-0-----	-001110000	0100000000	1010-00000	000100-?01	01010-00z0	
0100100?01	0111110000	1011000010	00000-0000	-100000000	-000000010	0000?0001-	000-000100	0000100001	
1000010001	1000000000	0002100100	000000----	--00010101	00001001?1	001-000000	0000010?01	00? ?? 00000	
Gasteropelecidae									
<i>Carnegiella strigata</i>									
-01----0-0	0010-11000	11-1100000	-?00100110	1000000-0-	011001----	1-00-----1	-0-----000	0--00-0---	
10-1000010	0011100000	1000000100	000--11011	0001000000	001-000101	-010001000	00z0000201	01010-0000	
0101000010	00111100-0	00100010010	0100000000	-100010100	000--00110	0-00?0111-	-100100000	0101100000	
0011000001	1001011z00	000201010z	00000110--	-000110101	0000100011	1100000000	0000010001	00? ?? 1zzz0	
<i>Engraulisoma taeniatum</i>									
01010010-0	0010-z0-00	z001100000	-000101110	000-000-0-	0110010010	-00001-000	0000000000	10z--00-11	
00-1---010	0010100000	1000000100	010-011000	0000000--0	001-000100	1010020000	0100000201	0101000000	
0101100001	01111100-0	??10010011	-000000-10	-1000z0110	1001000000	000000011-	--0-100000	1101100000	
1000000001	0010011000	0000000100	00000? ????	??00110101	00001100?1	1100000000	0000010?00	00? ??? ????	
<i>Thoracocharax stellatus</i>									
-01----0-0	0010-11000	11-1100000	-?00100100	1000000-0-	0110010000	1-01-1-0-1	-000---000	0-000-0---	
---1000010	0011100000	1000000100	0100011011	00011z0000	001-000001	-010101000	0000000201	0101000000	
0001000-00	00111000-0	0010010010	0110--0000	-100010100	000--001?0	0-00?0111-	---0100000	0101100001	
0011011101	1001011110	0002000101	00000110--	-000110101	0010100011	1000000000	0000110?00	00? ?? 11zz0	
Serrasalminidae									
<i>Metynnis cf. maculatus</i>									
01110010-1	0010100100	00z1100001	0000101110	0000000-0-	1000000000	100101-?-0	0010000000	0000000010	
00-1---210	0010000101	1000000100	010000--00	1000000--0	0001100000	1010000000	0000000?10	?1010000?0	
0100100101	0111100010	00100000010	0100000001	1100110110	0000000010	0000000001	0100000000	0001010001	
0000111111	010011111-	0002010001	000010----	--0000--0-	11101110?1	?010-00000	0100010?00	0000?11111	
<i>Piaractus mesopotamicus</i>									
01110010-1	0010100100	z011100001	0000101110	0000000-0-	0z00000000	1001000000	0011010000	1000000010	
0101---210	0000000101	1100000100	010000--00	1000000--0	0001000000	0010000000	0010000210	01010000?0	
0100100001	0111000010	0110010010	0110000001	1100110100	0100000010	0000000001	0110000000	0001100001	
0100011111	z100111000	0002010001	000010----	--0000--0-	11101000?1	1010000000	01000?0?00	00? ?? 11110	
<i>Serralmus maculatus</i>									
?011-010-1	10101?0100	10-1100001	0000101110	000?100-0-	0000000000	100101--00	0010000000	1000000110	
00-1---210	0010000101	1000000100	0-0-----	-000000--0	001-100000	0010000010	0000000210	01010000?0	
0100100001	0111100010	0111000010	0100000001	1100110100	0100000010	0000000001	0110000000	0001000001	
0100111111	0100111110	0002010011	000010? ???	??0000--0-	11101110?1	10100?0000	0100010?00	00? ?? 11111	
Alestidae									
<i>Alestes cf. macrophthalmus</i>									
0?0100?111	00??-?0100	10-1100000	-00?121?1?	000?000-?-	01000?100?	?????0?0?0	?01??1000?	11?0??0?11	
?-0---210	000101010?	1100000100	010?020000	0000000--0	0001000000	0000001000	?10?0?020?	?-01?00000	
01??100?11	0??0000000	???1000010	010?0000?1	?1?001?00?	?0?000010	001000000z	0??0000110	000?000001	
1100000011	0?00011000	0?01111000	000110----	--00?10100	00001110?1	?0000?0000	00000?0?00	0? ??? ????	
<i>Brycinus caroliniae</i>									
-?01??111?	001?-?0?00	11-1100000	-000121?1?	100?000-0-	0110000100	?000000000	101001000?	11? ??? ?0?11	
00-0---21?	0001010101	1100000100	010?020000	0000000--0	0001000000	0000001000	?100000201	?101?0?000	
?1??100?11	???1000000	???1000010	010?000?1	11?000000?	0?00000010	0010000001	0??000110	000?000001	
1100000011	0000010000	0001111?00	000110----	--00010100	0000111? ?1	1??00?0000	0000010?00	0? ??? 10000	
<i>Bryconethiops macrops</i>									
-101000111	001?-00100	1z-1100000	-000121?10	000?000-0-	010000100?	?00000?000	1?1001000?	1100?0?0?10	

Appendix 2
(Continued)

00-0---210	0001010101	1100000100	011-020000	0000000--0	0001000000	0000001000	?100000201	?10100?000
?1??100?11	?111000000	??110??010	010??00011	11?001?00?	0?00000010	001000000z	0100000111	0-00000001
1100000010	0?00011000	00011111000	000110----	--00010100	00001110?1	1??00?0000	00000?0?00	0?????????
<i>Chalceus macrolepidotus</i>								
01?10010-1	0011000100	10-1101001	000010z010	0000000-0-	0110000000	0001000000	0111110000	0100000011
00-1000-10	0001000101	1000000100	011-011010	0001111100	0001000000	0010001000	0000000201	?001000000
0111100?11	0001100000	0011000010	0100000011	1100000000	0000000010	0010000001	0100000110	0001000001
1101011011	1000000000	0000111100	000010----	--00010101	0000100011	1000000000	00000?0?00	00??111z0
<i>Micralestes stormsi</i>								
0111001111	0011-00100	10-1100000	-000101010	000?000-0-	0110001000	0000100001	-010001000	11z0000011
00-0---210	0011010111	1000000100	0100111000	0000000--0	0001000000	1010001000	0100000201	0101000010
0100100111	00111z0000	0011000010	0100000011	1100010100	0001000010	0010000000	0100000100	0000000001
1101000001	0100010000	00011111000	000110----	--00010100	00001100?1	1000000000	00000?0?00	00?????????
INGROUP — Characidae								
<i>Agoniatinae</i>								
<i>Agoniates anchovia</i>								
0101000110	0011000000	0011100001	0000100010	0000001000	0110010010	1-00000000	0011001000	00?0010010
0??1000-10	001?000000	1000000100	010001--10	?001111000	00?-00-001	-011101000	0000000201	?001001000
01010?1011	0001000001	0101000010	0100000011	11001100?	1001100010	0010000001	111?000000	1001100001
1001010011	1z01111100	0000?00101	00021?????	??00110000	00001001?1	1100000000	0000010?00	00?????????
<i>Salmininae</i>								
<i>Salminus brasiliensis</i>								
-1010000-0	1000000z00	1z-1100001	000010zz10	000?000-?-	0110000000	1201000000	101101000-	10000?0010
0111000-10	0010000000	1000000100	010001--11	0001111z00	0000000011	-011100000	?000000100	?001000010
z111100?01	0001000011	0101000010	0100000001	1100001000	0000000010	0000000001	0110000100	0001110001
1000010011	1000111z00	0000010101	010211????	??00012000	0000100001	1000000000	0000000?00	00??11000
<i>Acestrorhynchinae</i>								
<i>Acestrorhynchus pantaneiro</i>								
0101001z-z	1111000000	z0-0100001	0-01100010	0000001101	0111000010	1201000100	101z001000	0010000010
0111000-10	0010000000	1000000000	1-0-----	-001111000	0000000011	-0111000010	1010100200	?001001000
0111001011	0000002?11	0101000010	1100--1001	1100001100	1001000010	0010000000	0110000100	0001100001
10010100z1	1010111000	00000z0001	0z0210----	--0000-00	0000100011	1100001000	0000010?00	0000?11000
<i>Cynodontinae</i>								
<i>Rhaphiodon vulpinus</i>								
1101001100	0010000000	0010100001	0001001010	0000001101	011-010000	1-01000100	1010010001	00000-0000
0111000-10	0010000001	1000000000	1-0-----	-001111000	001-000011	-0111000001	1010100201	?001101000
1110100?11	0111002?11	0111000010	1111001000	-1?0001000	1000001110	00---0011-	-111000000	0101100001
1111010011	1011111110	000001000-	000210----	--0000--0-	z010100011	1110000000	0000010?00	00??11110
<i>Bryconinae</i>								
<i>Brycon falcatus</i>								
010100z0-1	00z1000100	0011100001	0-00100?10	000000z-0?	011000000?	??01000000	1111010000	10000?0010
0111000-10	000?000?01	1000000100	011-011010	1001111100	0001000z00	001?000000	?000000200	?001?00000
01??100?01	0001000010	0111000010	0100000001	1100011000	0000000010	001000000?	?110000100	0001110001
1000010011	1000111000	0000010101	000211????	??00012000	00101000?1	?????00000	00000?0?00	0????11000
<i>Brycon meeki</i>								
0?0100?0-1	00010??100	0011100001	0?00100?10	0000001???	010?000000	?001000000	100101000?	?0000?0?10
0?-1000-10	0000000?01	1000000100	011-01?010	?001111100	0001000?0?	?01000?000	?00000020-	?001000?00
0111100?01	00??0000?0	01?10?0010	0100000001	11?00z100?	?0000000?0	0010000000	01?0000100	0001100001
1000010011	1?00111100	0000011101	00021?----	--00????00	00?01?0?0?	???0000000	00000?0?00	0?????????
<i>Brycon orbignyianus</i>								
01010000-1	0011000100	0011100001	0000100?10	0000000-0-	0z00000000	1001000000	10z1010000	10000?0010
0111000-10	0000000101	1000000100	011-111011	1001111110	0001000000	0010z00000	1000000200	0001000010
0111100?01	0111000010	0111000010	0100000001	1100011000	0000000010	0000000000	0110000100	0001110001
1000010011	1000111z00	0000010101	00021?????	??00012000	00?0100001	1000001000	00000?0?00	00??11000
<i>Brycon pesu</i>								
0?0100z0-1	0011000100	11-1100001	0?00100010	1000001100	0110000000	1000000000	10z1010000	?000000010
0111000-10	0000000101	1000000100	011-011010	1001111100	0001000z00	001z000000	z000000200	00010000z0
0111100?01	0001100010	01110z0010	0100000001	1100010000	0000000010	0010000000	0100000100	00011z0001
1000010011	1000111000	0000010101	00021?----	--00012001	0010100?01	?1?0000000	00000?0?00	0000?11000
<i>Triportheus nematurus</i>								
01110000-1	0011000100	10-1100001	0000100000	0000001000	0110010001	0000001000	1000010000	1000100010
0111000210	0000000101	1000000100	011-010010	1001100100	0001000000	1010000000	z000010201	0101100000
0111000010	0001000010	0011000010	0100100011	1100010000	1000011110	0000-0011-	-110000000	1101100001
1001010011	1z00111100	0000010101	000210----	--00110100	0000100001	1100000000	0000010?00	00??11100
<i>Triportheus pantanensis</i>								
01110000-1	0011000100	10-1100001	0000100000	0000001000	0110010001	0000001000	1000010000	1000100010
0111000210	0000000101	1000000100	011-010010	1001100100	0001000000	1010000000	z000010201	0101100000
0111000010	0001000010	0011000010	0100100011	1100010000	1000011110	0000-0011-	-110000000	1101100001
1001010011	1z00111100	0000010101	000210----	--00110100	0000100001	1100000000	0000010?00	00??11100

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(Continued)

1001010011	1z00111100	0000010101	000210----	--00110100	0000100001	1100000000	0000010?00	00?0000-??
Iguanodectinae								
<i>Iguanodectes geisleri</i>								
01010010-1	0011000100	10-1100001	0000100010	000?111100	011?000000	-000001010	0110000000	1000000?10
0?11---200	0-11000101	1000100100	0100011010	0000000--0	001-0000?0	110000?100	?000001201	?101000010
01?1100?01	0111110000	?0?00z0010	0100000111	01000z1z?0	?001100010	00z000?z00	0100000100	0001100001
1000010001	10?0011000	0010010101	00021?????	??0000--00	00001-01?1	1100?0000	00001?0?00	10?0000000
<i>Piabucus melanostomus</i>								
11010010-1	0011000100	z001100001	0000100010	000?101100	0100000000	-000101010	0010000000	1010000110
0101011200	0-11000101	1000100100	000--11010	0001100110	001-000000	1100001100	0000001201	0101000z10
0100100101	0111100000	0010000010	0100000101	0100001010	0011000110	001000011-	-1z0000100	0101100000
1001000001	1z11111110	0010010101	00021?????	??0000--00	00001-01?1	0100000000	0000100?00	1?00000000
Bryconops clade								
<i>Bryconops affinis</i>								
01010010-1	0011000100	0011100001	0000100010	0000001100	0110000001	1001001000	0111010000	1010000011
00-1000210	0010000000	1000000100	010?01z010	00011001z0	001-000100	0010000000	0000000201	1001000010
0111100-11	0001100000	0111000010	0100000111	0100011000	0001000010	0010000000	0100000100	0001z00001
1000010011	0000111z00	0000010101	0102110000	0000112000	0000100001	1100000000	00000?0?00	00?0010000
<i>Bryconops melanurus</i>								
01010010-1	0011000100	0011100001	0000100010	0000001100	0110000001	120100z000	0111010000	1010000011
00-1000210	0010000000	1000000100	0100111010	00011001z0	001?000100	0011000000	0000000201	1001000010
0111100101	0001110000	0111000010	0100000111	0100011000	0001000010	0010000000	0100000100	0001000001
1000010011	0000111100	0000010101	01021?????	??00112000	0000100?01	??0?00000	00000?0000	0000010000
Heterocharacinae n. subf.								
<i>Heterocharax macrolepis</i>								
0011001101	0011000100	001110z001	0?0010000z	0000111100	0100000010	0000001001	-?00010000	10-0110110
0111000-10	0011001000	1000000000	0?0-----	-001111000	0000000-00	0011100000	0010000x00	?00000z0z0
0111100011	0001100000	0111000010	0100000111	011001010?	1001000010	0010000000	0101000100	?001100001
1000010011	01001111z0	0000010z01	000200----	--001????00	00001000?1	11000?0001	0000010000	00?0000000
<i>Hoplocharax goethei</i>								
0011001101	0011000100	z01110z001	0?001000zz	0000111100	0100000000	000001--11	-0000--000	10-00?0110
1101000-10	0011001000	1000000000	0?0-----	-001111000	0000000-00	0011000000	0010000x0-	?000000zz0
0100100011	01111z0000	0011000010	01000001z1	011001011?	-0z1000010	0000000000	0101000000	0001100000
1000000011	0000111z00	0000010101	001200----	--001????00	00001001?1	11000?0001	0000010000	00?0000000
<i>Lonchogenys ilisha</i>								
0011001101	0011000100	001110z00z	-?00100000	0000111100	0110000000	0000001000	0000010000	10-0010110
0111000-10	0011000000	1000000000	0?0-----	-001111000	0000000-10	0011000000	001000010-	1000000010
0111100011	0001100000	0111000010	01000001z1	011001011?	0001000010	0000000000	0101000100	0001100001
1000010011	01001111z0	0000010101	000200----	--001????0-	10001001?1	z1000?0001	0000010000	00?0000000
Jupiaba clade								
<i>Jupiaba mucronata</i>								
00110010-1	0011000?00	0011100001	000010000z	0000011100	0100000000	0001001011	-010000000	0010000110
0101000010	001000000z	1000000100	0100011010	00011z0110	001-000000	0010000000	z000000101	0001000110
0101100001	0?11z0000	00110?00?0	0100000101	01?0010100	1000000000	0000000001	0101000100	0-11110001
1000010000	0z00111z00	0000010101	00021?????	??00112000	0000100?1	??0?01000	00000?0?00	00?0000000
<i>Jupiaba scologaster</i>								
00110010-1	0011000100	0011100001	0000100000	0000011100	0100000000	0001001011	-010000000	0010000110
0101000010	0010000000	1000000100	0100111010	0001110110	001-000z00	0010000000	zz00000101	0001000110
0100100101	0001110000	0z11000010	0100000101	0100010100	1000000000	0000000001	0101000100	0-11110001
1000010000	0100111000	0000010101	000200----	--00112000	0000100001	1100000000	00000?0?00	00?0000000
Tetragonopterinae								
<i>Tetragonopterus argenteus</i>								
00110010-1	0011000100	0011100001	0000100000	0000011z00	0000000000	0001001011	-010010000	0010000110
0111000110	0010000000	1000000100	0100011010	00011z0100	001-001100	0010000000	0000000101	1001000110
0101000001	0001100000	0111000010	0100000101	0100010100	0000000000	0000000001	0101000100	0001110001
1000010000	01001111z0	0001010101	0z02110000	0001112100	0011100001	?100000100	0000010000	00?0011z00
Stethaprioninae								
<i>Gymnocorymbus ternetzi</i>								
00110010-1	0011000100	0011100001	000010000z	0000011100	1000000000	0001001011	-010000000	0010000110
0101-0010	0010000000	1000000100	0100011010	0001000100	001-001100	1010000000	0000000101	?001000110
0101000?01	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000000	0001110001
1000010000	0100111110	00110z0101	000201????	??0011200-	1011100001	1100000100	00000z0?00	0?0001z00
<i>Poptella paraguayensis</i>								
00110010-1	0011000100	0011100001	0000100001	0000011100	1000000000	0001001011	-010000000	0010000110
0101000010	0010000000	1000000100	0100011010	00011z01z0	001-001100	0010000000	0000000101	0001000110
0101z00101	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000000	0001011001
1000010000	0100111110	0001010101	000211?1??	?200112000	00z1100001	1100000z00	0000010?00	0-00?11000

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<i>Stethaprion erythropros</i>								
00110010-1	0011000100	0011100001	0000100001	000?011100	1000000000	0001001001	-010000000	0010000110
0101000010	0010000000	1000000100	0100011010	0001z00100	001-001100	0010000000	0000000101	?001000110
0101000?01	00?100000	00?1000010	0-00000101	01000101??	?000000000	0000000001	0101000000	0101011001
1000011000	0100111110	0001010101	0002111?--	-200112010	00111000?1	1??0?0000	00000?0000	0?????????
<i>Stichonodon insignis</i>								
0?110010-1	00110?0100	00?110?001	0000100?00	000?011100	100?000000	0000001011	-010000000	?110000110
0101---010	0011000000	1000000100	0100011010	0010000--0	001-001000	101000?000	?100000101	?001000100
0101000?01	000100000?	0011000010	0100000101	01010101??	?000000000	0000000001	01?10?0000	?001010001
1000011000	0100111100	0001010101	00021?????	??0011210-	10111000?1	???0?0000	00000?0?00	00?????????
<i>Hemigrammus clade</i>								
<i>Bario steindachneri</i>								
00110010-1	0011000100	10-1100001	0000100001	0000011z00	0110000000	000100z0?1	-010000000	01100?0110
0?1000010	0010000010	1000000100	0100011010	0001z001z0	001-000100	0010000000	0000000101	?001000110
0101000?01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001100001
1000010001	0000111000	0000010101	0002110101	120z111100	0011100001	1??0?00000	000z0?0?00	0?????????
<i>Deuterodon iguape</i>								
00110010-1	0011000100	z001100001	0000100001	0000011100	0110000000	0001000011	-01z000000	0010000110
0101010010	0010000001	1000000100	0100111010	0001100110	001-000000	0010000000	0z00000101	0001000110
0101z00?01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001010001
100001000z	0100111000	0000010101	00021?????	??00112000	0000100001	1100000000	00000?0?00	00?????????
<i>Deuterodon langei</i>								
00110010-1	0011000100	10-1100001	0000100?01	0000011100	0100000000	0001000011	-011000000	0010000110
0101011-10	0010000001	1000000100	0100111010	0001110110	001-000000	0010100000	z000000101	?001000110
0101000?01	0001100000	0111000010	0100000111	010001010?	1000000000	0001000001	0101000100	0001010001
1000010000	0100111000	0000010101	000210----	--00112000	0000100?01	???0?0000	0000000?00	00?????????
<i>Hasemania nana</i>								
001z0010-1	0011000-00	0001100001	0000100100	0000011100	0110000000	000001--11	-010000000	0010000110
10-1--0010	0010000000	1000000100	0100011010	000z000--0	001-000010	1010000000	0000000101	10010-0110
0101000101	00011z0000	0011000010	0100000101	0100010110	1000000000	0000000001	0001000000	0001110001
10000100-1	0000110000	1000010101	000200----	--00112000	00001000?1	1100000000	00000?0?0z	00???1z000
<i>Hemigrammus erythrozonus</i>								
00110010-1	0011000100	0011100001	0000100101	0000011100	0110000000	000101--11	-01000-000	00100?0110
10-1000010	0011000001	1000000100	0100011110	00011z0110	001-000000	1010000000	0000000101	1001000110
0101000001	00?1110000	0011000010	0100000101	0100010110	1001000000	0000000001	0001000z00	0001110001
1000010000	000011z000	0000010101	00020101z0	1000?12000	000z1000?1	?100000000	0000000?00	00???1zz00
<i>Hemigrammus cf. rhodostomus</i>								
00110010-z	0011000100	10-1100001	0000100001	0000011100	0110000000	0001001011	-010000000	0010000110
10-1--0010	0011000001	1000000100	0100011110	000z000100	001-000000	1010000000	0000000101	1001000110
0101000001	00?11z0000	0011000010	0100000101	0100010100	1001000000	0000000001	01010001z0	0001110001
1000010000	0000110000	0000010101	00020?????	??00112000	0001100001	1100000000	00000?0?00	00???11000
<i>Hemigrammus ulreyi</i>								
00110010-1	0011000100	0011100001	?000100001	0000011100	0100000000	0001001011	-010000000	0010000110
1101000010	0010000000	1000000100	0100011010	00011z0100	001-000100	1010000000	0000000101	1001000110
0101000001	00011z0000	0011000010	0100000101	0100010110	1001000000	0000000001	0101000100	0001110001
1000010000	0z00111000	0000010101	0002010000	1000112000	000?100001	110000-0z0	00000?0?00	00?????????
<i>Hemigrammus unilineatus</i>								
00110010-1	0011000100	00z1100001	0000100?01	0000011z00	0100000000	0001001011	-010000000	0010000110
10-1000010	0010000000	1000000100	0100011010	00011101z0	001-000z00	1010000000	0z00000101	?001?00110
0101z00?01	00011z0000	0011000010	0100000101	0100010110	100z000000	0000000001	0101000100	0001110001
100001000z	0000111100	000?0z0101	0002010000	0000112000	0001100001	1?????0010	0000000000	00???11100
<i>Hyphessobrycon elachys</i>								
00110z10-1	0011000100	0001100001	001-10010z	0000011z00	0110000000	000100-?-1	-01-0--01-	0-10000110
10-1---010	001--00000	1000000100	0100011010	0000000--0	001-000000	1010000000	0000000101	1001000110
0101000001	0111100000	1011000010	0100000101	0100010110	1001000000	0000000001	0001000000	0001100101
100001000z	000011z000	0000010101	000200----	--00112000	00001000?1	0100-20000	00000?0?00	00?????-??
<i>Hyphessobrycon eques</i>								
00110010-1	0011000100	0011100001	0000100101	0000011100	0100000000	00100z1011	-010000000	0110000110
10?1000010	0011000000	1000000100	0100011010	00011101z0	001-000010	1010000000	0000000101	1001000110
0101000001	0001100000	0111000010	0100000101	0100010110	1000000000	0000000001	01z1000100	0001110001
1000010000	0000111100	00010z0101	00020110--	-200112000	0000100001	1100110010	0000000?00	00???1zz00
<i>Hyphessobrycon herbertaxelrodi</i>								
00110010-1	0011000100	0001100001	0000100101	0000011100	0110000000	00010010-1	-010000000	0010000110
10-1000010	0010000000	1000000100	0100011010	0001110100	001-000100	1010000000	0z00000101	0001000110
0101z00001	0001110000	1011000010	0100000101	0100010110	1001000000	0001000001	0001000100	00011z0001
100001z000	0z00111000	0000010101	0002010000	1000112000	00001000?1	?100000000	0000000000	00???11100

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<i>Hypheobrycon pulchripinnis</i>								
00110010-1	0011000100	10-1100001	000010010z	0000011z00	0110000000	000001--01	-01z000000	0010000110
10-1000010	0011000000	1000000100	0100011010	0001100110	001-000000	1010000000	0000000101	1101000110
0101000001	0001110000	0011000010	0100000101	01000101z0	1001000000	0000000001	0101000100	0001110001
1000010000	0000111z00	0000010101	00020????	-?00112000	00001000?1	?100010010	0000000?00	00????1z000
<i>Hypheobrycon socolofi</i>								
00110010-1	0011000100	0001100001	000010010z	0000011100	z1z0000000	0010001011	-0100000000	0010000110
10-1000010	0011000000	1000000100	0100011010	0001110100	001-000000	1010000000	0000000101	1001000110
0101000z01	0001000000	0011000010	0100000101	0100010110	1000000000	0000000001	0101000100	0001110001
1000010000	0000111100	0001010101	0002010101	0200112000	0000100001	1100110010	00000?0?00	00????????
<i>Moenkhausia dichroua</i>								
00110010-1	0011000100	0011100001	0000100001	0000011100	0100000000	0001001011	-0100000000	0010000110
0101000010	0010000000	1000000100	0100010010	000zz00100	001-000100	1010000000	0000000101	0001000110
0101000101	0011000000	0011000010	0100000101	z101010100	0001000000	0000000001	0101000100	0001110001
100001000z	0100111z00	0000010101	0z0210----	--00112000	0001100001	1100000000	3000000?00	00???11000
<i>Moenkhausia cf. intermedia</i>								
00110010-1	0011000100	0011100001	000010000z	0000011100	0100000000	0001001011	-0100000000	0010000110
0101000010	0010000000	1000000100	0100011010	0001z00100	001-000100	1010000000	0000000101	1001000110
0101000101	0011000000	0011000010	0100000101	0101010100	1001100000	0000000001	0001000100	00011z0001
1000010000	0z00111000	0000010101	0002z0----	--00112000	0001100001	1100000000	3000000?00	00???11000
<i>Moenkhausia sanctaefilomenae</i>								
00110010-1	0011000100	0001100001	000010010z	0000011z00	0110000000	000000z011	-0100000000	0010000110
1101000010	001000000z	1000000100	0100011010	0001z00110	001-000100	1010000000	0000000101	?001000110
0101000?01	0001110000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0000111000	0000010101	0002z110--	--00111100	00011000?1	1100000000	0001000?00	000001z000
<i>Moenkhausia xinguensis</i>								
001100z0-1	0011000100	0011100001	0000100001	0000011100	0100000000	0001001011	-01z000000	0z10000110
0101000010	0010000000	1000000100	0100011010	0001z00110	001-000100	0010000000	0000000101	0001000110
0101000101	0001100000	0z11000010	01000001z1	0100010100	1000000000	0000000001	0101000100	0001010001
1000010000	0100111000	0000010101	00021110--	--00112100	0001100001	1100000000	0000000000	00????????
<i>Paracheirodon axelrodi</i>								
00110110-1	0011000100	0011101001	0000100101	0000011100	0110000000	000100---1	-01000-000	0010000-10
10-1--1010	0011000000	1000000100	000--11110	0001000110	001-000000	1010000000	0000000101	1101--0110
0101100001	z001100000	0011000010	0100000101	0100010100	1001000000	0000000001	0001000100	0001100001
100001000z	000001z000	0000010101	000201????	??00????00	0000100?1	?100-20000	00000?0?00	00?0?1zz00
<i>Pristella maxillaris</i>								
00110010-1	0011000100	00z1100001	0000000100	0000z11100	0110000000	0010001011	?01000--00	0110000-10
10-100001z	0011000000	1000000100	010-011010	00011zz000	001-001000	1010100000	0000000101	1001000110
0101000001	z0z1100001	0111000010	0100000101	0100010100	1001000000	0000000001	0101000100	0001110001
1000010000	0000111000	00000z0101	0002010000	1000112000	0001100001	0100000010	0000000000	00????1zz00
<i>Probolodus heterostomus</i>								
00110010-z	0011000100	0001100001	0000100101	0000011100	0100000000	0001001011	-01z000000	0010000110
0??1000010	0010000000	1000000101	000--1--00	00011z0100	001-000000	1010000000	0000000101	?001000110
0101z00?01	z001100000	0011000010	0100000101	0100010100	1001000000	0000000001	0111000100	0001110001
100001000z	0100111100	0000010101	0002110100	0000112000	0000100001	1100?00000	00000?0?00	00????11000
<i>Thayeria boehlkei</i>								
00110010-1	0011000100	00z1100001	0000100001	0000011100	0110000000	0001001011	-01000001-	0010000110
10-1--0010	0010000001	100000-100	0100011010	0001000100	001-000100	1010000000	0z00000101	1001000110
0101000101	00011z0000	0011000010	0100000101	0100010100	0001000000	0000000001	0001000100	0001110001
1000010000	0000110000	0000010101	000200----	--00112000	00011000?1	1100000000	20000?0?00	00???11000
<i>Thayeria obliqua</i>								
00110010-z	0011000100	10-1100001	0000100001	0000011100	0110000000	0001001011	-0100000000	0010000110
10-1--0010	001000000z	1000000100	0100011010	000z000100	001-000100	1010000000	0000000101	1001000110
0101000?01	1001100000	0011000010	0100000111	0100010100	0001000000	0001000001	0001000100	0001100001
1000010000	0000110000	0000010101	000200----	--00112000	00011000?1	1100?00000	20000?0?00	00????1z000
<i>Astyanax clade</i>								
<i>Astyanax abramis</i>								
00110010-1	0011000100	0001100001	0000100100	0000010-0-	0z00000000	0001000001	-0110000000	0010000110
0101---110	001000011?	1000000100	0100010010	0000000--0	001-000z00	0010000000	0000000100	0001000110
0101000?01	0011z00000	0010000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010000	0100111100	0000010101	0002010001	0000012000	0000110001	1100001000	0010010000	01????11000
<i>Astyanax cf. abramis</i>								
00110010-1	0011000100	0001100001	0000100100	0000010-0-	0z00000000	0001000001	-0110000000	0010000110
0101---110	0010000111	1000000100	0100010010	0000000--0	001-000000	0010000000	000000010z	00z1000110
0101000001	0001z00000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0100111100	0000010101	0002010z00	0000012z00	0000110001	1100001000	0010010000	01????????
<i>Astyanax asuncionensis</i>								
00110010-1	0011000100	0001100001	0000100100	0000010-0-	0100000000	0001001001	-0110000000	0010000110

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0101---110	0010000111	1000000100	0100010010	0000000--0	001-000000	0010000000	000000010z	?0z1000110
0101000?01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0100111100	0000010101	0002010000	0000012z00	0000110001	1100001000	0010010000	01????11000
<i>Astyanax cf. asuncionensis</i>								
00110010-1	0011000100	0001100001	0000100100	0000010-0-	0100000000	0001001001	-011000000	0010000110
0101---110	0010000111	1000000100	0100010010	0000000--0	001-000z00	0010000000	0000000101	0001000110
0101z00001	0001100000	0011000010	01z0000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0100111z00	0000010101	0002010101	0000012z00	0000110001	1100001000	0010000000	01?????????
<i>Astyanax chico</i>								
00110010-1	0011000100	0001100001	0000100100	0000011000	0100000000	0001001001	-01z000000	0010000110
0101--0110	0010000011	1000000100	0100111010	00010001z0	001-000000	0010000000	0000000101	?001000110
0101000101	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111000	0000010101	0002010100	0000112000	0000110001	1100000000	0000010000	00?????????
<i>Astyanax correntinus</i>								
00110010-1	0011000100	0011100001	0000100100	000001z000	0z00000000	0001001001	-010000000	0010000110
01z1--0110	0010000011	1000000100	0100110010	0001000110	001-000000	0010000000	0000000101	0001000110
0101000101	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010000	0100111100	0000010101	00020100??	??00112000	0000100001	110000z000	0000000000	01?????????
<i>Astyanax cf. eigenmanniorum1</i>								
00110010-1	0011000100	0011100001	0000100100	0000011000	0100000000	0001001001	-010000000	0010000110
0101--0110	0010000010	1000000100	0100111010	00010001z0	001-00z000	0010000000	0000000101	0001000110
0101z00101	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111000	0000010101	0002010000	0000112000	0000100001	1100000000	00000?0000	00?????????
<i>Astyanax cf. eigenmanniorum2</i>								
00110010-1	0011000100	0001100001	000010010z	0000011000	0100000000	0001001001	-010000000	0010000110
0101--0110	001000001z	1000000100	0100111010	00010001z0	001-000000	0010000000	0000000101	0001000110
0101000z01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111000	0000010101	0002010000	0000112000	0000100001	1100000000	00000?0000	00?????????
<i>Astyanax endy</i>								
00110010-1	0011000100	0001100001	0000100100	0000011000	0100000000	0001001001	-010000000	0010000110
0101000110	001000001z	1000000100	0100111010	0001z001z0	001-000000	0010000000	0000000101	0001000110
0101000z01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111000	0000010101	0002010000	0000112000	0000110001	1100000000	0000000000	00?????????
<i>Astyanax latens</i>								
00110010-1	0011000100	0001100001	000010010z	000001z000	0100000000	0001001011	-010000000	0010000110
0101000110	00100000zz	1000000100	0100011010	00011z0100	001-000100	1010000000	0000000101	0001000110
0101000z01	0001000000	0011000010	0100000101	01000101z0	1000000000	0000000001	0101000100	0001110001
1000010001	0100111100	0000010101	0002010000	0000112000	00001000?1	1100000000	0000000000	00?????????
<i>Astyanax cf. lineatus</i>								
00110010-z	0011000100	0001100001	0000100100	0000010-0-	0100000000	0001000001	-011000000	0010000z10
0101--0110	0010000111	1000000100	0100010010	00010001z0	001-000z00	0010000000	0000000101	?101000110
0101000?01	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0100111z00	0000010101	0002010100	0000012000	0000110001	1100000000	0000000000	0100?11000
<i>Astyanax mexicanus</i>								
00110010-1	0011000100	z001100001	0000100100	000?011000	0100000000	0001000001	-010000000	0010000110
0101--0110	001000001z	1000000100	0100011010	0001000110	001-000000	1010000000	0000000101	0001000110
0101000001	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	01z1000100	0001110001
100001000z	0100111000	0000010101	0002010000	0000112000	0000100001	1100000000	00000?0000	00????1z000
<i>Astyanax paris</i>								
00110010-1	0011000100	0001100001	0000100100	0000011000	0100000000	0001000001	-010000000	0010000110
0101000110	0010000001	1000000100	0100011010	00011z0100	001-00z100	0010000000	0000000101	0001000110
0101000001	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	01010001z0	00011z0001
1000010001	0100111000	0000010101	000200----	--00112000	0000100001	1100000000	0000000000	00?????????
<i>Astyanax pelegri</i>								
00110010-1	0011000100	0001100001	0000100100	0000011000	0100000000	0001001001	-010000000	0010000110
0111--0110	0010000111	1000000100	0100010010	0001000110	001-000000	0010000000	0000000101	0101000110
0101000101	0001000000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010000	0100111110	0000010101	0002010000	0000012000	0000110001	1100000000	0000000000	01?????????
<i>Astyanax puka</i>								
00110010-1	0011000100	0001100001	000010010z	0000011000	0100000000	0001001001	-010000000	0010000110
0101--0110	001000001z	1000000100	0100111010	0001000110	001-000000	0010000000	0000000101	0001000110
0101000101	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
100001000z	0100111z00	0000010101	0002010000	0000112000	0000110001	1100000000	0000000000	00?????????
<i>Astyanax cf. rutilus</i>								
00110010-1	0011000100	0011100001	0000100100	0000011000	0100000000	0001001001	-010000000	0010000110
0101--0110	00100000zz	1000000100	0100z11010	0001000110	001-001000	1010000000	0000000101	0001000110
0101000101	0001000000	0011000010	0100000101	z100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111100	0000010101	0002010000	0000112000	0000100001	1100000000	0000000000	00?????????

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<i>Astyanax troya</i>								
00110010-1	00z1000100	0001100001	000010010z	0000011000	0100000000	0001000001	-011000000	0010000110
0101--0110	0010000011	1000000100	0100111010	0001000110	001-000000	0010000000	0z00000101	0001z00110
0101000z01	00011z0000	0111000010	0100000101	0100010100	1000000000	0000000001	01z1000100	0001110001
100001000z	0100111000	0000010101	0002010100	0?00112000	0000110001	110000z000	00000z0000	00z???????
"Bryconamericus" <i>scleroparius</i>								
00110010-1	0011010100	10-1100001	0000100100	0000010-0-	0100000000	0000000001	-011000000	0010000110
0101000110	0010000011	1000000100	010z011000	0001100110	001-000000	0010000000	0000000201	0001000110
0101000001	00011z0000	0011000010	0100000101	0100010100	1000000000	0000000001	0111000100	0001110001
1000010001	0100111100	0000010101	00021?????	??00112000	0000100001	1100000000	00000?0?00	00z???????
"Hyphessobrycon" <i>anisitsi</i>								
00110010-1	0011000100	0001100001	000010010z	0000011000	0100000000	0001001001	-010000000	0010000110
10?1000110	001000001z	1000000100	0100011010	0001z001z0	001-000000	0010000000	0000000101	0001000110
0101000001	00011z0000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110001
1000010001	0100111000	0000010101	0002010000	0000112000	0000100001	1100000000	0000000000	00z??11000
"Hyphessobrycon" <i>bifasciatus</i>								
00110010-1	0011000100	0001100001	0000100100	000001z000	0100000000	0001001011	-010000000	0010000110
10-1--0110	0011000000	1000000100	0100111010	0001000110	001-000000	1010000000	0000000101	0001000110
0101000101	00011z0000	0011000010	0100000101	0100010110	1000000000	0000000001	01z1000100	0001110001
1000010000	0100111100	0000010101	0002010000	0000112000	0000100001	1100010100	0000000000	00z??11000
"Hyphessobrycon" <i>luetkenii</i>								
00110010-1	0011000000	0001100001	0000100100	0000011000	0100000000	000100---1	-01-0--01-	0010000110
10?1000110	0011000000	1000000100	0100111010	0001100110	001-000000	1010000000	0000000101	0001000110
0101000001	0001100000	0011000010	0100000101	z100010110	1000000000	0000000001	0101000000	0001110001
1000010001	0z00111100	0000010101	00020111--	-200112000	0000100001	z100000000	0000000000	00z???????
<i>Markiana nigripinnis</i>								
001100z0-1	00z1100100	0001100001	0000101100	0000010-0-	0z01000000	0100000001	-011010000	1010z00z10
0101---210	0010000111	1000000100	0100011000	0000000--0	001-000000	0010000000	0000000101	0101110110
0101000001	0001100000	0011000010	0100000101	0100010100	1000000000	0000000001	0110000100	00011z0001
1000010001	0100111110	0100010101	00021110--	-001102-00	0011110001	1000000000	0000000000	01z??11100
<i>Psellogrammus kenedyi</i>								
00110010-1	00110000100	0001100001	000010010z	0000011000	0000000000	0001001011	-010000000	0010000110
z101---110	0010000111	1000000100	0100010010	0000000--0	001-000000	1010000000	0000000101	0101000110
0101000z01	0001100000	0011000010	0100000101	01000101z0	1000000000	0000000001	0101000100	0001110001
1000010000	0100111110	0001010101	00020110--	-010012000	0000110001	1100-00000	0000000000	01z??11000
Rhoadsiinae								
<i>Carlana eigenmanni</i>								
00110010-z	0011000100	z001101101	0000100100	0000011100	0100000000	000001--11	-01-000000	0010000110
10-100z-1z	1011000000	1000000100	000--11110	00011zz111	101-0000z0	001zz00000	0000000101	1001000110
0101000001	0111110000	0011000010	0100000101	z1000101z?	?000000000	0000000001	0111000100	00011z0101
1000010001	0100111100	0000010101	0002z10000	00001????00	0000100?1	1?0?000000	00000?0000	00z???????
<i>Nematocharax venustus</i>								
00110010-1	0011000100	0011100001	0000100100	0000011100	0100000000	0001000011	-010000000	0010000110
10-1000010	001000000z	1000000100	0100111110	000111111?	001-000000	101zz00000	0000000101	1001000110
0101100001	0001110000	0011000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001110101
1000010000	0000111z00	0000010101	000201?1??	??001????00	0001100?1	??0?000000	00000?0000	00000?0???
<i>Rhoadsia altipinna</i>								
00010010-0	0011000100	z011101101	0000100100	0000111100	0z00000000	0000010011	-010000000	0010000z10
10-101z01z	1011000000	1000000100	0100011110	00011zz111	101-0000z0	001zz00000	0000000101	1001000110
0101000?01	0011100000	??11000010	0100000101	0100010100	1000000000	0000000000	0111000100	0001110101
1000010001	0100111100	0000010101	000200----	--001????00	00001000?1	11?0-00000	00000?0?00	0z???????
Characinae								
<i>Acestrocephalus sardina</i>								
00010010-0	1?11000000	z011100001	000010zz00	000?010-0-	0100000000	0201000101	-01z010001	00100z0110
0101000-10	001000000z	100001?000	110001--00	0001111000	0000000-11	-011100000	1010000100	0001100100
1100100?01	0011110001	0111000010	1101010101	110001011?	1100000000	0000000001	011?000100	0001100001
1000010000	00011111z0	0000010101	0z0z2?????	??20102-00	0010100111	1100??0000	0000010?00	00z???????
<i>Bryconexodon juruena</i>								
001100z??0	z001000100	0011100001	0000100001	0000011100	0101000010	0101000001	-011010000	0010000110
0101000-10	001000000z	1000000101	0-0?01----	-0011110000	000000--00	0010000000	0000000101	0001000110
0100100001	0011110000	0111000010	01000001z1	010001010?	1000000000	000z000001	01?1000100	0001110001
1000010001	0000111000	0000010101	000211????	??00112000	0000100?1	??0?0?0000	0000000?00	00z???????
<i>Charax stenopterus</i>								
z0110010-0	1011000000	0011100001	0000100100	000011z-00	0000000000	02010z1011	-010000001	0010000110
00-1000-10	0011000000	10000001000	1?0-----	-0011110000	011-000011	-011100000	?010000101	1001--0100
0100100001	0001110001	0111000010	1101010101	1100010110	1110000000	0000000001	0111000100	0001100001
1000010000	0101111110	0010010101	0002010000	0-00102-0-	1000100111	1100100000	0000000000	00z???????

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<i>Cynopotamus argenteus</i>								
100100z0-0	1111000000	0011100001	0000101100	0000010-0-	1101000000	0201000101	-010010001	0010010110
0111000-10	0010000000	1000010000	1?0-?-----	-001111000	001-000011	-011100000	1010000100	0001100100
1101100001	00111z01-1	0111000010	1101010101	1100011110	1z10000000	0000000001	0111000100	0001100001
1000010000	0z01111110	0010010101	01020?????	-?20102-00	0010100111	1100001000	00000?0?00	00???11100
<i>Galeocharax humeralis</i>								
z0010010-0	1011000000	10-1100001	0001101000	0000010-0-	0101001000	0201000101	-010010001	0010z10110
0111000-10	0010000000	1000010000	1?0-----	-001111000	0000000011	-011100000	1010000100	0001z00100
1100100001	00111z01-1	0111000010	1101010z01	110001z110	11z0000000	0000000001	0111000100	0001100001
1000010000	0101111110	0000010101	0102110000	0020102-00	0010100111	1100-00000	0000010?00	00???11100
<i>Phenacogaster tegatus</i>								
00110010-0	0011000100	001110z001	0000100100	0000111000	0100000000	0201001011	-010000000	0010000110
10-1000-10	0011000000	1000000100	0100011011	0001111000	001-000000	1010000000	0z10000101	1001000110
0101000001	0001110001	0111000010	0101000101	1100010110	1000000000	0000000001	0101000100	0001100001
100001000z	0101111110	0000010101	00020112--	-000112000	0000100001	1100100000	00000?0100	00?????????
<i>Roebooides bonariensis</i>								
10110000-1	1011000000	0011100001	0000101100	0000110-0-	0001000000	020101-001	-011010001	0010000110
0111000-10	0010000000	1000001001	0-0-01--11	0001111000	001-000011	-011100000	1010000100	0001100100
0100100001	0001100001	0111000010	1101010101	1100010110	1110000000	0000000001	0111000100	0001110001
1000010000	0101111110	0011010101	0z021?????	?00012000	0010100111	1100101000	0000000?00	00???11100
<i>Roebooides paranensis</i>								
10110000-1	1011100000	0011100001	0000100100	0000111000	0001000000	020101-001	-011010001	00100z0110
0111000-10	0010000000	1000001001	0-0-0---??	0001111000	001-000011	-011000000	1010000101	0001000100
0100100101	00011z0001	0111000010	1101010101	1100010110	1z10000000	000z000001	0111000100	00011z0001
1000010000	0101111110	0011010101	0002z1-???	?0011200-	1010100111	1100100000	0000000000	00???11100
<i>Exodon paradoxus</i>								
00110010-z	0011000100	10-1100001	0000100100	0000011100	0100000010	0201000001	-011010000	0010000110
0101000-10	0010000000	1000000001	0-0-----	0001111000	0000000-01	-011100000	1000000101	0001000110
0100z00001	0011110000	0111000010	0100000101	0100010100	1000000000	0000000001	0101000100	0001010001
100001000z	0100111000	0000010101	000210----	--00012000	0000100001	1110000000	000?0?0?00	00???11100
<i>Roeboexodon geryi</i>								
00110010-0	0011100100	00111100?1	0001100100	0000011100	01z000001?	0-00000001	-0100z00?0	0010000110
0??1000010	001--0000z	10000-0101	0-----	0001111000	001-000000	1011100000	-000000101	?001000110
0100100?01	0001110000	0011000010	0100000111	0100010100	1001000000	0000000001	0101000100	0001100001
1000010001	0000111000	0000010101	000200----	--00112000	00001?0?1	1100100000	00000?0?00	0?????????
<i>Bramocharax clade</i>								
<i>Bramocharax bransfordii</i>								
0?111010-1	0011000100	0001100001	0000100100	0000011100	0110000000	0001000001	-010000000	00100?0110
0??1000-10	001000001z	1000000100	0100011010	0001111110	001-000000	0011000000	0000000101	0001000110
0101000?01	0001100000	0111000010	0100000101	0100010100	1000000000	0000000001	0111000100	0001110001
100001000z	0100111100	0000010101	000201????	?00112000	0000100?01	1??0000000	00000?0?00	00?????????
<i>Hollandichthys multifasciatus</i>								
00110010-z	z011000100	0001100001	000010z100	0000010-z-	0100000000	120101--11	-010-00000	0010000110
10-1000-10	001000000z	1000000100	0100011010	0001111100	001-0000z1	-011100000	0000000101	10010-0110
0100100z01	00011z000z	0111000010	0100000101	z100010101	1000000000	0000000001	0111010000	00011z0001
1000010001	0100111100	0000010101	0002010010	0000112000	0000100?01	1??0?00000	0000000000	0011111000
<i>Characidae N. gen. N. sp.</i>								
00111010-1	0001000100	0001100001	0000100100	0000011000	0100000000	0201000001	-010000000	0010000010
0101000-10	0010000001	1000000100	0100011010	0001111100	001-000000	0011000010	1000000100	0001z10110
0101000001	0001100000	0111000010	0100000101	z100010100	1000000000	0000000001	0111000100	0001110001
1000010001	0100111000	0000010101	0002110000	0000112000	0000100001	1100000000	00000?0000	00?????????
<i>Oligosarcus bolivianus</i>								
00111010-z	0101000100	00z1100001	0000100100	0000011000	0100000000	0201000101	-010000001	0010000110
0101000-10	0010000001	1000000100	1-0-----	0001111100	001-000101	-011100010	1000000100	0001110110
0101000101	0001100001	0111000010	0100000101	0100010100	1000000000	0000000001	0111000100	0001110001
1000010001	0000111000	0000010101	0002110011	0000112000	0000100001	1100000000	0000010000	00?????????
<i>Oligosarcus cf. jenkinsii</i>								
00111010-1	0101000z00	z0z1100001	0000100100	0000011000	0100000000	0201000101	-010010001	0010000110
0101000-10	0010000001	1000000100	1-0-----	0001111100	001-000101	-011100010	1000000101	0001110110
0101000101	0001100001	0111000010	0100000101	0100010100	1000000000	0000000001	0111000100	00011z0001
1000010001	0000111z00	0000010101	00021100z1	0000112000	0000100001	1100000000	0000010000	00???11000
<i>Pseudochalceus kyburzi</i>								
00110010-1	0011000100	z001100001	0000100100	0000011100	0z00000000	000001--11	-0-0000000	0010000110
10-1000-10	001000000z	1000000100	0100011010	0001111100	001-000z11	-011100000	0000000101	0001000110
0101000001	0001100000	1011000010	1100000101	0100010101	1000000000	0000000000	0111000100	0001110101
1000010001	0z00111100	0000010101	000200----	--00112000	00??100?01	??0?0?0000	0000?00?00	00000?????

Appendix 2
(Continued)

<i>Nematobrycon</i> clade									
<i>Nematobrycon palmeri</i>									
00110010-z	0011000100	10-1100001	1000100101	0000z11100	0100000000	000001--11	-010000000	0-10000110	
0??1000-10	001z000011	1000000100	0100011000	00?1111100	001-000000	1010000000	0000000101	?101000110	
010??00?01	00111z0000	1011000010	0100000101	0100010100	1000000000	000z000001	0101000100	0001100001	
1000010001	0000111100	0000010101	000200----	--001???00	00?0100??1	???0?0000	0000???01	0000011000	
<i>Gymnocharacinae</i> n. def.									
<i>Coptobrycon bilineatus</i>									
00110010-0	0011010100	0001100001	001-10010z	0000010-0-	011000----	---?00---1	-0-----1-	00?--00-10	
10-1---010	001--0000z	1000000100	010-011100	0000000--0	001-000000	1010000000	0z00000101	01010-0110	
0100000001	0z111z0000	1011000010	0100000101	01000101z?	1000000000	1000000001	010-000000	0001110000	
1000010001	0000110000	1000010101	0002z0----	--001???00	00001000?1	1?0?0?0001	0000001?01	00? ????????	
<i>Grundulus cochae</i>									
0011011?-0	0011010100	0001100001	1000100100	0000010-?-	0110000000	0--100---1	-01-0--01-	00?--?0---	
10-1000-10	001100000z	1000000000	000--1--11	00?1111000	0z1-000010	1010000000	?000000101	?101000110	
0101000?01	01111z0000	1011000010	0100000101	01?00z0100	1000000000	100000000z	0101000000	0001110001	
1000010001	1000110000	0000010101	000200----	--0011200-	1000100?1	??0?0?0000	0000001?01	0? ????????	
<i>Gymnocharacinus bergii</i>									
00110010-0	011-010z00	0001100001	1000100100	0000010-0-	0110000-00	0--1-0---1	-010001000	?0?0000110	
0--1000010	0011000001	1000000110	0100111100	0001100110	001-000000	1010000000	0000000101	0001000110	
0100100001	0111100000	1011000010	0100000101	0100000100	1000000000	1000100000	1101000000	0001110001	
1000010001	1010110000	0000010101	0z0200----	--001???0-	10001100?1	?100000000	00000?0?01	00? ????????	
<i>Aphyocharacinae</i> n. def.									
<i>Aphyocharax anisitsi</i>									
00110010-0	0111011110	10-110000-	-100001100	0100111001	0110000000	010001-001	-010001100	0z10000110	
1101000010	0111101000	1000000100	000--1--10	00111z0000	001-000000	1010000000	0000000101	0101000110	
0101000?01	0001110000	0011000010	0100000101	0100010110	1001000000	0001000z00	1100000000	0001100001	
1000010001	000011z000	0000010101	000201001-	1000112000	0000100001	1100000000	1000000100	00?0? ??????	
<i>Aphyocharax dentatus</i>									
00110010-0	0111011100	10-110000-	-100001100	0100111001	0110000000	010001-001	-010001100	0010000110	
1101000010	0111101000	1000000100	000--1--1z	0011110000	001-000000	1010000000	0100000101	010100011z	
0101000001	0001110000	0011000010	0100000101	0100010110	1001000000	0001000000	1100000100	0001100001	
1000010001	0000111000	0000010101	0002010000	0000112000	0000100001	11z0000000	1000000?00	00? ??11000	
<i>Aphyocharax nattereri</i>									
00110010-0	0111011100	00z110000-	--00001100	0100110-0-	0110000000	010001-0-1	-01000-11-	0-10000110	
10-1000-10	0111100000	1000000100	000--1--10	0011110000	001-000000	1010000000	0000000101	?001000110	
0101000001	0001110000	0011000010	0100000101	0100010110	1001000000	0001000000	110?000z00	0001100000	
1000010001	0000111000	0000010101	000y010000	0000112000	0000100001	11?0000000	0000000?00	0000? ??????	
<i>Inpaichthys kerri</i>									
00110010-1	00110-0100	10-1100001	1-00000100	0000011010	0110100000	010001---1	--1-0-0000	0010000110	
10-1000010	001100000z	1000000100	000--1--1z	0011110100	001-000000	1010000000	0001000101	1101000110	
0101000001	0001110000	0011000010	0100000101	0100010110	1000000000	0000000001	0101000000	00011z0001	
100001z001	0000111000	0000010101	000200----	--00112000	00001000?1	0100000000	00000?0?00	00? ??11100	
<i>Paragoniates alburnus</i>									
00110010-0	0011011100	10-110000-	?100001100	000?10-0-	01000??1?0	01?00000?1	-010001100	0?10000110	
1101000-10	0?11?00000	1000000100	0z0--11---	00?1111100	001-000000	101000?00	?0000?0101	?0100?110	
01010?0?01	00??100000	0011000010	0100000101	01000101?-	?001000100	0001000zz-	-?0000100	?001100001	
1000010001	1001111110	0001010101	000200????	?001??000	00101000??	?100?0000	00000?0?00	00000?0???	
<i>Phenagoniates macrolepis</i>									
00110010-0	0111011100	z001100001	0-00001100	000?z10-?-	0100000100	0100000011	-010000100	00100?0110	
1101110-10	0?10100000	1001000100	000--11110	00?1111100	001-000000	1110000000	0000000101	?101000110	
0101010?01	0001110000	0011000010	0100000101	01000111?-	1001000000	000100000-	-100000000	?001100000	
1000000001	1001111110	0001010101	00020?????	?000002-00	00?01100?1	1?000?0000	0000010?01	00? ????????	
<i>Prionobrama paraguayensis</i>									
00110010-0	0111011100	10-110000-	-100001100	0000111001	0110000100	010001---1	-010001100	0010000110	
1101000-10	0011100000	1000000100	000-----11	0011111000	001-000000	1010000000	0100000101	0101000110	
0101010001	0001100001	0011000010	0100000101	010001011-	0001100000	000101000-	0100000000	0001100000	
1000000001	0001111100	0001000101	0002010010	0000112000	00001000?1	0100000000	0000010?00	0000011100	
<i>Xenagoniates bondi</i>									
00110010-0	0111011100	10-110000-	-100001100	0000110-1-	010000?100	010?00?0?1	-0?0001100	0?1??0110	
0??1110-?0	0?1??0011?	1001000100	000--11110	0001111100	001-000000	1110000?10	0000000101	?101000110	
0100-10001	0001110000	0011000010	0100000101	0100011110	1001100000	0000000z1-	-??0000000	?001100000	
1000000001	1011111110	0001010101	000200????	?00112000	0000111?1	1??0?00000	00000?0?00	00000?0???	
<i>Aphyoditeinae</i> n. def.									
<i>Aphyocharacidium bolivianum</i>									
00110010-z	0011000100	10-1101001	1000100100	001-011000	0110000000	0100001011	-010000000	0010000110	
00-1000011	0011000100	1000000100	000--11111	0011110100	0100000000	1010000000	0000000101	1101000110	
0101000101	0011110000	0011000010	0101000101	01000101z?	1001000000	0000000001	0101000100	0001100001	

Appendix 2
(Continued)

1000010000	0000z1100z	0000010101	0z02010010	10001???00	00001000?1	z??0100000	00000?0100	00????????
<i>Aphyodite grammica</i>								
00110010-1	0011000100	0001101001	0000100100	0000011z00	0110000000	010101--11	-010000000	0010000110
10-1000011	0011000000	1000000100	000--1--11	00?1z00000	011-000000	1010000000	0000000101	1101000110
0101000?01	0011100000	0011000010	0100000101	0100010110	1001000000	0001000001	0101000100	00011z0001
1000010001	0000111000	0000010101	00020?????	??00112000	00011001?1	1100100000	00000?0?00	00????????
<i>Axelrodia lindeae</i>								
00110010-z	0011000100	0011101001	0000100100	001-011000	0110000000	0-010010-1	-010000000	0010000110
10-1000011	0011000000	1000000000	000--1--11	--11110000	011-010000	1010000000	00z0000-01	11010-0110
0100100001	0001110000	1010000010	0101000101	010001011?	10010000-0	0-00000001	0101000000	0001100001
1000010000	0000111z01	0000010101	1z12010011	00001???00	0000100?1	z??0100000	00000?0100	00????????
<i>Microschemobrycon casiquiare</i>								
00110010-0	0011000100	10-1101001	0000100100	00z0011z00	0110000000	0100000011	-010000000	0011--0110
10-1000011	0011000000	1000000100	000001--11	0011110100	011-000000	1010000000	0100000101	1101z00110
0101000101	0011110000	0011000010	0100000111	0100010110	1001000000	0000000001	0101000100	0001110001
1000010000	000011z000	0000010101	00020?????	??00112100	000z100001	1100100000	00000?0?00	00???00000
<i>Parecbasis cyclolepis</i>								
00110010-z	0011000100	10-1101001	0000100100	0000011100	0100000000	0100000001	-010000000	01100?0110
0??1--011	0011001000	1000000100	000-----11	0010000--0	011-000000	1010000000	0000000101	?001000110
0101000?01	0111000000	0011000010	0100000111	0101010100	1001000000	0000000001	0101000100	00010z0001
1000010000	0100111000	00000z0101	00020?????	??00112000	00011000?1	1100?00000	00000?0?00	0?????????
<i>Cheirodontinae</i>								
<i>Cheirodon interruptus</i>								
00110010-0	0011010100	10-1101001	-000100100	0000011000	0110000000	0100001011	-010000000	0-10000110
10-1--1011	0011001000	1000000110	000--11110	0001000110	001-000010	1010000000	0z01000101	01010-0111
0101000z01	z111100000	0011000010	0100000101	0100010110	1000000000	0000000001	0101000000	0001110001
1000010001	000011z000	0000010101	1112010011	0000112000	00001000?1	1100100000	0000010100	00000?????
<i>Odontostilbe microcephala</i>								
00110010-0	0011010100	10-1101001	0000100100	0000011000	0110000000	0100001001	-010010000	0010000110
0101001011	0011001000	1000000110	000--11110	0001100110	001-000010	1010000000	0101000101	0101000111
0101000101	0111100000	0011000010	0100000101	0100010110	1001000000	0000000001	0101001100	0001110011
1000010001	0000111000	0000010101	0002010001	0000112000	0000100001	1100100000	0000000100	0????11100
<i>Odontostilbe paraguayensis</i>								
00110010-0	0011010100	10-1101001	000010010z	0000011000	0100000000	0100001001	-010000000	0110000110
0101001011	0011001000	1000000110	000--11110	0001100110	001-0000z0	1010000000	0101000101	0101000111
0101000001	0001110000	0011000010	0100000101	0100010110	1001000000	0001000001	0101001100	0001110011
1000010000	0100111000	0000010101	0002010001	0000112000	0000100001	0100100000	00000z0100	0000011100
<i>Odontostilbe pequirá</i>								
00110010-0	0011010100	10-1101001	-000100100	0000011000	0110000000	0100001001	-010000000	0010000110
0101001010	0011001000	1000000110	000--11110	0001100110	001-000000	1010000000	0z0z000101	?101000110
0101000001	0001100000	0011000010	0100000101	0100010110	1001000000	0000000001	0101001100	0001110011
100001000z	0000111000	0000010101	0002010001	0000112000	0000100001	1100100000	0000000100	0000011100
<i>Prodontocharax melanotus</i>								
00110010-0	00110z0100	10-1101001	100010010z	000?011000	0110000000	0100001011	-010000000	0z10000110
0101010-11	001100100z	1000000100	000--11110	00011111z0	101-000000	1010000000	0101000101	1101000110
0101100001	1111z00000	0011000010	0100000101	0100010110	1001000000	0000000001	0101001100	0001110001
1000010001	0100110000	0000010101	00020100z0	0000112000	00001000?1	0100100000	0000000100	00????????
<i>Serrapinnus calliurus</i>								
00110010-0	0011010100	10-1101001	000010010z	0000011000	0110000000	0100001001	-010000000	0110000110
10-1001011	0011001000	1000000110	000--11110	0001100110	001-000010	1010000000	0101000101	0101000111
0101000001	1001110000	0011000010	0100000101	0100010100	1001000000	0000000001	0101000100	0001110001
1000010000	0100111001	0000010101	1112010011	0100112000	0000100001	0100100000	00000z0100	0000011100
<i>Stevardiinae n. def.</i>								
<i>Acrobrycon tarijae</i>								
00110010-0	0011010100	00z1100001	1000100100	0001011000	0110000000	0000000011	-010000000	0011--0110
0101000010	001000001z	1000000100	0100011000	0001110100	001-000000	0010000000	0z00000101	0011000110
0101000001	0001100000	0011000010	0100000101	0100010z00	1001000000	0000000000	0101000100	0001100000
1000000001	1000111z00	0000010101	0002010311	0000112000	0000100001	1100000000	0000000110	00111?????
<i>Attonitus ephimeros</i>								
00110010-0	0111010100	z0-1100001	1000100100	0001010-0-	0110000000	0100000011	-010001000	0011--0110
0101000011	0011000001	1000000100	0100011100	0001110100	001-000000	0010001000	0100000101	0101000110
0100000101	0111110000	1011000010	0100000101	01000101?0	1001100000	0000000000	0101000100	0001100000
1000000001	0000110000	0000010101	0002010011	0000112000	0000100001	1110000000	00000?0100	00100?????
<i>Aulixidens eugeniae</i>								
0011001?-z	0010010100	10-1100001	0000100100	0001011000	0110000000	0100000011	-010000000	0011--0110
0100--011	0011000011	1000000100	000--11100	0000000--0	001-001000	1010010000	?100000101	?101000110
0101000?01	1011110000	1011000011	-100000101	0100010110	1001000000	000z000000	0001000100	000110000z
1000000001	0000111000	0000010101	0002010011	1000112000	0001110?1	??0?000000	0000000?00	00????????

Appendix 2
(Continued)

<i>Bryconamericus agna</i>								
00110010-0	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-0100000000	0011--0110
01010z0010	0011000111	1000000100	0100111000	0001100110	001-000000	0010000000	0100000101	0101000110
0101000001	0111110000	0011000010	0100000101	0100010100	1001000000	000z000000	0101000100	0001100000
1000000001	0000111000	0000010101	0002010000	0000112000	0000110001	1100000000	0000000100	00z???????
<i>Bryconamericus beta</i>								
00110010-z	0011010100	z0-1100001	100010010z	0001011000	0110000000	0100000011	-01000z000	0011--0110
0101000010	0010000111	1000000100	0100z11000	0001100110	001-000000	0010000000	0100000101	0101000110
0101000001	0111110000	0011000010	0100000101	0100010110	1001000000	0000000000	0101000100	0001100000
100000000z	0000111z00	0000010101	00020100z0	0000112000	000z110001	1100000000	00000?0?00	00z???????
<i>Bryconamericus exodon</i>								
00110010-0	0011010100	00z1100001	1000100100	0001011000	0110000000	0100000011	-0100000000	0011--0110
0101000010	0010000111	1000000100	0101011000	0001100100	001-000000	0010000000	0100000101	01z1000110
0101z00001	0001110000	0011000010	0100000101	0100010110	1001100000	0000000000	0001000100	0001100000
100000000z	0000111000	0000010101	0002z1? ???	? ?00112000	0000110001	1100000000	30000?0100	00z??11100
<i>Bryconamericus cf. exodon</i>								
00110010-0	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-0100000000	0011--0110
0101000010	0010000111	1000000100	0101011000	0001100100	001-000000	0010000000	0100000101	01z1000110
0101000001	z011100000	0011000010	0100000101	0100010110	1001100000	0000000000	0001000100	0001100000
1000000001	0000111000	0000010101	0002010010	0000112000	0000110001	1100000000	0000000100	00z???????
<i>Bryconamericus cf. iheringii</i>								
00110010-0	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-01000z0z0	0011--0110
0101000010	0011000011	1000000100	0100011000	00011z0100	001-000000	0010000000	0z00000101	0101000110
0101000001	1111100000	0011000010	0100000101	0100010100	1001000000	0000000000	0101000100	0001100000
1000000001	000011z000	0000010101	0002010111	0000112000	0000110001	1100000000	0000000100	000??11100
<i>Bryconamericus mennii</i>								
00110010-0	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-01000z000	0011--0110
0101000010	0010000z11	1000000100	0100011000	00011z0100	001-000000	0010000000	0100000101	0101000110
0101000001	0001110000	0011000010	0100000101	0100010100	1001000000	0000000000	0101000100	0001100000
100000000z	0000111000	0000010101	000200----	--00112000	0000110001	1100000000	0000000?00	00z0? ??????
<i>Bryconamericus cf. rubropictus</i>								
00110010-0	0011010100	0011100001	1000z00100	0001011000	0110000000	0100000011	-01000z000	0011--0110
0101000010	0011000011	1000000100	01000110z0	0001110100	001-000000	0010000000	0z00000101	0101000110
0101000001	1111110000	0011000010	0100000101	01000101z0	1001000000	0000000000	0101000100	0001100000
1000000001	0000111000	0000010101	0002010011	0000112000	0000110001	1100000000	0000010000	00z???????
<i>Bryconamericus rubropictus</i>								
00110010-0	0011010100	00z1100001	1000100100	0001011000	0110000000	0101000011	-01000101-	0011--0110
00-1000010	0011000011	1000000100	0100011000	00011z0100	001-000000	0010000000	0z00000101	0101000110
0101000001	11111z0000	0011000010	0100000101	0100010110	1001000000	0000000000	0101000100	0001100000
1000000001	0000110000	0000010101	0002010111	0000112000	0000110001	1100000000	0000010000	00z???????
<i>Bryconamericus thomasi</i>								
00110010-0	0011010100	00z1100001	1000100100	0001011000	0110000000	0100000011	-010001000	0011--0110
00-1000010	0011000011	1000000100	0100011000	00011z0100	001-000000	0010000000	0z00000101	0101000110
0101000001	1111110000	0011000010	0100000101	0100010100	1001000000	0000000000	0101000100	0001100000
1000000001	000011z000	0000010101	0z0z010111	0000112000	0000110001	1100000000	00000z0100	00z???????
<i>Creagrutus anary</i>								
00110010-1	0011010100	0001110001	1000100100	0001011000	0110000000	0100000011	-010001000	0010000110
0101010010	0010000111	1000000100	011-010000	00011z0100	001-000000	0110000000	0100000101	0101z00110
0100100001	0001100000	1010000010	0100000101	z100010100	1001100000	0000100000	0001000100	0001000000
1000000001	01000z0000	0000010101	01020110--	-000112000	0000111001	0000000000	00000?0?00	00z???????
<i>Creagrutus cf. taphorni</i>								
00110010-0	0011010100	0001110001	0000100100	000?011000	0110000000	0101000011	-010001000	0010000110
0??1010010	0010000111	1000000100	011-011000	00011z0100	001-000000	0110000000	?100000100	?101?00110
010??00?01	?0?1110000	1010010010	0100000101	01000101??	?001100000	0001100000	0101000100	0001100000
100000000z	0z000z0000	0000010101	0102010011	0000112000	00001110?1	11000?0000	00000?0?00	0z???????
<i>Cyanocharax alburnus</i>								
00110010-z	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-0100000000	0011--0110
0101000010	001000001z	1000000100	01000110z0	00011z0100	001-000000	1010000000	0100000101	0101000110
0101000001	0z11100000	0011000010	01z0000111	0100010100	1001000000	0000000000	0101000000	0001100000
1000000001	0000111000	0000010101	00020100??	?000112000	0000100001	1100000000	00000?0100	00z???????
<i>Diapoma speculiferum</i>								
00110010-0	0011010100	0001100001	1000100100	0001011000	0110000000	0100000011	-0100000000	0011--0110
10-1000010	0010000011	1000000100	0100011000	0001110100	001-000000	1010000000	0100000101	0101000110
0101000101	z001100000	0011000010	01000001z1	0100010100	1001000000	0000001000	0001000000	0001100000
1000000001	0011111100	0000010101	00020100??	0000112000	0000100001	1100000000	00000?0010	00111? ?????

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<i>Diapoma terofali</i>								
00110010-0	0011010100	0001100001	1000100100	000101z000	0110000000	0100000011	-010000000	0011--0110
10-1000010	001000001z	1000000100	01000110z0	00011z0100	001-000000	0010000000	0100000101	01z1000110
0101000101	0011100000	0011000010	0100000101	0100010100	1001000000	000z001000	0101000000	0001100000
100000000z	0011111100	0000010101	0002010011	0000112000	0000100001	1100000000	00000?0010	00111?????
<i>Hemibrycon dariensis</i>								
001100z0-z	0011010100	0001100001	1000100100	0000011000	0110000000	0100000011	-010000000	0011--0110
0101000010	0010000011	1000000100	010zz11000	0001110110	001-000100	0010000000	0000000101	0011000110
0101000001	0001110000	0011000010	0100000101	0100010100	1001000000	000000000z	0101000100	0001100000
1000000001	0000111100	0000010101	00020?????	??00112000	0000100001	1100000000	00000?0?00	0000??????
<i>Hemibrycon surinamensis</i>								
00110010-0	0011010100	0001100001	1000100100	0000011000	0110000000	01000000?1	-01???0000	0011--0110
0??1000-10	0010000011	1000000100	010z0110z0	0001111100	001-000100	0010000000	0000000101	0011000110
0101000?01	00011z0000	0011000010	0100000101	010001010?	1001000000	0000000001	0??1000100	0001100000
1000000001	0000111100	0000010101	000201????	??00112000	0000100001	1100000000	00000?0?00	00? ???????
<i>Knodus breviceps</i>								
00110010-z	0011010100	10-1100001	0000100100	0001011000	0110000000	010000z011	-010000000	0011--0110
0??1000010	0010000111	1000000100	010z011000	0001100110	001-000000	0010000000	0100000101	?101000110
0101000?01	0111110000	0011000010	01z0000101	0100010100	1001000000	0000000000	0001000100	0001100000
1000000001	000011z000	0000010101	00020100z0	0000112000	0001110001	???0?00000	00000?0?00	00???11100
<i>Mimagoniates rheocharis</i>								
00110010-z	00110-0?00	0001100001	??0000010z	0000z11000	0110000000	11000z-011	-010?00?00	0-1?--0-10
1--1000010	0010000010	1000000100	0100011010	0001110100	001-000000	0010000000	0z00000101	01z10-0110
0101100?01	00011z0000	0011000010	0100000101	010001010?	1001000000	0000001000	01010z0000	0001100001
0000010001	1001111100	0000010101	0002012011	0000112000	000-1000?1	1??0?00000	0000000010	00111?????
<i>Nantis indefessus</i>								
00110010-0	0011010100	0001100001	1000100100	0001010-0-	0110000000	0-010z-011	-01000z000	0011--0-10
00-1010010	0011000001	1000000100	0100011010	0001110100	001-000000	1010000000	0z00000101	0101000110
0101000001	0111110000	0011000010	0100000101	0100010100	1000000000	0000000000	01z1000100	0001100000
1000000001	00001z0000	0000010101	0002012011	1-00112000	0000100001	1100000000	00000z0000	00? ???????
<i>Nantis cf. indefessus</i>								
00110010-0	0011010100	0001100001	1000100100	0001010-0-	0110000000	0-0100-011	-010001010	0011--0-10
00-1010010	0011000001	1000000100	0100011010	0001110100	001-000000	1010000000	0z00000101	0101000110
0101000001	01111100-0	0011000010	01z0000101	0100010100	1000000000	0000000000	01z1000100	0001100000
1000000001	00001z0000	0000010101	0002012011	0-00112000	0000100001	1100000000	00000?0000	00? ???????
<i>Odontostoechus lethostigmus</i>								
00110010-z	0011010100	10-1100001	0000100100	0001011000	0110000000	0100000011	-010001000	0011--0110
0101010010	0011000011	1000000110	000--11110	0001110110	001-000000	0010000000	0100000101	0101000110
0101000?01	01111z0000	0011000010	01000001z1	010001010?	1001000000	0000000000	0101000100	0001100000
1000000001	000011z000	0000010101	0002z1001z	z000112000	0000110001	1??0000000	0000000000	00? ???????
<i>Piabina argentea</i>								
00110010-0	10z1010100	0001110001	0000100100	0001011000	0110000000	0100000011	-01000z000	0010000110
01010z0010	0010000111	1000000100	01z-010000	0001100100	001-000000	0010000000	0100000101	0001000110
0111000001	0001100000	1011010010	0100000101	0100010110	1001100000	0000000000	0101000100	0001100000
1000000001	000011z000	00000z0101	000201001?	0000112000	00001110?1	z110000000	0000000?00	00???11100
<i>Pseudocorynopoma doriae</i>								
00110010-0	0011010100	0001100001	0000100100	0001000-0-	0110000000	0100000011	-0100-0000	0011--0110
0101000010	001z00001z	1000000100	010001101z	00011z01z0	001-000000	1010000000	0000000201	0101000110
0101000001	?001100000	00110z0010	0100000101	0100010100	1001000100	0000001100	010-000000	0001100101
1000000001	1001111110	0001010101	00020110--	-000112000	0000100001	1100000000	0000000010	00111?????

Appendix 3

Common synapomorphies obtained in the trees used to construct the final hypothesis. Node numbers are those assigned by TNT, corresponding with those of Figs 1–3. Under each node both stability and support measures are stated. Stability measures consider all the range of explored parameters, while support measures were calculated for $K = 10$, under implied weighting. Those measures are, respectively, GC values as stability measure, relative frequencies, GC values as support measure, and relative Bremer support. Cases where support measures are (artificially) negative are indicated with a dash (–), whereas stability measures are indicated as negative.

Node 164: Characoidei (100/100/83/20)	Char. 222: (0) > (1)	(100/100/38/13)	Char. 271: (0) > (1)
Char. 36: (3) > (0)	Char. 231: (1) > (0)	Char. 9: (0) > (1)	Node 162: Parodontidae
Char. 168: (0) > (2)	Char. 260: (1) > (0)	Char. 182: (1) > (0)	(100/100/100/55)
Char. 175: (1) > (0)	Char. 330: (0) > (1)	Char. 305: (0) > (1)	Char. 7: (1) > (0)
	Node 163:	Some trees:	Char. 11: (0) > (1)

- Char. 16: (0) > (1)
 Char. 20: (0) > (1)
 Char. 36: (0) > (1)
 Char. 41: (0) > (1)
 Char. 71: (0) > (1)
 Char. 96: (0) > (1)
 Char. 113: (0) > (1)
 Char. 163: (0) > (1)
 Char. 197: (0) > (1)
 Char. 230: (0) > (1)
 Char. 235: (0) > (1)
 Char. 242: (1) > (0)
 Char. 252: (1) > (0)
 Char. 259: (1) > (0)
 Char. 292: (0) > (1)
 Char. 345: (0) > (1)
 Node 167:
 (0/86/11/9)
 Char. 21: (1) > (0)
 Char. 74: (0) > (1)
 Char. 76: (0) > (1)
 Char. 179: (0) > (1)
 Char. 297: (0) > (1)
 Node 166: **Anostomoidea**
 (100/100/96/42)
 Char. 143: (0) > (1)
 Char. 153: (1) > (0)
 Char. 168: (2) > (0)
 Char. 199: (0) > (1)
 Char. 207: (0) > (1)
 Char. 209: (1) > (0)
 Char. 332: (1) > (0)
 Char. 345: (0) > (2)
 Node 165:
 (30/88/52/12)
 Char. 205: (0) > (1)
 Char. 208: (0) > (1)
 Node 169:
 (47/95/10/16)
 Char. 171: (1) > (0)
 Char. 272: (1) > (0)
 Char. 279: (1) > (0)
 Char. 282: (1) > (0)
 Char. 331: (0) > (1)
 Some trees:
 Char. 294: (0) > (2)
 Node 168: **Crenuchidae**
 (100/100/100/44)
 Char. 37: (1) > (0)
 Char. 47: (0) > (1)
 Char. 64: (0) > (1)
 Char. 87: (0) > (1)
 Char. 143: (0) > (1)
 Char. 149: (0) > (1)
 Char. 159: (0) > (1)
 Char. 164: (0) > (1)
 Char. 183: (0) > (1)
 Char. 185: (1) > (0)
 Char. 230: (0) > (1)
 Char. 315: (0) > (1)
 Char. 317: (0) > (2)
 Char. 318: (1) > (0)
 Char. 334: (0) > (1)
 Char. 347: (0) > (1)
 Some trees:
 Char. 38: (1) > (0)
 Char. 204: (1) > (0)
- Node 173:
 (100/100/78/21)
 Char. 8: (1) > (0)
 Char. 25: (0) > (1)
 Char. 100: (1) > (0)
 Char. 111: (0) > (1)
 Char. 242: (1) > (0)
 Char. 259: (1) > (0)
 Char. 266: (1) > (0)
 Char. 325: (0) > (1)
 Node 180: **Erythroidea**
 (100/100/93/33)
 Char. 24: (1) > (0)
 Char. 34: (0) > (1)
 Char. 41: (0) > (1)
 Char. 70: (0) > (1)
 Char. 118: (1) > (0)
 Char. 135: (0) > (1)
 Char. 136: (0) > (1)
 Char. 300: (1) > (0)
 Char. 350: (0) > (1)
 Char. 356: (1) > (0)
 Char. 357: (1) > (0)
 Some trees:
 Char. 332: (1) > (0)
 Node 172: **Characoidea**
 (100/100/69/16)
 Char. 57: (1) > (0)
 Char. 89: (0) > (1)
 Char. 226: (0) > (1)
 Char. 264: (0) > (1)
 Char. 286: (0) > (1)
 Char. 287: (0) > (1)
 Char. 295: (1) > (0)
 Some trees:
 Char. 333: (1) > (0)
 Node 171: **Gasteropelecidae**
 (100/100/100/60)
 Char. 56: (0) > (1)
 Char. 66: (0) > (1)
 Char. 73: (1) > (0)
 Char. 105: (0) > (1)
 Char. 143: (0) > (1)
 Char. 206: (0) > (1)
 Char. 248: (0) > (1)
 Char. 249: (0) > (1)
 Char. 255: (0) > (1)
 Char. 262: (0) > (1)
 Char. 315: (0) > (1)
 Some trees:
 Char. 110: (1) > (0)
 Char. 204: (1) > (0)
 Char. 228: (0) > (1)
 Char. 258: (1) > (0)
 Node 170:
 (100/100/100/44)
 Char. 2: (1) > (0)
 Char. 3: (0) > (1)
 Char. 17: (0) > (1)
 Char. 37: (1) > (0)
 Char. 41: (0) > (1)
 Char. 70: (0) > (1)
 Char. 81: (1) > (0)
 Char. 130: (0) > (1)
 Char. 150: (0) > (1)
 Char. 157: (0) > (1)
 Char. 185: (1) > (0)
- Char. 190: (1) > (0)
 Char. 238: (0) > (1)
 Char. 247: (0) > (1)
 Char. 273: (0) > (1)
 Char. 274: (0) > (1)
 Char. 281: (0) > (1)
 Char. 284: (0) > (1)
 Some trees:
 Char. 192: (1) > (0)
 Node 179:
 (100/100/-/16)
 Char. 10: (0) > (1)
 Char. 30: (0) > (1)
 Char. 64: (0) > (1)
 Char. 98: (0) > (2)
 Char. 220: (0) > (1)
 Char. 279: (0) > (1)
 Char. 305: (0) > (1)
 Some trees:
 Char. 76: (0) > (1)
 Char. 108: (0) > (1)
 Node 186: **Serrasalminidae**
 (100/100/100/48)
 Char. 53: (1) > (0)
 Char. 126: (1) > (0)
 Char. 131: (0) > (1)
 Char. 169: (0) > (1)
 Char. 170: (1) > (0)
 Char. 199: (0) > (1)
 Char. 225: (0) > (1)
 Char. 278: (0) > (1)
 Char. 282: (0) > (1)
 Char. 316: (1) > (0)
 Char. 321: (0) > (1)
 Char. 322: (0) > (1)
 Char. 323: (0) > (1)
 Char. 342: (0) > (1)
 Char. 359: (0) > (1)
 Some trees:
 Char. 3: (0) > (1)
 Char. 15: (0) > (1)
 Char. 184: (1) > (0)
 Char. 228: (0) > (1)
 Char. 258: (1) > (0)
 Char. 298: (1) > (0)
 Char. 333: (0) > (1)
 Char. 358: (0) > (1)
 Node 185:
 (100/100/90/26)
 Char. 66: (0) > (1)
 Char. 145: (0) > (1)
 Char. 275: (0) > (1)
 Char. 288: (0) > (1)
 Char. 326: (0) > (1)
 Char. 327: (0) > (1)
 Char. 360: (0) > (1)
 Some trees:
 Char. 76: (1) > (0)
 Node 184: **Alestidae**
 (100/100/39/16)
 Char. 61: (1) > (0)
 Char. 82: (0) > (1)
 Char. 90: (0) > (1)
 Char. 157: (0) > (1)
 Char. 189: (0) > (1)
 Char. 287: (1) > (0)
 Char. 295: (0) > (1)
- Char. 297: (0) > (1)
 Char. 300: (1) > (0)
 Some trees:
 Char. 219: (0) > (1)
 Node 183:
 (100/100/99/30)
 Char. 8: (0) > (1)
 Char. 30: (1) > (0)
 Char. 57: (0) > (1)
 Char. 64: (1) > (0)
 Char. 94: (1) > (0)
 Char. 106: (0) > (1)
 Char. 162: (0) > (1)
 Char. 264: (1) > (0)
 Char. 276: (1) > (0)
 Char. 304: (0) > (1)
 Char. 326: (0) > (1)
 Some trees:
 Char. 294: (0) > (1)
 Char. 298: (1) > (0)
 Node 182:
 (100/100/99/37)
 Char. 36: (0) > (2)
 Char. 112: (0) > (1)
 Char. 126: (1) > (2)
 Char. 127: (1) > (0)
 Char. 153: (1) > (0)
 Char. 195: (1) > (0)
 Char. 327: (0) > (1)
 Node 181:
 (100/100/90/12)
 Char. 53: (1) > (0)
 Char. 287: (0) > (1)
 Node 178: **Characidae**
 (100/100/42/12)
 Char. 37: (1) > (0)
 Char. 47: (0) > (1)
 Char. 227: (0) > (1)
 Char. 288: (0) > (1)
 Char. 304: (0) > (2)
 Char. 318: (1) > (0)
 Char. 329: (1) > (0)
 Some trees:
 Char. 21: (1) > (0)
 Char. 92: (0) > (1)
 Char. 135: (0) > (1)
 Char. 172: (1) > (0)
 Char. 193: (1) > (0)
 Char. 317: (0) > (2)
 Node 177:
 (100/100/12/6)
 Char. 7: (1) > (0)
 Char. 71: (0) > (1)
 Char. 93: (0) > (1)
 Char. 136: (0) > (1)
 Char. 137: (0) > (1)
 Char. 195: (1) > (0)
 Char. 199: (0) > (1)
 Char. 253: (0) > (1)
 Some trees:
 Char. 74: (0) > (1)
 Char. 183: (0) > (1)
 Char. 202: (0) > (1)
 Char. 281: (0) > (1)
 Node 176:
 (100/100/47/17)
 Char. 10: (1) > (0)

Char. 62: (0) > (2)	Char. 64: (1) > (0)	Char. 151: (0) > (1)	(100/100/100/51)
Char. 150: (0) > (1)	Char. 67: (0) > (1)	Char. 152: (0) > (1)	Char. 8: (0) > (1)
Char. 154: (0) > (1)	Char. 74: (1) > (0)	Char. 153: (1) > (0)	Char. 73: (1) > (0)
Char. 155: (0) > (1)	Char. 85: (0) > (1)	Char. 158: (0) > (1)	Char. 118: (1) > (0)
Char. 200: (0) > (1)	Char. 136: (1) > (0)	Char. 167: (0) > (1)	Char. 137: (0) > (1)
Char. 203: (1) > (0)	Char. 137: (1) > (0)	Char. 192: (0) > (1)	Char. 138: (1) > (0)
Some trees:	Char. 166: (0) > (1)	Char. 204: (1) > (0)	Char. 143: (1) > (0)
Char. 108: (1) > (0)	Char. 172: (0) > (1)	Char. 293: (0) > (1)	Char. 154: (0) > (1)
Char. 110: (1) > (0)	Char. 175: (0) > (1)	Char. 316: (1) > (0)	Char. 163: (0) > (1)
Node 175:	Char. 185: (1) > (0)	Char. 345: (0) > (1)	Char. 174: (1) > (0)
(100/100/57/38)	Char. 189: (0) > (1)	Char. 351: (0) > (1)	Char. 189: (0) > (1)
Char. 8: (0) > (1)	Char. 190: (1) > (0)	Some trees:	Char. 223: (0) > (1)
Char. 81: (1) > (0)	Char. 202: (1) > (0)	Char. 64: (1) > (0)	Char. 305: (1) > (0)
Char. 177: (0) > (1)	Char. 215: (0) > (1)	Char. 76: (1) > (0)	Char. 340: (0) > (1)
Char. 189: (0) > (1)	Char. 219: (0) > (1)	Char. 108: (0) > (1)	Some trees:
Char. 231: (0) > (1)	Char. 227: (1) > (0)	Char. 172: (0) > (1)	Char. 45: (0) > (1)
Char. 274: (0) > (1)	Char. 236: (0) > (1)	Char. 193: (0) > (1)	Char. 64: (1) > (0)
Some trees:	Char. 237: (0) > (1)	Char. 279: (1) > (0)	Node 215:
Char. 21: 0(1) > (0)	Char. 238: (0) > (1)	Char. 281: (0) > (1)	(73/96/6/12)
Node 174:	Char. 248: (0) > (1)	Char. 328: (0) > (1)	Char. 93: (0) > (1)
(100/100/98/61)	Char. 249: (0) > (1)	Node 277: Bryconops clade	Char. 183: (0) > (1)
Char. 7: (0) > (1)	Char. 258: (1) > (0)	(100/100/99/25)	Char. 202: (0) > (1)
Char. 24: (1) > (0)	Char. 261: (0) > (1)	Char. 60: (0) > (1)	Some trees:
Char. 34: (0) > (1)	Char. 262: (0) > (1)	Char. 72: (0) > (1)	Char. 69: (1) > (0)
Char. 50: (0) > (1)	Char. 274: (0) > (1)	Char. 90: (0) > (1)	Node 203:
Char. 68: (0) > (1)	Some trees:	Char. 148: (0) > (1)	(100/100/63/5)
Char. 118: (1) > (0)	Char. 21: (0) > (1)	Char. 302: (0) > (1)	Char. 81: (1) > (0)
Char. 121: (0) > (1)	Char. 61: (1) > (0)	Char. 357: (1) > (0)	Char. 178: (0) > (1)
Char. 163: (0) > (1)	Char. 127: (1) > (0)	Some trees:	Char. 234: (1) > (0)
Char. 165: (0) > (1)	Char. 151: (0) > (1)	Char. 74: (0) > (1)	Char. 239: (1) > (0)
Char. 197: (0) > (2)	Char. 223: (0) > (1)	Char. 92: (1) > (0)	Char. 250: (0) > (1)
Char. 211: (0) > (1)	Char. 231: (0) > (1)	Char. 171: (0) > (1)	Char. 266: (0) > (1)
Char. 217: (0) > (1)	Char. 243: (1) > (0)	Char. 183: (0) > (1)	Char. 280: (1) > (0)
Char. 283: (0) > (1)	Char. 315: (0) > (1)	Char. 202: (0) > (1)	Some trees:
Char. 298: (1) > (0)	Char. 317: (2) > (0)	Node 204:	Char. 76: (1) > (0)
Char. 316: (1) > (0)	Char. 318: (0) > (1)	(100/100/91/34)	Char. 279: (1) > (0)
Node 189: Bryconinae	Node 188:	Char. 2: (1) > (0)	Node 292: Jupiaba clade
(82/97/17/6)	(100/100/66/14)	Char. 3: (0) > (1)	(100/100/67/32)
Char. 103: (1) > (0)	Char. 143: (0) > (1)	Char. 39: (1) > (0)	Char. 139: (0) > (1)
Char. 123: (0) > (1)	Char. 179: (0) > (1)	Char. 70: (0) > (1)	Char. 263: (0) > (1)
Char. 131: (0) > (1)	Char. 218: (0) > (1)	Char. 168: (2) > (1)	Node 202:
Some trees:	Char. 221: (1) > (0)	Char. 227: (1) > (0)	(4/97/-/4)
Char. 108: 0(1) > (1)	Some trees:	Char. 228: (0) > (1)	Char. 185: (1) > (0)
Char. 144: (0) > (1)	Char. 67: (0) > (1)	Char. 243: (1) > (0)	Char. 306: (0) > (1)
Node 297:	Char. 83: (0) > (1)	Char. 254: (0) > (1)	Node 220:
(100/100/100/43)	Char. 234: (0) > (1)	Some trees:	(73/97/33/6)
Char. 3: (0) > (1)	Node 187: Iguanodectinae	Char. 46: (0) > (1)	Char. 52: (1) > (0)
Char. 39: (1) > (0)	(100/100/100/51)	Char. 53: (1) > (0)	Char. 147: (0) > (1)
Char. 56: (0) > (1)	Char. 99: (1) > (0)	Char. 61: (1) > (0)	Char. 148: (0) > (1)
Char. 60: (0) > (1)	Char. 115: (0) > (1)	Node 216: Heterocharacinae	

Appendix 4

Results across the explored parameters. Trees used to construct the final hypothesis are in bold. Similitud index (the complement of Farris distortion index; tcomp) was used as the main criterion to define the range of trees to construct the final consensus; note that the hypothesis with higher value of similarity according to SPR distances (sprdiff) is also included in this range of solutions. “Order” is the average ranking of optimality of a tree from the most-parsimonious set of each parameters set; lower is better.

	K	Steps	No. of trees	Fit	Tcomp	Sprdiff	Order
Analysis under IW							
k1	4.52895	2163	4	137.87971	0.92410	0.87000	11.05
k2	5.31659	2163	4	128.40554	0.92410	0.87000	11.05
k3	6.25426	2162	4	118.91134	0.92395	0.86667	11.64
k4	7.38933	2135	2	109.31589	0.94819	0.89429	8.41

Appendix 4
(Continued)

	<i>K</i>	Steps	No. of trees	Fit	Tcomp	Sprdiff	Order
k5	8.79148	2135	2	99.54851	0.94819	0.89429	8.41
k6	10.56754	2129	2	89.58764	0.94876	0.89810	9.27
k7	12.89008	2125	2	79.37617	0.94953	0.90619	8.14
k8	16.05718	2117	1	68.83640	0.94510	0.89619	8.95
k9	20.63187	2117	1	57.87469	0.94510	0.89619	8.95
k10	27.82067	2113	1	46.41089	0.94090	0.88095	10.73
k11	40.76052	2106	1	34.29356	0.93005	0.84667	14.14
Analyses under SL							
k1	7.29000	2188	1	1382.06029	0.93381	0.89190	13.32
k2	8.37000	2184	1	1430.87624	0.93386	0.89190	11.50
k3	9.65000	2184	1	1481.59369	0.93310	0.89667	11.50
k4	11.19000	2171	1	1533.95385	0.93219	0.89286	9.95
k5	13.09000	2168	1	1588.56253	0.93038	0.88905	10.77
k6	15.49000	2167	1	1645.83377	0.93119	0.89762	11.27
k7	18.61000	2156	1	1705.32576	0.93381	0.88333	10.64
k8	22.87000	2139	2	1766.62069	0.93667	0.90524	7.50
k9	29.00000	2137	1	1828.39040	0.93519	0.89714	8.68
k10	38.64000	2132	1	1891.52603	0.93495	0.89286	9.32
k11	55.96000	2112	1	1952.84349	0.91433	0.85238	14.64