# DISTRIBUTIONAL PATTERNS OF FRESHWATER FISHES IN COASTAL ATLANTIC DRAINAGES OF EASTERN BRAZIL: A PRELIMINARY STUDY APPLYING PARSIMONY ANALYSIS OF ENDEMISM

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Freshwater fishes constitute an excellent subject to access historical biogeography of continental waters. They are unable to survive in salt water or estuarine conditions and have a limited ability to disperse over underlying hydrographic basins. Furthermore, watersheds, such as high mountains, are often regarded as effective dispersal barriers for the fish fauna. To study the distributional patterns over eastern Brazilian coastal drainages, a parsimony analysis of endemism (Morrone, 1994) was carried out, using the distributional ranges of 145 taxa (83 informative) in 28 geographical units, all of them are coastal drainages between the mouth of the rio São Francisco basin and the mouth of the laguna dos Patos system. Geographical units are river Basins, drainages flowing to the same bay, or small neighboring drainages with similar fish fauna. The "São Paulo" unit is represented by small rivers draining into São Paulo state coast above rio Ribeira de Iguape, and the "Rio de Janeiro" unit consists of coastal rivers draining to the Ilha Grande and the Sepetiba Bays. The analyzed taxa are either strictly intolerant to salt water (eg. Siluriformes and Characiformes) or rather strictly confined to fresh water (eg. Poeciliidae-*Phalloptychus* and Cichlidae-*Crenicichla*). Distributional data were taken from bibliography of recently revised taxa, complemented by additional collecting data from the fish collection of Museu de Ciências e Tecnologia da PUCRS (MCP). Supraspecific taxa were used only when phylogenetic relationships were available and when the group was endemic from the analyzed region (eg. "subgroup B" of *Spintherobolus* in Weitzmann & Malabarba, 1999). The distribution of the species was considered as 1 for presence and 0 for absence in each geographical unit and the cladogram was rooted on a hypothetical area with absence of all species. The parsimony analysis was carried out using the implicit enumeration algorithm with the software TNT version 1.1 (Goloboff et al., 2003). A single most parsimonious tree was found (152 steps, CI=54, RI=79). Two great sister areas could be identified in the southern portion of the eastern Brazilian coast (Fig. 1). The "South" clade formed by Maquiné, Três Forquilhas, Mampituba, and Araranguá Basins was previously delimited as an area of endemism by Reis & Schaefer (1998). In the present study, this area is extended up to the rio Tubarão drainage (Fig. 1), which is its north limit. The sister area, here called "Southeast" (Fig. 1), is formed by the geographical units of Cubatão Sul (south), Itajaí-Açu, Itapocú, Babitonga, Guaratuba, Paranaguá, and Ribeira de Iguapé (north). The "South" and "Southeast" clades are physically separated from each other by the Serra do Tabuleiro (Fig. 1), a formation composed of elevated mountains (up to 1000 m above sea level) almost extending to the coastal line. The Serra do Tabuleiro watershed, seems to be an effective biogeographical barrier, isolating the fish fauna of "South" and "Southeast" clades. The "East" clade (Fig. 1) includes the river drainages from the north of São Paulo state to the rio Itanhém drainage in the south of Bahia. This region presents a somewhat heterogeneous fauna and might not be considered an endemic area. However, two large areas sharing several taxa seem to demonstrate a pattern of recent faunal interchange. One of them is comprised by the main drainage of the rio Paraíba do Sul plus adjacent geographical units, and the other one is formed by rio Doce and the nearby drainages of São Mateus and Mucurí basins. In northern portion, the rio Paraguaçu drainage has a high number of autapomorphies (endemic species) and is the most basal member of the "North" clade. This clade, also formed by de Contas, Pardo, and Jequitinhonha drainages is the sister group of all other geographical

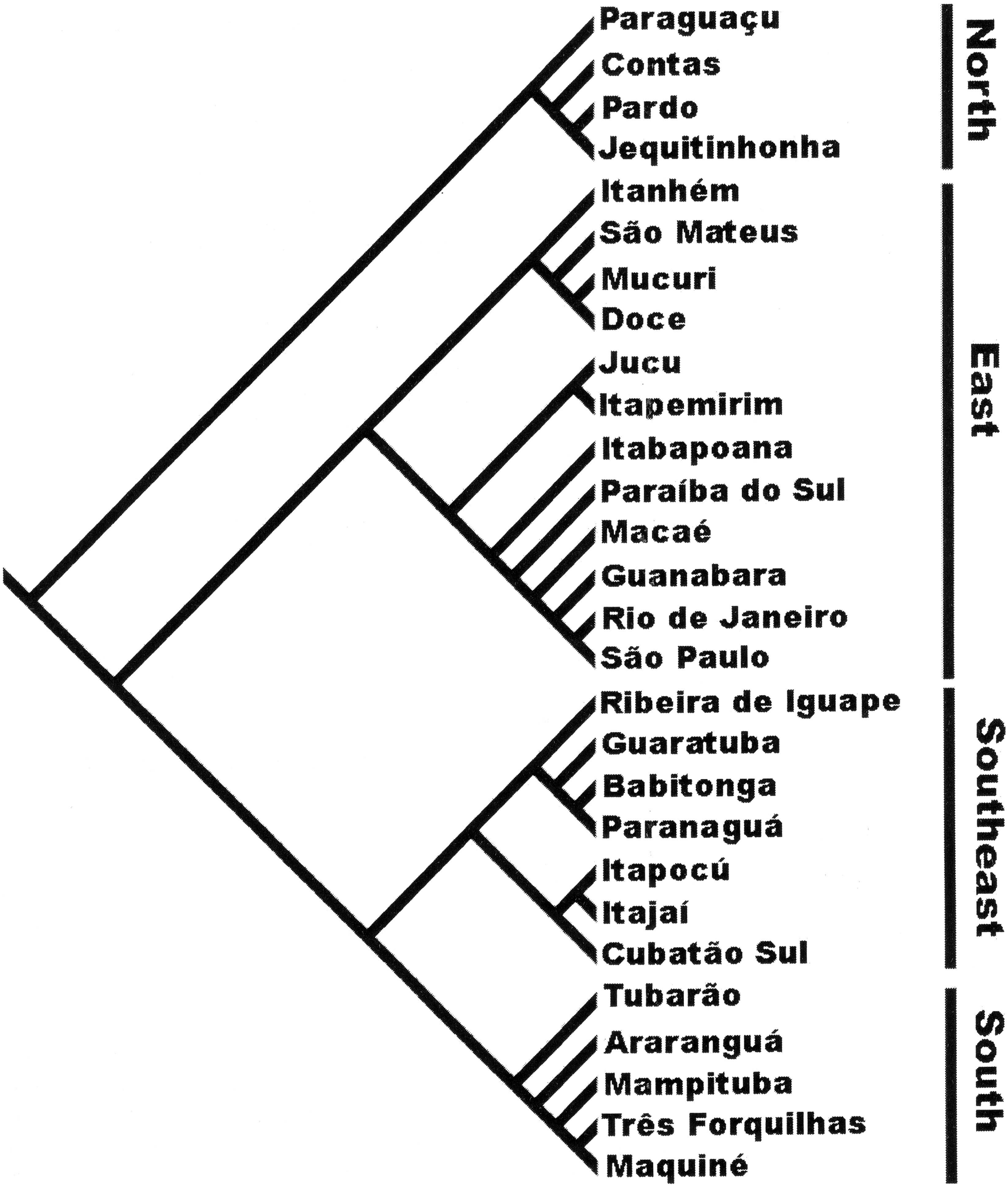

**Fig. 1**. Optimal tree obtained with PAE.

units and contains some basal taxa within Trichomycteridae (Copionodontynae in the Paraguaçu river drainage) and Doradidae (*Weirtheimeria* in the Jequitinhonha and Pardo drainages and *Kalyptodoras* in the Paraguaçu drainage). The relatively basal "North" clade (Fig. 1) is separated from the remaining derived geographical units by the widely distributed *Mimagoniates microlepis* (area synapomorphy). Weitzmann et al. (1988) discussed that the distribution of *M. microlepis* and several other taxa are result of the fluctuations in the sea level during the Pleistocene, allowing during low sea levels periods, the dispersal of freshwaters fishes across the much more extensive costal plains. Nevertheless, fluctuations in the sea level during the Pleistocene could not explain all fish distribution in the eastern coastal drainages. As discussed by Ribeiro (2006), the faunal interchange, caused by capture streams events between the headwaters of eastern Atlantic drainages and the adjacent areas of tributaries of the La Plata system and the rio São Francisco Basin, seem to be the principal mechanism forming the freshwater fish fauna of the coastal drainages. The analysis of the fish fauna of the tributaries of the La Plata system, rio São Francisco Basin and the inclusion of these areas as geographical units in a future study will permit a better understanding of the complex biogeographic patterns of this region.

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# EVOLUCIÓN DE PEQUEÑAS INVERSIONES RECURRENTES EN ADN DE CLOROPLASTO: UN CASO DE ESTUDIO EN ANGIOSPERMAS

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Las inversiones que involucran grandes regiones del genoma de cloroplasto se conocen hace más de 20 años (eg. Palmer, 1985). Sin embargo, la amplia ocurrencia de pequeñas inversiones que involucran alrededor de 4-20 pares de bases, ha sido sólo recientemente reconocida (eg. Kim & Lee, 2005). Estas inversiones están siempre asociadas a una estructura secundaria particular del ADN: una estructura de lazo y tallo en la cual la inversión se verifica en el lazo de la misma. El tallo se forma debido a la existencia de secuencias repetidas invertidas de alrededor de 10 pares de bases. Los estudios realizados hasta el momento han sugerido que la ocurrencia de estas inversiones se vería afectada por el grado de estabilidad de la estructura de lazo-tallo, estimada por la energía libre asociada a la misma. Sin embargo esta hipótesis no ha sido puesta a prueba. En este trabajo evaluamos esta hipótesis en una inversión recientemente descubierta en el genero *Prosopis* (Catalano et al., en prensa) en la región no codificante ubicada entre los genes *trnS* y *psbC*. Para ello se utilizó un método filogenético comparativo modificado del originalmente desarrollado por Maddisson (1990). Como dicho método considera caracteres binarios, el valor de energía fue discretizado clasificando los valores en baja y alta energía libre. La energía libre fue optimizada de diferentes modos: (i) como un carácter continuo (ii) como un carácter binario (iii) evaluando las secuencias ancestrales de esta región del genoma para cada nodo y derivando los valores de energía libre para cada una de dichas secuencias. Para la optimización de la inversión se desarrolló un