Killi-Data Wassup n°13

Overview of Killifish research output

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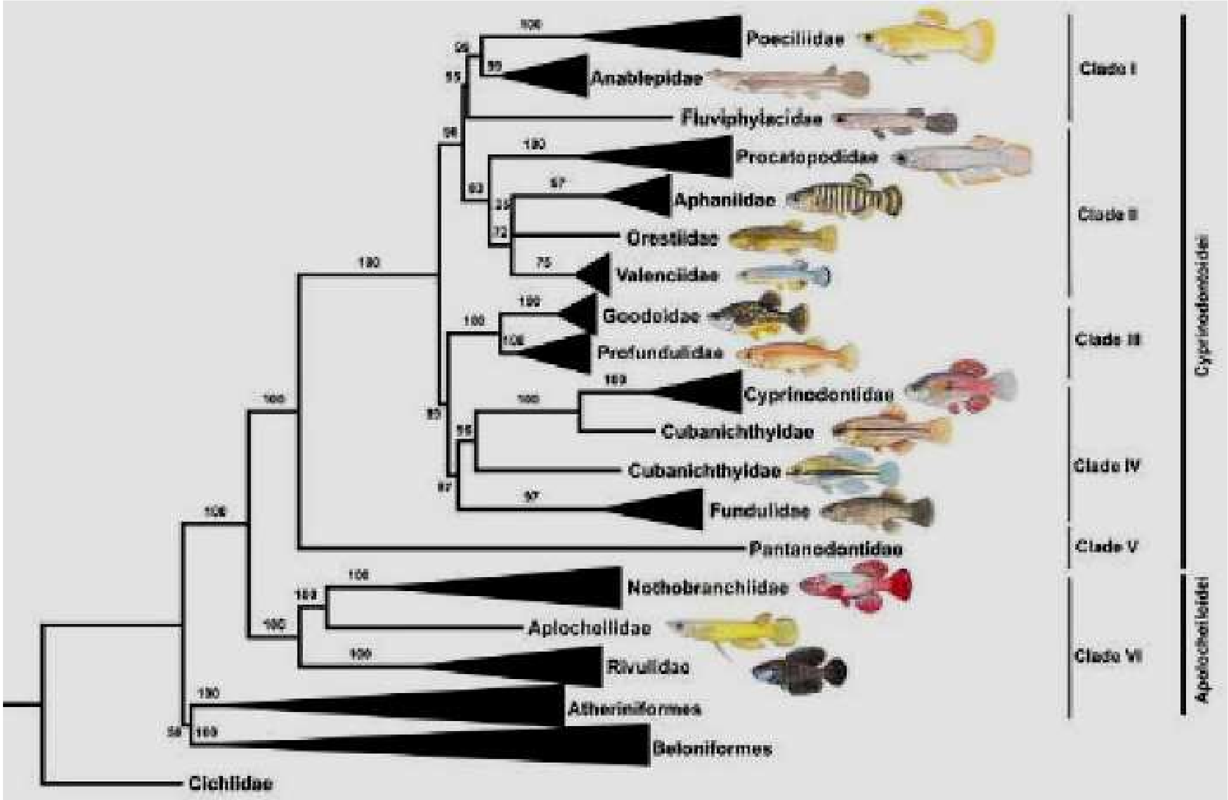
INTRODUCTION

Within this (short) time frame of present Wassup, the menu contains (1) some new species, 3 in *Rivulus* s.l., as *anitae*, *falconi* and *katukina*, from Brasilian Amazon, 1 lampeye as *Lacustricola margaritatus*, previously misidentified *pumilus* (by Seegers or Wildekamp), from Victoria and Kyoga lakes basins, Tanzania and Uganda, (2) a major finding, the first evidence of significant sex changes in annual oviparous fish *Millerichthys robustus* (female to male), the produced males being sexually active and prolific, (3) the pessimistic monitoring of the dramatic (a disaster) decline (16 pops, 14 years) of *Valencia letourneuxi* and *robertae* in Greece, (4) the first rediscovery, previously unknown live (and with types presumably lost) of *Kryptolebias campelloi*, (5), for not-only aquarists (as food for thought) the unparalleled experiment comparing bloodworms and 4 commercial diets vs. wild protein profile for *Nothobranchius furzeri* (the winner is a surprise, and not the bloodworms), and (6) last, an inevitable but major première i.e., for the first time, molecular data show synonymizations of species diagnosed in a modern way and by morpho characters, in genus *Phalloceros* (livebearers), that is the exact reverse to routine (= disclosing new molecular species or revalidating synonyms).

However, 2 additional taxonomic publications needs a broader coverage because they raise more general questions (although not new, but confirmation of past major issues) and they manage them differently (by letting aside taxonomical consequences).

First, the molecular study (with multigene sequences) by Amorim, an ex-student coached by Costa, raises again the now standard situation of the incompatibility of results between molecular data and morphological data, here applied to the very large *micropus* group in *Rivulus* s.l. according to latest evidence (or in genus *Anablepsoides* according to them) ; the authors claim their results are new notably in terms of understanding bio-geography and different from initial molecular papers (Murphy, Thomerson & Collier, 1999, Hrbek & Larson, 1999, Hrbek et al., 2004) for the same group ; indeed, their bootstrap values are remarkably much more solid and the sampling of species is larger (still not complete), but the global picture of the tree is not that different, notably the tree is divided into 2 main branches, one for western components (in Peru, Bolivia and Brasil up to Manaus), one for eastern components (from lower Amazon and the Guyana shield up to Martinique), whatever the morphology is, notably the *atratus* group is nested within western components (and notably the Andean foothill species, *jucundus*, is molecularly related to the *atratus* superspecies with no shared morphological characteristics), the *urophthalmus* and *hartii* groups are mixed according to biogeography (vicariant speciation), but not to morphology (with few shared morphological characteristics) ; as usual now molecular and morphological data are irreconcilable and even the authors do not even try (they just ignore morphological issues, what else can they do? and that is something new again, i.e. to produce solid results but without new taxonomic proposals and without new traditional diagnoses), unlike in the past ; the other issue of that work is on molecular outgroups and here the readers must not be confused : the authors select 3 outgroups (*Cynodonichthys*, *Atlantirivulus*, *Melanorivulus*) plus *Kryptolebias* and show by that selection that the studied group of 26 species is phylogenetic (encompassing 4 generic morphological names *Anablepsoides* s.s., *Oditichthys*, *Benirivulus*, now not molecularly phylogenetic) but this must not imply that their whole sample (*Anablepsoides* in the authors' sense, *Cynodonichthys*, *Atlantirivulus*, *Melanorivulus*) is phylogenetic, on the contrary several recent works published and yet un-published by US teams show that there are annual groups nested withing the *Rivulus* sub-units, then the putative reshuffling of genus *Rivulus* into several molecular genera or subgenera is still in front of us (with a major sampling problem, since, according to Costa, the extremely important *Prorivulus* lineage is extinct).

Second, the new molecular revision by Piller et al. goes further into splitting families of Cyprinodontiformes, from 14 (still recently… and only 7, just a decade ago) to 16 (Anablepidae [in K-D, Anablepsidae], Aphaniidae Aplocheilidae, Cubanichthyidae, Cyprinodontidae, Fluviphylacidae, Fundulidae, Goodeidae, Nothobranchiidae, Orestiidae, Pantanodontidae, Poeciliidae, Procatopodidae, Profundulidae, Rivulidae, and Valenciidae, introducing 2 new families, upgraded from previous subfamilies (Cubanichthyidae and Orestiidae [in K-D, Orestiadidae]), but to-date their proposals seem not to be followed by international bodies (it is still very early and from their results another derived option could be selected with 6 families only, corresponding to their large clades (see their figure further, copyrighted by the authors) and K-D will delay necessary decisions in F-G N (https://www.killi-data.org/list-names-familygroup.php), but the new paper using a new discriminating technique of analysis (https://www.anchoredphylogeny.com) exemplifies new findings, notably that *Cubanichthys* is heterophyletic, because the species *pengelleyi* is closer to Cyprinodontidae than Cubanichthyidae (with *cubensis* and possibly the un-studied *martae* from Columbia) but the authors do not go further by revalidating genus *Chriopeoides* because they consider their molecular data on the 2 sp., *cubensis* and *pengelleyi*, are incomplete (a move that K-D has already -then rightly, if so- chosen since at least 2009 based on unpublished molecular data, as far back as the turning of last century) and that (another trichotomy), the sub-branch with *Aphanius* et al., *Orestias* et al., and Valenciidae is not strong enough.



In conclusion, both present works by Brasilian and North-American researchers (as new strategies or as interim moves?) propose new incremental molecular evidence but do not discuss-assign morphological diagnoses and do not conclude in terms of taxonomic shifts (further splits or revalidations).

Is it an interim strategy ? or does it imply a decided divorce between morphology and genetics, permanently or for how long? Time will tell.

Post-scriptum : a renown dedicated aquarist writing for his association has just raised the question if only molecular data can be considered as phylogenetic (i.e., singly representing evolutionary relationships and natural lineages from ancestry to extant forms), implying that previous methods are not phylogenetic, then would be artificial or un-natural, and that present molecularists, only, do tackle the issue of evolution in taxonomy ; since my answer is not temporary and not anecdotal it may be worth sharing it herein ; no, molecular data are definitely not the only tool to show true evolution and they are for sure not the ultimate tool in taxonomy, which does not minimize their output and contribution in our better understanding of evolution of killifish (and of all living beings, including plants) since over 30 years ; indeed, all taxonomists since the first, Linnaeus (and even before without taxa binominal naming), have been struggling to understand evolution and to accommodate naming (the pyramid from superorder to species) in consequence (even when for some time they erroneously use abdominal characters as phylogenetic at a very high level, during a period in 19th century) ; during modern times, various methods have incrementally been used and all are considered as phylogenetic, giving already, with detailed morphology, then micromorphology, then karyology, a good picture of evolutionary paths in killifish with some gaps in details that cladists, then computerized taxonomists, then molecularists (early or late comers) try to solve (always with a still imperfect picture (for example, do not forget that cladism is basically claiming phylogeny and uses for the first time words like plesiomorphic and apomorphic, new technical words just to speak of primitive and derived levels in previous taxonomy) ; after all, nobody knows if full genome will give the ultimate picture of phylogeny, simply because there may be elsewhere in cells, today unknown, information that can be of high importance to understand phylogeny, and in addition because even the ultimate sampling of myriads of species shall always miss one, known or unknown or even extinct that shake the molecular tree as unstable and not coherent ; yes all taxonomical approaches are aimed to be phylogenetic and up to a point they are indeed (molecular improvement would not have been possible without phylogenetic data of the past) ; what makes a (but not the) difference is today that we have to learn to adapt to new evidence and, like for cladism, learn new vocabulary words, such as molecular species (a species defined by no difference with others of similar appearance except genetic data)… just imagine the surprise for Linnaeus and generations of taxonomists, all dead (and so respectable in reference to our still imperfect knowledge) if some individual could talk to them and mention molecular species!

SELECTION OF PUBLICATIONS (last in, first out)

- Reichard, M., Janac, M., Blazek, R., Zak, J., Alila, O. D., & Polacik, M. [Reichard et al. analyse *Nothobranchius* biodiversity from 127 pools across 7 local regions in lowland Eastern Tanzania over 2 years ; this study tackles a major general issue of the causes of sympatry, expansion, species diversifications and assemblages within a focus of a limited geographical region in lowlands, although it is the richest in terms of speciation in Tanzania (for genus *Nothobranchius*) and even if it is based on a very high number of collecting localities ; the authors decompose beta diversity (compositional species differences between local pools within a region) into nestedness (defined as the number of decreasing fills, or NODF) and turnover components ; a total of 15 species form local assemblages containing 1 to 6 species ; most *Nothobranchius* species are endemic to 1 or 2 adjacent regions ; regional diversity is highest in Ruvu, Rufiji and Mbezi regions ; nestedness is significant in Ruvu and Rufiji, with shared core (*melanospilus*, in almost all pools, *eggersi*, *janpapi*) and common (*ocellatus*, *annectens*) species, and distinctive rare species ; . nestedness apparently results from selective colonization rather than selective extinction {which is a major new finding}, and local species richness is negatively associated with altitude {a confirmation} ; *Nothobranchius* assemblages in the Mbezi region are not nested, and have many endemic species and the highest beta diversity driven by species turnover ; Mbezi region contains highest diversity and many endemic species (not less than 5), apparently due to repeated colonizations of the region rather than local diversification ; on the contrary, Wami region (12 pools with *Nothobranchius* present) contains only a single species (widespread *melanospilus*) ; highest beta diversity is found in Mbezi region, strongly driven by species turnover while Rufiji and Ruvu regions have similar beta diversity, but it is primarily driven by nestedness in Ruvu region and by species turnover in Rufiji region ; understanding of how nestedness and turnover are linked to beta diversity is important for defining optimal conservation strategies. 2022. E.E., https://onlinelibrary.wiley.com/doi/epdf/10.1002/ece3.8990] {Jean Huber, 24-June-2022} <°))))>< <°))))>< <°))))><

- Moncayo, R.E., J.A. De La Cruz, E.L. Lopez, P.L. Del Monte, M.M.A. Diaz, A.T. Chacon, A.G. Ramirez, O.D. Dominguez & J.P.H. Ramirez. [Moncayo et al. show high density of CrE *Hubbsina turneri* {K-D maintained in *Girardinichthys*} along niche type and low fecal coliforms ; the livebearing killifish *Hubbsina turneri* (Buen, 1940) within a monotypic genus {or *Girardinichthys turneri* and *ireneae*, as valid, if not its junior synonym} is herein studied as a model species in a historical context at varying locations ; initially the species (or the twin species) occur(s) only in the Lerma-Chapala basin, the main lake complex in Mexico, but it has (have) not been collected from lago Cuitzeo and now is restricted to lago Zacapu {*ireneae* s.s.} (both lakes are jointed at the Pliocene-Pleistocene boundary by wide channels related to morphotectonic structures and then are separated during the Pleistocene-Holocene period) ; the 2 lakes' contrasting abiotic/biotic characteristics (water depths, temperature, chemical data) provide distinguishing factors to describe some species distribution limits along chemical ion gradients ; estimated extirpation dates in lago Cuitzeo have occurred, after detailed evidence, between years 2013 and 2018, linked to an abrupt drop in lake volume, water quality degradation, increased biotic interactions within macrophytes habitats with native and introduced {alien} species, and fisheries bycatches {as a consequence of human poor -or silly- behaviors and to other Goodeidae competition such as sympatric *Zoogoneticus quitzeoensis* and *Alloophorus robustus*} ; current restricted range derives from the draining of the larger lake, forcing the remaining populations to small spring-fed remnants ; recent samplings have resulted in a low number of individual ; high *turneri* density is related to low hardness and low presence of fecal coliform bacteria, to medium depth and high suspended solids, and high oxygen concentration ; the authors suggest the implementation of 3 actions to preserve the remaining Zacapu ecosystem: (1) protect spring zones and regulate the water extraction for the conservation of aquatic biodiversity, (2) restoration of the littoral areas, and (3) adapt decision-making initiatives of the lake use and urban development to long-term objectives to preserve the ecosystem structure and function. 2022. F.inB., https://www.imrpress.com/journal/FBL/27/5/10.31083/j.fbl2705165/htm] {Jean Huber, 9-June-2022} <°))))>< <°))))>< <°))))><
- Dominguez, O.C., S.C. Valdez, T.M.C. Muñoz, J.H. Huber & M. Reichard. [Dominguez et al. first evidence protogynous functional hermaphroditism (female-to-male) in annual killifish, *Millerichthys robustus* ; sex change (sequential hermaphroditism) has evolved repeatedly in teleost fishes but is unreported scientifically in oviparous Cyprinodontiformes (it is frequent among livebearers notably in genus *Xiphophorus* or sword-tails) ; here the authors document with lab behavior experiment sustained by gonad cell study that in an annual killifish (*Millerichthys robustus*) from temporary pools in Mexico,

functional protogynous hermaphroditism (female-to-male sex change) occurs in 60% replicates, when groups of 5 females interact and have a visual and olfactory cue of a male ; the study is stemmed from the observation that in natural (wild) populations, adults with intersex coloration and gonads are disclosed (even if rare) ; in further details the lab experiment {easily duplicable by aquarists} shows that only one female changes sex in any given replicate, that sex change never occurs in isolated females and that protandrous (male-to-female) hermaphroditism is not recorded ; besides gradual changes in behavior, coloration and gonad structure are evidenced during the sex change process and secondary (trans) males do spawn successfully after 75 days {note : an innovative and pioneering experiment that should be duplicated, notably on *Pseudepiplatys annulatus*, already aquarium reported as a similar sex changer}. 2022. N.S.R., https://www.nature.com/articles/s41598-022-12947-2.pdf] {Jean Huber, 4-June-2022}
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- Dekker, M.L., L.M. van Son, K.M. Leon-Kloosterziel, A. Hagmayer, A.I. Furness, J.L. van Leeuwen & B.J.A. Pollux. [Dekker et al. show in both *Poeciliopsis retropinna* and *turrubarensis* that superfetation may promote polyandry and reproductive skew ; superfetation, the ability to carry several overlapping broods at different developmental stages in a single female, has evolved independently multiple times within the live-bearing fish family Poeciliidae and today in extant species, but its (putative) evolutionary advantages remain unclear ; then the authors test, in 2 Poeciliidae superfetatious congeners, *Poeciliopsis retropinna* and *turrubarensis*, a group of 25 females per species from freshwater streams in Costa Rica and they genetically (from hundreds of embryos) find a high frequency of unique sires in both species and even that the mean number of sires within females (bearing multiple broods) is higher than the number of sires within separate broods, plus other differences (in the proportion of offspring sired by each male), suggesting an unequal reproductive success of sires (i.e. reproductive skew) mostly originated from differences in paternal contribution between, rather than within broods and implying extensive polyandry. 2022. JEB, https://onlinelibrary.wiley.com/doi/pdf/10.1111/jeb.14019] {Jean Huber, 4-June-2022}
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- Souto-Santos, I.C.A., W.B. Jennings & P.A. Buckup [The Buckup team shows that in left-sided *Phalloceros* sp., morpho-distinct *aspilos* and *tupinamba* are molecular synonyms of *leptokeras* ; the sinistral *Phalloceros* group {with dominantly left oriented urogenital papilla in female} consists of 3 congeners, *aspilos*, *leptokeras* and *tupinamba*, that inhabit the Paraiba do Sul Basin and coastal drainages in southeastern Brasil, showing large hooks in medial portion of the gonopodial appendices in male ; the authors molecularly study mitochondrial (COI and Cytb) and nuclear (RAG1) haplotypes of 36 specimens sampled from 11 localities including the type localities of the 3 species and their results show that those 3 nominal taxa are not molecularly separable and they consider 2 of them as synonyms, with *leptokeras* being designated as the single valid species in the group {there are about 19 other congeners that are not sinistral} ; further, the geographic expansion of fused *leptokeras* lineage stems in the coastal region ca. 2.3 MYA following a palaeo-drainage model. 2022. ZJLS, https://academic.oup.com/zoolinnean/advance-article-abstract/doi/10.1093/zoolinnean/zlac030/6591851] {Jean Huber, 29-May-2022} <°))))><
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- Fuller, R.C., K.E. McGhee, B. Sandkam, M. Schrader & J. Travis. [Fuller et al. show, in *Lucania goodei*, that genetically-controlled blue phenotype can override red-yellow phases (latter dominant) ; color phases in male *goodei*, represented by blue, red and yellow morphs, are common in all populations with blue males being more common in tannin-stained swamps (vs. clear springs) ; in lab, the authors combine crosses with a manipulation of light to explore how genetic variation and phenotypic plasticity shape these patterns ; results show that different coloration {phase} is attributable mainly to 2 axes of variation: (1) a red-yellow axis with yellow being dominant to red, and (2) a blue axis that can override red-yellow and is controlled by genetics, phenotypic plasticity, and genetic variation for phenotypic plasticity ; curiously, variation among populations in plasticity suggests it is adaptive in some populations, but not in others.

2022. Evol., https://onlinelibrary.wiley.com/doi/abs/10.1111/evo.14511] {Jean Huber, 29-May-2022} <°))))>< <°))))>< <°))))><

- Perkin, J.S., C.G. Montaña, E.J. Nogueira, B.B. Brandão, G.M.T. Mattox & K.W. Conway. [Perkin et al. first rediscover *Kryptolebias campelloi*, together with *marmoratus* group component and extend *Fluviphylax palikur* range ; the authors report on a detailed field survey in the rio Jacunda drainage of the Lower Amazon River basin, Para State, northeastern Brasil with a special focus on more miniature fishes (<26 mm in standard length) ; excellent outcome for Killifish because they collect 3 rare species, the lampeye *Fluviphylax palikur*, previously known from (french) Guyane and neighboring territories in Brasil up to the Amazon delta {not South of it}, and 2 *Kryptolebias* sp., one related to selfing hermaphrodite *marmoratus* (according to Mattox, pers. communication), the other as *campelloi* with strong range extension vs. type and only known locality, a sp. described by Wilson Costa as only fixed material and no known live pattern and supposedly related to *brasiliensis* from Rio de Janeiro, a huge distance away {further details expected soon}. 2022. N.I., https://www.scielo.br/j/ni/a/ZmsJPQbvhcffsNDXvHQTFxw/?lang=en] {Jean Huber, 23-May-2022} <°))))>< <°))))>< <°))))><
- Torres-Dowdall, J., S.J. Rometsch, J.V. Reyes, G. Aguilera, A.F. Kautt, G. Goyenola, A.C. Petry, G.C. Depra, W.J. da Graça & A. Meyer. [Torres-Dowdall et al. show that predominantly left sided *Jenynsia* sp., *sanctaecatarinae* and *obscura*, are scattered in molecular tree ; an interesting test that molecularly tackles a possible phylogeny of predominantly congeners with a left sided gonopodium vs. congeners with no polarity {Anablepsidae that include the southern genus *Jenynsia* show both left and right sided gonopodiums in male, often in equal proportion except a few species herein studied} and the results show that the evolution of genital asymmetry in 3 *Jenynsia* sp. where left-sided males are significantly more abundant than right-sided ones, is independent from the morphological characteristic (i.e. that in fully left-handed *sanctaecatarinae* and *obscura* and even if considered in 2 thirds left-handed *tucumana*, the character has appeared independently) {note : full article can be read freely at https://www.evolutionsbiologie-uni-konstanz.com/uploads/7/7/7/4/77747518/rspb.2022.0266.pdf }. 2022. PRSLB, https://royalsocietypublishing.org/doi/full/10.1098/rspb.2022.0266] {Jean Huber, 17-May-2022} <°))))>< <°))))>< <°))))><
- Kalogianni, E., Y. Kapakos, A. Oikonomou, S. Giakoumi & B. Zimmerman. [Kalogianni et al. monitor dramatic decline (16 pops, 14 years) of *Valencia letourneuxi* and *robertae* in Greece due to human impact ; freshwater fish biodiversity loss in Mediterranean basin is regarded as among the highest globally ; the authors re-assess the situation for population trends of two threatened freshwater killifish, in genus *Valencia* {the third congener, worldwide, being *hispanica* from Espana [Spain], also at risk of extinction for the same reasons}, with most modern methodologies such as Living Planet Index (LPI) and processes ; results show *letourneuxi* has been declining by 97.7% and *robertae* by 91.0% and it is due to water pollution, eutrophication and alien Eastern mosquitofish *Gambusia holbrooki* since long artificial introduction ; the authors conclude in pressing for conservation actions notably strict protection of lowland spring habitats, habitat improvement through changes in water management and agricultural practices, mosquitofish invasion prevention and mosquitofish impact mitigation measures, as well as translocation actions and captive breeding {the verdict is horrific and direct and indirect causes are only human failures and selfishness, never corrected even recently : not less than 16 sites of survey in 12 basins from Corfu island (type locality of *letourneuxi*) to Alfios river in mainland Greece, between 2005 and 2018, with little possibility to reverse the process, except in artificial refugia}. 2022. J.N.C., https://www.sciencedirect.com/science/article/abs/pii/S1617138122000644] {Jean Huber, 30-April-2022} <°))))>< <°))))>< <°))))><
- Reichard M., Blazek R., Zak J., Cellerino A., Polacik M. [The Reichard lab shows wild and lab life spans for 367 pops of 4 *Nothobranchius* sp. vary along behavior (aggressive vs. placid sp.) ; the objectives of present study is to test how sex differences in life span and ageing are modulated by social and environmental

factors, and by intrinsic differences between males and females (sex ratios), in many populations of 4 related *Nothobranchius* species from southern and central Mozambique (male aggression is known as markedly highest in *orthonotus*, followed by *furzeri* and *kadleci* and the lowest in *pienaari*) ; in the wild, females consistently outlive males ; in captivity (sex differences in life span and aging from 8 laboratory populations tested), sex-specific mortality depends on social conditions ; in social-housed experimental groups, male-biased mortality persists in 2 aggressive species, but ceases in 2 placid species ; then when social and physical contacts are prevented by housing all fish individually, male-biased mortality ceases in all 4 species (aging is similar per species, no matter of sex) ; no marker of functional aging, recorded in the study (lipofuscin accumulation, proliferative changes in kidney and liver) differs between males and females, despite their previously confirmed association with functional aging in *Nothobranchius* killifish ; in total, the authors show how sexual selection (especially sexually dimorphic behavior and coloration, and strength of male–male competitive interactions over access to mating) affects sex differences in life span and aging through multiple processes even within an ecologically and evolutionary discrete lineage, and that these effects are strongly moderated by social and environmental conditions. 2022. JAE, https://reichardlab.eu/pdf/MR165.pdf] {Jean Huber, 23-April-2022} <°))))>< <°))))>< <°))))><

- Zak, J., K. Roy, I. Dykova, J. Mraz & M. Reichard. [The Reichard lab compares bloodworms and 4 commercial diets vs. wild protein profile for animal research model *Nothobranchius furzeri* ; absence of a controlled diet is unfortunate for research in a promising model organism for ageing, the turquoise killifish and very short living organism, *Nothobranchius furzeri* Jubb, 1971 ; routinely captive *furzeri* are fed defrosted bloodworms but it is not known whether this is an optimal diet and it is not very practical compared to dry feed {note : juveniles are still fed 3 times per day with freshly hatched Artemia nauplii after 24 h from salt-water incubation} ; in present study, the authors estimate nutritional value of diet naturally ingested by wild fish and determine a fish-body amino acid profile as a proxy (best guess) for their nutritional requirements ; the authors then compare performance of aquarium fish fed between 4 commercial foods containing 46%–64% protein to that achieved with bloodworms (50% protein) and that of wild fish (wild fish meet an upper target with a high-protein diet, i.e. 60%, and this is supported by their superior performance on high-protein diets in captivity) ; in comparison to wild fish, a bloodworm diet leads to lower body condition, overfeeding, and male liver enlargement ; out of 4 dry commercial foods tested (2 brands for carnivorous fish species, 'Aller Infa' 0.4 mm (ALR, starter feed; Aller Aqua, Germany) and 'Skretting Vittalis' 2.5 mm (SKR, grow-out feed; Skretting, Norway), and 2 brands for omnivorous species, 'SAK MIX', 0.4–0.6 mm (SAK, pet-fish feed; Exot Hobby, Czech Republic) and 'Coppens Orange' 3 mm (COP, broodstock feed; Alltech, Netherlands), fish fed with 'Aller' match wild fish in body condition and liver size, and is comparable to bloodworms in terms of growth and fecundity (other multiple detrimental effects are observed with defrosted bloodworms). 2022. JFB, https://reichardlab.eu/pdf/MR168.pdf] {Jean Huber, 23-April-2022} <°))))>< <°))))>< <°))))><
- Piller, K.R., Parker, E., Lemmon, A.R. & Lemmon, E.M. [Piller et al. molecularly show a 100 killifish solid tree in no less than 16 families, with distinct Cubanichthyidae and Orestiadidae ; evolutionary relationships among the families within order Cyprinodontiformes, based on different molecular and morphological data sets, are still uncertain ; the authors then use a targeted approach, anchored hybrid enrichment, to investigate the phylogenetic relationships among the families within Cyprinodontiformes, involving not less than 100 specimens and an average of 244 loci per spm and newest phylogenetic processes (RaxML and ASTRAL) ; as usual now, 2 well-established clades (suborders Cyprinodontoidei and Aplocheiloidei) are recovered as monophyletic and unusual position of genus *Pantanodon* (Pantanodontidae) is confirmed ; results from this study provide a {more} robust, with still 2 uncertainties in sub-branches, (1) in Cubanichthyidae vs. Cyprinodontidae hypothetically due to gaps in molecular sequences of the 2 tested sp., *cubensis* and *pengelleyi*, and (2) in an ambiguous lineage encompassing European genera *Aphanius* s.l. and *Valencia*, plus the Andean genera in Peru-Chile, *Orestias* and *Pseudorestias* {notes : previous papers

give broadly similar results (identical for the 2 suborders, Cyprinodontoidei and Aplocheilodei) but only (sic) 14 families, there are also major surprises, notably 2 trichotomies, one for the 2 Cubanichthyidae members, unlike recent findings by Costa but like unpublished molecular data used in K-D, and one for *Aphanius* et al., *Orestias* et al., and Valenciidae, this time rather congruent with recent works by Iranian teams, and it cannot be anticipated whether international databases will jump into that 16 families or not, or will regard the 6 proposed clades as nodes for family levels}. 2022. MPE, https://www.sciencedirect.com/science/article/abs/pii/S1055790322000951] {Jean Huber, 22-April-2022} <°)))>< <°)))>< <°)))><

- Mustikasari, D., A. Nuryanto & S. Suryaningsih. [Mustikasari et al. disclose molecularly distinct pop of Bangka island, off Sumatra coast, Indonesia for *Aplocheilus panchax* ; previous studies divide Blue Panchax, *Aplocheilus panchax*, into 3 different clades, namely West, Central, and East clades, all over Asia from India to Vietnam and Indonesia, with populations from Indonesia belonging to Central and East clades ; the authors molecularly study, using the cytochrome c oxidase 1 (COI) gene, populations from pits with harsh conditions in Bangka Island, off-Sumatra, Indonesia, in order to compare them with standard populations (with normal ecological niche) and results are surprising with genetic distance within Bangka Island populations as less than 2%, whereas genetic distances between Bangka populations and other Indonesian and else populations are ranged from 103.87% to 122.10%, a clear genetic gap ; besides, 28 haplotypes with genetic divergence and variability are evidenced {still the authors consider only a single species and taxonomic unit all over huge range in Asia} [note : this study is a follow-up of a previous field study on newly discovered populations in abandoned ex-tin mining pits of different ages with same authors with reference as Mustikasari, D., S. Suryaningsih & A. Nuryanto. 2020. Morphological Variation of Blue *Panchax* (*Aplocheilus panchax*) Lives in different Habitat assessed using Truss Morphometric. Biosaintifika, 12 (3), 399-407]. 2022. Biodiversitas, https://www.smujo.id/biodiv/article/view/10618] {Jean Huber, 20-April-2022} <°)))>< <°)))>< <°)))><
- Nagy, B. & B.R. Watters. [Nagy and Watters describe *Lacustricola margaritatus*, misidentified *pumilus*, from Victoria and Kyoga lakes basins, Tanzania and Uganda ; the new species, previously identified erroneously, notably by Seegers or Wildekamp, as *pumilus* or *centralis*, 2 similar and isomorphic species distributed more southerly, inhabits small streams and swamps in lake Victoria basin in northwestern Tanzania and southern Uganda, and lake Kyoga basin in central Uganda and is documented by not less than a dozen of populations collected by the authors ; the diagnosis encompasses a combination of characters such as live male body color pattern with vertically-elongated iridescent light blue patches at scale centers, forming a striped appearance of dotted longitudinal lines on sides, with deeply colored unpaired fins as orange-brown in basal and median parts and a narrow black distal band, with a yellow base along Pectoral fin ; in both sexes, cephalic sensory system is open (entirely situated in open grooves) ; curiously both sexes show an inconspicuous post-opercular blotch which normally a characteristic of components of subgenus *Cynopanchax* {but the authors do not discuss that taxonomic issue} ; *Lacustricola margaritatus* differs from true *pumilus* {type species of genus and nominotypical subgenus *Lacustricola*} and *centralis* by morphometric and meristic characters, body and fin coloration, and cephalic sensory system. 2022. Zootaxa, https://mapress.com/zt/article/view/zootaxa.5128.1.2] {Jean Huber, 19-April-2022} <°)))>< <°)))>< <°)))><
- Amorim, P.F. & W.J.E.M. Costa [Amorim and Costa study molecular data of 26 species of genus *Anablepsoides* {K-D maintained as subgenus of *Rivulus*} along biogeography ; in the sense of the authors, genus *Anablepsoides* is a widely distributed Neotropical killifish genus found in shallow streams, in both dense forests and open areas, throughout northern and northeastern South America {it corresponds to 3 morpho-subgenera in Kill-Data, i.e., *Anablepsoides* s.s., *Oditichthys*, *Benirivulus*, or, 3 major morphospecies, the *micropus* group, with ca. 40 species, the large-sized *hartii* group with ca. 10 species and the diminutive *atratus* group with ca. 10 species, incongruent with those 3 generic units}, and the

molecular study involves 2 nuclear and 4 mitochondrial genes of 26 species {i.e. ca. half of the described species, therefore a solid but not ultimate sampling} ; however the authors concentrate their analyses on dating and originating their whole group as Early Miocene in an area corresponding to the Paleo-Amazon-Orinoco system, they consider 2 clades {and not 3 morpho-groups, pushing to confirm that subgenus *Benirivulus*, described by Costa in 2006, is irrelevant... as a consequence, *Benirivulus* is definitely considered as a synonym now, but it is impossible to reassign each taxon they study to a proper (?) molecular positioning and to harmonize their 2 clades with morphological groups, until a full revision of genus *Rivulus* s.l. with nearly 200 species, because they do not propose, and even ignore, or delay for a future publication, any taxonomic reorganization with diagnoses}. 2022. Z.S., https://onlinelibrary.wiley.com/doi/10.1111/zsc.12539] {Jean Huber, 13-April-2022} <°)))>< <°)))>< <°)))><

- Serra, W.S., F. Scarabino, M.P. Torres & G. Furtado. [Serra et al. report first record of *Austrolebias univentripinnis* in Cerro Largo, Uruguay (only known before from nearby Brasil) ; during a recent expedition to the lower Yaguarón river basin (northeastern Uruguay), the authors have collected the critically endangered killifish *Austrolebias univentripinnis* (this is only the sixth known population of the species), which represents the first record of this species for the country {this is not a surprise since 2 known localities in type area of the species are only a few kilometers away near Brasil border} ; detailed {well documented}morphometric are given and differences with topotypes are discussed (and *minor*) ; the new Uruguayan population does not extend significantly the area of distribution, and within the area, only one spot contains *Austrolebias reicherti*. 2022. H.N., https://fundacionazara.org.ar/img/revista-historia-natural/tercera-serie-volumen-11-3-2021/HN_11_3_19-29.pdf] {Jean Huber, 26-March-2022} <°)))>< <°)))>< <°)))><
- Sferco, E., G. Aguilera, J.M. Gongora & J.M. Mirande. [The Mirande team discovers fossil of *Jenynsia*, from upper Miocene lacustrine deposits in Catamarca, Argentina with new extinct sp. ; this a new additional record of a fossil in rich Argentina for livebearing genus *Jenynsia* {or related genera} and the live bearing breeding characteristics are then already present some 11.1 MYA ; the new species, named *herbsti*, after Dr. Rafael Herbst, prominent Argentinian-German palynologist, is described from rio Seco, located East of city of Santa María, in Catamarca province, based on many specimens of both females and sexually dimorphic males and a phylogenetic hypothesis is provided with a placement in nominal subgenus *Jenynsia* {like extant *alternimaculata*, *darwini*, *lineata*, *luxata*, *maculata*, *obscura*, *onca*, *sanctaecatarinae*, *sulfurica*, *tucumana*}, however, it is also recovered as forming a clade with extinct *Sachajenynsia pacha* ; according to the authors, the new findings and interpretations challenge the mostly marine-driven diversification of *Jenynsia* and the new taxon is older than predicted by the published estimations. This study reinforces the hypothesis that sexual reproduction by means of internal fertilization was already well-established in the Miocene for Anablepsidae. 2022. J.V.P., https://www.tandfonline.com/doi/abs/10.1080/02724634.2022.2039168] {Jean Huber, 13-March-2022} <°)))>< <°)))>< <°)))><
- Nielsen, D.T.B., J.W. Hoetmer & E. Vandekerkhove. [Nielsen et al. describe *Anablepsoides falconi* and *katukina* {K-D maintained in *Rivulus*} both from Acre state, N.E. Brasil, related to *limoncochae* ; both are known from each type area only, distant by about 140 km ; the authors solely define the *limoncochae* group by male color pattern following Costa (2010), oblique transverse stripe on middle of Dorsal fin, rows of red spots or stripes posteriorly extending to Caudal fin base, contact organs on scales of sides and they assign 13 taxa to the group, including species fully lineated sp. but not *micropus*, and it is agreeable even if it is artificial {in K-D, the group is much larger, holding some 38 valid sp., including the 2 new ones, *bahianus*, *bibosi*, *caurae*, *cearensis*, *chapare*, *christinae*, *corpulentus*, *cryptocallus*, *deltaphilus*, *elongatus*, *erberi*, *falconi*, *hoetmeri*, *intermittens*, *iridescens*, *jari*, *katukina*, *lanceolatus*, *limoncochae*, *lineasoppilatae*, *luitalimae*, *lungi*, *mazaruni*, *micropus*, *ophiomimus*, *parlettei*, *peruanus*, *roraima*, *rubrolineatus*, *stagnatus*,

taeniatus, *tessellatus*, *tocantinensis*, *urophthalmus*, *urubuiensis*, *vieirai*, *xanthonotus*, *xinguensis*} ; according to the authors, *katukina* is separated by color pattern of male, with purplish blue body sides, presenting 3 interrupted red longitudinal lines, composed by small red dots, whereas *falconi* {dedicated to friend and famous aquarist Francisco Falcon, not collector this time} differs from the other species of the *limoncochae* species group by a short, rounded, upturned snout, and fewer Pectoral fin rays. 2022. Aqua, [https://aqua-aquapress.com/product/aqua-281_anablepsoides-*limoncochae*/](https://aqua-aquapress.com/product/aqua-281_anablepsoides-limoncochae/)] {Jean Huber, 7-March-2022} <°))))>< <°))))>< <°))))><

Nielsen, D.T.B., J.W. Hoetmer & E. Vandekerkhove. [Nielsen et al. describe *Laimosemion anitae* {K-D maintained in *Rivulus*} from Brasil, related to similarly patterned *leticia*, *ubim* ; the new sp. belongs to subgenus *Owiyeye*, hypothesized to be closely related to *leticia* and *ubim* {then probably to a component of miniature sp. group named *romeri*} ; according to the authors, *anitae* differs from other species of that subgeneric group by a unique color pattern in live male, with overall background color of trunk and head orange-brown, sides of body with brown background and 4 thin light blue stripes from opercular region to caudal peduncle ; note : the description is a huge surprise because even if the authors do not quote previous work for Manaus fauna {ref.: Rohde, F., S. Smith & D. Smith. 2021. Collecting *Rivulus* near Manaus, Brazil: A George Maier Fund Award. Journal of the American Killifish Association, 54 (1) (June): 1-24, 50 figs.} the male and the female of *anitae* look strikingly similar to a fish from Manaus, i.e. not less than 1500 km away, in a very different drainage and in a northern tributary of Amazon river, then the 2 fish are either belonging to the same name, and our knowledge of *Rivulus* systematics needs to be reshuffled greatly or to 2 molecular distinct sp., and systematics based on morph bear very little usefulness. 2022. Aqua, [https://aqua-aquapress.com/product/aqua-281_laimosemion-*anitae*/](https://aqua-aquapress.com/product/aqua-281_laimosemion-anitae/)] {Jean Huber, 7-March-2022} <°))))>< <°))))>< <°))))><

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