

The GENETICS Table in FishBase

Karyological and cellular DNA content data (see Fig. 1) are important for studies of the genetics and systematics of fishes.

Fields

Locality: Refers to where the samples used were collected.

Country: Refers to the country of the sampling locality.

Sex: Refers to sex of samples used (unsexed, female, male or mixed).

Sex-determining mechanism: Gives information on how males and females of the species are designated (choices include xx-xy, xx-xo, etc. for those with sex chromosomes or no sex-associated heteromorphic chromosomes).

Tissue(s) Used: Refers to tissue(s) used for the chromosomal study.

Chromosome number: Fields are provided for the haploid/gametic and the diploid/zygotic chromosome number. If the chromosome number is variable, the range is provided in the diploid/zygotic chromosome number fields.

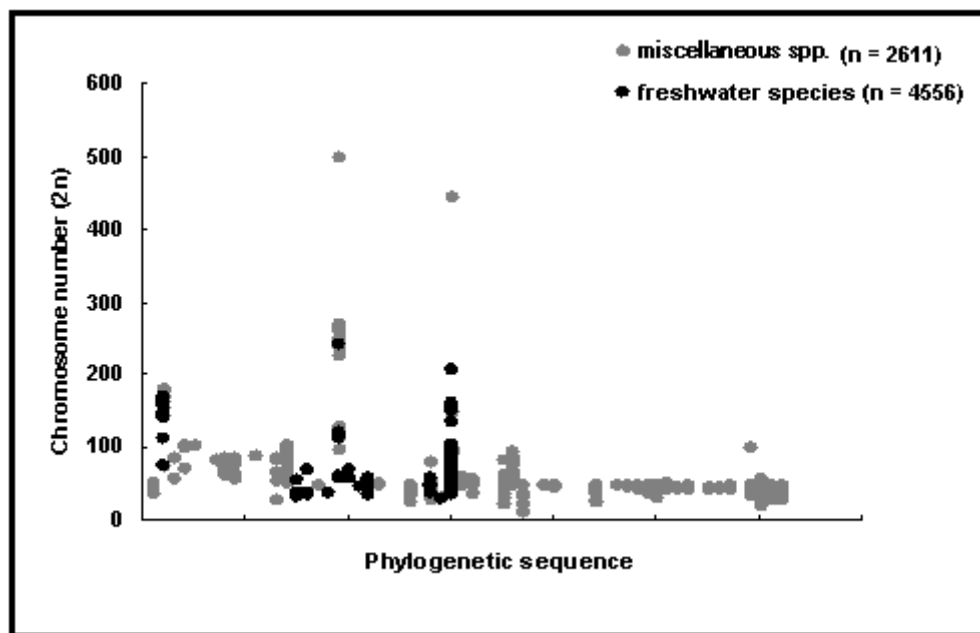


Fig. 1. Chromosome number of freshwater fishes compared with that of miscellaneous species arranged in phylogenetic sequence from primitive (left) to modern (right). Note the decrease in chromosome number and variance for modern groups. See Box 1 for a discussion of this graph.

Chromosome types: Gives the numbers of chromosomes of different types:

- metacentric: chromosomes whose centromeres are approximately midway between each end, thereby forming two chromosome arms of similar length;
- submetacentric: chromosomes whose centromeres are not at the middle of the chromosome (ratio of long arm to short arm is approximately 2:1);
- subtelocentric: chromosomes with a more terminally placed centromere, forming very unequal chromosome arms (ratio of long arm to short arm is approximately 3:1);
- telocentric/acrocentric: chromosomes whose centromeres appear to be at the very tip of the chromosome;
- meta-submetacentric: metacentric and submetacentric chromosomes.
- subtelo-acrocentric: subtelocentric and acrocentric chromosomes.

Chromosome arm number: Gives the total number of chromosome arms, which is largely dependent on the chromosome types (e.g., a metacentric chromosome will have two arms while a telocentric chromosome will only have one).

Genetic marker(s): States whether genetic marker(s) exist in the species and the choices are yes and no. A marker is a phenotypic characteristic (e.g., allozyme, chromosome band, etc.) that can be used to infer the genotype of an organism.

DNA content: Gives the specific haploid cellular content (in picograms). If references exist with values different from those in this field, they are placed in the remarks field.

DNA sequencing: States where DNA sequencing has been done for the species and the choices are yes and no.

Mt DNA analysis: States where DNA sequencing has been done for the species and the choices are yes and no.

Remarks: For miscellaneous comments, e.g., presence of structural rearrangements, specialized chromosomal features, sex-determining mechanism, polyploidization and, if any, other morphological markers.

Status

To date, the GENETICS table covers more than 7,800 records for 2,600 species with information extracted from over 3,000 references.

Sources

We used published references, checklists of chromosome numbers and karyotypes of different groups of fish aside from the database of Dr. Victor Arkhipchuk (1999) of Ukraine. Major

sources include the Fish Chromosome Atlas of the National Bureau of Fish Genetic Resources (India) NBFGR (1998) and Klinkhardt et al. (1995).

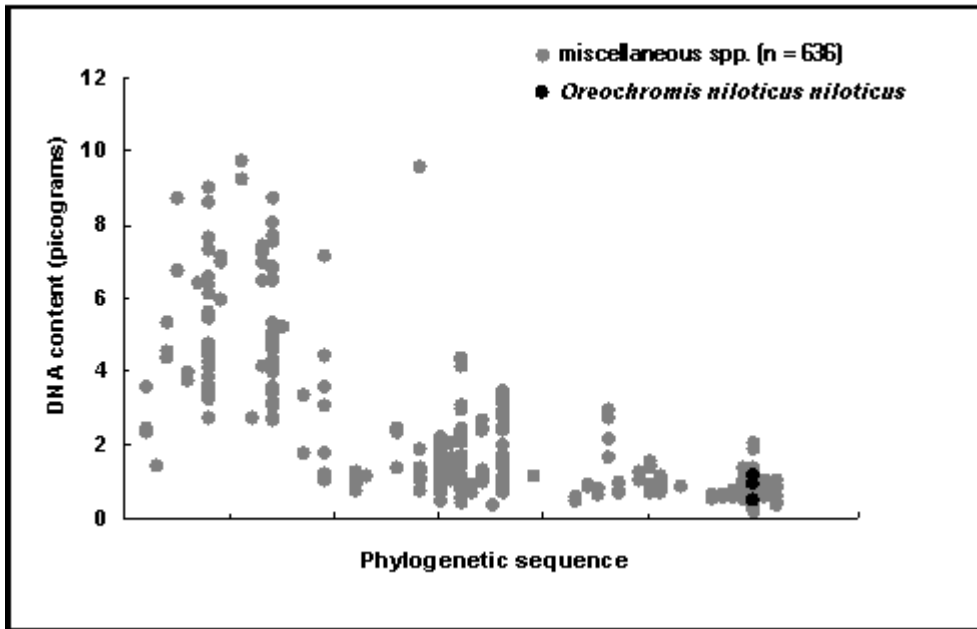


Fig. 2. DNA cell content of *Oreochromis niloticus niloticus* and miscellaneous species. Note that the decrease in DNA content from primitive (left) to modern groups (right) is similar to the independent decrease in chromosome numbers (Fig. 1).

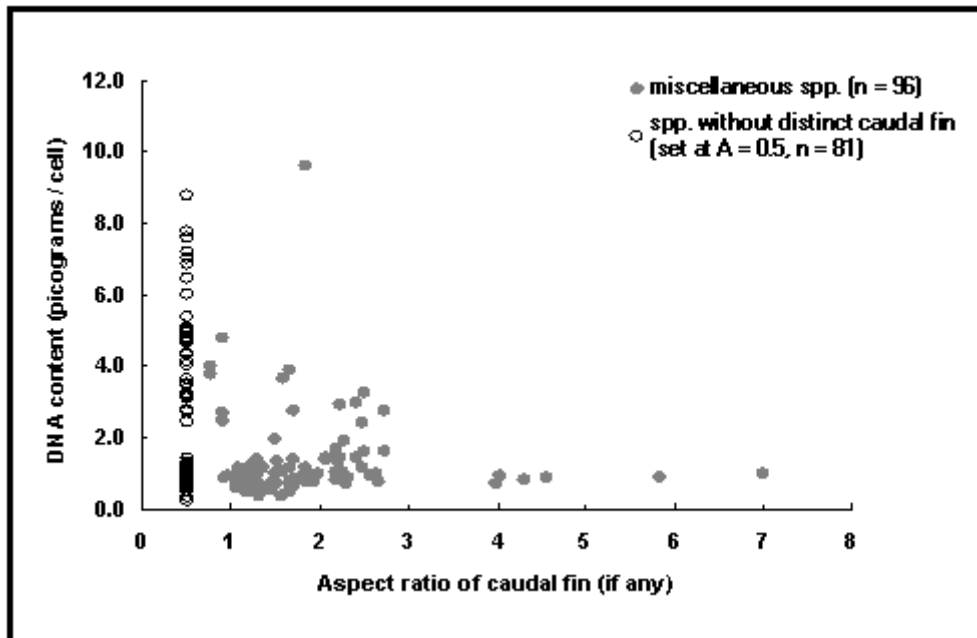


Fig. 3. DNA cell content as a measure of cell size vs. aspect ratio of caudal fin (A) as a measure of activity. See Box 1 for a discussion of this graph.

Box 1. DNA, cell size and fish swimming.

The DNA (deoxyribonucleic acid) content of plant and animal cells is extremely variable and few generalizations have emerged which can be used to predict the amount of DNA in the cells of a given group of organisms.

The most powerful of the existing generalizations is that the DNA content of cells tend to vary with cell size, suggesting a rough proportionality between the amount of DNA per cell, and the amount of living cellular material involved in various syntheses controlled by that DNA.

This generalization implies essentially that DNA content per cell, as recorded in the relevant field of the GENETICS table is a measure of cell size (see Cavalier-Smith 1991).

Given the tendency for organisms with large cells to have low metabolic rates, and conversely (von Bertalanffy 1951), animals with large cells (e.g., lungfishes, which reduce their metabolic rate during aestivation) will tend to have lots of DNA per cell (Thompson 1972).

In fishes, there is a clear pattern for chromosome numbers and for DNA (and hence cell size) to decline with derivedness, with perch-like fishes (high order number in Nelson's (1994) classification) exhibiting a much lower range of DNA contents than more generalized, primitive forms (Hinegardner and Rosen 1972 and see Fig. 2). [Note that chromosome number and DNA content are not correlated, as indicated by Cavalier-Smith (1991) and confirmed by a FishBase graph not reproduced here.]

This may be thought to be the result of metabolic constraints, with fish cell size (and thus DNA content) declining with the evolution of high metabolic performance, such as displayed, e.g., by tunas (Cavalier-Smith 1991).

However, as also pointed out by Cavalier-Smith (1991), there is a lower limit to the size of cells: the fact that capillaries (which are formed by single cells) cannot have a diameter much smaller than that of red blood cells.

Combining all the above, one can hypothesize that a plot of DNA content vs. the caudal aspect ratio of fish (an index of metabolic intensity, see the SWIMMING table) should have on the left side of the plot a wide range of DNA content associated with low aspect ratios (including aspect ratio set at 0.5, to represent fish which do not use the caudal fin as their main organ of propulsion, and which tend to have low metabolic rates), and, on the right side of the plot, a narrow range of (low) DNA content associated with high aspect ratios. Fig. 3 displays these features, thus corroborating hypotheses linking DNA content—via cell size—to metabolic rate.

References

- Cavalier-Smith, T. 1991. Coevolution of vertebrate genome, cell and nuclear sizes, p. 51-86. *In* G. Ghiara et al. (eds.) Symposium on the evolution of terrestrial vertebrates. Selected Symposia and Monographs. U.Z. I. 4, Modena.
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Internet

You can create a list of all species with available data by selecting the **Genetics** radio button in the 'Information by Topic' section of the Search Page.

In the 'Species Summary' page you get to GENETICS-related information by clicking on the Genetics link under the 'More information' section. In addition, species genome or nucleotide information in GenBank can be accessed by clicking 'GenBank' under Internet Sources.

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References

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