The ELECDAT Table in FishBase

Information based on electrophoresis has been arranged in three tables: the ELECSTUDIES table gives an overview of the studies that have been conducted on different populations of a certain species; the ELECDAT table shows the loci that have been investigated in a certain study; and the ELECSUB table contains the alleles that have been detected at a certain locus.

Together, the tables provide information on the genetic structure and variability of both natural and cultured fish populations. This is important for species/strain selection for aquaculture and will help the management and conservation programs for natural stocks.

As more data are entered in this table, it will become possible to identify research gaps (i.e., important species that have been little studied) and the most appropriate methods and reporting formats for the genetic characterization of various species.

The tables contain allele frequencies from electrophoretic studies of fish populations, both wild and cultured. They also contain information on the enzymes, the total number of loci studied, the tissues and the buffer systems used, heterozygosity values and proportions of polymorphic loci. The fields of the tables are:

Fields

Locality and Country: Refer to the site where the specimens were collected.

Sample source: Refers to whether specimen came from captivity or open waters.

Total loci: States the number of loci examined.

The **Observed heterozygosity** is the proportion of individuals in a population that are heterozygous at a given number of loci. An individual with two different alleles at a particular locus is called a heterozygote. An individual is called a homozygote when two alleles at a particular locus are the same.

The **Expected heterozygosity**, on the other hand, is the proportion of individuals which are prospective heterozygotes based on the allele frequencies and assuming Hardy-Weinberg equilibrium. These are computed for every locus, population and species and help to indicate, for example, the potential for selective breeding (see Fig. 1).

Polymorphic loci: refer to the number of loci in a sample found to be polymorphic divided by the total number of loci examined (see Fig. 1). To standardize the data, the 95% criterion is used here, wherein a locus is considered polymorphic if the frequency of the most common allele does not exceed 0.95. If the data refer to the 99% criterion, this is indicated in the comment field.

Enzyme: Includes names, abbreviations, and numbers recommended for enzymes and other proteins commonly analyzed in fish genetics work. The names and numbers used are based on the

nomenclature recommended by the International Union of Biochemistry's Nomenclature Committee (Shaklee et al. 1990).

Locus: Refers to the specific position or location of a gene on the chromosome. A gene is a specific length of DNA occupying a locus. A locus is called monomorphic if only one allele is known, and polymorphic when different alleles can occur in a locus. Where two or more loci are involved in producing different forms of a protein (isozymes), the most anodal locus is designated as 1, the next 2, and so on. Sometimes the locus is designated by letters, the most anodal is designated as A, the next B, etc.

Tissue: The type of tissue sample used for electrophoresis. The available choices are: skeletal muscle; visceral muscle; heart; kidney; liver; blood; mucus; eye lens; whole body; others. The last choice refers to tissues that are specified in the **Comment** field.

Method used: Refers to the type of electrophoretic method used. Gel electrophoresis is one of the most common methods for studying the genetic variation of individuals at both strain and species levels. Four choices are given: starch gel; polyacrylamide gel; sodium dodecyl sulfate; other methods.

Buffer system: Refers to the electrophoretic buffer system used for clear resolution of specific proteins and enzymes. The fifteen buffer systems most commonly used are described by Boyer et al. (1963), Ridgway et al. (1970), Shaw and Prasad (1970), Selander et al. (1971), and Clayton and Tretiak (1972).

pH: Refers to the acidity of the buffer system used.

Samples: Gives the number of samples per site or per population screened.

An **Allele** is one of several alternative forms of a specific gene. Alleles are distinguished by their protein products (enzymes) during electrophoresis. The relative electrophoretic mobility of enzymes in a zymogram is expressed in terms of numbers. Relative mobilities are calculated based on the most common allele, which is considered **100** (or **-100** for a cathodal locus). A minus sign is assigned to any allele exhibiting cathodal mobility.

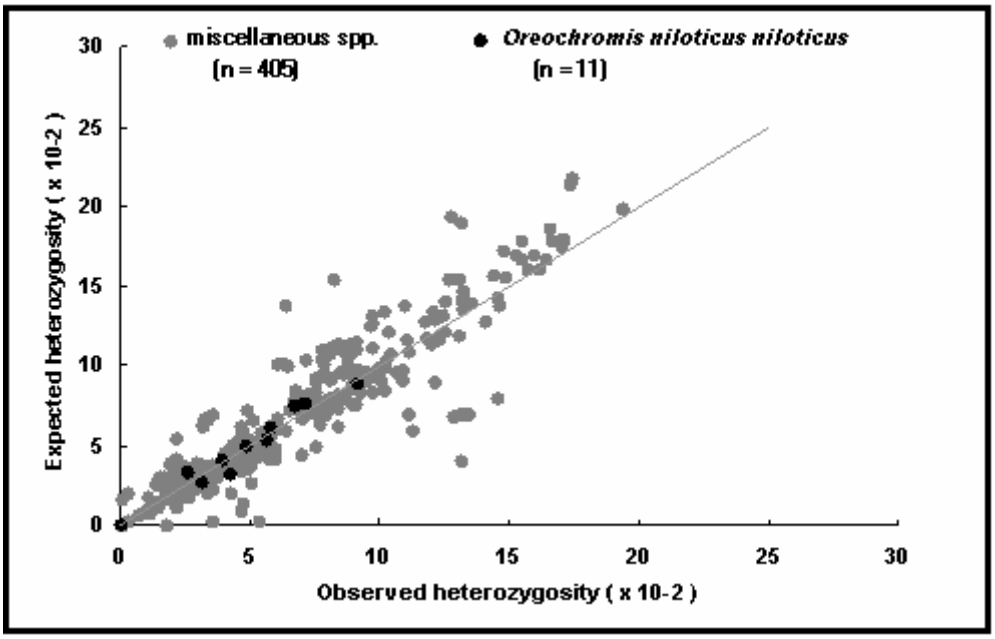

Fig. 1. Expected vs. observed heterozygosity of *Oreochromis niloticus niloticus* (black dots) and miscellaneous fishes. The line represents 1 : 1 ratios. Values well above the line may be the result of inbreeding. Values well below the line may result from crossing of strains.

The **Allele frequency** at a given locus is calculated using the following formula: frequency of allele **A** = 2 (frequency of genotype **AA**) + (frequency of genotype **Aa**) / **2n,** where **n** = number of individuals screened.

Status

The tables currently hold over 15,400 records (one record represents alleles at a single locus) of allele frequencies for over 1100 studies of over 250 species. The updating of this table in collaboration with and using the references identified by Skibinski et al. (1991) has made it the largest repository of data on the genetic variability of fishes.

Graphs

Several graphs can be generated from this table showing:

- the correspondence line between expected and observed heterozygosity (see Fig. 1); examines whether genetic variability (H and P) has been reduced in captive populations relative to populations from open waters;
- the relationship between DNA content and phylogenetic order following Nelson's *Fishes of the World* (1994) (see Fig. 2 of GENETICS table);
- the relationship between chromosome number and DNA content; and
- the relationship between DNA content and aspect ratio of the caudal fin (see Fig. 3 and Box 1 of the GENETICS table chapter for an explanation of this graph).
- These are however not yet available on on the web.

Sources

Important references used so far are Winans (1980), McAndrew and Majumdar (1983), Macaranas et al. (1986, 1995), van der Bank et al. (1989), Carvalho et al. (1991) and Pouyaud and Agnèse (1995).

To achieve a complete coverage of the allele frequencies and related information on fish so far published is a rather daunting challenge and will involve resolving the problems posed by lack of standardization among publications, which still precludes pooling of data (Agustin et al. 1993, 1994).

Internet

You can create a list of all species with available data by selecting **Allele frequencies** radio button in the 'Information by Topic' section of the 'FishBase Search page'. From the Species Summary page, you get to electrophoretic data by clicking the **Allele frequencies** link in the 'More information' section.

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