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PHYLOGENETIC RELATIONSHIPS AMONG NINE SPECIES FROM THE GENUS *FUNDULUS* (CYPRINODONTIFORMES, FUNDULIDAE) INFERRED FROM SEQUENCES OF THE CYTOCHROME *B* GENE.—The New World cyprinodontiform family Fundulidae comprises one extinct genus, *Parafundulus*, and five extant genera: *Adinia, Fundulus, Leptolucania, Lucania,* and *Plancterus* (Parenti, 1981). *Fundulus* is the most speciose genus of the family with approximately 35 recognized species. Three to five subgenera within *Fundulus* have been recognized: *Fundulus, Fontinus, Plancterus, Xenisma,* and *Zygonectes* (Farris, 1968; Parenti, 1981; Wiley, 1986). Parenti (1981) considered *Plancterus* to be a separate genus. The few phylogenies of species of *Fundulus* that have been hypothesized are somewhat contradictory (Cashner et al., 1992).

Our laboratory has been involved in biochemical aspects of the biology of *Fundulus heteroclitus* for 15 years (Powers et al., 1993). To develop a phylogenetic framework for comparative studies with other members of the genus, a better understanding of phylogenetic relationships existing among different species of *Fundulus* is needed. In this study, we used nucleotide sequence data from the mitochondrially encoded cytochrome *b* (cyt *b*) gene to infer phylogenetic relationships among nine species of *Fundulus.* The cyt *b* gene was chosen because it has been informative in phylogenetic inference at various taxonomic levels (Meyer et al., 1990; Meyer and Wilson, 1990; Birt-Friesen et al., 1992).

*Materials and methods.*—Cyt *b* sequences for *F. heteroclitus* and *F. parvipinnis* were taken from Bernardi et al. (1993). The sequence for *P. zebrinus* was provided by C. Grant of the University of Nevada at Las Vegas (UNLV). Specimens of *F. olivaceus, F. chrysotus, F. catenatus, F. notatus, F. dispar,* and *F. lima* were collected from natural populations. Collection localities are given in Materials Examined. DNA was extracted from liver tissue following Bernardi and Bernardi (1990).

The polymerase chain reaction (Saiki et al., 1988) was used to amplify a 270 base pair (bp) region of the cyt *b* gene starting at amino acid