ulation, has been observed in the clear-nosed skate, *Raja eglanteria* (E. L. Libby and P. W. Gilbert, 1960, unpubl.) and the southern stingray, *Dasyatis americana* (Brockman, 1975). Reed and Gilmore (1981) saw similar behavior in the roughtail stingray, *D. centroura,* but copulation was not observed. After an extensive examination of the functional morphology of the clasper of *U. jamaicensis,* LaMarca (1964) concluded that any mating position other than abdomen-to-abdomen was highly unlikely for this species based on the length and angle of flexion of the clasper.

Like many species of skates and rays, *U. jamaicensis* has sexually dimorphic dentition in which the upper male teeth are more pointed and curved than the female teeth (Bigelow and Schroeder, 1953). This has been suggested to be an adaptation for the biting and holding behavior by the male during copulation (McEachran, 1977; McCourt and Kerstitch, 1980).

According to Wourms (1977), there are three basic types of annual reproductive cycles in chondrichthyan fishes: (1) year-round, (2) partially defined annual cycles with one or two peaks, and (3) well-defined annual or biennial cycles. An example of the latter is the California round stingray, *U. halleri,* which has one major reproductive season in late May through early July for most individuals (Babel, 1967). It is unknown whether its Atlantic congener, *U. jamaicensis,* has a similar reproductive strategy. The only other observations of *U. jamaicensis* in breeding condition come from two captured specimens both collected in March (Beebe and Tee-Van, 1928; Bigelow and Schroeder, 1953). Along with the present observation, these suggest a possible reproductive peak in Feb. and March.

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COMPLETE SEQUENCE OF THE MITOCHONDRIAL CYTOCHROME *b* GENE IN THE CHERRYFIN SHINER, *LYTHRURUS ROSEIPINNIS* (TELEOSTEI: CYPRINIDAE).—The mitochondrially encoded cytochrome *b* (cyt *b*) gene of the cherryfin shiner, *Lythrurus roseipinnis,* was sequenced using asymmetric primer-concentration ratios (Gyllensten and Erlich, 1988; Allard et al., 1991) to generate polymerase chain reaction (PCR) amplified cyt *b* DNA fragments (White et al., 1989), which were sequenced via the dideoxy chain-termination method (Sanger et al., 1977). PCR-primers external to the cyt *b* gene were designed from conserved, flanking tRNA genes (Irwin et al., 1991) and were modeled after published cyt *b* sequences of white sturgeon (Brown et al.,

TABLE 1. COMPLETE NUCLEOTIDE SEQUENCE AND INFERRED AMINO ACID SEQUENCE OF THE CYTOCHROME *b* GENE OF *Lythrurus roseipinnis*. Numbering is from the origin of the gene, i.e., base 1 of the cyt *b* gene of *L. roseipinnis* corresponds to position 14,747 of human mtDNA. Letters above the sequence are commonly used symbols for amino acids (Stryer, 1988).

	M A S L R K T H P L M K I A N D A L V D L
1	ATGGCAAGCCTACGAAAAACCCACCCACTTATAAAAATCGCTAATGACGCATTAGTCGACCTT
	P T P S N I S A M W N F G S L L G L C L I
64	CCAACACCATCCAATATCTCAGCAATATGAAACTTCGGATCCCTGCTGGGATTGTGTCTAATT
	T Q I L T G L F L A M H Y T S D I S T A F
127	ACTCAGATCTTAACTGGATTATTCCTAGCCATACACTACACCTCCGACATCTCGACCGCATTT
	S S V T H I C R D V N Y G W L I R N M H A
190	TCATCCGTCACACATATTTGCCGTGACGTCAACTATGGTTGACTTATTCGAAATATACATGCC
	N G A S F F F I C I Y M H I A R G L Y Y G
253	AACGGAGCATCATTTTTCTTCATCTGTATTTATATACATATTGCTCGCGGTCTTTACTACGGA
	S Y L Y K E T W N I G V V L L L L V M M T
316	TCTTACCTATACAAAGAAACCTGAAACATTGGAGTTGTTCTACTTCTTCTAGTTATGATAACC
	A F V G Y V L P W G Q M S F W G A T V I T
379	GCCTTTGTAGGCTACGTACTCCCATGAGGCCAAATGTCCTTTTGAGGTGCCACCGTTATTACA
	N L L S A V P Y M G D T L V Q W I W G G F
442	AACCTCCTGTCAGCAGTACCTTACATAGGGGATACTCTTGTGCAATGGATCTGAGGGGGCTTT
	S V D N A T L T R F F A F H F L F P F V I
505	TCAGTAGATAACGCAACACTAACCCGATTTTTCGCCTTCCACTTCTTGTTCCCCTTCGTCATC
	A G A T V L H L L F L H E T G S N N P A G
568	GCCGGTGCAACCGTTCTCCACTTACTATTTCTACATGAGACAGGGTCAAACAACCCCGCCGGG
	L N S D A D K I S F H P Y F S Y K D L L G
631	TTAAACTCTGATGCGGATAAGATCTCCTTCCACCCCTACTTCTCCTATAAAGACCTTCTTGGC
	F V L M L L A L T S L T L F S P T L L G D
694	TTCGTCCTAATACTGCTGGCTCTTACATCTCTGACGTTGTTCTCCCCCACCTTACTCGGCGAC
	P E N F T P A N P L V T P P H I Q P E W Y
757	CCAGAAAACTTCACCCCAGCAAACCCGCTGGTTACCCCACCACACATTCAACCTGAGTGATAC
	F L F A Y A I L R S I P N K L G G V L A L
820	TTCCTGTTCGCCTACGCCATCCTACGATCTATTCCGAATAAGCTAGGCGGAGTCCTAGCACTA
	L F S I L V L L V V P I L H T S K Q R G L
883	TTATTCAGTATCCTGGTACTATTGGTGGTTCCAATTTTACACACCTCAAAACAACGAGGACTA
	T F R P I T Q F L F W T L V A D M I I L T
946	ACCTTCCGACCCATCACCCAATTCCTATTCTGAACTCTAGTAGCAGATATAATTATTCTGACA
	W I G G M P V E H P Y I I I G Q V A S V L
1009	TGAATCGGAGGCATACCTGTAGAACACCCATATATCATCATTGGCCAGGTCGCCTCGGTTCTG
	Y F A L F L L L A P L A G W A E N K A L K
1072	TACTTTGCACTATTCCTCCTCCTCGCCCCACTCGCCGGGTGAGCAGAGAATAAAGCATTGAAA
	W A
1135	TGAGCTT

1989) and common carp (Araya et al., 1984). The external primer sequences were as follows, where the letters L and H refer to the strand designation (light and heavy, respectively) and the numbers reflect the position of the 3′ base relative to the human mitochondrial genome (Anderson et al., 1981): L14724 (5′-GTGACTTGAAAAACCACCGTTG-3′); H15915 (5′-CAACGATCTCCGGTTTACAAGAC-3′). Primers within the cyt *b* gene were based on sequences obtained from cherryfin shiner and other cyprinid species. The cyt

TABLE 2. NUCLEOTIDE (ABOVE DIAGONAL) AND AMINO ACID (BELOW DIAGONAL) SEQUENCE DIVERGENCE (IN PERCENT) OF THE CYTOCHROME *b* GENE AMONG FIVE VERTEBRATE SPECIES. Nucleotide sequence divergence is based on a two-parameter model (Kimura, 1980). Amino acid sequence divergence is based on inferred amino acid sequences.

	1	2	3	4	5
1. Cherryfin shiner	—	33.1	36.9	38.5	44.3
2. White sturgeon	15.0	—	33.2	34.0	39.5
3. *Xenopus laevis*	22.4	19.5	—	35.9	38.1
4. Cow	24.0	24.0	23.2	—	34.1
5. Human	29.3	29.3	28.2	20.8	—

b sequence for *L. roseipinnis* (Table 1) represents the first complete sequence of the cyt *b* gene in a neopterygian fish. The EMBL accession number for the cyt *b* sequence of *L. roseipinnis* is X66456.

The complete nucleotide and inferred amino acid sequences of the cyt *b* gene of *L. roseipinnis* were compared to those published for white sturgeon, frog (*Xenopus*), cow, and human (Anderson et al., 1981, 1982; Roe et al., 1985; Brown et al., 1989). Estimated divergence values (Table 2) indicate that cyt *b* amino acid sequences in the two fishes are more similar than might be expected on the basis of elapsed evolutionary time. The two fish taxa (sturgeon and cyprinid) represent paleopterygian and neopterygian lineages, respectively, that have been separated for 190–200 million years (Grande and Bemis, 1991); whereas cow and human represent lineages that have been separated for only 65–70 million years (Benton, 1990). The amino acid sequence for *Xenopus* also appears to be more similar to the other vertebrates than might be expected, given that the amphibian and mammalian lineages have been separated for over 350 million years (Benton, 1990). These results are consistent with the hypothesis (Thomas and Beckenbach, 1989) that amino acid substitutions may be functionally or otherwise constrained in mitochondrial protein-coding genes of cold-blooded vertebrates.

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DIEL COLOR PHASE CHANGES IN THE CONEY, *EPINEPHELUS FULVUS* (TELEOSTEI, SERRANIDAE).

Many piscivorous fishes (e.g., stonefish, lizardfish, and flatfish) have cryptic coloration that reduces their chances of being detected by potential prey (Hobson, 1975). The groupers (subfamily Epinephelinae) are common predators on Caribbean coral reefs that exhibit a wide variety of patterns and colorations to match their surroundings (Townsend, 1929; Smith, 1971). Variation in coloration can also be under the individual's behavioral control to enable rapid camouflaging. This ability occurs in many fishes and is so common that it has apparently been attributed to some fishes without observational proof (Cott, 1957). We report here observations of normal diel color phase changes in a species in which the changes were previously thought to occur only due to excitement.

Study species.—Coneys (*Epinephelus fulvus*) are small groupers common in the western Atlantic in shallow water (5–20 m deep) near coral patches (Smith, 1971). They are known to exhibit at least four color patterns (or phases) in nature, as illustrated in Townsend (1929, plate 9). One of the phases consists of a uniformly dark brown body with faint blue-black spots. Although some authors (e.g., Thompson and Munro, 1978) have reported that coneys from deep water are red, they actually appear brown underwater because under normal conditions there is very little red light below 10 m on coral reefs (Jerlov, 1976). In a second color phase, the dorsal part of the body is dark brown or black, and the ventral part of the body is creamy white. Between the black-and-white areas, there is a clear demarcation that runs from the tip of the snout to the dorsal part of the caudal peduncle (Smith, 1971). In the third pattern (xanthic coloration), the body is a uniform bright yellow. The fourth "sleep" pattern consists of irregular bars and blotches and occurs when the individual is at rest at night (Smith, 1971).

Individual fish can vary between the all-brown and black-and-white phases (Smith, 1958), whereas xanthic coneys are apparently not capable of color change (Townsend, 1929). In coneys, the yellow color is probably the result of a single recessive gene (Smith, 1971) unlike xanthism in a congener *E. drummondhayi*, which is simply an ontogenetic phase (Ross, 1988). Here we discuss only the all-brown and black-and-white patterns, because no xanthic coneys were observed during this study.

Methods.—Using SCUBA, we observed coneys almost daily from 12–29 Aug. 1991 at Playa Bengé off the northwest coast of Bonaire, Netherlands Antilles (12°8′N, 68°25′W). The site (depth 8 m) consists of a soft sandbed approximately 50 m in diameter surrounded by coral reefs (van Duyl, 1985; map B3). Fish around the sandbed were habituated to the presence of divers because we had been using the site for behavioral studies of green razorfish, *Xyrichtys splendens* (Nemtzov, 1992). A diver swam slowly around the perimeter of the sandbed and recorded the coloration of each coney observed as all brown, black and white, or intermediate between these two. We noted the time at the beginning of each survey and used it to identify the survey. We conducted 36 (8–10 min) surveys between 0700 h and 1735 h. A mean (± SD) of 20.3 ± 4.7 (range 13–34) coneys were recorded on each survey. During the study, the sun rose at 0640 h and set at 1850 h (±5 min).

Results and discussion.—Most coneys observed during the early morning and late afternoon hours exhibited black-and-white coloration, whereas most of those seen near midday were all brown (Fig. 1). There was a significant difference between the proportion of fish in either color phase for every survey (G-test, $P < 0.05$) except for the surveys conducted at 0930 h and 1615 h (G-test, $P > 0.8$ and $P > 0.99$, respectively). At these two times, there were approximately equal proportions of fish in the two phases. The proportion of fish with intermediate coloration was highest (Fig. 2) near these two times, namely, at 0915 h and 1540 h.

These observations show that the intermediate coloration is a transition between the all-brown and black-and-white phases. Thus, the