EARLY LIFE HISTORY AND RESURGENCE OF SNOOK (FAMILY CENTROPOMIDAE) IN TEXAS

A Thesis

by

CHRISTOPHER JACOB CHAPA

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

May 2012

Major Subject: Wildlife and Fisheries Sciences

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Approved by:

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ABSTRACT

Early Life History and Resurgence of Snook (Family Centropomidae) in Texas. (May 2012)

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Chair of Advisory Committee: Dr. Andre M. Landry, Jr.

The resurgence of Texas' snook (Family Centropomidae) recreational fishery is coupled with an uncertainty as to what species occur in State waters, a limited understanding of life history, and habitat needs of its constituents. This study described species composition and early life history aspects of juvenile (< 100 mm SL) centropomids taken in bag seine collections in estuarine and freshwater habitats along the upper, middle, and lower coast of Texas during 2006 to 2010. *Centropomus* specimens (n = 548) captured from 41 locations across the Texas coast as well as congeners from Mexico (n = 24), Florida (n = 7), and Costa Rica (n = 3) were used in a genetics- and meristic-based determination of species composition, growth rates, range of hatching dates, geographic distribution, and habitat association.

Genetic analyses of the mitochondrial DNA 16s ribosomal RNA gene and the mitochondrial control region (D – loop) validated the presence of smallscale fat snook (*C. parallelus* Poey, 1860, n = 333), common snook (*C. undecimalis* Bloch 1792, n = 212) and Mexican snook (*C. poeyi* Chavez, 1961, n = 3) in Texas, with the last of these validations representing the first known record of this species in Texas. AMOVA of 16s

and D – loop sequences failed to detect genetic differentiation within Texas for *C. parallelus* and *C. undecimalis*. However, AMOVA for 16s and D – loop *C. undecimalis* sequences did yield significant genetic differences between Texas and Mexico against those from Florida and Costa Rica.

Juvenile centropomids (< 100 mm SL) in Texas occupied backwater habitats with dissipated currents similar to those of Florida congeners (tidal sloughs, freshwater habitats, and structured shorelines). Coastal ranges of these species differed with *C. parallelus* taken from the Rio Grande to West Galveston Bay, whereas *C. undecimalis* was captured from the Rio Grande northward near Palacios. Three *C. poeyi* were captured at only two locations (Laguna Vista and Port Aransas). Daily growth rates varied between species and capture years, with these ranging from 0.22 to 0.97 mm d^{-1}. Analyses of hatch-date distribution suggest centropomids in Texas begin spawning in August and continue it through late September into mid-November.

DEDICATION

To my parents.

ACKNOWLEDGEMENTS

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Thanks also go to my colleagues in Dr. Landry's Sea Turtle and Fisheries Ecology Research Laboratory, Drs. Tasha Metz and Kim Reich, and Bill Dailey, and Josh Parks for their assistance. My appreciation also goes out to Dr. Rooker's Fisheries Ecology Lab, Dr. Brinkmeyer's and Dr. Schwarz's Coastal Health and Estuarine Microbiology Lab and Seafood Safety Lab. Additionally, I would like to thank the entire staff of the Perry R. Bass Marine Fisheries Research Center for their genetics help and guidance and Dr. Juan Carlos Perez from El Colegio de la Frontera Sur for his hospitality and fish finding skills in Campeche, Mexico. In particular I would like to thank Joel Anderson, Bill Karel, Britt Bumguardner, Rudy Salazar, Dustin Roberts, Ryan Schloesser, Luke Murphy, Shane Cantrell, The Snook Foundation, Fishing Guide Ernest Cisneros, Dr. Jim Ditty, and Randy Blankinship for their help either in the field or laboratory. I also want to extend my gratitude to the Southeast Texas Sportfishing Association, McDaniel Charitable Foundation, Texas A&M at Galveston Marine Biology Department and Graduate Office for their financial support and to the students who were willing to go into the field with me.

Finally, thanks to my mom and pop for their encouragement and to Katrina for her patience and love.

NOMENCLATURE

‰	parts per thousand
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
d	days
GOM	Gulf of Mexico
LLM	Lower Laguna Madre
mtDNA	mitochondrial DNA
NJ	neighbor joining
PCR	polymerase chain reaction
SL	standard length
TAMUG	Texas A&M University at Galveston
TL	total length
TPWD	Texas Parks and Wildlife Department

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CHAPTER I

INTRODUCTION

Snook are a monogenetic group of fishes (genus *Centropomus*) comprising the Family Centropomidae (Nelson 2006). Twelve constituent species occur in tropical and subtropical coastal waters of the American Atlantic and Pacific; none occur in both oceans (Rivas 1986, Aliaume et al. 1997, Tringali et al. 1999b, Orrell 2003). Centropomids are distributed in the American Atlantic from Florida (Atlantic and Gulf coasts), Greater and Lesser Antilles, southern coast of the Gulf of Mexico (GOM), continental Caribbean coast southward to Brazil (Shafland & Foote 1983, Rivas 1986, Howells et al. 1990, Pope et al. 2006). Although *Centropomus* species have been reported from Cape Hatteras, North Carolina and Port Aransas, Texas, their distribution in northern latitudes is limited by thermal intolerance, with few fish occurring in water cooler than 7 to 12 °C (Cooley 1974, Shafland & Foote 1983, Matlock & Osburn 1987, Howells et al. 1990). Nearly all descriptions of juvenile and adult centropomid life history demonstrate constituent species' use of brackish and freshwater tidal sloughs as nurseries for feeding, protection, growth, and overwintering (Volpe 1951, Marshall 1958, Martin & Shipp 1971, Fore & Schmidt 1973, McMichael et al. 1989, Blewett et al. 2006).

Largescale fat snook (*Centropomus mexicanus* Bocourt, 1886), smallscale fat

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This thesis follows the style of Bulletin of Marine Science.

snook (*C. parallelus* Poey, 1860), and common snook (*C. undecimalis* Bloch, 1792) are the only known representatives of six centropomid species with an Atlantic distribution assumed to inhabit Texas coastal waters (Mark Fisher & Randy Blankenship, TPWD, pers. comm., Martin & King 1991). *Centropomus undecimalis* exhibits the widest geographical range of all species in the genus and is the model for centropomid distribution (Figure 1.1). Swordspine snook (*C. enserferus* Poey, 1860), tarpon snook (*C. pectinatus* Poey, 1860), and Mexican snook (*C. poeyi* Chavez, 1961) exhibit a more restricted distribution and are not known from Texas, possibly as a result of their inability to tolerate variable environmental conditions (Rivas 1986, Tringali et al. 1999a, Tringali et al. 1999b).

Centropomid populations supported a commercial fishery in Texas during the early 20th century (Marshall 1958, Matlock & Osburn 1987, Alvarez-Lajonchère & Taylor 2003). Annual commercial landings in Texas peaked at 104,451 kg in 1928 followed by steady declines through 1961 (113 kg), after which no landings were reported (Matlock & Osburn 1987). Texas Parks and Wildlife Department prohibited the commercial capture and sale of centropomids in 1987 and set bag and size restrictions that were subsequently modified in 1991 and 1996. Current fisheries regulations in Texas for all *Centropomus* species include a one-fish bag limit per day and a slot limit of 61.0 to 71.1 cm (24 to 28 inches).

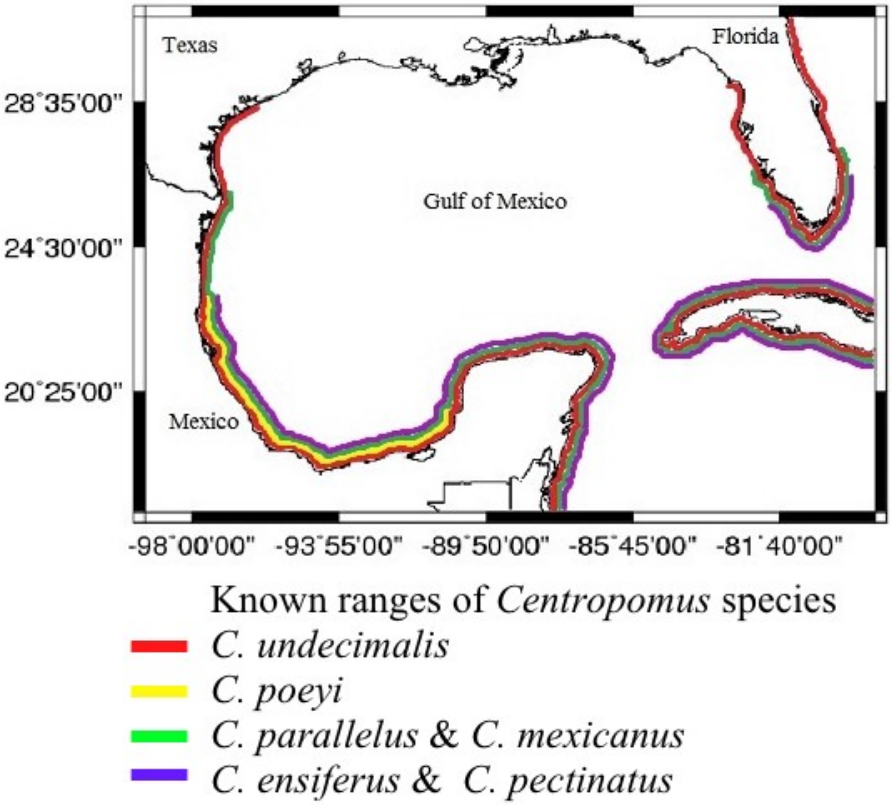

Figure 1.1. Distribution of the six recognized *Centropomus* species in the western Atlantic (Rivas 1986).

Centropomid Life History

Centropomus undecimalis and *C. parallelus* exhibit relatively similar life histories (Volpe 1951, Alvarez-Lajonchère et al. 2002a, Temple et al. 2004, da Silva Rocha et al. 2005, Tsuzuki et al. 2007a, Tsuzuki et al. 2007b), whereas comparable documentation for other centropomids is lacking. These species are estuarine-dependent, protandric hermaphrodites, maturing first as males within one year of age and later converting to females 2.5 – 3.5 years old (McMichael et al. 1989, Taylor et al.

2000, Muller & Taylor 2006, Alvarez-Lajonchère & Tsuzuki 2008). All female centropomids are considered sexually mature on the assumption they have developed directly from males that have previously participated in spawning events (Taylor et al. 2000). Females migrate to high salinity regions at the mouths of passes, canals, and ocean inlets just offshore during the spring and summer to spawn (Volpe 1951, Marshall 1958, Tucker & Campbell 1988, Peters et al. 1998b, Taylor et al. 1998), with this activity influenced by water temperature, salinity, tidal current and moon phase (Table 1.1, Taylor et al. 1998, Yanes-Roca et al. 2009). The biogenic need to spawn near tidal passes was confirmed by (Ager et al. 1976) who reported that *C. undecimalis* requires saltwater for sperm activation, after which fertilized eggs depend on salinities of 28 ‰ or greater for buoyancy that ensures optimal developmental conditions (Chapman 1987, Peters et al. 1998a). The necessity for higher salinities during spawning has also been confirmed for *C. parallelus* (Alvarez-Lajonchère et al. 2002b, Alves et al. 2006, Alvarez-Lajonchère & Tsuzuki 2008, Cerqueira & Tsuzuki 2009) and *C. poeyi* (Carvajal 1975).

Table 1.1. Status of information on spawning dynamics of Atlantic *Centropomus* species.

Species	Spawning Season	Location	Citation
Centropomus ensiferus	NA	NA	-
Centropomus mexicanus	NA	NA	-
Centropomus parallelus	June – August	Veracruz	(Chavez 1963)
	Spring – Summer	Brazil	(Santos et al. 2009)
Centropomus pectinatus	NA	NA	-
Centropomus poeyi	July – August	Veracruz & Campeche	(Carvajal 1975)
Centropomus undecimalis	June – July	SW Florida	(Volpe 1951)
	June – November	SW Florida	(Marshall 1958)
	July – October	SE Florida	(Tucker & Campbell 1988)
	April – December	SW Florida	(McMichael et al. 1989)
	April – October	SE & SW Florida	(Taylor et al. 1998)

NA, no information currently available

Centropomid larvae occur mainly in open waters near spawning locations but are eventually transported by tidal flow and currents to nursery habitats (Peters et al. 1998a). Settlement-sized centropomids (6 to 7 mm SL) spend their first months of life utilizing freshwater and marine marshes, seagrasses, and mangrove prop-root habitats (Tolley et al. 1987, Aliaume et al. 1997, Alvarez-Lajonchère & Tsuzuki 2008), primarily feeding on crustaceans (Fore & Schmidt 1973, Gilmore et al. 1983, Muller & Taylor 2006). Spatial distribution of these new recruits depends on circulation patterns and habitat suitability of each estuary. (Peters et al. 1998b) suggested that the low salinity requirement for newly settled *C. undecimalis* is misleading, by observing settlement sized (> 6 mm SL) *C. undecimalis* in polyhaline waters (18 to 30 ‰). Like their larval counterparts, juvenile centropomids prefer low-energy habitats and sporadically occur under overhanging vegetation and within submerged structure of freshwater tributaries and estuaries (Peters et al. 1998a, Peters et al. 1998b, Stevens et al. 2007). With growth, *Centropomus* species move from shallow riparian habitats to seagrass meadows, mangrove fringe, and deeper estuarine waters such as passes, nearshore reefs, jetties, and beachfronts (Muller & Taylor 2006).

Study Justification

The Texas centropomid fishery vanished 50 years ago; however, reopening of the Rio Grande and recent occurrence of milder winters may have facilitated a resurgence of populations of one or more *Centropomus* species from Mexico into Texas waters where they occupy the northern limit of their range in the western GOM. Increasing reports of centropomids taken by anglers, TPWD fisheries-independent and fisheries-dependent

surveys, and Texas A&M University at Galveston Field Ichthyology (MARB 312) classes confirm this reappearance. Fisheries-independent surveys conducted by TPWD since 1975 have yielded only a small number of centropomids tentatively identified as three species that are at the northern limit of their range in the western GOM (*C. undecimalis* $n = 532$, *C. mexicanus* $n = 111$, and *C. parallelus* $n = 48$; Mark Fisher, TPWD, pers. comm.). All published studies on the genus *Centropomus* in Texas refer only to *C. undecimalis* and are limited to ecologically-related articles that describe freeze related mortalities (Gunter 1941, 1951, Moore 1976, Holt & Holt 1983), sporadic occurrence (Springer & Pirson 1958, Moore 1975), and surveys of the LLM (Breuer 1962), Baffin Bay (Breuer 1957), South Bay (Hook 1991), and the Rio Grande (Breuer 1970, Edwards & Contreras-Balderas 1991). These studies coupled with TPWD data provide little information on the species composition, recruitment patterns, or habitat requirements that sustain constituent species. Lack of the aforementioned information and the need to manage an emerging fishery prompt the study described herein to identify species composition, extent of the spawning season, and age structure and growth characteristics.

Research Objectives

Research described herein characterized early life history and ecology of the Family Centropomidae in Texas, with specific objectives to:

- determine species composition in Texas waters;
- identify early recruitment habitats into which initial settlement occurs;
- determine age, growth and hatch-date distribution of juvenile centropomids recruiting to Texas waters.

CHAPTER II

GENETIC ANALYSIS OF *CENTROPOMUS* SPECIES IN TEXAS COASTAL WATERS

Introduction

Systematic reviews and revisions have classified *Centropomus* on the basis of morphology (Greenfield 1975, Rivas 1986, Orrell 2003); however, misidentification of species is common among researchers and field technicians unfamiliar with constituents of the Family Centropomidae. Rivas' (1986) thorough evaluation of centropomid classification examined multiple meristic and morphological characteristics differentiating these species. Although complete, Rivas' identification key lacks the ability to correctly identify centropomids < 100 mm SL due to unstable characteristics found within constituent life history stages. Since many *Centropomus* species co-occur over the range of the genus it is necessary to correctly identify juveniles to ensure that systematically valid studies of early life history, recruitment, and growth are conducted (Tringali et al. 1999a). Determination of molecular genetic data supporting morphological classification of centropomids provided by Rivas has been accomplished through allozyme electrophoresis and sequencing of the mitochondrial DNA 16s ribosomal RNA (rRNA) gene (Tringali et al. 1999a).

Currently, TPWD has identified *C. mexicanus*, *C. parallelus*, and *C. undecimalis* occurring in Texas bay systems through routine fisheries-dependent and fisheries-independent sampling efforts. The three *Centropomus* species occurring in Texas waters

look similar and are difficult to distinguish from one another. Confirmation of two Centropomus species' presence in Texas coastal waters has been verified through genetics (*C. parallelus*; Martin & King 1991) and historical data (*C. undecimalis*; Moore 1975, Holt & Holt 1983, Matlock & Osburn 1987, Pope et al. 2006). However, the occurrence of *C. mexicanus* in Texas waters is questionable, as no taxonomic investigation has been conducted to confirm such a presence. Additionally, mere mention of *C. mexicanus* in the scientific literature is restricted to Rivas' (1986) centropomid identification key, a report of this species' feeding habits in Brazil by (Sazima 2002) and genetic investigations conducted by (Tringali et al. 1999a) & (Seyoum et al. 2005). Based on mtDNA data, (Tringali et al. 1999a) identified *C. mexicanus* and *C. parallelus* as sister species, differing by only 1% divergence. Morphological analysis conducted by (Rivas 1986) separates these two species through overlapping scale counts (Table 2.1). Possible reasons for limited information on *C. mexicanus* could stem from the smaller sizes attained by this species (maximum 43 cm, common to 18 cm TL; Rivas 1986), cryptic behavior and associated capture difficulty within its habitat or misidentification as another species.

Centropomus parallelus is a commercially valuable species in Central and South America due to characteristics (robustness, resistance to disease, tolerance to high stocking densities, and euryhalinity) that foster culture success (Ribeiro & Tsuzuki 2010). Despite this commercial importance, limited genetic investigations involving *C. parallelus* have been conducted (Martin & King 1991, Tringali et al. 1999a, Prodocimo et al. 2008). Conversely, the recreationally popular *C. undecimalis* has been extensively

studied, with numerous genetic assessments characterizing restrictive gene flow (Donaldson & Wilson 1999, Tringali & Leber 1999, Seyoum et al. 2005), divergence rate (Donaldson et al. 1993), and genetic markers (Wilson et al. 1997); however, all of these were limited to Florida's centropomid fishery.

Table 2.1. Morphological comparison between *Centropomus mexicanus* and *Centropomus parallelus* derived from Rivas (1986).

Quantitative Characters	*Centropomus mexicanus*	*Centropomus parallelus*
Ray count		
First dorsal	VIII	VIII
Second dorsal	I + 10	I + 10
Anal fin	III + 6	III + 6
Pectoral fin	15	15
Scale count		
Lateral line	68 – 79	79 – 92
Second dorsal fin to lateral line	10 – 16	10 – 16
Anal fin to lateral line	12 – 16	13 – 18
Scales around caudal peduncle	24 – 28	26 – 31
Gill raker count		
Lower limb	11 – 12	11 – 12

Although TPWD has developed and implemented a sound sampling program to assess the health of Texas' marine fisheries, considerable portions of the state's estuary systems go uninvestigated due to sampling difficulties in constituent habitats. Ecologically important groups such as the Family Centropomidae whose various life history stages use habitats not sampled by TPWD are poorly known from both a taxonomic and natural history perspective. Such a lack of information is problematic for strategic management of Texas' centropomid stocks and the fisheries that may harvest these stocks. Additionally, implementation of a regional management plan for spotted

seatrout (*Cynoscion nebulosus* Cuvier, 1830) in the LLM (lowering bag and possession limits from ten to five) may redirect recreational fishing pressure toward the developing centropomid fishery in Texas. The possibility of misidentification of unknown *Centropomus* species occurring in Texas justifies the necessity for genetic analyses of constituent species. A common perception is that two or more *Centropomus* species are utilizing Texas estuaries. Effective, long-term management of Texas' centropomid populations will depend upon an understanding of the species' constituency and their genetic structure. This chapter assesses species composition of centropomids in Texas, with specific attention to:

- species identity of juvenile centropomids found in Texas waters;
- genetic diversity of each species;
- morphological characteristics that aid in field identification of centropomids.

Materials and Methods

Study Areas

Juvenile centropomids were collected at spatially restricted wetland sloughs, boat ramps, and other tidal- and freshwater- influenced habitats from Carancahua Bay (Palacios, Texas) to the Rio Grande (US – Mexico border). Selection of each collection site was based on historical data generated by TPWD and TAMUG as well as published (Breuer 1962, 1970, Pezold & Edwards 1983, Contreras-Balderas et al. 2002, Pope et al. 2006) and anecdotal reports of larval and juvenile centropomid occurrence. Collection sites were classified according to regions along the upper (Galveston to Matagorda Bay), middle (San Antonio Bay to Corpus Christi), and lower Texas coast (Port Mansfield to

Boca Chica) that are divided into two major climatological zones (temperate and subtropical). The only temperate climate collection site was located in the upper coast region, within the upper reaches of Carancahua Bay south of Palacios. The remaining study areas were located within the Aransas and LLM estuaries that exhibited subtropical climates. The Aransas estuary housed the middle coast collection sites that included Goose Island State Park (Rockport), Redfish Bay (at two locations along SH 361, Stedman Island), and a drainage ditch located in the city of Aransas Pass on SH 35. Lower coast collections were conducted from the southernmost portion of the LLM and included the Arroyo Colorado (and surrounding drainages), Laguna Vista, San Martin boat ramp and channel, Mexiquita Flats, Padre Island Coast Guard Station (northwest of the Brazos Santiago Pass) and Boca Chica (Rio Grande and surrounding sloughs).

Sampling Protocol

Bag seine tows were conducted biweekly at the aforementioned study sites from April to November 2006, September 2007 to January 2008, and September 2009 to January 2010 to increase sample size for genetic and age-growth analysis. Standardized and randomized tows of a 9.1 m long by 1.2 m deep bag seine with 0.6 cm bar mesh wings and a 0.3 cm bar mesh 1.2 x 1.2 x 1.2 m bag were used to sample juvenile centropomids. Three (15.2 m long x 6.0 m wide) standardized tows were conducted at each collection site to generate CPUE data on spatial and temporal occurrence. This sampling protocol was complemented by randomized bag seine sampling that took two forms: 1) a minimum of 30 minutes of non-standardized effort with the aforementioned bag seine at each collection site to characterize centropomid occurrence in any habitat

type not sampled during standardized sampling and to capture additional centropomids for age growth analysis; and 2) non-standardized effort conducted at sites and habitats other than those described previously in response to additional information on possible centropomid settlement grounds that was received during the study. Fin clippings from centropomids from Jacksonville, Florida; Barra del Colorado, Costa Rica; Campeche, Campeche, Mexico; and Frontera, Tabasco, Mexico were used as sources of additional DNA material for genetic analysis. Additional samples were obtained through hook and line sampling from LLM guides and local anglers. Subsequently, in January 2010, cold-killed centropomids from the upper Texas coast also were obtained for genetic analysis.

Meristic Analysis

All centropomids captured were kept on ice for transport to the laboratory where they were processed immediately or frozen for subsequent analysis. Species identification to the lowest possible taxon relied on keys by (Greenfield 1975), (Rivas 1986), (McEachran & Fechhelm 1998), and (Orrell 2003). Each specimen was enumerated SL and TL were measured to the nearest millimeter, and with meristic counts recorded as follows: Spines and soft rays in the first and second dorsal and anal fins were counted. Scale counts followed Rivas' (1986) protocol wherein lateral line, second dorsal to lateral line, and anal fin to lateral line scale counts were recorded. These morphological characteristics were examined for potential differences to aid in identification of centropomid species found in Texas.

DNA Isolation

Genetic identification of centropomids to the species level was performed in collaboration with TPWD's Perry R. Bass Marine Fisheries Research Center in Palacios following the protocols of (Tringali et al. 1999a) and (Anderson & Karel 2009). A single eyeball was removed from each centropomid to isolate DNA using Qiagen DNeasy Blood and Tissue Kit (Qiagen Inc., Valencia, California, USA) and PUREGENE DNA Isolation Kit (Gentra Systems Inc., Minneapolis, Minnesota, USA), following the manufacturers' protocols, with final rehydration values between 75 and 100 μL. Determination of quantity and purity of DNA was analyzed through spectrophotometry using a NanoDrop 1000 (NanoDrop Tech., Wilmington, Delaware, USA). Isolated DNA samples were stored at -20 °C.

PCR Reactions

PCR primers specific to the 16s rRNA (16s) region were designed using sequence data from previously published studies to investigate genetic identification in centropomids. The mitochondrial DNA control region (D – loop) was also characterized; data from the D – loop sequences, because of the substantially higher levels of variation, and thus resolution, compared to 16s data, were used to test a subsample of centropomids to identify any cryptic speciation and finer phylogeographic partitioning. Sequencing of 16s and D – loop was conducted according to protocols developed by(Tringali et al. 1999a) and (Anderson & Karel 2009). Amplifications of template DNA were conducted via PCR under a modified touchdown protocol by using Ready-To-Go PCR beads (GE Healthcare, Piscataway, New Jersey, USA) on a Techne

Genius thermocycler (Techne Inc., Princeton, New Jersey, USA). Reactions consisted of 1 μL of template DNA (50 ng/μL), one Ready-To-Go bead, and 24 μL of forward and reverse primer cocktail (0.4 μM standard concentration of each primer), for a total of 25 μL. The touchdown PCR protocol utilized for all reactions consisted of the following: an initial single denaturation period of 2 minutes at 95 °C, 10 cycles of initial amplification (95 °C for 30 seconds; 55 °C for 30 seconds, lowering 1 °C each cycle; and 72 °C for 1 minute), 20 cycles of primary product amplification (95 °C for 30 seconds; 55 °C for 30 seconds; and 72 °C for 1 minute, adding 3 seconds of extension per cycle), and a final extension period of 7 minutes at 72 °C. The primer sequences used for 16s PCR were: 16Sar (5'-CGCCTCTTTATCAAAAAC-3') and 16Sbr (5'-CCGGTCTGAACTCAGATCACG-3') (Palumbi 1994, Tringali et al. 1999a). The primer sequences used for D – loop PCR were: L15990 snk (5'-TACCGTCAACTCCCAAAGCTA-3') and CRSNOOK4H (5'-CTGCCCTCTGGAAATAATGCTRGGC-3').

PCR products were purified using ExoSAP-IT (USB, Cleveland, Ohio, USA) to free DNA of excess primers and nucleotides. Following the manufacturer's recommendations, 5 μL of PCR product were mixed with 2 μL of enzyme and placed on a thermocycler for 15 minutes at 37 °C, followed by an inactivation step for 30 minutes at 80 °C.

Sequencing Reactions

Sequencing reactions were carried out according to (Anderson & Karel 2009) using 10 μL volumes by means of Genomelab Quick Start Master Mix DTCS (Beckman Coulter Inc., Fullerton, California, USA). Primers for sequencing were the same as those used in PCR. Cycle sequencing parameters consisted of 30 cycles of denaturing at 96 °C for 20 seconds, annealing at 50 °C for 20 seconds, and extension at 60 °C for 4 minutes. Sequencing reactions were precipitated by adding 1/20 volume of a cocktail containing 2 μL sodium acetate (3M), 2 μL EDTA (100mM) and 1 μL glycogen, followed by 2 volumes of 95% ethanol, and centrifuged at 3,700 rpm for 30 minutes to form pellets. Resulting pellets were then rinsed twice with a 70% ethanol, dried, and rehydrated by using a formamide sample loading solution (Beckman Coulter, Fullerton, California, USA). Finally, sequences were separated and analyzed on a Beckman CEQ8000 capillary sequencer (Beckman Coulter, Fullerton, California, USA) using default sequencing module parameters. Examination of raw sequences for base-calling errors was trimmed manually. Forward and reverse traces for each sequence were aligned using Sequencher version 4.2 (Gene Codes Corp., Ann Arbor, Michigan, USA), and haplotypes were characterized only for those sequences that contained overlapping forward and reverse reads.

Genetic Analysis

Positive identification of centropomid species was confirmed via BLAST searches through GenBank (GenBank accession numbers: U85008, U85012, U85014, U85016, U85017, U85018; Tringali & Leber 1999) coupled with gene trees

reconstructed in MEGA 5.0 (Tamura et al. 2011). Gene tree structure was determined via NJ based on Tamura-Nei distances, as well as Maximum Likelihood (ML) distances among haplotypes. Statistical support for branching patterns was tested by bootstrap consensus. DnaSP v5.10 (Librado & Rozas 2009) was used to obtain genetic diversity estimates, including haplotype diversity (*h*), nucleotide diversity (π), number of pairwise nucleotide differences (k), number of haplotypes (*m*), and segregating sites (S) for all centropomid species identified. Parsimony-based haplotype networks were constructed from the data using MEGA 5.0 (Tamura et al. 2011). Nested Clade Analysis was performed using the TCS program and statistical parsimony (v1.13; Clement et al. 2000) and to subsequent phylogeographic inference. The degree of genetic variation among samples of each centropomid species identified was measured with analysis of molecular variance (AMOVA) using Arlequin 3.5.1.2 (Excoffier & Lischer 2010). Estimates of gene flow and genetic differentiation among sampling areas were based on Wright's F_{ST} using Arlequin.

Results

Identification of Centropomids

Overall, 580 centropomid specimens were examined for genetic analyses and meristic comparisons. Distribution of samples collected for genetic analysis is listed in Tables 2.2, 2.3 and Figure 2.1. Centropomids identified included *Centropomus parallelus*, *C. poeyi*, and *C. undecimalis*. Meristic comparisons were not useful in distinguishing among juveniles (< 100 mm SL) due to lateral line scale counts that were difficult to determine due to incomplete and/or missing scales. However, anal fin to

lateral line and second dorsal to lateral line counts were relatively easy to perform but did not accurately separate species due to overlapping values. Physical characteristics described by (Greenfield 1975), pelvic fins reaching past the anus in *C. parallelus* and not reaching past the anus in *C. poeyi* and *C. undecimalis*, was useful.

Nucleotide sequences of 16s ranged from 621 bp for *C. parallelus*, 609 bp for *C. poeyi*, and 628 bp for *C. undecimalis*; sequences were aligned and trimmed to 475, 535, and 483 bp, respectively. Sequence submissions to GenBank (using BLAST) revealed matches with three species: *C. parallelus*, *C. poeyi*, and *C. undecimalis*. Consensus sequences for each species identified (*C. parallelus n* = 337, *C. poeyi n* = 4, and *C. undecimalis n* = 239) were generated and aligned against the six recognized Atlantic centropomid representatives from GenBank (Figure 2.2; Tringali et al. 1999a) to assure positive genetic identification.

Table 2.2. Catch distribution of Texas centropomids.

Site #	County	Location	Latitude N	Longitude W	*C. parallelus* (*n*)	*C. poeyi* (*n*)	*C. undecimalis* (*n*)
1	Galveston	Hitchcock Diversionary Canal	29 20.134	95 01.417	1	-	-
4	Brazoria	Bastrop Bayou	29 05.598	95 16.940	4	-	-
7	Brazoria	Oyster Creek	29 00.059	95 18.070	1	-	-
8	Brazoria	Intracoastal waterway	28 57.850	95 17.533	1	-	-
9	Brazoria	Brazos River	28 52.803	95 22.780	1	-	-
13	Jackson	Carancahua Bay	28 44.252	96 24.121	10	-	1
14	Matagorda	Matagorda Bay	28 43.593	95 47.124	2	-	-
21	Nueces	Redfish Bay	27 53.637	97 07.676	10	-	-
22	Nueces	Redfish Bay at Stedman Island	27 53.341	97 07.063	9	-	3
23	Nueces	Aransas Pass	27 53.566	97 09.188	37	1	8
28	Willacy	Port Mansfield	26 33.822	97 16.590	2	-	-
30	Cameron	Arroyo Colorado	26 20.998	97 23.483	94	-	25
32	Cameron	Laguna Vista	26 05.705	97 17.024	88	2	79
33	Cameron	Lower Laguna Madre	26 04.461	97 12.878	3	-	-
34	Cameron	Lower Laguna Madre	26 04.356	97 09.994	5	-	-
35	Cameron	Mexiquita Flats	26 04.044	97 11.659	3	-	1
36	Cameron	South Bay	26 01.529	97 10.272	20	-	22
38	Cameron	Lake San Martin	26 00.125	97 17.913	17	-	12
40	Cameron	Rio Grande (6 km from mouth)	25 57.613	97 11.116	28	-	-
41	Cameron	Rio Grande (mouth)	25 57.556	97 08.810	3	-	55

Table 2.3. Locations of *Centropomus* species captured outside of Texas.

Locality	Collector	Capture date	Latitude N	Longitude W	*C. parallelus* (*n*)	*C. poeyi* (*n*)	*C. undecimalis* (*n*)
Barra del Colorado, Costa Rica							
	A. Landry	January 2006	10 46.170	83 35.566	-	-	3
Jacksonville, Florida							
	M. Hanke	October 2008	30 28.801	81 28.841	-	-	7
Frontera, Tabasco, Mexico							
	C. Chapa	January 2010	18 31.773	92 39.224	4	-	7
San Pedro, Tabasco, Mexico							
	C. Chapa	January 2010	18 30.646	92 39.034	-	1	-
Campeche, Campeche, Mexico							
	C. Chapa	January 2010	19 50.506	90 32.039	-	-	12

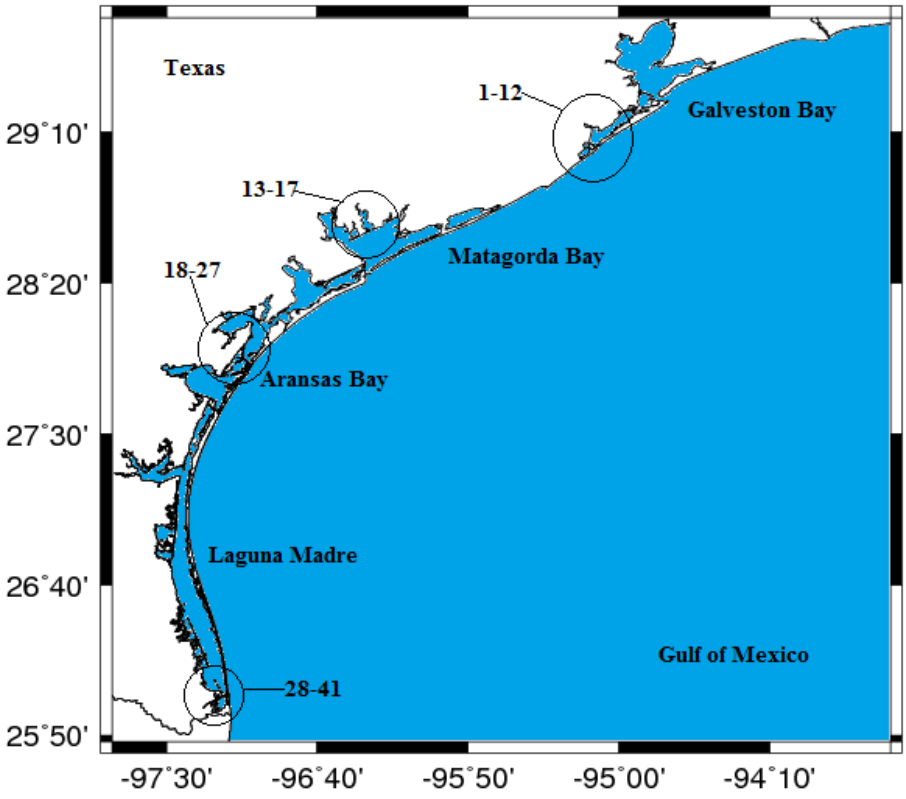

Figure 2.1. Map of the Texas Gulf coast, illustrating study site locations (numbered) within major bay systems. Refer to Table 2.3 to identify numbered sites.

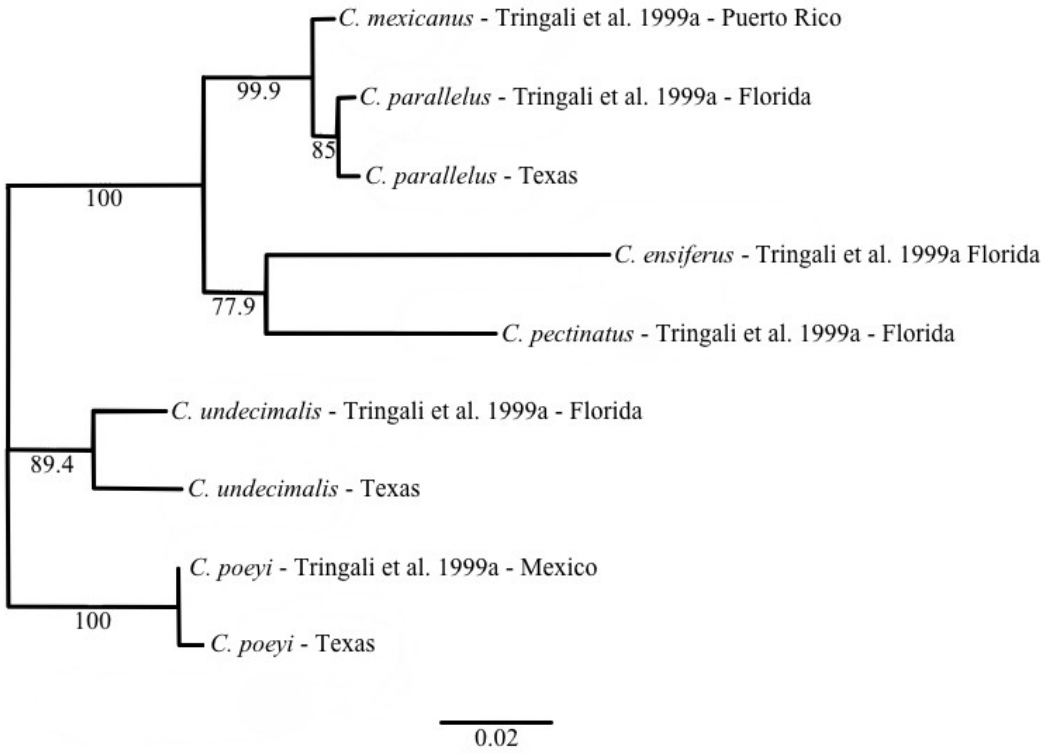

Figure 2.2. NJ tree, using the Maximum Composite Likelihood method, identifying Texas captured *Centropomus parallelus*, *Centropomus poeyi*, and *Centropomus undecimalis* 16s mtDNA consensus sequences with 16s mtDNA sequences from (Tringali et al. 1999a). Bootstrap values above 50% are shown.

Patterns of Variation in the mtDNA 16s Gene

The 475 bp region of the 16s gene for 337 assayed *C. parallelus* identified six variable positions, seven haplotypes, and six polymorphic sites; of which two were parsimoniously informative that corresponded to six transitions and zero transversions. Base frequencies of the 16s region for *C. parallelus* were 28.6% for A, 24.8% for C, 21.7% for G, and 24.8% for T. One haplotype (par – 1) was widely distributed throughout Texas and Mexico and represented 97% of all samples taken (Table 2.4, Figure 2.3). The remaining six haplotypes (par – 2 through par – 7) were restricted to Texas' LLM, with low overall haplotype diversity (h = 0.053) and nucleotide diversity (π = 0.000) differing by less than one substitution event. The absence of genetic differentiation among all localities of *C. parallelus* 16s is result of a dominant haplotype found throughout, thus a regional AMOVA was not executed.

Table 2.4. Haplotype relative frequency, distribution, and polymorphic sites contained within the 475bp segment of the 16s gene among *Centropomus parallelus* collected from Texas and Mexico. Identical bases (.) are shown.

Haplotype	Texas			Mexico	Total	Polymorphic Sites					
	Upper	Middle	Lower			38	141	192	267	388	424
	n = 18	*n* = 52	*n* = 263	*n* = 4	*n* = 337						
par – 1	1.000	1.000	0.966	1	0.973	A	G	G	G	C	T
par – 2	0	0	0.004	0	0.003	.	.	.	A	.	.
par – 3	0	0	0.004	0	0.009	.	.	.	.	T	.
par – 4	0	0	0.004	0	0.003	.	.	.	.	.	C
par – 5	0	0	0.008	0	0.003	G	.	.	.	.	.
par – 6	0	0	0.004	0	0.006	.	A	.	.	.	.
par - 7	0	0	0.011	0	0.003	.	.	A	.	.	.

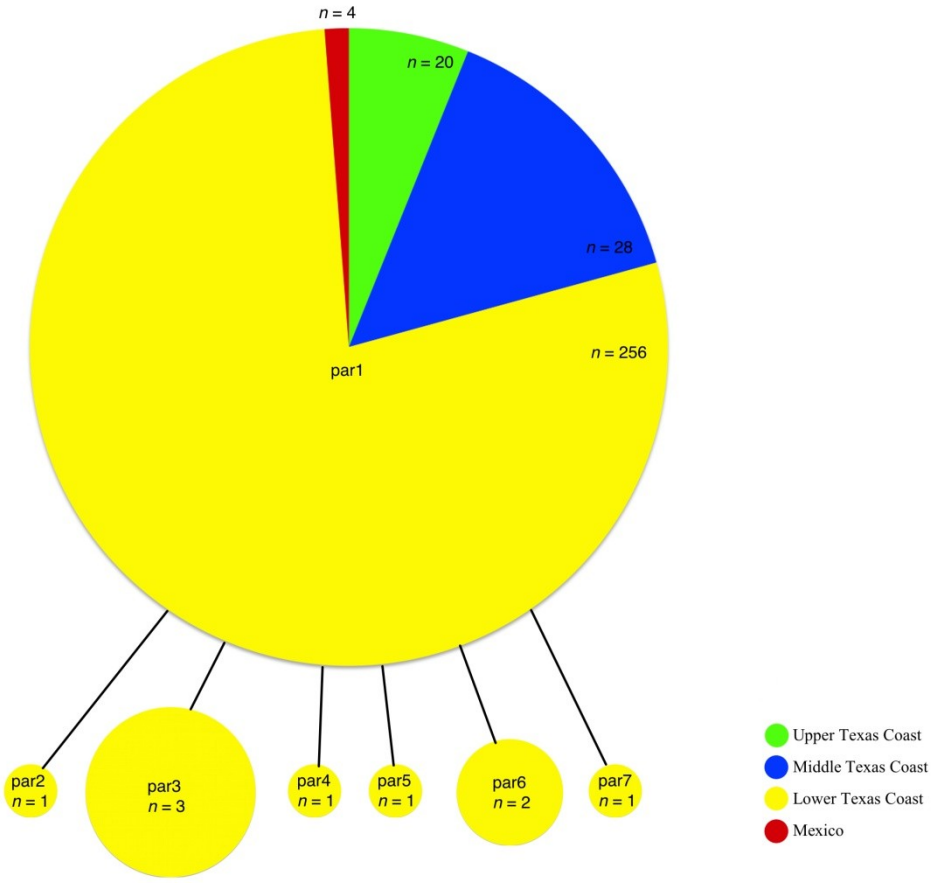

Figure 2.3. TCS network of the seven *Centropomus parallelus* 16s mtDNA haplotype sequences.

The 535 bp region of 16s sequenced from four *C. poeyi* specimens revealed three haplotypes and two variable sites corresponding to two transitions. Base frequencies for the four *C. poeyi* were: A = 28.5%, C = 26.9%, G = 22.1%, and T = 22.4%. Haplotype diversity was high ($h = 0.833$); distribution and frequency of *C. poeyi* haplotypes are shown in Table 2.5. Low nucleotide diversity for *C. poeyi* ($\pi = 0.001$) was similar to that for all centropomids sampled, possibly due to the reduced number of substitution events. AMOVA was not conducted on *C. poeyi* 16s data due to small sample size ($n = 4$).

Of the three species identified using 16s sequences, the 483 bp region of *C. undecimalis* was the most variable. A total of 12 variable sites, corresponding to 12 transitions and one transversion, generated 15 haplotypes (Table 2.6). The base frequencies were 29.7% for A, 26.1% for C, 20.4% for G, and 23.8% for T. Two haplotypes were most common (und – 1 and und – 2), each with frequencies greater than 0.05% that accounted for 90.3% of all *C. undecimalis* sampled. The remaining 13 haplotypes occurred at a frequency lower than 1%. Basic haplotype diversity estimates for each species and region sampled are provided in Table 2.7.

Table 2.5. Haplotype relative frequency, distribution, and polymorphic sites contained within the 535bp segment of the 16s gene among *Centropomus poeyi* collected from Texas and Mexico. Identical bases (.) are shown.

Haplotype	Texas		Mexico	Total	Polymorphic Sites	
	Middle	Lower			5	5
					4	5
	***n* = 1**	***n* = 2**	***n* = 1**	***n* = 4**	1	7
poe – 1	0	0.500	0	0.250	A	G
poe – 2	1.000	0	0	0.250	G	A
poe – 3	0	0.500	1.000	0.500	.	A

Table 2.6. Haplotype relative frequency, distribution, and polymorphic sites contained within the 483bp segment of the 16s gene among *Centropomus undecimalis* collected from Texas, Florida, Costa Rica, and Mexico. Identical bases (.) are shown.

Haplotype	Texas			Florida	Costa Rica	Mexico	Total	Polymorphic sites											
	Upper	Middle	Lower					40	136	184	196	202	207	226	235	299	333	343	349
	n=1	*n*=17	*n*=192	*n*=7	*n* = 3	*n* = 19	*n*=239												
und – 1	0	0.235	0.344	0.857	1.000	0.316	0.356	T	G	A	G	T	A	T	C	C	G	A	G
und – 2	1.000	0.706	0.557	0.143	0	0.526	0.548	.	.	.	.	.	.	.	.	.	.	.	A
und – 3	0	0	0.026	0	0	0	0.021	.	.	G	.	.	.	.	.	.	.	.	A
und – 4	0	0	0.005	0	0	0	0.004	.	.	.	.	.	.	.	.	.	.	.	C
und – 5	0	0	0.005	0	0	0	0.004	.	.	.	.	.	.	.	T	.	.	.	.
und – 6	0	0	0.021	0	0	0.105	0.025	.	.	.	.	.	.	.	.	.	.	G	.
und – 7	0	0	0.005	0	0	0.053	0.008	.	A	.	.	.	.	.	.	.	.	.	A
und – 8	0	0	0.005	0	0	0	0.004	.	.	.	A	.	.	.	.	.	.	.	.
und – 9	0	0	0.005	0	0	0	0.004	.	.	.	.	.	G	.	.	.	.	.	A
und – 10	0	0	0.005	0	0	0	0.004	C	.	.	.	.	.	.	.	.	.	.	.
und – 11	0	0	0.005	0	0	0	0.004	.	.	.	.	.	.	.	.	T	.	.	A
und – 12	0	0	0.005	0	0	0	0.004	.	.	.	.	.	.	C	.	.	.	.	.
und – 13	0	0	0.005	0	0	0	0.004	.	.	.	.	C	.	.	.	.	.	.	.
und – 14	0	0	0.005	0	0	0	0.004	.	.	.	.	.	G	.	.	.	.	.	.
und – 15	0	0.059	0	0	0	0	0.004	.	.	.	.	.	.	.	.	.	A	.	A

Table 2.7. Summary of haplotype diversity statistics of 16s for all *Centropomus* species including sample size (*n*), segregating sites (S), number of haplotypes (*m*), haplotype diversity (*h*), nucleotide diversity (π) and pairwise nucleotide differences (k).

Species	*n*	S	*m*	*h*	π	k
Centropomus parallelus	337	6	7	0.053	0.000	0.053
Texas – upper	20	0	1	0	0	0
Texas – middle	50	0	1	0	0	0
Texas – lower	263	6	7	0.067	0.000	0.068
Mexico	4	0	1	0	0	0
Centropomus poeyi	4	2	3	0.833	0.002	0.002
Texas – middle	1	0	1	0	0	0
Texas – lower	2	1	2	1.000	0.002	1.000
Mexico	1	0	1	0	0	0
Centropomus undecimalis	239	12	15	0.574	0.001	0.668
Texas – upper	10	2	3	0.600	0.001	0.002
Texas – middle	8	1	2	0.250	0.000	0.250
Texas – lower	192	11	14	0.573	0.001	0.671
Mexico	19	3	4	0.643	0.002	0.795
Florida	7	1	2	0.286	0.000	0.286
Costa Rica	3	0	1	0	0	0

AMOVA results for Texas *C. undecimalis* yielded no significant genetic differentiation for 16s between regions of capture (Table 2.8), most likely due to the shared haplotypes across regions. Virtually all variation (100%) is within the population ($p = 0.36$). An expanded AMOVA investigation across Gulf (Texas versus Costa Rica, Mexico, and Florida individually) identified differences between Florida/Costa Rica and Texas samples. The comparison of *C. undecimalis* from Texas and Florida yielded a significant ($p = 0.01$) proportion of variation between populations at 22.02%. Similarly, AMOVA revealed additional differences between Mexico and Florida populations ($p = 0.04$, Variation = 21.91%). A haplotype network tree displaying the distribution of *C. undecimalis* haplotypes sampled in this study is found in Figure 2.4.

Table 2.8. Summary of AMOVA results of *Centropomus undecimalis* 16s mtDNA.

Species	Source of variation	d.f.	Percentage of variation (*p*)
Centropomus undecimalis			
			Texas (upper vs. middle vs. lower)
	Between populations	2	-0.43 (0.36)
	Within populations	207	100.43
			Texas vs. Mexico
	Between populations	1	-1.29 (0.57)
	Within populations	227	101.29
			Texas vs. Florida
	Between populations	1	**22.02 (0.01)**
	Within populations	215	77.89
			Mexico vs. Florida
	Between populations	1	**21.91 (0.04)**
	Within populations	14	78.09
			Texas vs. Costa Rica
	Between populations	1	**29.89 (0.04)**
	Within populations	211	70.11
			Costa Rica vs. Mexico
	Between populations	1	27.73 (0.09)
	Within populations	20	72.27

Bold items indicate significant difference

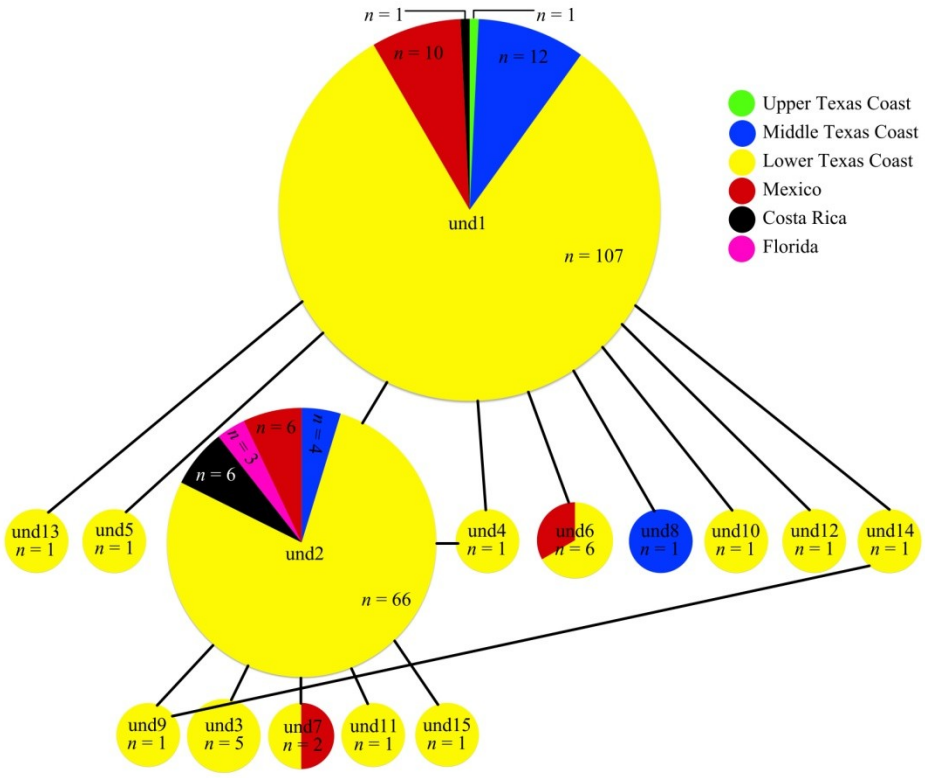

Figure 2.4. TCS network of the 15 *Centropomus undecimalis* 16s mtDNA haplotype sequences.

D – loop

The length of the mitochondrial control region (D – loop) for both *C. parallelus* and *C. undecimalis* resulted in 500+ bp sequences with multiple (ten plus) tandem repeats for each species (Table 2.9) thus, sequences were aligned and edited manually, resulting in 181 bp and 152 bp sequences for *C. parallelus* and *C. undecimalis*, respectively.

Table 2.9. Repeated sequences found in mitochondrial control region (D – loop) for *Centropomus parallelus* (41 bases) and *C. undecimalis* (39 bases)

Species	Repeated Sequence
C. parallelus	TACATAAAGTGTATGCCCCTGACATACTATAATGGTGGTAA
C. undecimalis	GGTGATTATACATAGAATGTATAATTTATCATCATATAT

Variation in the 181 bp segment of the mitochondrial control region (D – loop) was analyzed for 82 *C. parallelus.* Forty-eight polymorphic sites were found, with six transversions and 46 transitions. Haplotype diversity was high, as expected due to rapid evolution and divergence of the D – loop sequence (Table 2.10). A total of 47 haplotypes was observed, with the most common haplotype (Dpar – 1) accounting for 25.6% of the sample (Table 2.11). Specimens representing Dpar – 1 all came from the LLM and Aransas Pass collection sites. AMOVA results of *C. parallelus* D – loop sequences identified no significant differences among regions at any level (Table 2.13). The results of these AMOVAS (upper coast versus middle, upper versus lower, and middle versus lower) suggest a lack of regional genetic differentiation (Figure 2.5).

A segment 152 bp long of the D - loop was characterized for seventy-four *C. undecimalis*. The segment contained 27 polymorphic sites corresponding to four transversions and 28 transitions. Similar to the D-loop of *C. parallelus*, the D – loop of *C. undecimalis* is characterized by relatively low nucleotide diversity values within samples, indicating that haplotypes are closely related concurrent with high values of haplotype diversity (Table 2.10). There were 24 haplotypes with two haplotypes, Dund – 4 and Dund – 5, accounting for 38.2 and 14.9% of the sample, respectively (Table 2.12). The two most common *C. undecimalis* haplotypes (Dund - 1 and Dund - 2)

consisted of samples largely from LLM and Aransas Pass collection sites. Frequencies of all other haplotypes for both species were less than 10%. Many *C. undecimalis* haplotypes were not detected in the GOM; for instance, Dune – (1,2,6,8, and 20) was restricted to Florida and Costa Rica, and these were highly divergent from the majority of haplotypes present in Texas and Mexico. The NJ tree developed for *C. undecimalis* D – loop haplotypes indicated divergence between Texas samples and those from Costa Rica and Florida (Figure 2.6). AMOVA for *C. undecimalis* revealed similar results for intrastate comparisons of D – loop analysis, with no significant variation ($p = 0.06$) between middle and lower coast populations, suggesting a lack of genetic population structure within Texas (Table 2.13). Comparisons between Texas *C. undecimalis* and Florida conspecifics illustrated significant difference among populations ($p = 0.00$), with 20.5% of the genetic variation among Texas and Florida. Lastly, a comparison of Texas *C. undecimalis* to Costa Rica conspecifics yielded similar significant difference results among groups ($p = 0.00$).

Table 2.10. Summary of D - loop haplotype diversity statistics for 156 *Centropomus* specimens including sample size (*n*), segregating sites (S), number of haplotypes (*m*), haplotype diversity (*h*), nucleotide diversity (π), and pairwise nucleotide differences (k).

Species		*n*	S	*m*	*h*	π	k
Centropomus parallelus	**Texas**	82	48	47	0.929	0.023	4.154
	Texas – upper	2	6	2	1.000	0.034	6.000
	Texas – middle	8	13	6	0.928	0.025	4.392
	Texas – lower	72	47	44	0.928	0.023	4.095
Centropomus undecimalis	**Texas**	74	27	24	0.820	0.027	3.787
	Texas – middle	6	7	5	0.766	0.021	2.933
	Texas – lower	58	19	17	0.755	0.012	1.593
	Florida	7	13	4	0.714	0.028	3.905
	Costa Rica	3	3	2	0.667	0.014	3.905

Table 2.11. Haplotype distribution and frequency of *Centropomus parallelus* D - loop sequences.

Haplotype	Texas			Total
	Upper	Middle	Lower	
	n = 2	*n* = 8	*n* = 72	*n* = 82
Dpar – 1	0	0.250	0.264	0.256
Dpar – 2	0	0	0.014	0.012
Dpar – 3	0	0	0.014	0.012
Dpar – 4	0	0	0.014	0.012
Dpar – 5	0	0	0.014	0.012
Dpar – 6	0	0.125	0.014	0.024
Dpar – 7	0	0.250	0.042	0.061
Dpar – 8	0	0	0.014	0.012
Dpar – 9	0	0	0.014	0.012
Dpar – 10	0	0	0.014	0.012
Dpar – 11	0	0	0.014	0.012
Dpar – 12	0	0	0.014	0.012
Dpar – 13	0	0.125	0.014	0.024
Dpar – 14	0	0	0.014	0.012
Dpar – 15	0	0	0.014	0.012
Dpar – 16	0	0	0.014	0.012
Dpar – 17	0	0	0.028	0.024
Dpar – 18	0.50	0	0	0.012
Dpar – 19	0	0	0.014	0.012
Dpar – 20	0	0.125	0.028	0.037
Dpar – 21	0	0	0.028	0.024
Dpar – 22	0	0	0.014	0.012
Dpar – 23	0	0	0.028	0.024
Dpar – 24	0	0	0.014	0.012
Dpar – 25	0	0	0.014	0.012
Dpar – 26	0	0	0.014	0.012
Dpar – 27	0	0	0.014	0.012
Dpar – 28	0	0	0.014	0.012
Dpar – 29	0	0	0.014	0.012
Dpar – 30	0	0	0.014	0.012
Dpar – 31	0	0	0.056	0.049
Dpar – 32	0	0	0.028	0.024
Dpar – 33	0	0	0.014	0.012
Dpar – 34	0	0	0.014	0.012
Dpar – 35	0	0	0.014	0.012
Dpar – 36	0	0	0.014	0.012
Dpar – 37	0	0	0.014	0.012
Dpar – 38	0	0.125	0	0.012
Dpar – 39	0	0	0.014	0.012
Dpar – 40	0	0	0.014	0.012
Dpar – 41	0	0	0.014	0.012
Dpar – 42	0	0	0.014	0.012
Dpar – 43	0	0	0.014	0.012
Dpar – 44	0	0	0.014	0.012
Dpar – 45	0	0	0.014	0.012
Dpar – 46	0.50	0	0	0.012
Dpar – 47	0	0	0.014	0.012

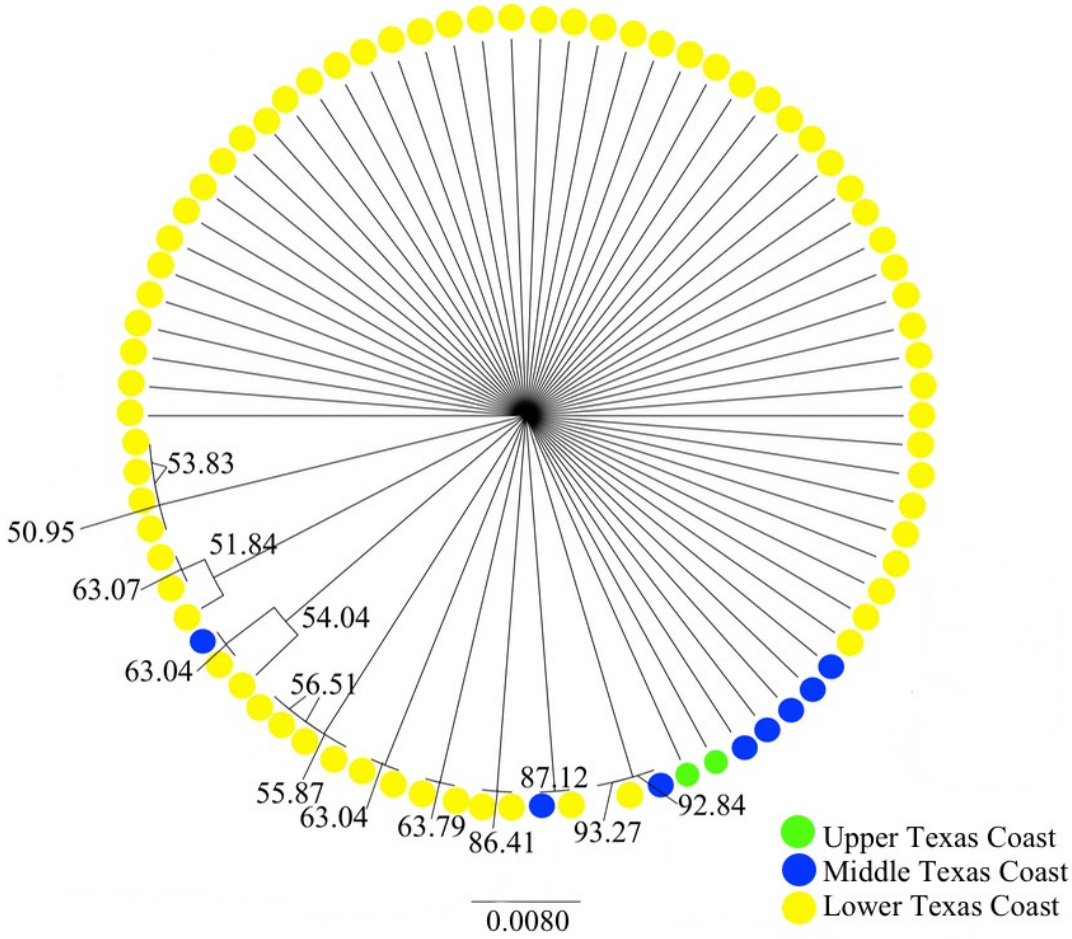

Figure 2.5. Unrooted NJ tree based on 47 *Centropomus parallelus* D - loop haplotypes from Texas using the Maximum Composite Likelihood method. Bootstrap values above 50% are shown by the nodes.

Table 2.12. Haplotype distribution and frequency of *Centropomus undecimalis* D - loop sequences.

Haplotype	Texas		Florida	Costa Rica	Total
	Middle	Lower			
	n = 6	*n* = 58	*n* = 7	*n* = 3	*n* = 74
Dund – 1	0	0	0.571	0.667	0.081
Dund – 2	0	0	0.143	0	0.014
Dund – 3	0.167	0.034	0	0	0.041
Dund – 4	0.333	0.466	0	0	0.392
Dund – 5	0.167	0.172	0	0	0.149
Dund – 6	0	0	0	0.333	0.014
Dund – 7	0	0.017	0	0	0.014
Dund – 8	0	0	0.143	0	0.014
Dund – 9	0	0.017	0	0	0.014
Dund – 10	0.167	0	0	0	0.014
Dund – 11	0	0.069	0	0	0.054
Dund – 12	0	0.034	0	0	0.027
Dund – 13	0	0.017	0	0	0.014
Dund – 14	0	0.034	0	0	0.027
Dund – 15	0	0.017	0	0	0.014
Dund – 16	0	0.017	0	0	0.014
Dund – 17	0	0.017	0	0	0.014
Dund – 18	0	0.017	0	0	0.014
Dund – 19	0	0.017	0	0	0.014
Dund – 20	0	0	0.143	0	0.014
Dund – 21	0	0.017	0	0	0.014
Dund – 22	0	0.017	0	0	0.014
Dund – 23	0	0.017	0	0	0.014
Dund – 24	0.167	0	0	0	0.014

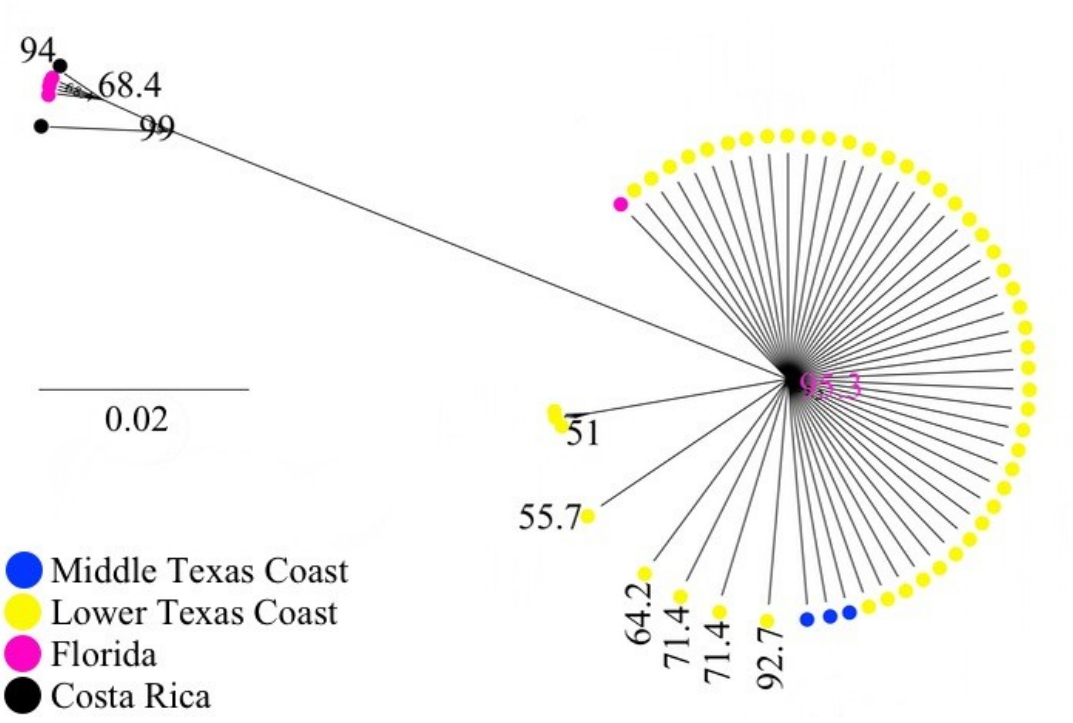

Figure 2.6. Twenty-four *Centropomus undecimalis* D – loop haplotypes displayed on an unrooted NJ tree using the Maximum Composite Likelihood method. Bootstrap values above 50% are shown by the nodes.

Table 2.13. Summary of AMOVA results of *Centropomus* species D – loop sequences.

Species	Source of variation	d.f.	Percentage of variation (*p*)
Centropomus parallelus			
			Texas (upper vs. middle vs. lower)
	Between populations	2	0.83 (0.35)
	Within populations	79	99.17
Centropomus undecimalis			
			Texas (middle vs. lower)
	Between populations	1	11.19 (0.06)
	Within populations	62	88.81
			Texas vs. Florida
	Between populations	1	79.26 (0.00)
	Within populations	1	20.74
			Texas vs. Costa Rica
	Between populations	1	84.43 (0.00)
	Within populations	1	15.57

Bold items indicate significant difference

Morphological Identification

Using results of the aforementioned genetic identification, a subset of 20 randomly selected individuals from *C. parallelus* and *C. undecimalis* and all three *C. poeyi* (< 100 mm SL) was examined to produce identification aids. Meristic analysis yielded morphological differences between all three species as described by (Greenfield 1975), where pelvic fins (P_2) in *C. parallelus* reach past the anus but fail to reach the anus in *C. undecimalis* and *C. poeyi* (Figures 2.7) Separation of *C. undecimalis* and *C. poeyi* can be differentiated by Rivas' (1986) use of first dorsal spine (D_1) counts, wherein *C. undecimalis* = 8 and *C. poeyi* = 7 (Figure 2.8).

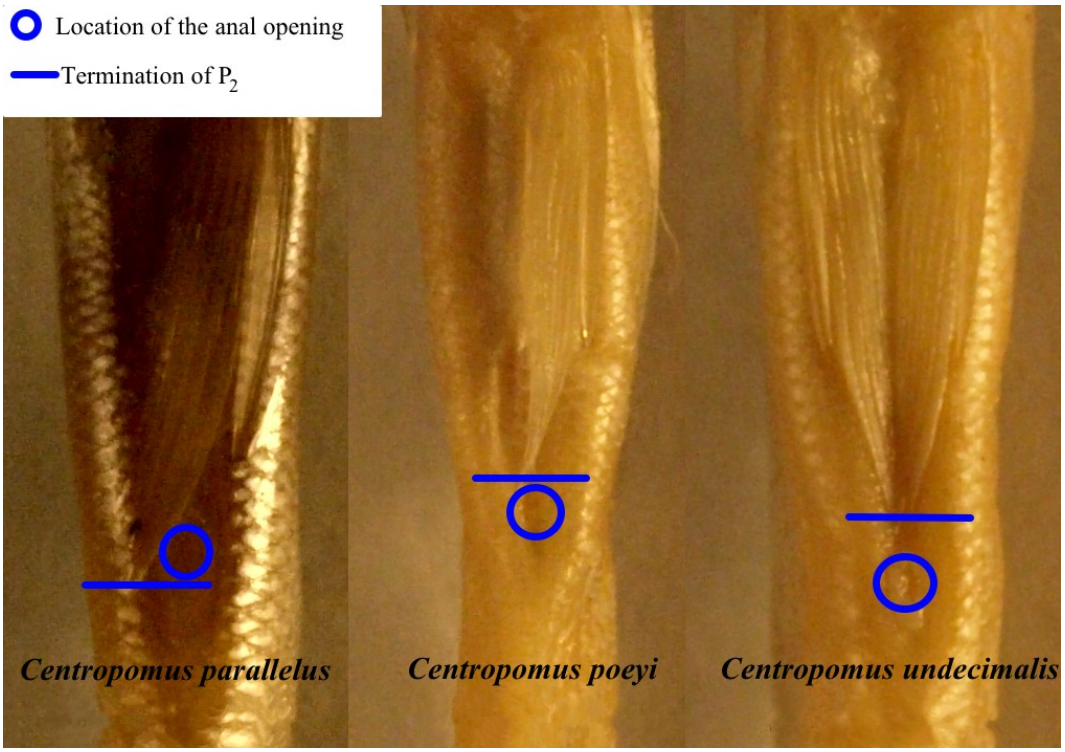

Figure 2.7. Ventral view of *Centropomus* species showing relationship of pelvic fin termination (P_2) to anal opening.

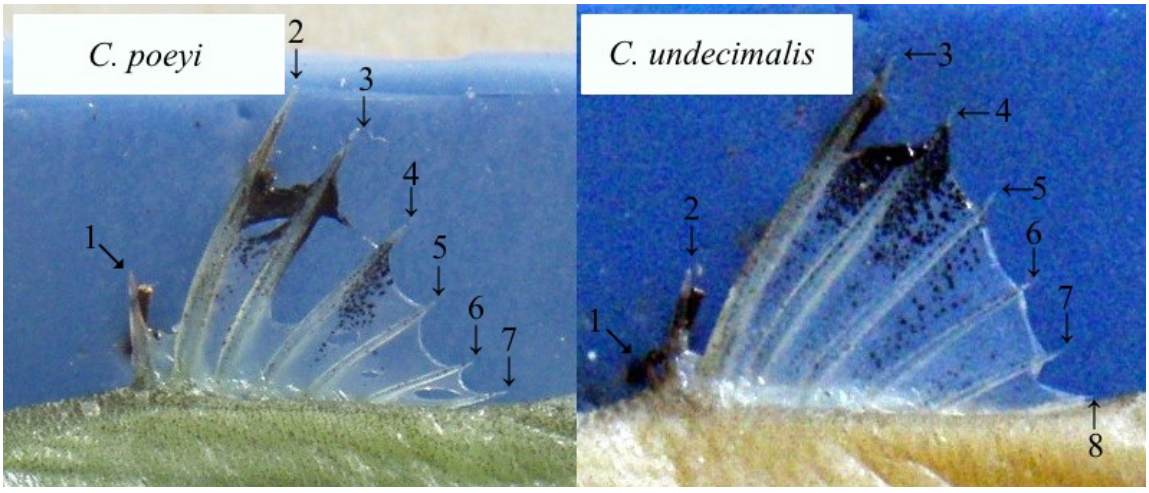

Figure 2.8. Images of dorsal fin spine counts for *Centropomus poeyi* and *Centropomus undecimalis* illustrating differences between species.

Discussion

Genetic analysis of the mtDNA16s gene from centropomids collected during this study yielded three species in Texas: *C. parallelus*, *C. poeyi*, and *C. undecimalis*. The presence of *C. mexicanus* could not be confirmed with mitochondrial data. The existence of *C. parallelus* in Texas waters was previously documented (Martin & King 1991). The occurrence of *C. undecimalis* in Texas is a presumption largely based on historical documentation and the common misconception that all centropomids in the state were *C. undecimalis* (Gunter 1941, 1951). The capture of only three *C. poeyi* in Texas 500 km from their closest established range (Carvajal 1975, Chavez 1981, Alvarez-Lajonchère & Tsuzuki 2008) provides little indication of a resident population in Texas. However, otolith microstructure analyses (Chapter 4) for two *C. poeyi* captured in Laguna Vista, Texas indicate that these specimens were spawned 80 to 90 days prior to their capture. Possible reasons for this species' presence in Texas include: 1) successful transport of larvae from resident spawning grounds in Mexico via long-shore currents, and 2) populations of *C. poeyi* have migrated further north along the Mexican coast and have colonized Texas waters.

Warmer winters may have facilitated a northern advancement of other centropomids into Texas waters may have also facilitated *C. poeyi*'s migration beyond their normal range into northern localities with suitable habitats. However, the only information about the possibility of *C. poeyi* conducting large-scale migrations is based on a small scale tagging study in the Papaloapan River system south of Veracruz, Veracruz, Mexico. (Chavez 1981) identified migrations of *C. poeyi* between the

Papaloapan and Grijalva River systems, where one specimen traveled 333 km south to the Grijalva River. The remaining *C. poeyi* that were recaptured in Chavez's study were found within the confines of the Papaloapan estuary, only migrating out of the river to the GOM during their reproductive season to spawn. The single *C. poeyi* found in the Grijalva River suggests that *C. poeyi* and possibly all centropomids are not limited to a single estuary and freely move from one estuary to another. Additionally, the migration patterns of Florida's Atlantic *C. undecimalis* are known to migrate up to 350 km along the Atlantic coast (Tringali & Bert 1996). Migration patterns identified by Chavez (1981) and Tringali & Bert (1996) indicate that settlement into new estuaries is possible if new habitats are adequate for establishment.

The low genetic diversity and shared haplotypes found within Texas' *C. parallelus* 16s suggest a lack of genetic population structure; most likely all Texas *C. parallelus* are from an expanding population originating from Mexico. Haplotype par – 1 accounted for 328 of the 337 (97.3%) *C. parallelus* examined in this study, and could be considered as the genetic hub from which all different *C. parallelus* haplotypes develop. Specimens from this haplotype ranged from the northernmost collection site of any centropomid captured in this study (Freeport, Texas) to the most southern collection site (Frontera, Tabasco, Mexico). The remaining haplotypes (par – 2 through par – 7) were represented by few individuals (less than two in most cases) and were only found in the LLM.

AMOVA results for 16s *C. undecimalis* specimens within Texas and Mexico region yielded no significant genetic variation; however, variation was found within

Texas and Florida/Costa Rica comparisons. These results suggest that centropomids from Texas are reproductively isolated from those in Florida and Costa Rica. The separation between populations utilizing of 16s mtDNA haplotypes is notable, since (Tringali & Bert 1996) found differences between Atlantic and Gulf populations of *C. undecimalis* in Florida utilizing the entire mtDNA nucleotide sequence. AMOVA for the 16s *C. poeyi* samples were not conducted due to small sample size ($n = 4$); however it is important to note that the single sample from Frontera, Tabasco, Mexico shared a haplotype with a specimen from Laguna Vista, Texas. The shared haplotype suggests a potential connection between Mexico and Texas populations. Size and age of *C. parallelus* and *C. undecimalis* (Chapter 4) captured in this study provide evidence that recruits found in Texas stem from a resident spawning population rather than from long-range dispersal that is strongly dependent on favorable long-shore currents.

D –loop sequences were perceived as a diagnostic tool to identify any potential hybridization or cryptic speciation within *C. parallelus* and the potential probability of the occurrence of *C. mexicanus*. However, the D – loop sequence analysis of *C. parallelus* stocks present in Texas revealed no genetic differentiation, suggesting that *C. parallelus* populations could be treated as a single genetic stock. *Centropomus undecimalis* exemplified the same lack of genetic differences among Texas populations; however, analysis of D – loop data revealed differences between the samples of Texas and Mexico against those from Florida and Costa Rica.

The absence of genetic population structure between both *C. parallelus* and *C. undecimalis* within Texas can be explained by the reproductive patterns of these species.

Spawning strategies documented for centropomids (spawning at the mouths of passes) allow for dispersion of these species, thus facilitating gene flow; however, a noticeable decrease in genetic differentiation is expected for new or invading populations.

Conclusion

This study successfully confirmed the identification of early juveniles of three centropomid species (*C. parallelus*, *C. poeyi*, and *C. undecimalis*) in Texas waters. The lack of population structure resolvable by 16s data most likely reflects the highly conserved nature of this mitochondrial gene. D – loop AMOVA of *C. undecimalis* indicated significant differences between Texas and Florida/Costa Rica populations, a finding supported by the separation shown on the NJ tree (Figure 2.6) and nucleotide diversity for each clade (Texas dominant clade $\pi = 0.012$ and Florida/Costa Rica clade $\pi = 0.008$). Along with these differences, the potential for differences between Texas and Mexico should be investigated for both *C. parallelus* and *C. undecimalis* using satellite markers. Genetic validation aided in morphological identification of species captured in Texas. Termination of P_2 in relation to the anal opening separates *C. parallelus* from *C. poeyi* and *C. undecimalis*, and D_1 counts separated the latter two species from one another. This separation follows a combination of identification characteristics given in keys developed by (Greenfield 1975) and (Rivas 1986), and should assist fisheries biologists in correctly identifying similar looking centropomids.

Sources of centropomid recruits to Texas populations have yet to be determined and could originate from distant spawning grounds and not a contribution from resident populations. An assessment of sources and pathways of centropomid populations into

Texas waters remains to be conducted. Otolith microstructure analyses (Chapter 4) insinuate a proximal spawning population, and additional otolith chemistry studies could also aid in determination of origins and possible separate populations. Further morphometric and molecular analyses are necessary to interpret population structure, relationships, origins, and possible morphological or genetic divergence of centropomids in Texas. Additionally, examination of a larger sample size of *Centropomus* species from ecologically- and geographically-diverse locations along the Texas coast, spanning multiple spawning seasons across several years, is necessary to clarify genetic diversity on a regional basis. Continued genetic analysis will elucidate the population structure of centropomids and assess the potential for additional species occurring in Texas waters.

CHAPTER III

DISTRIBUTION AND OCCURRENCE BY HABITAT OF *CENTROPOMUS* SPECIES IN TEXAS

Introduction

The Texas Gulf shoreline stretches 595 km from the Sabine River to the Rio Grande, and spans seven major and five minor estuaries covering one million hectares. These estuaries serve an important role by providing habitats, nurseries, food, and spawning grounds for estuarine dependent fishes (Blaber & Blaber 1980, Boesch & Turner 1984, Adams et al. 2006). Despite their importance, Texas estuaries are confronted with significant problems related to anthropogenic alterations of freshwater inflow (Longley 1994, Adams et al. 2009) and habitat loss (Bell et al. 1988, Rozas et al. 2007, Engle 2011) that impact fish assemblages. Additionally, the susceptibility of Texas estuaries to severe climatic impacts due to regional climate and coastal geology (Larkin & Bomar 1983, Montagna et al. 2011) can affect fish population structure.

Changes in global temperatures are occurring more rapidly (IPCC 2008), intensifying impact on sea surface temperature and subsequently affecting estuarine ecosystems. Population cycles, fish kills, and range expansions have been linked with fluctuations in water temperature (Gunter 1941, Matlock & Osburn 1987, Enfield et al. 2001, Hare & Able 2007). The eastern equatorial Pacific and Texas' Gulf coast represent excellent examples where temperature shifts have resulted in changes in fish community structure. Climatic variability along the Texas coast investigated by (Tolan

& Fisher 2009) determined that the presence of gray snapper (*Lutjanus griseus* Linnaeus, 1758) in inshore waters of Texas is related to increased water temperatures. Additional studies support the interplay between estuarine biological expansions and climate change (Barber & Chavez 1983, Oviatt 2004, Preston 2004, Roessig et al. 2004, Winder et al. 2011).

Members of the Family Centropomidae are semicatadromous, stenothermic, euryhaline, and protandric hermaphroditic group of species represented by a single genus *Centropomus* (Tringali & Leber 1999) inhabiting subtropical and tropical waters of North and South America (Gilmore et al. 1983, Rivas 1986). Although one species (*C. undecimalis*) has been collected as far north as New York (Schaefer 1972), centropomids occur mostly from Florida south to Rio de Janeiro, Brazil along the Atlantic and throughout Mexico, and in Texas from Port Aransas southward to the US – Mexico border (Marshall 1958, Seaman & Collins 1983, Rivas 1986).

Centropomus undecimalis' intolerance of low water temperature has been historically cited for southern Texas being this species' northernmost limit in the western GOM (Tucker & Campbell 1988). Juvenile and adult *C. undecimalis* have been collected in 14.2 to 35.6 °C waters in Florida (Marshall 1958, Fore & Schmidt 1973, McMichael et al. 1989). Four reports have identified centropomids as unresponsive, stunned, or killed as a result of winter cold events throughout their distributional range in Texas waters (Gunter 1941, 1951, Moore 1976, Holt & Holt 1983). Temperature tolerances of all centropomids may vary throughout their range due to genetic composition, salinity, size, and diet (Shafland & Foote 1983, Howells et al. 1990).

This chapter describes habitat and distribution of juvenile *Centropomus* species captured for the genetics and age growth portions of this study. The experimental design deployed during this study did not allow for analysis of CPUE due to sporadic sampling frequency and severely limited catch (<2%) in standardized tows prerequisite to determining CPUE. Specific objectives of this chapter were to:

- identify habitats used by settled centropomids;
- identify habitats utilized by juvenile centropomids.

Materials and Methods

Juvenile centropomids were collected at wetland sloughs, boat ramps, and other tidal- and freshwater- influenced habitats from Carancahua Bay (Palacios) to the Rio Grande (US – Mexico border). Selection of each collection site was based on historical data generated by TPWD and TAMUG as well as published and anecdotal reports of larval and juvenile centropomid occurrence (Martin & King 1991, Pope et al. 2006). Collection sites were classified according to upper, middle, and lower regions of the Texas coast and divided into two major climatological zones (temperate and subtropical; Figure 3.1). The temperate climate collection area was located in the upper coast region within the Galveston and Matagorda Estuary Systems. Upper coast collection sites included Caney Creek (south of Sargent), Tres Palacios River (at its intersection along FM 521), upper reaches of Carancahua Bay (near FM 35), and Lavaca Bay (near Port Lavaca).

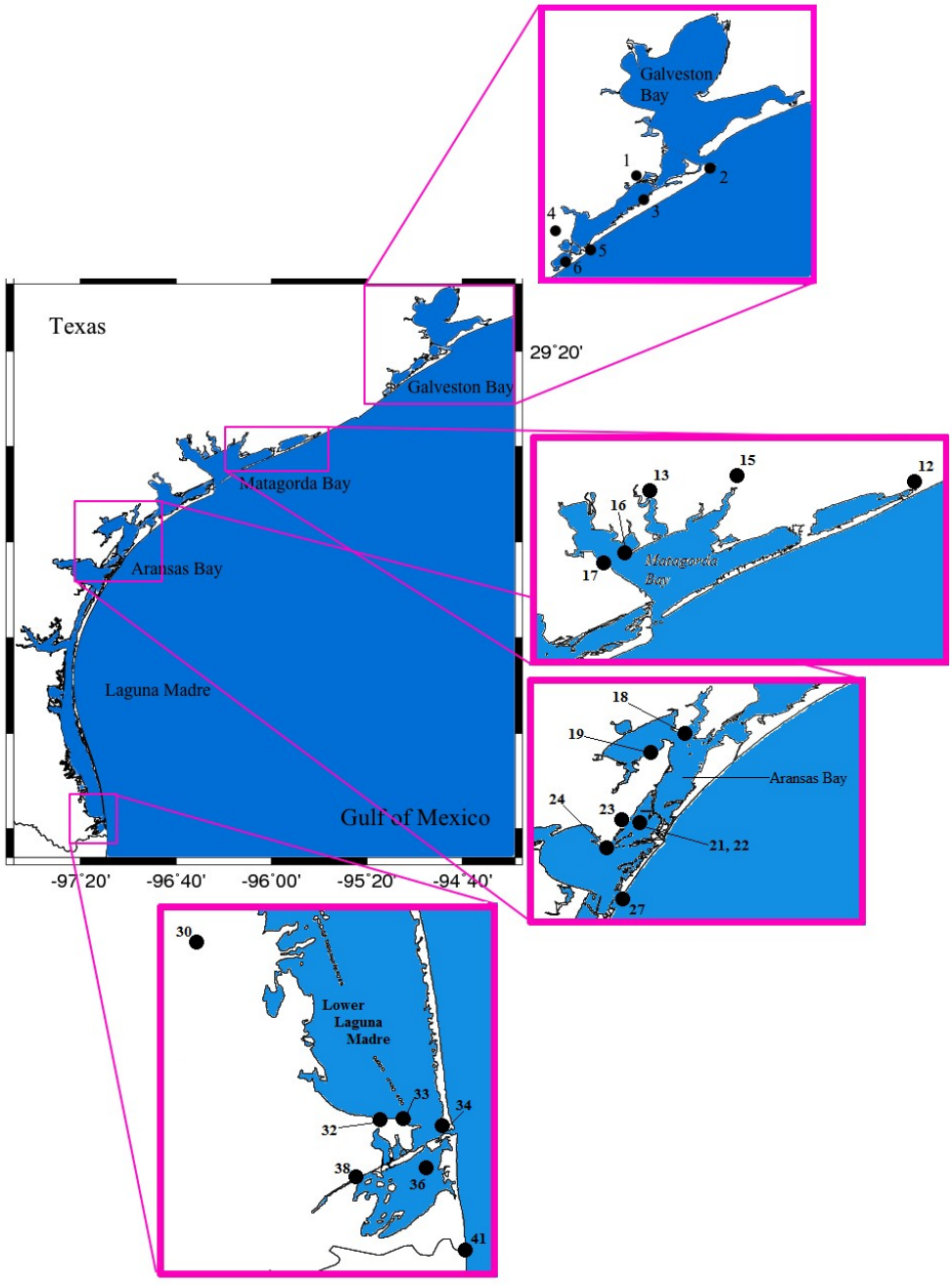

Figure 3.1 Texas sampling sites. Numbers correspond to sites labeled in Table 3.1.

Remaining study areas were located within the Aransas and LLM Estuary Systems that featured subtropical climates. The Aransas Estuary represented the middle coast collection site that included Goose Island State Park (Rockport), Redfish Bay (at two locations along SH 361, Stedman Island), and a drainage ditch located in the city of Aransas Pass on SH 35. Lower coast collections were conducted from the southernmost portions of the LLM Estuary System and included the Arroyo Colorado (and surrounding drainages), Laguna Vista, San Martin boat ramp and channel, Mexiquita Flats, Padre Island Coast Guard Station (northwest of the Brazos Santiago Pass), and Boca Chica (Rio Grande and surrounding sloughs). Complete information regarding all sample locations is listed in Table 3.1. Sampling protocol was the same as that described in Chapter 2.

Hydrographic data taken during each collection included: 1) dissolved oxygen content (mg/L) and water temperature (°C) using an YSI 550 DO meter (YSI Inc., Yellow Springs, OH, USA); 2) wind speed (meters per second) and air temperature (°C) using an EA-3010 anemometer (La Crosse Technology Ltd., La Crosse, WI, USA); 3) salinity (‰) using an SR6 Salinity Refractometer (Aquatic Ecosystems Inc., Apopka, FL, USA); and 4) turbidity (cm) using a 20 cm Secchi disk (Aquatic Ecosystems Inc., Apopka, FL, USA). Habitat characteristics including shoreline vegetation, submerged aquatic vegetation, bottom structures and obstructions were documented and photographed to aid in determination of settlement habitats of *Centropomus* species.

Table 3.1. Geographical information for all sites sampled.

Site #	County	Location	Region of the Texas coast	Latitude	Longitude
1*	Galveston	Diversionary Canal	Upper	29 20.134 N	95 01.417 W
2	Galveston	East Lagoon	Upper	29 19.209 N	94 45.489 W
3	Galveston	West Galveston Bay	Upper	29 12.725 N	94 57.409 W
4*	Brazoria	Bastrop Bayou	Upper	29 05.598 N	95 16.940W
5	Brazoria	San Luis Pass	Upper	29 04.728 N	95 07.847 W
6	Brazoria	Christmas Bay	Upper	29 02.928 N	95 09.933 W
7*	Brazoria	Oyster Creek	Upper	29 00.059 N	95 18.070 W
8	Brazoria	Intracoastal Waterway	Upper	28 57.850 N	95 17.533 W
9	Brazoria	Brazos River	Upper	28 52.803 N	95 22.780 W
10	Brazoria	San Bernard River	Upper	28 52.586 N	95 28.171 W
11	Matagorda	Tres Palacios River	Upper	28 47.147 N	96 08.977 W
12	Brazoria	Caney Creek	Upper	28 46.329 N	95 38.063 W
13	Jackson	Carancahua Bay	Upper	28 44.252 N	96 24.121 W
14*	Matagorda	Matagorda Bay	Middle	28 43.593N	95 47.124W
15	Matagorda	Turtle Creek	Upper	28 43.251 N	96 16.417 W
16	Calhoun	Lavaca Bay	Upper	28 39.898 N	96 34.378 W
17	Calhoun	Lavaca Bay	Upper	28 38.297 N	96 36.659 W
18	Aransas	Aransas Bay	Middle	28 07.677 N	96 59.164 W
19	Aransas	Copano Bay	Middle	28 05.747 N	97 03.137 W
20	Aransas	Little Bay	Middle	28 01.854 N	97 02.341 W
21	Nueces	Redfish Bay	Middle	27 53.637 N	97 07.676 W
22	Nueces	Redfish Bay	Middle	27 53.341 N	97 07.063 W
23	Nueces	Aransas Bay	Middle	27 53.566 N	97 09.188 W
24	San Patricio	Nueces Bay	Middle	27 51.515 N	97 21.193 W
25	Nueces	Redfish Bay	Middle	27 50.396 N	97 07.734 W
26	Nueces	Corpus Christi Bay	Middle	27 45.010 N	97 09.003 W
27	Nueces	Packery Channel	Middle	27 37.592 N	97 12.987 W
28**	Willacy	Lower Laguna Madre	Lower	26 34.193 N	97 25.637 W
29	Willacy	Creek West of Port Mansfield	Lower	26 30.221 N	97 29.320 W
30	Cameron	Arroyo Colorado	Lower	26 20.998 N	97 23.483 W
31	Cameron	Harlingen Shrimp Farm	Lower	26 08.097 N	97 18.017 W
32	Cameron	Laguna Vista	Lower	26 05.705 N	97 17.024 W
33	Cameron	Lower Laguna Madre	Lower	26 04.461 N	97 12.878 W
34	Cameron	Lower Laguna Madre	Lower	26 04.356 N	97 09.994 W
35	Cameron	Mexiquita Flats	Lower	26 04.044 N	97 11.659 W
36	Cameron	South Bay	Lower	26 01.529 N	97 10.272 W
37	Cameron	Bahia Grande	Lower	26 00.826 N	97 16.537 W
38	Cameron	Lake San Martin	Lower	26 00.125 N	97 17.913 W
39	Cameron	Port Brownsville	Lower	25 57.795 N	97 24.123 W
40	Cameron	Rio Grande (6 km upstream)	Lower	25 57.613 N	97 11.116 W
41	Cameron	Rio Grande (mouth)	Lower	25 57.556 N	97 08.810 W

* centropomids were collected at this location after January 2010 freeze event

** centropomids were collected at this location after October 2009 red tide event

Results

Environmental Conditions

Water temperature differed significantly with presence or absence of centropomids ($p = 0.03$) across all collections. Mean water temperature values at collection sites where centropomids were present was 23.3 °C and ranged from 12.5 to 33.1 °C (Table 3.2). Collection sites where centropomids were not captured displayed a slightly wider temperature range (10.9 to 32.4 °C) while averaging 25.1 °C. Water temperature varied seasonally, with mean readings highest in summer (29.2 °C) and declining steadily from 23.4 to 18.8 °C during fall and winter, respectively. Centropomid presence or absence was not related to salinity or DO levels, as attested by non-significant ANOVA results (salinity p =0.10, DO $p = 0.08$). Mean salinity readings did not differ significantly among seasons or regions but displayed significant variation ($p = 0.007$) among years 2006 (21.3 ‰, $n = 16$), 2007 (24.5 ‰, $n = 23$), 2008 (22.8 ‰, $n = 2$), and 2009 (24.9 ‰, $n = 3$). Conforming to seasonal variability in water temperature, salinity averaged 22.4, 15.0 and 21.0 ‰ in winter, summer and fall, respectively. Regional salinity differences followed trends in the amount of freshwater inflow along the Texas coast, with mean salinities increasing from upper (16.5 ‰) to middle (19.6 ‰), and finally the lower coast (21.9 ‰). Dissolved oxygen concentrations, averaging 6.14 mg/L coast wide and ranging from 2.28 to 11.86 mg/L at collection sites, failed to exhibit significant differences between regions, seasons, years, and presence or absence of centropomids.

Table 3.2. Summary for hydrographic parameters at sites sampled where centropomids were present or absent, arranged by region and overall.

	Upper			
	Present		**Absent**	
	***n* = 4**		***n* = 36**	
	Mean	Min – Max	Mean	Min - Max
Temperature (°C)	17.8	12.6 – 23.7	26.1	19.9 – 32.4
Salinity (ppt)	16.5	5.0 – 35.0	18.7	0.0 – 34.0
Dissolved O_2 (mg/L)	5.81	4.46 – 6.43	6.55	2.75 – 9.89
	Middle			
	Present		**Absent**	
	***n* = 11**		***n* = 49**	
	Mean	Min – Max	Mean	Min - Max
Temperature (°C)	21.9	12.5 – 31.6	25.3	12.8 – 31.9
Salinity (ppt)	21.2	0.0 – 38.0	25.1	3.0 – 41.0
Dissolved O_2 (mg/L)	6.60	3.04 – 10.38	7.04	2.75 – 11.86
	Lower			
	Present		**Absent**	
	***n* = 27**		***n* = 31**	
	Mean	Min – Max	Mean	Min - Max
Temperature (°C)	24.8	18.4 – 33.1	25.3	10.9 – 30.6
Salinity (ppt)	21.9	3.3 – 40.0	28.8	0.0 – 50.0
Dissolved O_2 (mg/L)	6.63	2.28 – 11.27	6.63	2.48 – 11.40
	Overall			
	Present		**Absent**	
	***n* = 42**		***n* = 116**	
	Mean	Min – Max	Mean	Min - Max
Temperature (°C)	23.5	12.5 – 33.1	25.1	10.9 – 32.4
Salinity (ppt)	21.3	0.0 – 40.0	24.2	0.0 – 50.0
Dissolved O_2 (mg/L)	6.16	2.28 – 11.27	6.78	2.48 – 11.86

Species Distribution

Centropomus parallelus captured during this study ranged from 10 to 411 mm SL (size mode: 27 mm SL), and *C. undecimalis* captured ranged from 12 to 271 mm SL (size mode: 27 mm SL; Table 3.3, 3.4). *Centropomus parallelus* was taken from the Freeport/Brazos River area to the Rio Grande. Distribution of *C. undecimalis* ranged from its northernmost capture site near Palacios south to the Rio Grande. Collections were dominated by *C. parallelus* at all sites except for those conducted at the Rio Grande. *Centropomus undecimalis* was found at the mouth of the Rio Grande whereas

only *C. parallelus* was found up river; however, this observation was based on a single up river collection. Twenty-seven percent of collections with any centropomid contained at least two *Centropomus* species, revealing that Texas centropomids co-occur over their range during early life history. Additionally, the current study identified the occurrence of one new species, *Centropomus poeyi*, previously unknown from Texas. Three specimens of *C. poeyi* captured were 52, 55, and 62 mm SL. Two *C. poeyi* were captured at Laguna Vista on 10 November 2007 and the remaining conspecific was captured at the Aransas Pass ditch on 26 October 2007.

Table 3.3. Percent composition of *Centropomus* species listed by region of capture along the Texas coast.

	Upper	Middle	Lower
C. parallelus	95%	74%	57%
C. poeyi	0%	1%	1%
C. undecimalis	5%	25%	42%

Table 3.4. Size distribution of all *Centropomus* species by region capture along the Texas coast.

Centropomus parallelus	***n***	**Min**	**Max**	**Average**
Upper	20	20	376	150.4
Middle	50	16	160	63.6
Lower	243	10	411	37.6
Centropomus poeyi	***n***	**Min**	**Max**	**Average**
Middle	1	-	-	62
Lower	2	52	55	53.5
Centropomus undecimalis	***n***	**Min**	**Max**	**Average**
Upper	1	-	-	27
Middle	17	34	271	65.6
Lower	172	12	113	47.6

Habitat Utilization

Ninety-four percent of the 506 Texas centropomids captured were < 100 mm SL (mean: 38.4 mm; mode: 21 mm; range: 10 to 100 mm SL; Table 3.5). Habitats utilized by these centropomids varied broadly, making the characterization of primary habitat use difficult. Smallest centropomids (5 to < 15 mm SL, 5.0% of the catch) were collected in shallow, sheltered riverine or drainage areas with mud substrates in the Arroyo Colorado and a sewage effluent ditch at Laguna Vista. The Arroyo is one of few freshwater tributaries to the LLM and serves to support riparian, freshwater wetland, and estuarine habitats. The Laguna Vista effluent ditch was primarily influenced from discharge of the Laguna Madre Water District and received additional influence from tidal exchange with the LLM during high tides. No submerged vegetation was found at either site; furthermore, constituent habitats were proximate to complex structures such as boat ramps, debris, and bulkheads. Scattered shoreline vegetation included black mangrove (*Avicennia germinans*), saltmeadow cordgrass (*Spartina patens*), and spike grass (*Distichlis spicata*). Each of these areas contained habitat described as early settlement sites for centropomids in Florida (Gilmore et al. 1983, McMichael et al. 1989, Peters et al. 1998a).

Table 3.5. Size distribution of *Centropomus* species < 100 mm SL by region along the Texas coast.

C. parallelus	*n*	Range	Mode	Average
Upper	11	20 – 69	29	40.9
Middle	46	16 – 95	48	57.7
Lower	231	10 – 76	21	27.3
C. poeyi	***n***	**Range**	**Mode**	**Average**
Middle	1	-	-	62
Lower	2	52, 55	-	53.5
C. undecimalis	***n***	**Range**	**Mode**	**Average**
Upper	1	-	-	27
Middle	16	34 – 78	52	52.8
Lower	168	12 – 100	27	46.1

Post-settlement sized centropomids (>15 to 50 mm SL, 65.2% of the catch) occurred across three distinct habitats: predominantly freshwater, semi-isolated sloughs and ditches, and complex structure. Freshwater-influenced sites (Arroyo Colorado, Carancahua Bay, and a slough 6.5 km from the mouth of the Rio Grande) were protected backwater habitats with dissipated currents and a soft mud/silt substrate. Sites with semi-isolated ditch and slough habitats included Laguna Vista, Aransas Pass, and tidal sloughs near Redfish Bay and mouth of the Rio Grande. Laguna Vista and Aransas Pass sites were influenced primarily by storm drain discharge from surrounding communities and local sewage treatment plants. Each of these habitats was frequently isolated from their respective estuary during low tide and exhibited soft muddy substrates. The post-settlement size class was routinely captured in the vicinity of structure provided by shoreline vegetation such as prop roots and rhizomes of black mangroves, palms (*Sabal* and *Serenoa* spp) and man-made structures consisting of debris and culverts. Largest centropomids (50 mm SL and greater) were captured across multiple habitat types previously described for smaller size classes at Aransas Pass and Laguna Vista.

Discussion

Statistical support from CPUE data was lacking, three percent of all centropomids captured were the result of standardized sampling. However, habitats used by settlement-sized and early juvenile centropomids were identified. The tendency for settlement-sized *Centropomus* species to occupy backwater habitats with dissipated currents is similar to that observed for *C. undecimalis* in Florida (Peters et al. 1998a, Peters et al. 1998b). Texas juvenile centropomids were captured in habitats comparable to those of tidal sloughs described by (Fore & Schmidt 1973) and (McMichael et al. 1989), freshwater habitats identified by (Volpe 1951) and (Gilmore et al. 1983), and utilization of shoreline vegetation as protective structure described by (McMichael et al. 1989). Similarities found between Florida and Texas conspecifics during early life are noteworthy; however, there is little documentation to support that all phases of Texas centropomid life history are analogous to that observed elsewhere.

Two of the three centropomid species captured during this study (*C. parallelus* and *C. undecimalis*) dominated capture totals. The aforementioned dominance and expanded range exhibited by *C. parallelus* was unexpected, given the fact this species composed < 7% of TPWD's fisheries-independent centropomid catch data. Temperature tolerances for *C. parallelus* have yet to be determined; however, this species' wide geographical distribution across the Texas coast may imply it has greater tolerance of cooler water than does *C. undecimalis*. However, both *C. parallelus* and *C. undecimalis* were found in water temperatures as low as 12.6 ºC, which has been documented as the upper boundary of *C. undecimalis'* lower lethal temperature (Shafland & Foote 1983,

Howells et al. 1990). The geographical range of *C. poeyi* has been reviewed by (Chavez 1961) and (Rivas 1986) and consists of a restricted distribution along the Mexican Gulf coast from Tampico, Tamaulipas to Campeche, Campeche, Mexico (Chavez 1961, 1981, Rivas 1986, Orrell 2003). The potentially similar spawning habits shared by all centropomids (Chavez 1963, Carvajal 1975, Taylor et al. 1998) could have aided in the widespread dispersion of *C. poeyi* larvae outside their native range through pelagic larvae dispersal.

Relatively mild winters were an additional factor that may have allowed for apparent northward expansion of centropomids captured in this study. Above-average winter temperature minima across Texas estuaries during the past decade (Tolan & Fisher 2009, Montagna et al. 2011) may have benefitted centropomids, allowing for increased settlement, survival, and growth rates. Other species that are sensitive to low winter temperatures (*Lutjanus griseus* and *Avicennia germinans*) are flourishing in Texas estuaries (Sherrod & McMillan 1981, Tolan & Fisher 2009). Several exogenous factors other than temperature per se may influence centropomid settlement in Texas waters, including reduced frequency of freeze events (Sherrod & McMillan 1981, Hare & Able 2007, Tolan & Fisher 2009, Montagna et al. 2011), genetic change (Tringali & Bert 1998, Tringali et al. 2008), essential habitat availability (Blaber & Blaber 1980, Aliaume et al. 1997, Peters et al. 1998a, Stevens et al. 2007), and freshwater sources (Volpe 1951, Fore & Schmidt 1973, Peters et al. 1998b).

Conclusion

Although *C. parallelus* and *C. undecimalis* have been previously reported to inhabit Texas coastal waters (Moore 1975, Martin & King 1991), the present study is the first to document the geographical distribution and habitat types used by early life history constituents of these species. The geographical distributions of these two species overlap one another, although that of *C. parallelus* is broader. Lack of captures north of Palacios may indicate *C. undecimalis'* use of nursery grounds and developmental habitat in Texas is limited to that along the middle and lower coast. Lastly, this study's capture of multiple life history stages at various collection sites mandate that thorough investigations be conducted on the biology and ecology of *Centropomus* species in Texas to provide information prerequisite to developing successful management practices.

CHAPTER IV

AGE, GROWTH, AND HATCH-DATE DISTRIBUTION OF JUVENILE SMALLSCALE FAT SNOOK (*CENTROPOMUS PARALLELUS*) AND COMMON SNOOK (*CENTROPOMUS UNDECIMALIS*) IN TEXAS

Introduction

The Family Centropomidae consists of inshore tropical euryhaline species that are valued recreationally in Texas and Florida and support important food fisheries in Central and South America (Roberts et al. 1999, García-Galano et al. 2003, da Silva Rocha et al. 2005, Jackson & Ockelmann-Lobello 2006, Lemos et al. 2006). Increased abundance (TPWD fisheries-independent and fisheries-dependent collection data, Mark Fisher, TPWD, pers. comm.) and growing recreational popularity of centropomids in Texas have failed to motivate comprehensive examination of constituent species' life history, including age and growth analysis. Considerable life history data exist for centropomids in Florida; however, the majority of studies reported on the genus *Centropomus* in Texas are based on opportunistic capture (Martin & King 1991, Pope et al. 2006) and reflect sporadic occurrence of *C. undecimalis* (Springer & Pirson 1958, Moore 1975). Studies on growth and developmental biology of *Centropomus* species present in Texas are needed to effectively characterize and manage nursery areas utilized by constituent taxa.

Information on growth and development of *C. parallelus* is limited to aquaculture studies in Central and South America (Alvarez-Lajonchère et al. 2002a,

Temple et al. 2004, da Silva Rocha et al. 2005, Tsuzuki et al. 2007a, Tsuzuki et al. 2007b) that indicate its spawning parameters and embryonic development are similar to those of *C. undecimalis* (Alvarez-Lajonchère et al. 2002a, Cerqueira & Tsuzuki 2009). Summer spawning of *C. parallelus* has been reported by (Chavez 1963) in Veracruz, Veracruz, Mexico while comparable results were obtained via histological examination by (Santos et al. 2009) in Brazil (Table 4.1). Reported size at age data for *C. parallelus* are the result of aquaculture pilot studies and reflect little information on naturally occurring growth rates. A synopsis of these data is presented in Table 4.2.

Table 4.1. Status of information on spawning dynamics of Atlantic *Centropomus* species.

Species	Spawning season	Location	Citation
Centropomus ensiferus	NA	NA	-
Centropomus mexicanus	NA	NA	-
Centropomus parallelus	June – August	Veracruz	(Chavez 1963)
	Spring – Summer	Brazil	(Santos et al. 2009)
Centropomus pectinatus	NA	NA	-
Centropomus poeyi	July – August	Veracruz & Campeche	(Carvajal 1975)
Centropomus undecimalis	June – July	SW Florida	(Volpe 1951)
	July – November	SW Florida	(Marshall 1958)
	July – October	SE Florida	(Tucker & Campbell 1988)
	April – December	SW Florida	(McMichael et al. 1989)
	April – October	SE & SW Florida	(Taylor et al. 1998)

NA denotes no information available

Table 4.2. Reported size (SL & TL) at age (days) for *Centropomus parallelus* from aquaculture studies in Mexico and Brazil.

Age	SL (SD) (mm)	TL (SD) (mm)	Citation
28	9.6 (1.4)	-	(Alves et al. 2006)
48	14.2 (1.12)	-	(Alves et al. 2006)
56	-	22.7 (NA)	(Corrêa & Cerqueira 2007)
66	29.7 (2.53)	-	(Cerqueira et al. 1995)
76	26.4 (0.3)	-	(Tsuzuki et al. 2007b)
88	57.6 (0.1)	-	(Alvarez-Lajonchère et al. 2002b)
90	-	52.4 (1.4)	(Alvarez-Lajonchère et al. 2004)
106	32.1 (0.22)	-	(Tsuzuki et al. 2007b)
126	38.2 (0.13)	-	(Tsuzuki et al. 2007b)
156	70.0 (5.7)	-	(Tsuzuki et al. 2008)
190	-	112.0 (1.4)	(Ribeiro & Tsuzuki 2010)

There are numerous studies involving spawning patterns (Taylor et al. 1998, Roberts et al. 1999, Taylor et al. 2000), early development (Lau & Shafland 1982), and growth of *C. undecimalis* (McMichael et al. 1989, Peters et al. 1998b, Aliaume et al. 2000, Taylor et al. 2000). The most comprehensive study on *C. undecimalis* spawning was conducted by (Taylor et al. 2000) who observed female oocyte maturation extending from April – October throughout Florida. Age determination of larval and early juvenile *C. undecimalis* (3.5 to 22.0 mm SL) was conducted under laboratory conditions by (Lau & Shafland 1982) who determined growth rates increase gradually with increasing size from 0.15 to 0.50 mm d^{-1}. Studies of juvenile *C. undecimalis* (15 to 150 mm SL) from southern Florida reported growth rates of 0.9 to 1.0 mm d^{-1} (Fore & Schmidt 1973, Gilmore et al. 1983). Reported growth rates for juvenile C. undecimalis in the wild ranged from 0.5 to 1.0 mm $d^{-1}$and 0.41 to 0.67 mm d^{-1} for western Florida (McMichael et al. 1989) and Puerto Rico (Aliaume et al. 2000).

Age, growth, and hatch-date distribution of juvenile *C. parallelus* and *C. undecimalis* from Texas as determined by otolith microstructure analysis are characterized in this chapter. Although general patterns of centropomid spawning and age growth characteristics are known (Taylor et al. 1998), no study has been conducted to determine these characteristics for *Centropomus* species in Texas waters. Specific objectives were to:

- estimate age and model age and growth of *C. parallelus* and *C. undecimalis*;
- assess spatial and temporal variation in growth of these species;
- determine hatch-date distribution of spawning centropomids;
- compare growth rates of Texas centropomids with those published for *C. undecimalis*.

Materials and Methods

Sample Processing

All *C. parallelus* and *C. undecimalis* were sampled, identified, and processed as described in Chapter II. Juvenile centropomids captured for otolith analysis were kept on ice for transport to the laboratory where they were processed immediately or frozen for subsequent analysis. Individual specimens were measured to the nearest 1.0 mm SL and, when possible, TL.

Otolith Microstructure Analysis

Sagittal otoliths were removed, cleaned and processed following protocols developed by (Secor et al. 2002), while those for age and growth analysis follow procedures developed by (Aliaume et al. 2000) for *C. undecimalis*. One sagitta from

each centropomid was randomly selected for age determination and mounted in Struer's Resin (EPOES/EPOAR; Struers Inc., Cleveland, Ohio, USA). Otoliths were then sectioned along a transverse plane, adjacent to the core, using a Buehler IsoMet 1000 Precision Saw (Buehler, Lake Bluff, Illinois, USA). Each otolith section containing the core was fixed to a 27 mm x 46 mm petrographic slide (Lakeside Microscope Accessories, Monee, Illinois, USA) with Crystal Bond (Armeco Products Inc., Ossining, New York, USA), sanded on Buehler CarbiMet paper discs (320, 400, 600 and 800 grit) and polished with Buehler 0.3 μm MicroPolish Alumina on a microcloth following techniques reported by (Rooker et al. 2004).

Sectioned and polished otoliths were examined through transmitted light on an Olympus BX41 compound microscope at 40X magnification. Image analysis software Image Pro Plus (version 4.5, Media Cybernetics Inc.) was utilized to enumerate daily growth increments, beginning at the core and counting along the sulcus to the otolith edge. Ages were based upon the average of two independent counts conducted by a single reader. In the event of a mean difference of counts greater than 10%, a third count was taken for age estimation. If the third count was within 10% of one of the prior readings, the mean of the two was used for analysis. If the third count differed by 10% or more, the otolith was not used for analysis. A random subsample of *C. parallelus* and *C. undecimalis* otoliths (n = 25) was read by a second independent reader to ensure quality control in ageing techniques. Validation of daily increment formation has been conducted for *C. undecimalis* in aquaculture and wild specimens (Tucker & Warlen

1986, McMichael et al. 1989, Joyeux et al. 2001) and, thus, was not performed in this study.

Age, Growth, and Hatch-date Analysis

Centropomus species greater than 100 mm SL were considered too large for effective sampling in this study, and therefore were not included in age and growth analysis. Growth of centropomids was determined by otolith-derived age estimates and length data (*C. parallelus n* = 168, *C. undecimalis n* = 113). Length-length conversion regression (SL & TL) relationships were calculated for comparison with other studies conducted on *C. undecimalis*. Length-frequency histograms for *C. parallelus* and *C. undecimalis* were generated by categorizing lengths into 5-mm increments to determine the size distribution of juvenile centropomids sampled by species.

Linear regression was applied to otolith-derived age data to determine growth rates (*C. parallelus n* = 171, *C. undecimalis n* = 114) using the following equation:

1. *Standard length = slope*age* (days) + *y-intercept*

To complete hatch-date distributions, ages were also predicted for individuals with unreadable otoliths (*C. parallelus n* = 119, *C. undecimalis n* = 72). Equations predicting age of individuals were developed for each year (Table 4.3). Daily instantaneous growth was estimated utilizing an exponential model:

2. $L_t = L_0 e^{gt}$

Where L_t = length (mm SL) at time t (days); L_0 = the estimated length at hatching; g = the daily instantaneous growth coefficient; and t = otolith-derived age in days.

Table 4.3. Equations for predicting age of individuals with unreadable otoliths.

	n	Linear Equation	r^2
Centropomus parallelus			
2006	24	*Predicted age = 1.1593SL + 34.644*	0.95
2007/2009	141	*Predicted age = 1.3756SL + 29.262*	0.83
2008	4	*Predicted age = 1.687SL + 36.148*	0.62
Centropomus undecimalis			
2006	79	*Predicted age = 0.8506SL + 38.124*	0.73
2007	17	*Predicted age = 0.9234SL + 29.838*	0.90
2009	16	*Predicted age = 0.9335SL + 60.759*	0.21

All statistical analyses were preformed on SPSS 17.0 (IBM Corp., Somers, New York, USA), and significance was accepted at the $\alpha = 0.5$ level. Temporal and spatial variation in environmental parameters was analyzed across year, season, and region using one-way analysis of variance (ANOVA); however, these analyses were not used to evaluate variations in growth due to unequal sampling effort across 2006 – 2009. Analysis of covariance (ANCOVA) was used to assess intra- and inter-annual variability of growth by comparing growth of each species captured across years (covariate: age).

Results

Centropomid Otolith Structure and Age Determination

Sagittal otoliths of *C. parallelus* and *C. undecimalis* were similar in appearance: elliptical in shape and concavo-convex with a deep sulcus on the medial surface. Otoliths from both species exhibited a rounded rostrum differing along the margins of the antirostrum and dorsal surface and the path of the sulcus groove. Thin transverse cross-sections of each otolith revealed a singular central primordia, followed by alternating translucent and opaque zones (Figure 4.1) indicating the formation of daily growth increments. The counting path of transverse-sectioned otoliths consisted of a

dorso-ventral path from the core to increments that were followed to the sulcus, continuing counts to the otolith edge.

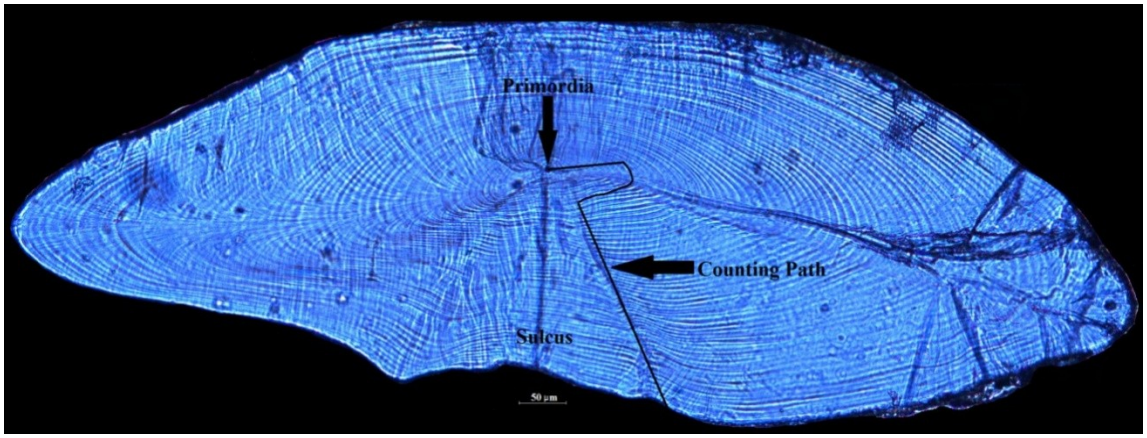

Figure 4.1. Transverse, polished section of *Centropomus parallelus* otolith (29 mm SL; 67 d).

Catch Composition

Juvenile centropomids collected from Texas coastal waters during 2006 – 2009 (n = 474) were used for age and growth analysis (Table 4.4). Only 284 otoliths (*C. parallelus* n = 169, *C. poeyi* n = 2, and *C. undecimalis* n = 113) were included in otolith microstructure analysis (Table 4.5). Seven otoliths were excluded from the analysis because of reader disagreement while the remaining otolith complement (n = 185) was either unreadable or destroyed during the polishing process. Quality control of reader accuracy indicated high reader agreement between the primary reader and the second independent reader based upon linear regression:

3. *Primary reader age = 0.9855 * Second reader + 1.4515* $r^2 = 0.98$

Table 4.4. Number, size range, and capture year of all juvenile centropomids used in age structure and growth analysis. Size range given in millimeters of SL.

Upper								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	5	27 – 32	0	-	0	-	6	20 – 69
C. undecimalis	1	27	0	-	0	-	0	-
Middle								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	6	16 - 90	25	48 – 95	6	45 – 65	9	35 – 79
C. undecimalis	9	34 - 61	0	-	0	-	7	49 – 78
Lower								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	24	12 - 47	207	10 – 76	0	-	0	-
C. poeyi	0	-	2	52, 55	0	-	0	-
C. undecimalis	112	14 - 87	34	12 - 100	0	-	21	48 - 94

Table 4.5. Number, size range, and capture year of the 284 otoliths used in age structure and growth analysis. Size range given in millimeters of SL.

Upper								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	3	27 - 32	0	-	0	-	5	20 – 69
C. undecimalis	1	27	0	-	0	-	0	-
Middle								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	6	16 – 90	16	48 – 95	4	45 – 65	5	35 – 49
C. undecimalis	6	70 - 90	0	-	0	-	4	49 – 61
Lower								
	2006		**2007**		**2008**		**2009**	
	n	Range	*n*	Range	*n*	Range	*n*	Range
C. parallelus	15	13 - 47	115	10 - 76	0	-	0	-
C. poeyi	0	-	2	52, 55	0	-	0	-
C. undecimalis	72	14 – 72	17	12 - 83	0	-	12	48 – 91

Centropomid Length and Age Distribution

Standard length of centropomids examined for age and growth (Figure 4.2) ranged from 10 to 100 mm (*C. parallelus*: 10 to 95 mm SL, mean 32.6, SD = 17.5; *C. undecimalis*: 12 to 100 mm SL, mean 46.6, SD = 20.1). Intra-annual differences in mean length of centropomids were observed across *C. parallelus* (ANOVA, $p < 0.001$) and *C. undecimalis* (ANOVA, $p < 0.001$); smallest mean lengths were observed in September for *C. parallelus* (24.4 mm SL, SD = 20.3) and October for *C. undecimalis* (39.3 mm SL, SD = 18.2). Largest individuals of both species were captured in March (*C. parallelus*: 66.5 mm SL, SD = 17.7; and *C. undecimalis*: 62.5 mm SL, SD = 11.0).

Centropomid ages ranged from 36 to 168 d (*C. parallelus* 36 to 168 d, mean = 74.6, SD = 26.0; *C. undecimalis* 37 to 164 d, mean = 80.2, SD = 24.5). Intra-annual differences in mean ages of centropomids were observed across species, *C. parallelus* (ANOVA, $p < 0.001$) and *C. undecimalis* (ANOVA, $p < 0.001$); youngest mean ages corresponded to length distributions (*C. parallelus*: 59.4 d, SD = 29.4, September; and for *C. undecimalis*: 67.6 d, SD = 14.7, October). Oldest centropomids for both species were captured in March (*C. parallelus*: 120.5 d, SD = 24.7; *C. undecimalis*: 119.3 d, SD = 17.4). The length-length regressions for *C. parallelus* and *C. undecimalis* were significantly different (ANCOVA, intercepts test, $p < 0.001$); relationships between SL and TL are presented in Table 4.6.

Table 4.6. Relationship between SL and TL of *Centropomus parallelus* and *Centropomus undecimalis* <100 mm SL.

$Y = a + bX$						
Y	**X**	***n***	**Species**	***a***	***B***	r^2
SL	*TL*	277	*C. parallelus*	-0.124	0.773	0.99
SL	*TL*	188	*C. undecimalis*	0.277	0.776	0.99
TL	*SL*	277	*C. parallelus*	0.379	1.288	0.99
TL	*SL*	188	*C. undecimalis*	0.021	1.278	0.99

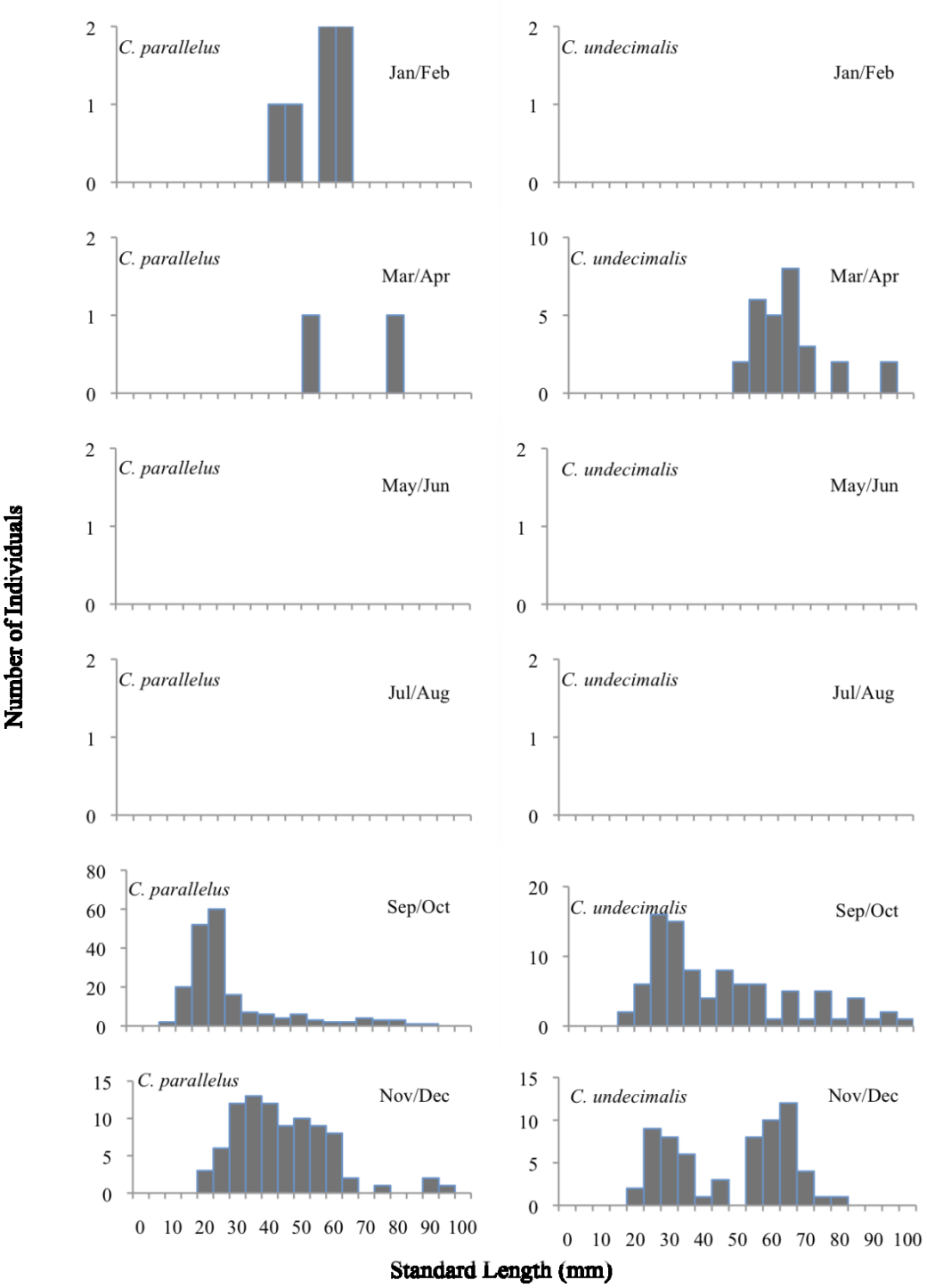

Figure 4.2. Bimonthly length frequency distribution of *Centropomus parallelus* and *Centropomus undecimalis* from 2006 through 2009.

Age and Growth

Centropomus parallelus growth rate was similar (0.61 mm d^{-1}, r^2= 0.83) during 2007 (n = 131) and 2009 (n = 10; ANCOVA slopes p = 0.397, ANCOVA intercept p = 0.335). Inter-annual variation (Figure 4.3, 4.4) in *C. parallelus* growth was detected in 2006 (n = 24, 0.82 mm d^{-1}, r^2 = 0.95) and 2008 (n = 4, 0.37 mm d^{-1}, r^2 = 0.63). A linear growth equation was fitted to length-age data to produce an overall growth description for all years *C. parallelus* were captured:

4. $SL = 0.6026 * age - 12.277$ [n = 169, r^2 = 0.84]

Centropomus undecimalis displayed inter-annual variation in growth across all years sampled (ANCOVA slopes $p < 0.001$; Figure 4.5, 4.6). Growth of *C. undecimalis* in 2006, based on the largest number (n = 79) of otoliths examined, was 0.86 mm d^{-1} (r^2 = 0.73). This species' highest growth rate occurred in 2007 (n = 17, 0.97 mm d^{-1}, r^2 = 0.90) while 2009 yielded the lowest (n = 16, 0.22 mm d^{-1}, r^2 = 0.21). Overall growth of juvenile *C. undecimalis* was described by the linear equation:

5. $SL = 0.6227 * age - 4.1629$ [n = 112, r^2 = 0.70]

Centropomus parallelus data from 2007/2009 were further analyzed to examine the influence of geographic location on growth from three different regions (upper, middle, lower coast). No significant differences were detected in 2007/2009 *C. parallelus* growth across these regions (ANCOVA slopes p = 0.150, ANCOVA intercept p = 0.636). Geographical influence on growth for 2006 *C. parallelus* was not detected among regions sampled (ANCOVA slopes p = 0.092, ANCOVA intercept p = 0.097). Collections in 2008 were all made at a single location (Aransas Pass); consequently, the

influence of geographical distribution could not be assessed. No geographic or intra-annual effect was detected for *C. undecimalis* (ANCOVA slopes $p = 0.081$, ANCOVA intercept $p = 0.069$).

Hatch dates for both *Centropomus* species, based on otolith-based and predicted age, indicate centropomids captured in Texas are the result of spawning that occurs from late May to early December. A unimodial hatch-date distribution was observed for *C. parallelus*, represented by a single peak in late August (Figure 4.7). Alternatively a bimodial hatch-date distribution was observed for *C. undecimalis*, with a major peak in early September and a minor peak in mid-November.

Centropomus poeyi Age Characteristics

Three *Centropomus poeyi* were captured in two locations (Aransas Pass, $n = 1$; Laguna Vista, $n = 2$) in 2007. Specimen identification was based on genetic analysis of 16s mtDNA described in Chapter II. On October 26, a 62 mm SL *C. poeyi* was captured in Aransas Pass (San Patricio County). Age of this specimen was not determined due to destruction of both sagittal otoliths during the polishing process. Two other *C. poeyi* were captured in Laguna Vista (Cameron County) on November 10 that measured 52 and 55 mm SL (aged 90 and 79 d, respectively). Hatch dates for Laguna Vista specimens were August 12 and 23.

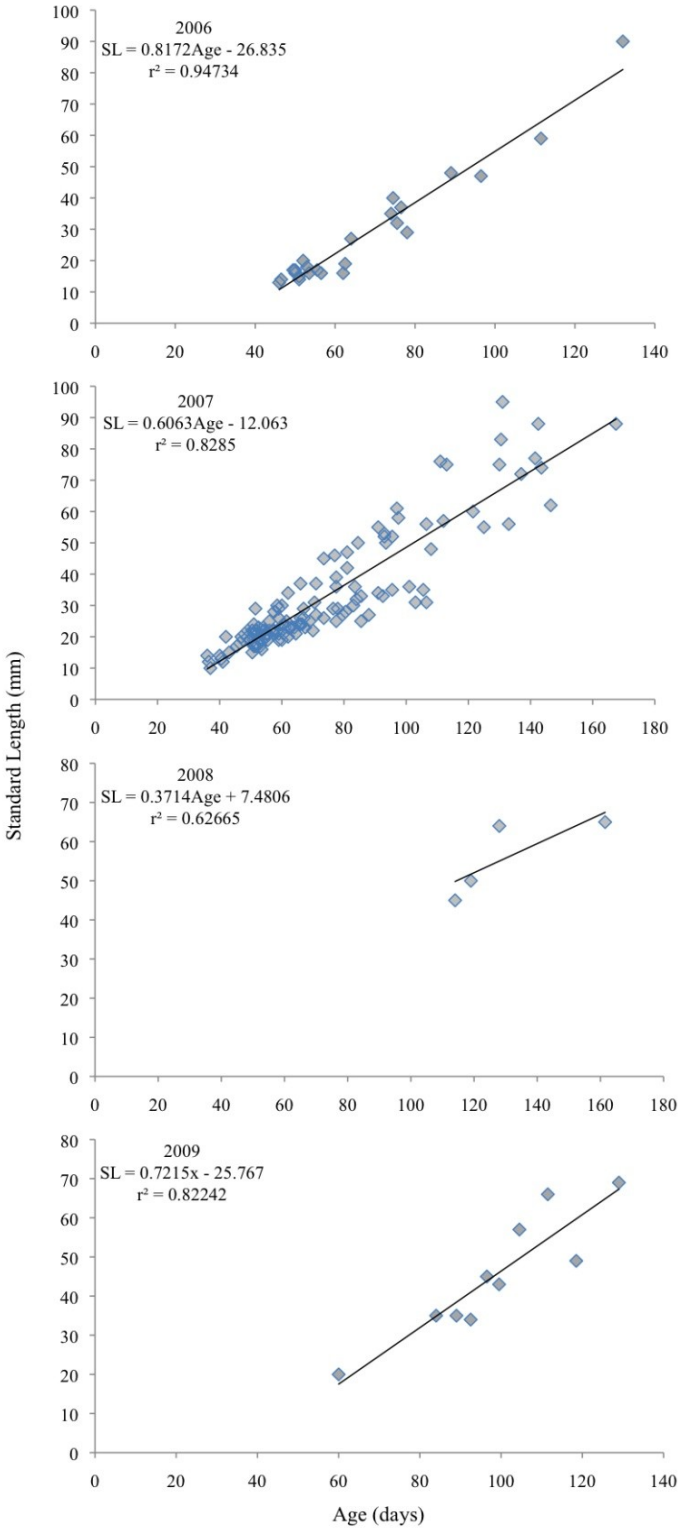

Figure 4.3. Size at age relationships by year for *Centropomus parallelus* (<100 mm SL) from Texas.

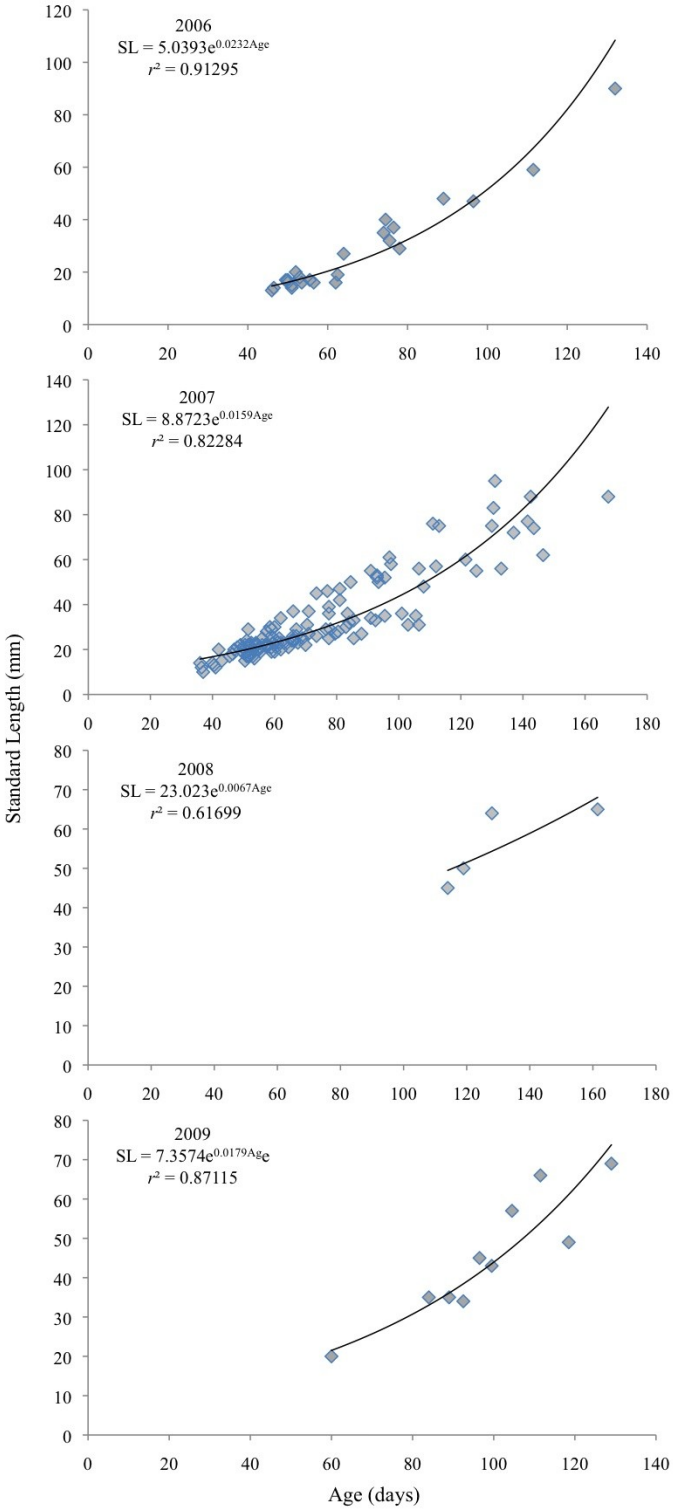

Figure 4.4. Exponential growth comparison in SL among years sampled for *C. undecimalis* (<100 mm SL) from Texas.

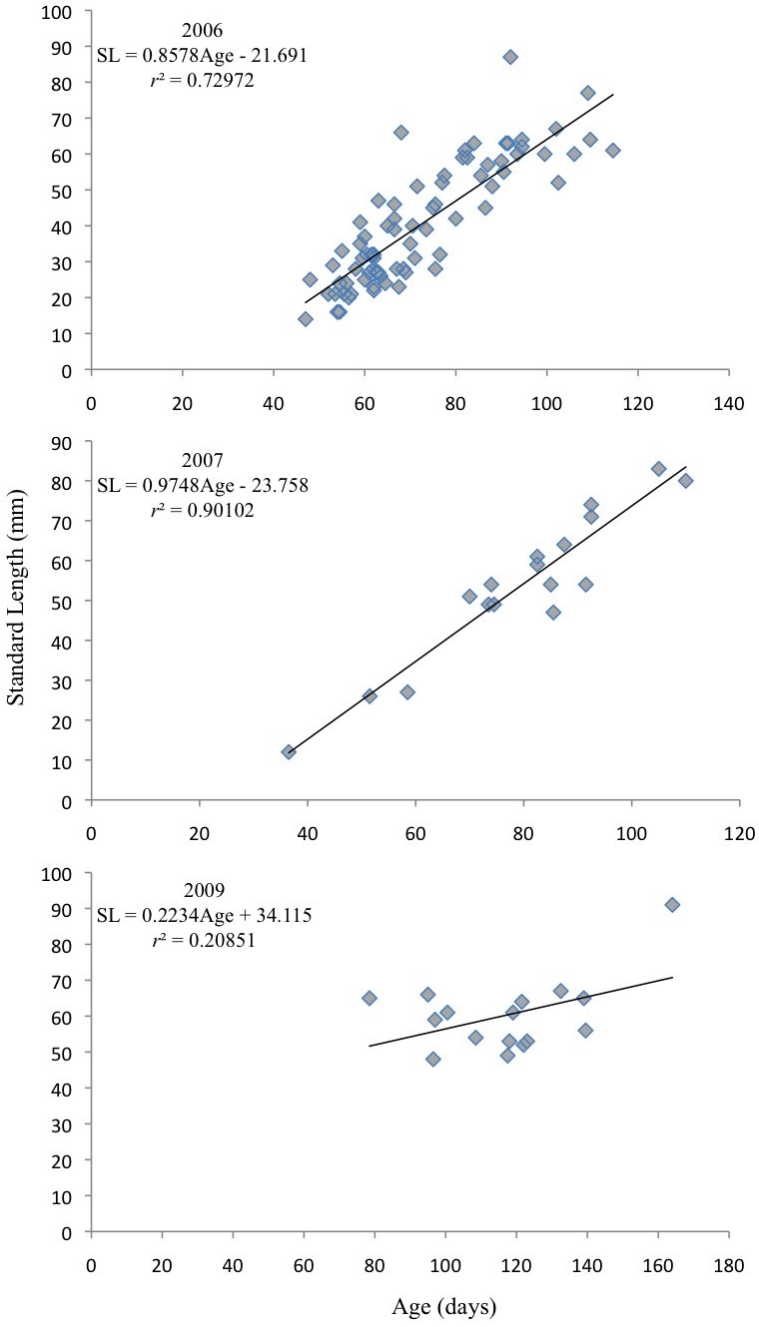

Figure 4.5. Size at age relationships by year for *Centropomus undecimalis* (<100 mm SL) from Texas.

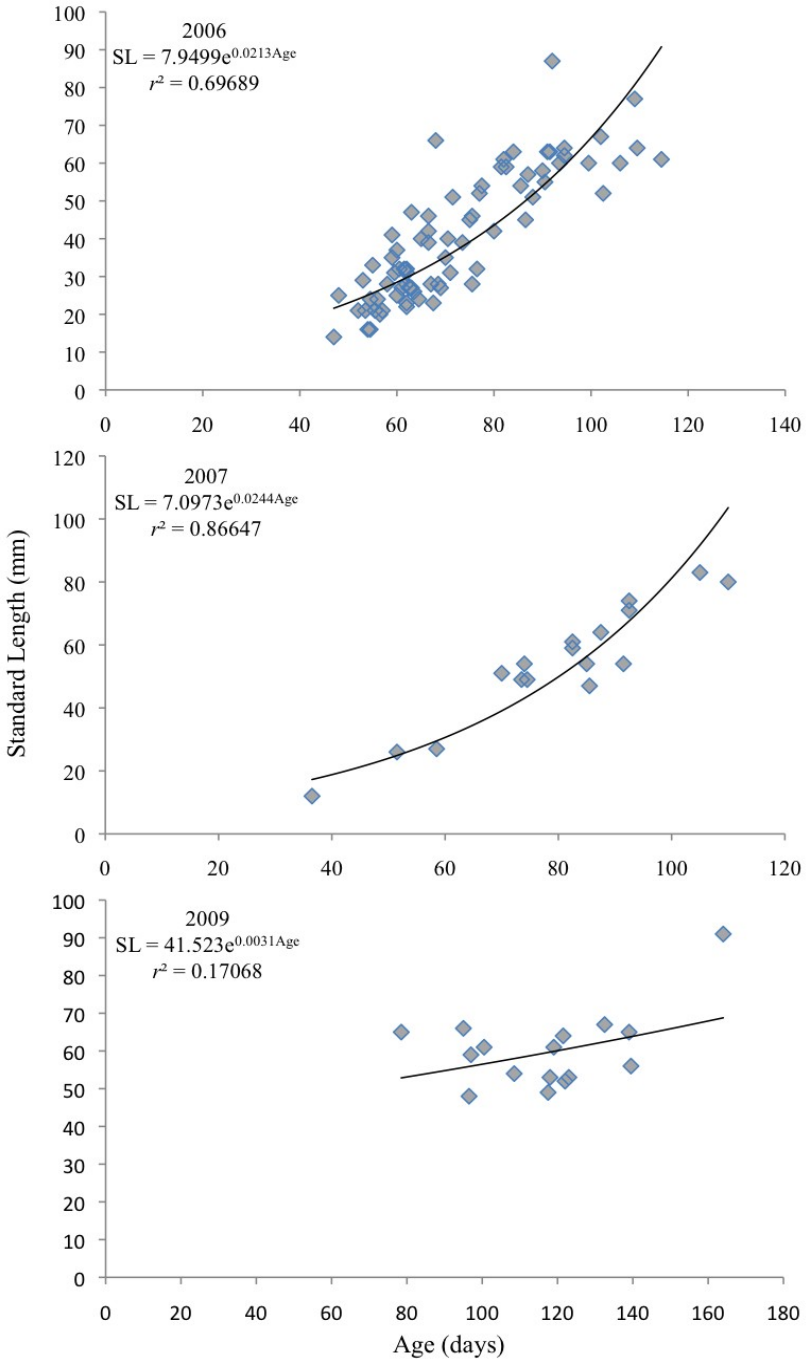

Figure 4.6. Exponential growth comparison in SL among years sampled for *C. undecimalis* (<100 mm SL) from Texas

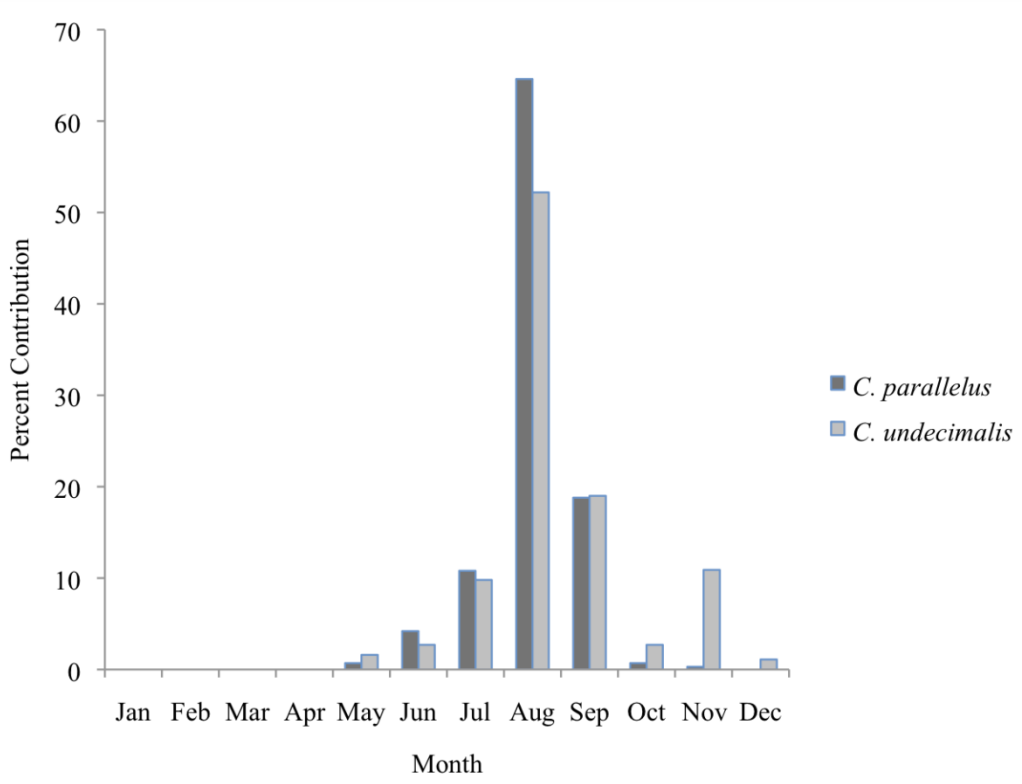

Figure 4.7. Monthly hatch-date distribution for *Centropomus* species from Texas coastal waters.

Discussion

All specimens in age and growth analysis were captured via unmethodical sampling conducted at opportunistic times of the year that would yield highest abundances. Mortality estimates based on age and abundance (i.e., catch curves) were not determined due to discontinuity in capture efforts. Most centropomids from upper and middle coast collection sites were captured via single-day sampling trips that

allowed for repeated effort but resulted in low yield (upper $n = 12$, middle $n = 62$). Lower coast collection sites, not regularly sampled due to logistical limitations associated with the distance and time required to get to these sites, yielded the highest catch of centropomids ($n = 399$). Therefore, the ability for this study to quantify growth rates other than differences among years was limited. The finding that *C. parallelus* exhibited significantly higher growth in 2006 ($n = 24$) than it did in 2007 ($n = 131$) may be the result of a smaller sample size in 2006. However, differences in instantaneous growth rates for specimens of similar age (46 to 56 days) across 2006 and 2007 were negligible (0.06 mm d^{-1}). Additionally, comparison of overall growth rate for both species yielded similar slopes (ANCOVA, slopes, $p = 0.832$) yet different intercepts (ANCOVA, intercepts, $p < 0.001$).

The smallest specimens captured (10 to 15 mm SL) for both species in this study indicate that larvae and early juveniles along the Texas coast spend approximately the first 30 to 40 days in the plankton (planktonic larval duration) before settling into nursery grounds. This finding is not much different from that of (Gilmore et al. 1983), (McMichael et al. 1989), (Peters et al. 1998a), and (Adams & Wolfe 2006) who concluded that settlement sizes range from 13 to 25 mm SL for *C. undecimalis*. However, this study and that of the aforementioned studies were conducted years apart and on opposite sides of the GOM; additionally, differences observed could be accounted for by sampling gear, temperature regimes, and habitats. Spawning activity has been documented for higher salinity waters of inlets, mouths of coastal rivers, and secondary embayments in Florida (Tolley et al. 1987, Tucker & Campbell 1988, Taylor

et al. 1998) and could support inshore spawning of centropomids in Texas. The hypersaline environment of Texas' LLM is a possible inshore spawning ground that could provide quick access to proximal settlement habitats for juvenile centropomids. The only major freshwater source for the LLM is the Arroyo Colorado, a distributary of the Rio Grande no longer connected to the river. The Arroyo Colorado serves as a major drainage of the Lower Rio Grande Agricultural District (Onuf 1996) and seemingly provides characteristic *C. undecimalis* habitat described by (McMichael et al. 1989) and (Fore & Schmidt 1973). Alternatively, it is anticipated that centropomids in Texas spawn near inlets such as the Mansfield Channel, Brazos Santiago Pass, or the Rio Grande, thus following Florida's centropomid spawning pattern.

Centropomus parallelus Growth

Determination of growth rate of smallest *C. parallelus* captured was relevant only for 2007 catches. Length-specific growth rate of the 2007 *C. parallelus* (36 to 46 days old ranging from 10 to 20 mm SL) averaged 0.27 mm d^{-1}. These *C. parallelus* were considered settlement sized according to (Peters et al. 1998a) who categorized settlement size for *C. undecimalis* as 15 mm SL. Although inter-annual differences in growth was observed, variability in seasonal growth was not observed for a single year-class of centropomid. Nonetheless, four *C. parallelus* captured in January 2008 (winter) displayed a significantly lower growth rate (ANCOVA, slopes, $P < 0.001$; 0.37 mm d^{-1}) when compared to that of conspecifics sampled in other years. This estimate of winter growth rate, however, should be viewed with caution owing to the small sample size involved. However, this species' stenothermic nature (Marshall 1958) and determination

of seasonally influenced growth rates of *C. undecimalis* (McMichael et al. 1989) render it plausible that all centropomids achieve faster growth over the summer. Although a literature review provided no estimates of growth rates in *C. parallelus*, eight aquaculture trials (Cerqueira et al. 1995, Alvarez-Lajonchère et al. 2002b, Alvarez-Lajonchère et al. 2004, Alves et al. 2006, Corrêa & Cerqueira 2007, Tsuzuki et al. 2007b, Tsuzuki et al. 2008, Ribeiro & Tsuzuki 2010) reported size at age data for *C. parallelus* (Table 4.2). Comparisons between findings of the current study and those from the eight trials show variable growth for certain age classes (Table 4.7). The apparent growth discrepancy between *C. parallelus* in Texas versus that recorded during aquaculture trials may be a result of several factors including wild versus laboratory-reared stock, genetic differentiation, water temperature, and food availability.

Table 4.7. Comparison of size at age data from 2007/2009 and various aquaculture studies of *Centropomus parallelus* (size in mm SL).

Age (days)	Texas coast		Aquaculture study
48	16.6	14.2	(Alves et al. 2006)
56	21.5	22.7*	(Corrêa & Cerqueira 2007)
66	27.5	29.7	(Cerqueira et al. 1995)
76	33.5	26.4	(Tsuzuki et al. 2007b)
88	40.8	57.6	(Alvarez-Lajonchère et al. 2002b)
90	42.0	52.4*	(Alvarez-Lajonchère et al. 2004)
106	51.6	32.1	(Tsuzuki et al. 2007b)
126	63.7	38.2	(Tsuzuki et al. 2007b)
156	81.7	70.0	(Tsuzuki et al. 2008)

* TL converted to SL from equations given in Table 4.5

Centropomus undecimalis Growth

Estimated growth of *C. undecimalis* along the Texas coast displayed variable rates across every year sampled. This could be due to small sample sizes during 2006, 2007, and 2009 (n = 76, 17, 16, respectively). Growth rate of smallest *C. undecimalis* (47 to 57 days, 14 to 29 mm SL) averaged 0.51 mm d^{-1} and was well above the instantaneous growth rate for equally sized *C. parallelus* (0.32 mm d^{-1} and 0.39 mm d^{-1}, respectively) for 2007 and 2006. This difference could be due to the larger size typically attained by *C. undecimalis* and an indication of faster growth (Rivas 1986, Tringali et al. 1999b). Failure to observe seasonal variation in growth in any year-class was probably due to lack of year-round capture. The winter capture of *C. undecimalis* in 2009 did not provide viable data to establish reduced growth rates (r^2 = 0.21); however, it could be assumed that slower growth rates occur during winter months.

Comparison of growth rates of *C. undecimalis* in this study with those of similar investigations revealed that estimated growth rates for 2006 constituents from Texas (0.85 mm d^{-1}) were similar to values reported in the literature. Faster growth rates were reported (through length frequency distribution analysis) for *C. undecimalis* for Ten Thousand Island, Florida (Fore & Schmidt 1973) and the Indian River Lagoon, Florida (Gilmore et al. 1983; 1.0 to 0.9 mm d^{-1}, respectively). Otolith-based estimates of SL growth for *C. undecimalis* from Tampa Bay, Florida (McMichael et al. 1989) varied between 0.5 and 1.0 mm d^{-1}.

Factors on Centropomid Growth

The habitat description for *C. undecimalis* by (McMichael et al. 1989) resembles that for habitats in which Texas centropomids were collected during this study. However, aside from inter-annual differences, this study did not detect differences in growth of centropomids among regions that could be temperature related. Upper and middle coast sites, when sampled, did not vary significantly in their temperature regimes (ANOVA, $p = 0.551$). However, comparison of lower coast water temperatures to the aforementioned regions (independently and combined) yielded statistical significance (ANOVA, $p < 0.001$). The impact of salinity on growth in this study was not assessed.

Temperature's influence on centropomid growth rates has been assessed under aquaculture trials for *C. parallelus* and *C. undecimalis* (Zarza-Meza et al. 2006) and with wild *C. undecimalis* (McMichael et al. 1989). These studies considered temperature a determinant factor in yielding growth variation (Neidig 2000, Alvarez-Lajonchère & Tsuzuki 2008, Cerqueira & Tsuzuki 2009), also observed in this study's capture of *C. parallelus* during 2008. However, this study's lack of year-round sampling and associated hydrographic data limits the ability to assess variability in growth across regions.

Hatch-date Distribution

The wide distribution of hatch dates for both species reflects a protracted spawning period. These species spawn earlier than Florida's *C. undecimalis* (Tucker & Campbell 1988, McMichael et al. 1989, Taylor et al. 1998) and Mexico's *C. parallelus* (Chavez 1963). Termination of spawning in Texas occurs in November and is similar to

that for Florida and Mexico conspecifics, and this implies that spawning behavior of *C. parallelus* and *C. undecimalis* throughout their North American range is generally similar. Initiation of spawning might be temperature dependent (Figure 4.8), when highest spawning peaks coincide with or near yearly maximum temperatures. However, (Chapman 1987), (Peters et al. 1998b), and (Yanes-Roca et al. 2009) reported that *C. undecimalis* in Florida spawned on either side of the new and full moon, correlating with stronger tides. This study found that spawning activity of 2007 *C. parallelus* and 2006 *C. undecimalis* corresponded with moon phase (Figure 4.9). Additionally, the bulk of the spawning during this period alternated between species, with the majority of C. *parallelus* hatched under a new moon whereas most *C. undecimalis* hatched under a full moon.

Conclusion

The present study has provided knowledge of centropomid growth and spawning periods in Texas that is considered prerequisite to strategic management of fisheries populations. Additionally, identification of growth characteristics is important to generate growth models that can be used to better understand population dynamics and facilitate effective management of these species. The findings of this study revealed that growth patterns for *C. parallelus* and *C. undecimalis* do not differ greatly from those of Florida *C. undecimalis* growth studies; however, further work is necessary to fully understand the settlement period of centropomids in Texas estuaries. Identifying spawning locations and the dynamics of spawning frequency of these species through acoustic telemetry tags and histological analysis should aid in discovery of other

proximal settlement habitats.

The comparisons made in this study of centropomid growth and hatch-date distributions should be further investigated due to the lack of year round sampling and the variations found among years sampled. Findings generated by the present study should be considered a starting point for TPWD to further pursue research on centropomid age growth characteristics. Even implementation of a small-scale mark and recapture project could aid TPWD in further understanding the growth, habitat use, and possible spawning characteristics of *Centropomus* species in Texas. Moreover, examination of young-of-the-year and juvenile mortality, linkages between spawning grounds, and additional larval recruitment locations should be the next step in the research.

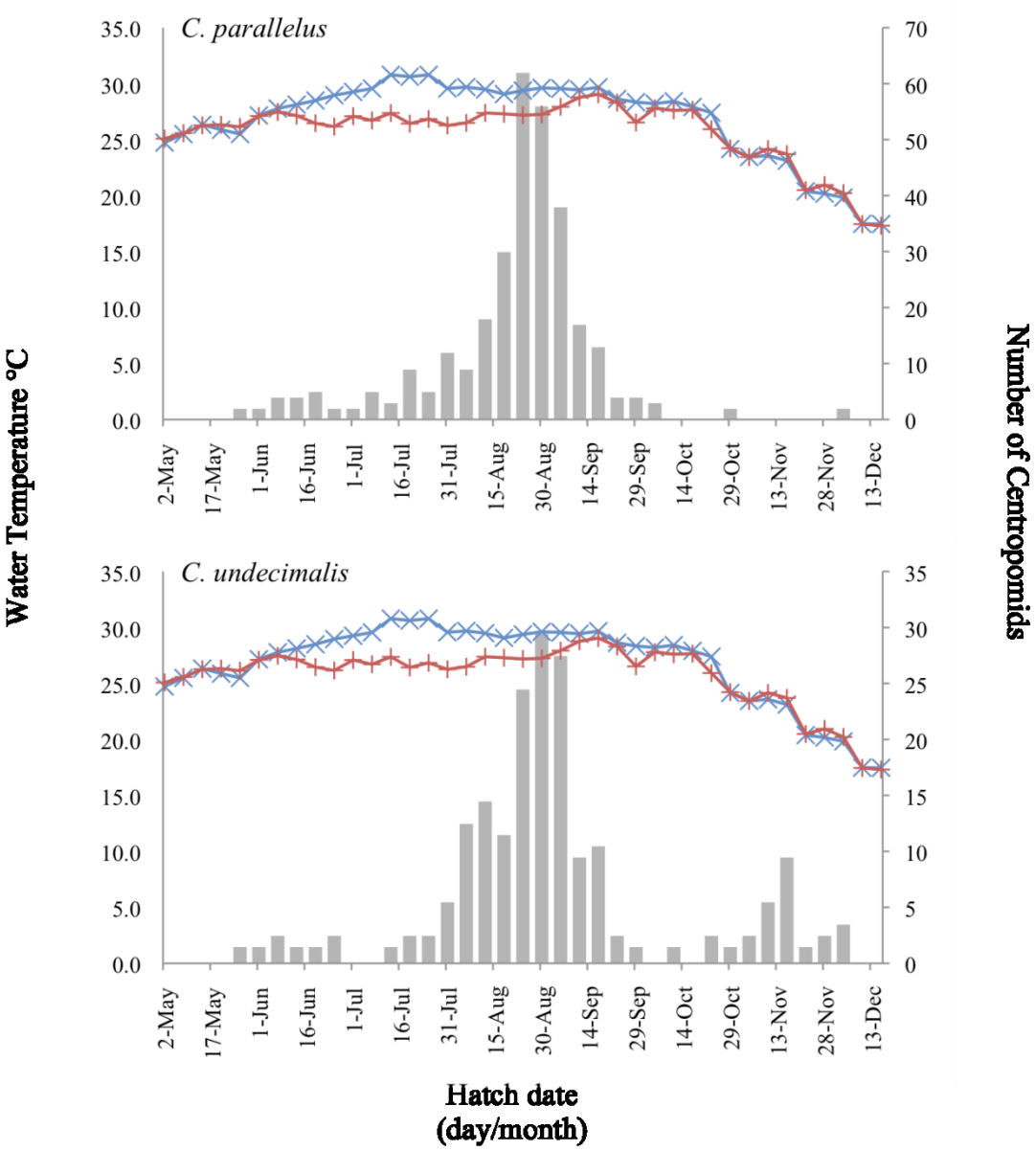

Figure 4.8. Weekly hatch-date distributions for *C. parallelus* and *C. undecimalis* in Texas. Comparisons shown are for mean weekly water temperatures from Aransas Pass (x) and South Padre Island (+) during 2006 - 2009.

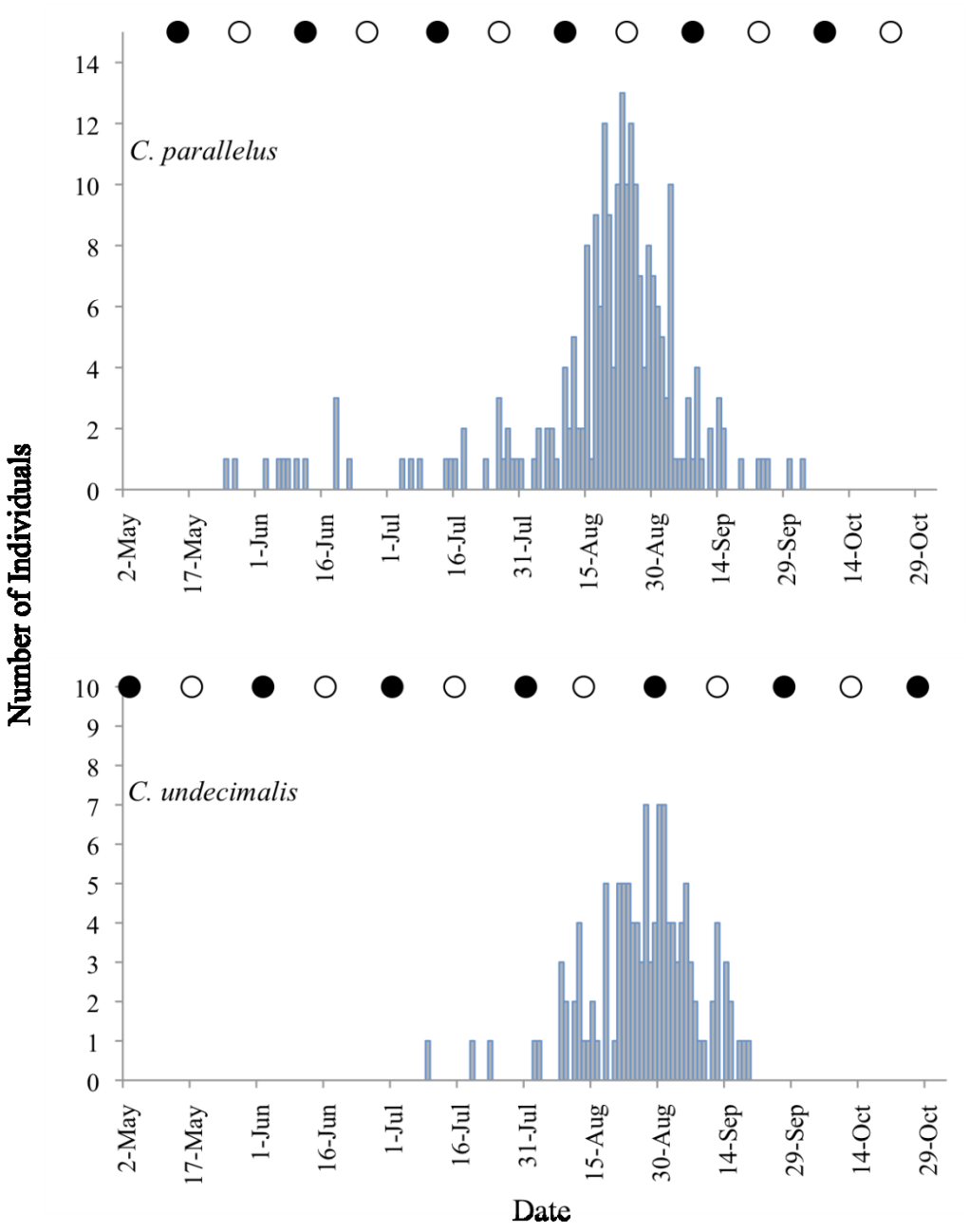

Figure 4.9. Daily hatch date distributions for *C. parallelus* (2007) and *C. undecimalis* (2006) collected from Texas coastal waters and moon phase (● = full moon; ○ = new moon) during their collection.

CHAPTER V

SUMMARY

- Genetic analyses of 548 Texas captured centropomids resulted in successful identification of *C. parallelus*, *C. poeyi*, and *C. undecimalis*.
- The capture of three *C. poeyi* is the first known occurrence of this species in Texas waters.
- AMOVA for D – Loop sequences revealed significant differences between Texas and Florida/Costa Rica populations.
- Morphological identification key developed by this study should aid fisheries biologist in correctly identifying *Centropomus* species.
- Geographic distribution between the two dominant species varies with *C. parallelus* capture range extending from the Rio Grande to Galveston, whereas *C. undecimalis* ranged was limited from the Rio Grande to Palacios.
- Faster growth rates were observed for *C. undecimalis* versus *C. parallelus* in Texas, additionally growth rates for Texas and Florida *C. undecimalis* assemblages.
- Texas spawning season ranges from August to September for *C. parallelus* and from August to November for *C. undecimalis*.

LITERATURE CITED

Adams A, Wolfe KR, Barkowski N, Overcash D (2009) Fidelity to spawning grounds by a catadromous fish *Centropomus undecimalis*. Marine Ecology Progress Series 389:213-222

Adams AJ, Dahlgren CP, Kellison GT, Kendall MS, Layman CA, Ley JA, Nagelkerken I, Serafy JE (2006) Nursery function of tropical back-reef systems. Marine Ecology Progress Series 318:287-301

Adams AJ, Wolfe RK (2006) Cannibalism of juveniles by adult common snook (*Centropomus undecimalis*). Gulf of Mexico Science 24:11-13

Ager LA, Hammond DE, Ware F (1976) Artificial spawning of snook. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies 166:158-166

Aliaume C, Zerbi A, Joyeux JC, Miller JM (2000) Growth of juvenile *Centropomus undecimalis* in a tropical island. Environmental Biology of Fishes 59:299

Aliaume C, Zerbi A, Miller JM, North C (1997) Nursery habitat and diet of juvenile *Centropomus* species in Puerto Rico estuaries. Gulf of Mexico Science 15:77-87

Alvarez-Lajonchère L, Cerqueira VR, dos Reis M (2002a) Desarrollo embrionario y primeros estadios larvales del robalo chucumite, *Centropomus parallelus* Poey (Pisces, Centropomidae) con interes para su cultivo. Hidrobiologica 12:89-100

Alvarez-Lajonchère L, Cerqueira VR, Silva ID, Araujo J, dos Reis M (2002b) Mass production of juveniles of the fat snook *Centropomus parallelus* in Brazil. Journal of the World Aquaculture Society 33:506-516

Alvarez-Lajonchère L, Cerqueira VR, Silva ID, Araujo J, dos Reis M (2004) First basis for a sustained juvenile production technology of fat snook *Centropomus parallelus* Poey. Hidrobiologica 14:37-45

Alvarez-Lajonchère L, Taylor RG (2003) Economies of scale for juvenile production of common snook (*Centropomus undecimalis* Bloch). Aquaculture Economics and Management 7:273-292

Alvarez-Lajonchère L, Tsuzuki MY (2008) A review of methods for *Centropomus* spp. (snooks) aquaculture and recommendations for the establishment of their culture in Latin America. Aquaculture Research 39:684-700

Alves TT, Cerqueira VR, Brown JA (2006) Early weaning of fat snook (*Centropomus parallelus* Poey 1864) larvae. Aquaculture 253:334-342

Anderson JD, Karel WJ (2009) A genetic assessment of current management strategies for spotted seatrout in Texas. Marine and Coastal Fisheries: Dynamics, Management, and Ecosystem Science 1:121-132

Barber RT, Chavez FP (1983) Biological consequences of El Niño. Science 222:1203-1210

Bell JD, Steffe AS, Westoby M (1988) Location of seagrass beds in estuaries: effects on associated fish and decapods. Journal of Experimental Marine Biology and Ecology 122:127-146

Blaber SJM, Blaber TG (1980) Factors affecting the distribution of juvenile estuarine and inshore fish. Journal of Fish Biology 17:143-162

Blewett DA, Hensley RA, Stevens PW (2006) Feeding habits of common snook, *Centropomus undecimalis*, in Charlotte Harbor, Florida. Gulf and Caribbean Research 18:1-14

Boesch D, Turner R (1984) Dependence of fishery species on salt marshes: The role of food and refuge. Estuaries and Coasts 7:460-468

Breuer JP (1957) An ecological survey of Baffin and Alazan Bays. Publications of the Institute of Marine Science, University of Texas 4:134-155

Breuer JP (1962) An ecological survey of the Lower Laguna Madre of Texas, 1953-1959. Institute of Marine Science 8:153-183

Breuer JP (1970) A biological survey of the tidewater areas of the Rio Grande. Project CF-2-1. (Job No 2), Coastal Fisheries Project Report 1969 and 1970 TPWD. Austin, Texas:127-139

Carvajal RJ (1975) Contribución al conocimiento de la biología de los róbalos *Centropomus undecimalis* y *C. poeyi* en la laguna de Términos, Campeche, México. Boletino del Instituto Oceanografico Universidad de Oriente, Cumana 14:51-71

Cerqueira VR, Macchiavello JAG, Brugger AM (1995) Produção de alevinos de robalo, *Centropomus parallelus* Poey, 1860, através de larvicultura intensiva em laboratório Proceedings of 7th Simpósio Brasileiro de Aqüicultura, Peruíbe, São Paulo, p 191-197

Cerqueira VR, Tsuzuki MY (2009) A review of spawning induction, larviculture, and juvenile rearing of the fat snook, *Centropomus parallelus*. Fish Physiology and Biochemistry 35:17-28

Chapman RW (1987) Changes in the population structure of male striped bass, *Morone saxatilis*, spawning in the three areas of the Chesapeake Bay from 1984 to 1986. Fishery Bulletin 85:167-170

Chavez H (1961) Estudio de una nueva especie de robalo del Golfo de Mexico Y redescripcion de *Centropomus undecimalis* (Bloch) (Pisc., Centropom.). Ciencia 21:75-83

Chavez H (1963) Contribucion al conocimiento de la biologia de los robalos, chucumite y constantino (*Centropomus* sp) del Estado de Veracruz. Ciencia 5:141-161

Chavez H (1981) Tagging of *Centropomus poeyi* in the Papalapan River Basin. Ciencia Pesquera 1:17-26

Clement M, Posada D, Crandall KA (2000) TCS: A computer program to estimate gene genealogies. Molecular Ecology 9:1657-1659

Contreras-Balderas S, Edwards RJ, Lozano-Vilano MDL, Garcia-Ramírez ME (2002) Fish biodiversity changes in the lower Rio Grande/Rio Bravo, 1953-1996. Reviews in Fish Biology and Fisheries 12:219-240

Cooley NR (1974) Occurrence of snook on the north shore of the Gulf of Mexico. Florida Scientist 37:98-99

Corrêa CF, Cerqueira VR (2007) Effects of stocking density and size distribution on growth, survival and cannibalism in juvenile fat snook (*Centropomus parallelus* Poey). Aquaculture Research 38:1627-1634

da Silva Rocha AJ, Gomes V, Van Ngan P, De Arruda Campos Rocha Passos MJ, Rios Furia R (2005) Metabolic demand and growth of juveniles of *Centropomus parallelus* as function of salinity. Journal of Experimental Marine Biology and Ecology 316:157-165

Donaldson EM, Devlin RH, Solar II, Piferrer F (1993) The reproductive containment of genetically altered salmonids. NATO ASI (Advanced Science Institute) Series, Series A, Life Sciences 248:113-129

Donaldson KA, Wilson RR (1999) Amphi-panamic geminates of snook (Percoidei: Centropomidae) provide a calibration of the divergence rate in the mitochondrial DNA control region of fishes. Molecular Phylogenetics and Evolution 13:208-213

Edwards RJ, Contreras-Balderas S (1991) Historical changes in the ichthyofauna of the lower Rio Grande (Rio Bravo del Norte), Texas and Mexico. The Southwestern Naturalist 36:201-212

Enfield DB, Mestas-Nuñez AM, Trimble PJ (2001) The Atlantic multidecadal oscillation and its relation to rainfall and river flows in the continental U.S. Geophysical Research Letters 28:2077-2080

Engle V (2011) Estimating the provision of ecosystem services by Gulf of Mexico coastal wetlands. Wetlands 31:179-193

Excoffier L, Lischer HEL (2010) Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. Molecular Ecology Resources 10:564-567

Fore PL, Schmidt TW (1973) Biology of juvenile and adult snook, *Centropomus undecimalis* in the Ten Thousand Islands. In: Carter MR, Burns LA, Cavinder TR, Dugger KR, Fore PL, et al. (eds) Ecosystems Analysis of the Big Cypress Swamp and Estuaries. Environmental Protection Agency Publication Number EPA 904/9-74-002, Atlanta pXVI-1 - XVI-18

García-Galano T, Gaxiola G, Pérez JC, Sánchez A (2003) Effect of feeding frequency on food intake, gastric evacuation and growth in juvenile snook, *Centropomus undecimalis* (Bloch). Revista de Investigaciones Marinas 24:10

Gilmore RG, Donahoe CJ, Cooke DW (1983) Observations of the distribution and biology of the east Florida populations of the common snook, *Centropomus undecimalis* (Bloch). Florida Scientist 46:313-336

Greenfield DW (1975) *Centropomus poeyi* from Belize, with a key to the western Atlantic species of *Centropomus*. Copeia 1975:582-583

Gunter G (1941) Death of fishes due to cold on the Texas coast, January, 1940. Ecology 22:203-208

Gunter G (1951) Destruction of fishes and other organisms on the south Texas coast by the cold wave of January 28-February 3, 1951. Ecology 32:731-736

Hare JA, Able KW (2007) Mechanistic links between climate and fisheries along the east coast of the United States: explaining population outbursts of Atlantic croaker (*Micropogonias undulatus*). Fisheries Oceanography 16:31-45

Holt SA, Holt GJ (1983) Cold death of fishes at Port Aransas, Texas: January 1982. The Southwestern Naturalist 28:464-466

Hook JH (1991) Seasonal variation in relative abundance and species diversity of fishes in South Bay. Contributions in Marine Science 32:127-141

Howells RG, Sonski AJ, Shafland PL, Hilton BD (1990) Lower temperature tolerance of snook, *Centropomus undecimalis*. Northeast Gulf Science 11:155-158

IPCC (2008) Climate change and water IPCC, Geneva

Jackson TL, Ockelmann-Lobello L (2006) Centropomidae: Snooks. In: Richards WJ (ed) Early stages of Atlantic fishes: an identification guide for the western central North Atlantic Vol 1. CRC Marine Biology Series, Boca Raton, p 1197-1206

Joyeux JC, Aliaume C, Zerbi A (2001) Brief communications - An alternative to validation of otolith microincrementation. Journal of Fish Biology 58:873-879

Larkin TJ, Bomar GW (1983) Climatic atlas of Texas. Texas Department of Water Resources Austin, Texas:151

Lau SR, Shafland PL (1982) Larval development of snook, *Centropomus undecimalis* (Pisces: Centropomidae). Copeia 1982:618-627

Lemos D, Netto B, Germano A (2006) Energy budget of juvenile fat snook *Centropomus parallelus* fed live food. Comparative Biochemistry and Physiology - A Molecular and Integrative Physiology 144:33-40

Librado P, Rozas J (2009) DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. Bioinformatics 25:1451-1452

Longley WL (1994) Freshwater inflows to Texas bays and estuaries: ecological relationships and methods for determination of needs, Vol. Texas Water Development Board and Texas Parks and Wildlife Department, Austin, Texas

Marshall AR (1958) A survey of the snook fishery of Florida, with studies of the biology of the principal species, *Centropomus undecimalis* (Bloch), Vol, Virgina Key, Miami, Florida

Martin JH, King TL (1991) Occurrence of fat snook (*Centropomus parallelus*) in Texas: evidence for a range extension. Contributions in Marine Science 32:123-126

Martin JR, Shipp RL (1971) Occurrence of juvenile snook, *Centropomus undecimalis*, in North Carolina waters. Transactions of the American Fisheries Society 100:2

Matlock GC, Osburn HR (1987) Demise of the snook fishery in Texas, USA. Northeast Gulf Science 9:53-58

McEachran JD, Fechhelm JD (1998) Fishes of the Gulf of Mexico, Vol. University of Texas Press, Austin

McMichael KM, Peters GR, Parsons GR (1989) Early life history of the snook, *Centropomus undecimalis*, in Tampa Bay, Florida. Northeast Gulf Science 10:113-125

Montagna P, Brenner J, Gibeaut J, Morehead S (2011) Coastal Impacts. In: Schmandt J, Clarkson J, North GR (eds) The impact of global warming on Texas. University of Texas Press, Austin

Moore RH (1975) Occurrence of tropical marine fishes at Port Aransas, Texas 1967-1973, related to sea temperatures. Copeia 1975:170-172

Moore RH (1976) Observations on fishes killed by cold at Port Aransas, Texas, 11-12 January 1973. The Southwestern Naturalist 20:461-466

Muller RG, Taylor RG (2006) The 2005 stock assessment update of common snook, *Centropomus undecimalis*, Vol. Fish and Wildlife Conservation Commission, Florida Marine Research Institute, St. Petersburg, FL

Neidig CL (2000) Techniques for spawning common snook: Broodstock handling, oocyte staging, and egg quality. North American Journal of Aquaculture 62:103-113

Nelson JS (2006) Fishes of the world, Vol. John Wiley, Hoboken, N.J.

Onuf CP (1996) Biomass patterns in seagrass meadows of the Laguna Madre, Texas. Bulletin of Marine Science 58:404-420

Orrell TM (2003) Centropomidae snooks. In: Carpenter KE (ed) The living marine resources of the Western Central Atlantic FAO Species identification guide for fishery purposes and American Society of Ichthyologists and Herpertologist p1286-1293

Oviatt C (2004) The changing ecology of temperate coastal waters during a warming trend. Estuaries and Coasts 27:895-904

Palumbi SR (1994) Genetic divergence, reproductive isolation, and marine speciation. Annual Review of Ecology and Systematics 25:547-572

Peters KM, Giordano SD, Adams JM, Fenwick RW, McWilliams RW, Berill NJ (1998a) Factors influencing the distribution of larvae of the common snook, *Centropomus undecimalis* (Bloch), in southwest Florida. Florida Marine Research Publications:33p

Peters KM, Matheson Jr RE, Taylor RG (1998b) Reproduction and early life history of common snook, *Centropomus undecimalis* (Bloch), in Florida. Bulletin of Marine Science 62:509-529

Pezold FL, Edwards RJ (1983) Additions to the Texas marine ichthyofauna, with notes on the Rio Grande estuary. The Southwestern Naturalist 28:102-105

Pope KL, Blankinship DR, Fisher M, Patino R (2006) Status of the common snook (*Centropomus undecimalis*) in Texas. Texas Journal of Science 58:325-332

Preston BL (2004) Observed winter warming of the Chesapeake Bay estuary (1949–2002): Implications for ecosystem management. Environmental Management 34:125-139

Prodocimo V, Tschá MK, Pie MR, Oliveira-Neto JF, Ostrensky A, Boeger WA (2008) Lack of genetic differentiation in the fat snook *Centropomus parallelus* (Teleostei: Centropomidae) along the Brazilian coast. Journal of Fish Biology 73:2075-2082

Ribeiro FF, Tsuzuki MY (2010) Compensatory growth responses in juvenile fat snook, *Centropomus parallelus* Poey, following food deprivation. Aquaculture Research 41:e226-e233

Rivas LR (1986) Systematic review of the perciform fishes of the genus *Centropomus*. Copeia 1986:579-611

Roberts SB, Jackson LF, King V W, Taylor RG, Grier HJ, Sullivan CV (1999) Annual reproductive cycle of the common snook: Endocrine correlates of maturation. Transactions of the American Fisheries Society 128:436-445

Roessig JM, Woodley CM, Cech JJ, Hansen LJ (2004) Effects of global climate change on marine and estuarine fishes and fisheries. Reviews in Fish Biology and Fisheries 14:251-275

Rooker JR, Landry AM, Geary BW, Harper JA (2004) Assessment of a shell bank and associated substrates as nursery habitat of postsettlement red snapper. Estuarine, Coastal and Shelf Science 59:653-661

Rozas LP, Minello TJ, Zimmerman RJ, Caldwell P (2007) Nekton populations, long-term wetland loss, and the effect of recent habitat restoration in Galveston Bay, Texas, USA. Marine Ecology Progress Series 344:119-130

Santos AA, Egami MI, Ranzani-Paiva MJT, Juliano Y (2009) Hematological parameters and phagocytic activity in fat snook (*Centropomus parallelus*): Seasonal variation, sex and gonadal maturation. Aquaculture 296:359-366

Sazima I (2002) Juvenile snooks (Centropomidae) as mimics of mojarras (Gerreidae), with a review of aggressive mimicry in fishes. Environmental Biology of Fishes 65:37-45

Schaefer RH (1972) First record of a snook from New York waters. New York Fish and Game Journal 19:182-183

Seaman W, Collins M (1983) Species profiles: Life histories and environmental requirements of coastal fishes and invertebrates (south Florida) - snook. US Fish Wildlife Service FWS/OBS-82/1116 US Army Corps of Engineers TR EL-82-4:16pp

Secor DH, Campana SE, Zdanowicz VS, Lam JWH, Yang L, Rooker JR (2002) Inter-laboratory comparison of Atlantic and Mediterranean bluefin tuna otolith microconstituents. ICES Journal of Marine Science 59:1294-1304

Seyoum S, Tringali MD, Sullivan JG (2005) Isolation and characterization of 27 polymorphic microsatellite loci for the common snook, *Centropomus undecimalis*. Molecular Ecology Notes 5:924-927

Shafland PL, Foote KJ (1983) A lower lethal temperature for fingerling snook, *Centropomus undecimalis*. Northeast Gulf Science 6:175-177

Sherrod CL, McMillan C (1981) Black mangrove, *Avicennia germinans*, in Texas: past and present distribution. Contributions in Marine Science 24:115-131

Springer VG, Pirson J (1958) Fluctuations in the relative abundance of sport fishes as indicated by the catch at Port Aransas, Texas, 1952-1956. Publications of the Institute of Marine Science, University of Texas 5:169-185

Stevens PW, Blewett DA, Poulakis GR (2007) Variable habitat use by juvenile common snook, *Centropomus undecimalis* (Pisces: Centropomidae): Applying a life-history model in a southwest Florida estuary. Bulletin of Marine Science 80:93-108

Tamura K, Dudley J, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Molecular Biology and Evolution submitted

Taylor RG, Grier HJ, Whittington JA (1998) Spawning rhythms of common snook in Florida. Journal of Fish Biology 53:502

Taylor RG, Whittington JA, Grier HJ, Crabtree RE (2000) Age, growth, maturation, and protandric sex reversal in common snook, *Centropomus undecimalis*, from the east and west coasts of south Florida. Fishery Bulletin 98:612-624

Temple S, Cerqueira VR, Brown JA (2004) The effects of lowering prey density on the growth, survival and foraging behaviour of larval fat snook (*Centropomus parallelus* Poey 1860). Aquaculture 233:205-217

Tolan JM, Fisher M (2009) Biological response to changes in climate patterns: Population increases of gray snapper (*Lutjanus griseus*) in Texas bays and estuaries. Fishery Bulletin 107:36-44

Tolley SG, Dohner ET, Peebles EB (1987) Occurrence of larval snook, *Centropomus undecimalis* (Bloch), in Naples Bay, Florida. Florida Scientist 50:34-38

Tringali MD, Bert TM (1996) The genetic stock structure of common snook (*Centropomus undecimalis*). Canadian Journal of Fisheries and Aquatic Sciences 53:974

Tringali MD, Bert TM (1998) Risk to genetic effective population size should be an important consideration in fish stock-enhancement programs. Bulletin of Marine Science 62:641-659

Tringali MD, Bert TM, Seyoum S (1999a) Genetic identification of centropomine fishes. Transactions of the American Fisheries Society 128:446-458

Tringali MD, Bert TM, Seyoum S, Bermingham E, Bartolacci D (1999b) Molecular phylogenetics and ecological diversification of the transisthmian fish genus *Centropomus* (Perciformes: Centropomidae). Molecular Phylogenetics and Evolution 13:193-207

Tringali MD, Leber KM (1999) Genetic considerations during the experimental and expanded phases of snook stock enhancement. Bulletin of National Research Institute of Aquaculture 1:109-119

Tringali MD, Seyoum S, Wallace EM, Higham M, Taylor RG, Trotter AA, Whittington JA (2008) Limits to the use of contemporary genetic analyses in delineating biological populations for restocking and stock enhancement. Reviews in Fisheries Science 16:111-116

Tsuzuki MY, Cardoso RF, Cerqueira VR (2008) Growth of juvenile fat snook *Centropomus parallelus* in cages at three stocking densities. Boletim do Instituto de Pesca 34:319-324

Tsuzuki MY, Cerqueira VR, Teles A, Doneda S (2007a) Salinity tolerance of laboratory reared juveniles of the fat snook *Centropomus parallelus*. Brazilian Journal of Oceanography 55:1-5

Tsuzuki MY, Sugai JK, Maciel JC, Francisco CJ, Cerqueira VR (2007b) Survival, growth and digestive enzyme activity of juveniles of the fat snook (*Centropomus parallelus*) reared at different salinities. Aquaculture 271:319-325

Tucker JW, Campbell SW (1988) Spawning season of common snook along the east central Florida coast. Florida Scientist 51:1-6

Tucker JW, Warlen SM (1986) Aging of common snook *Centropomus undecimalis* larvae using sagittal daily growth rings. Northeast Gulf Science 8:173-176

Volpe AV (1951) Aspects of the biology of the common snook, *Centropomus undecimalis* (Bloch) of southwest Florida, Vol. Marine Laboratory, University of Miami, Miami

Wilson RR, Donaldson KA, Frischer ME, Young TB (1997) Mitochondrial DNA control region of common snook and its prospect for use as a genetic tag. Transactions of the American Fisheries Society 126:594-606

Winder M, Jassby AD, Mac Nally R (2011) Synergies between climate anomalies and hydrological modifications facilitate estuarine biotic invasions. Ecology Letters 14:749-757

Yanes-Roca C, Rhody N, Nystrom M, Main KL (2009) Effects of fatty acid composition and spawning season patterns on egg quality and larval survival in common snook (*Centropomus undecimalis*). Aquaculture 287:335-340

Zarza-Meza EA, Berruecos-Villalobos JM, Vásquez-Peláez C, Álvarez-Torres P (2006) Experimental culture of snook *Centropomus undecimalis* and chucumite *Centropomus parallelus* (Perciformes: Centropomidae) in artisanal earthen ponds. Ciencas Marinas 32:219-227

APPENDIX A

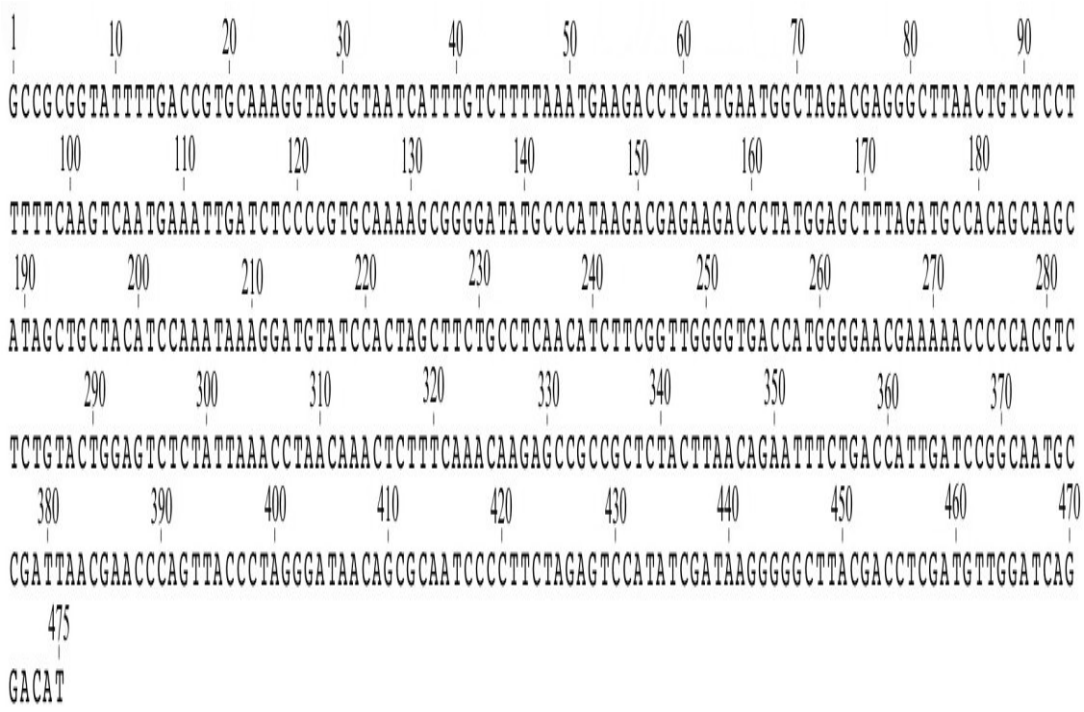

Figure A-1. Consensus sequence of the 475bp segment of Texas captured *Centropomus parallelus* 16s mtDNA gene.

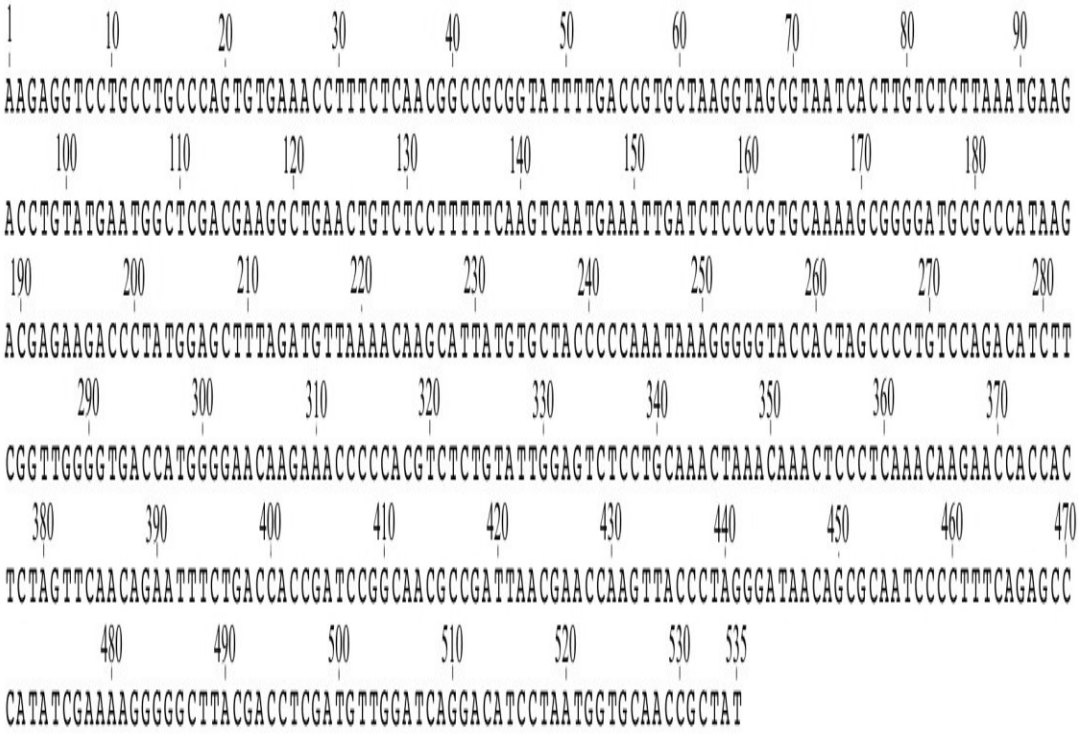

Figure A-2. Consensus sequence of the 535bp segment of Texas captured *Centropomus poeyi* 16s mtDNA gene.

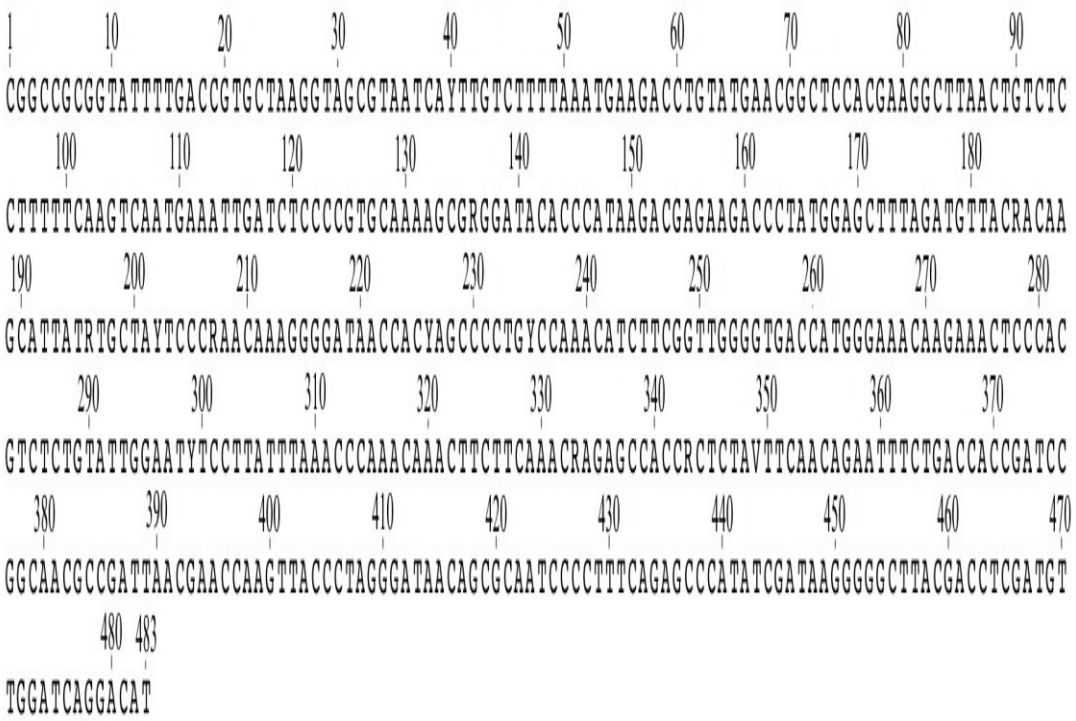

Figure A-3. Consensus sequence of the 483bp segment of Texas captured *Centropomus undecimalis* 16s mtDNA gene.

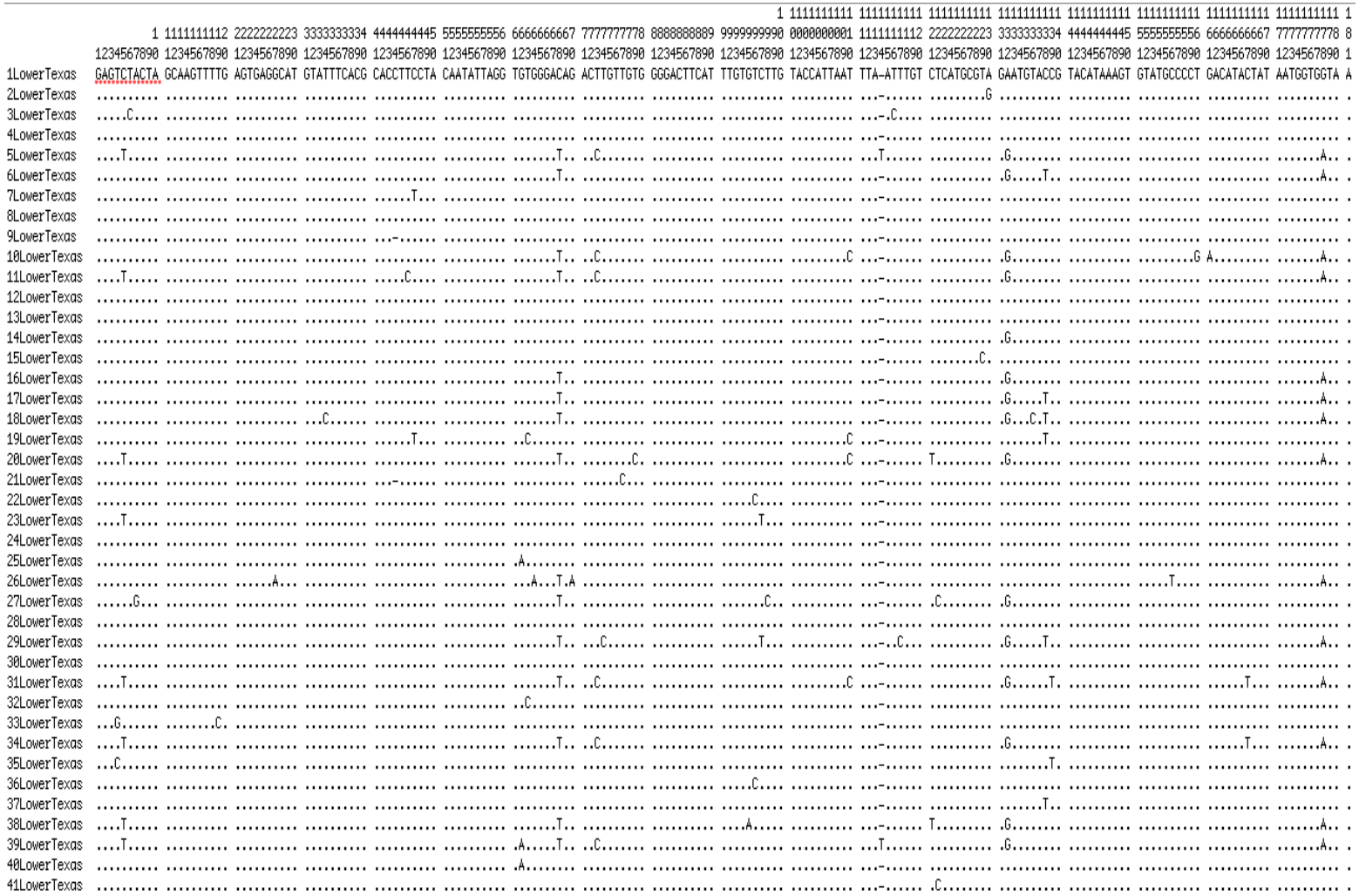

Figure A-4. Consensus alignment of 181bp long segment of the D – loop of 82 *Centropomus parallelus.*

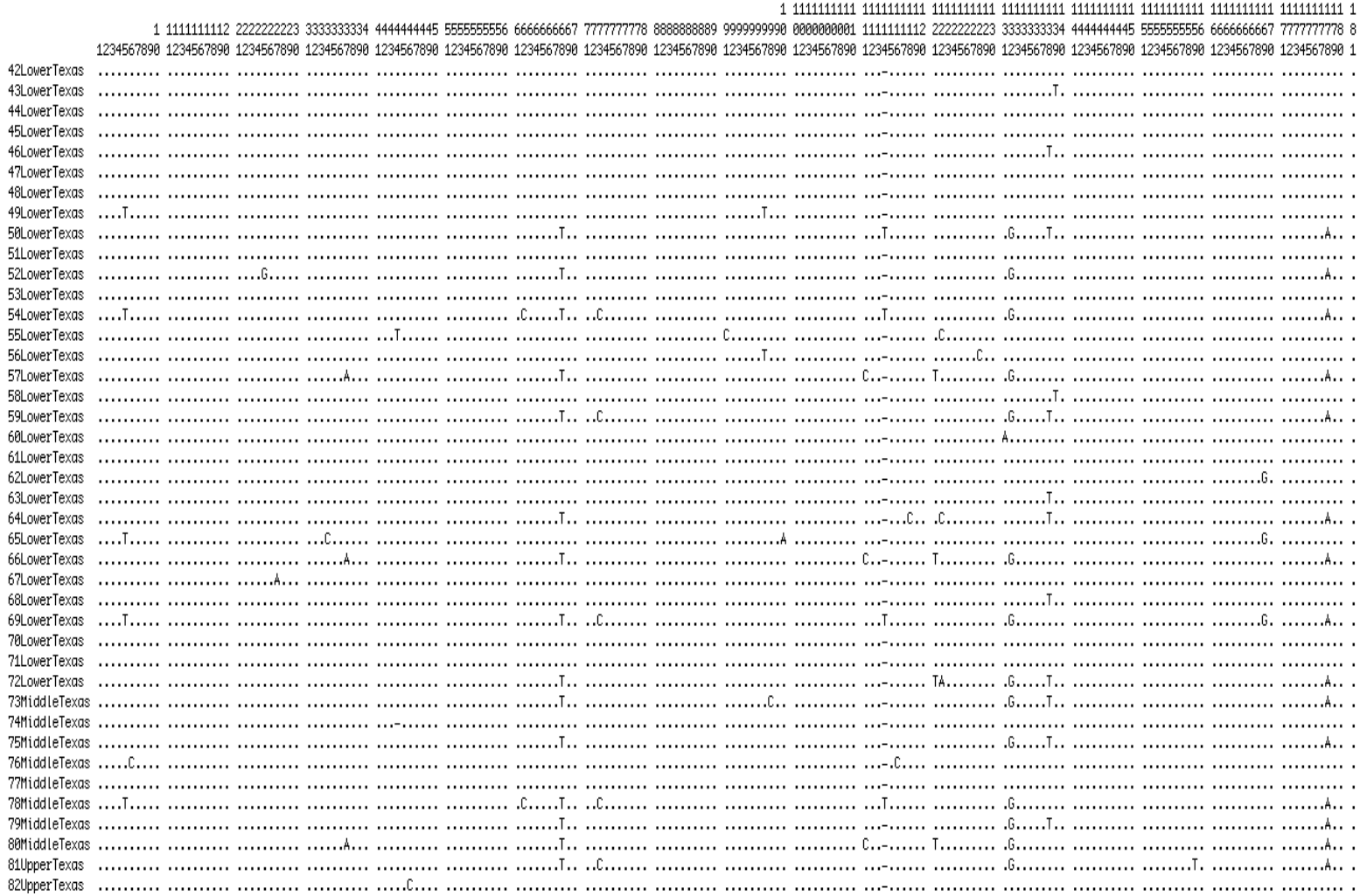

Figure A-4. Continued.

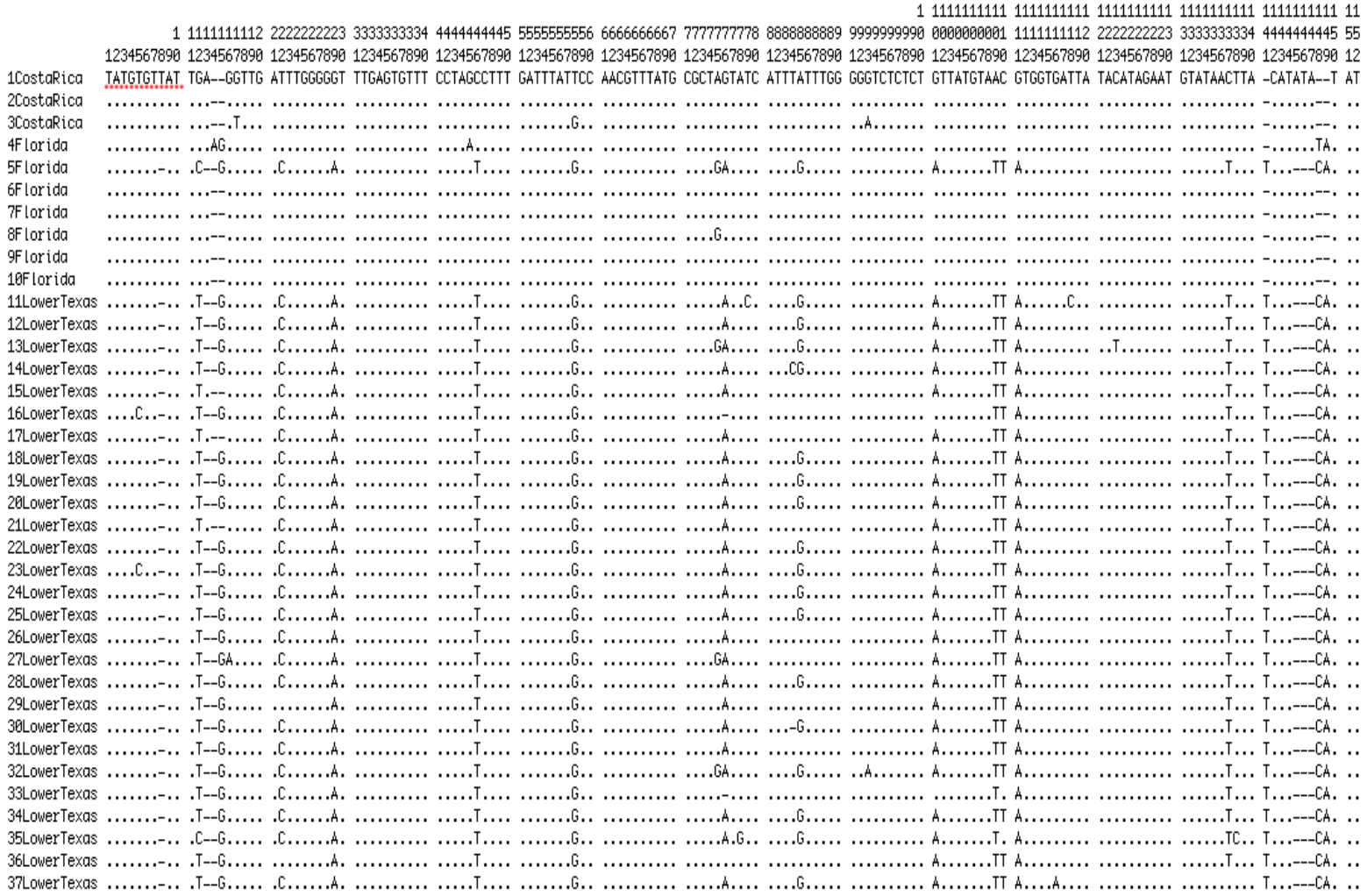

Figure A-5. Consensus alignment of 152bp long segment of the D – loop of 74 *Centropomus undecimalis*

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                                                                                                                         1 1111111111 1111111111 1111111111 1111111111 1111111111 11
                      1 1111111112 2222222223 3333333334 4444444445 5555555556 6666666667 7777777778 8888888889 9999999990 0000000001 1111111112 2222222223 3333333334 4444444445 55
             1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 12
38LowerTexas .......-.. .T.-G-.... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
39LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
40LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
41LowerTexas .......-.. .T--G....A .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
42LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
43LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
44LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
45LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
46LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... -.-...-CA. ..
47LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
48LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
49LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
50LowerTexas .......-.. .C--G..... .C......A. .......... .....T.... .......G.. .......... .....A.G.. ....G..... .......... A.......T. A......... .......... ......TC.. T...---CA. ..
51LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
52LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
53LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
54LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... .C..G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
55LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
56LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... ....GA.... ....G..... ..A....... A.......TT A......... .......... ......T... T...---CA. ..
57LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
58LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
59LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
60LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... ......A... ......T... T...---CA. ..
61LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......T. A......... .......... ......T... T...---CA. ..
62LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
63LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .....G.... ......T... T...---CA. ..
64LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... ....GA.... ....G..... .......... A.......TT A......... ..T....... ......T... T...---CA. ..
65LowerTexas .......-.. .T--G..... ........A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
66LowerTexas .......-.. .T--G..... ........A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
67LowerTexas .......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
68LowerTexas .......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
69MiddleTexas.......-.. .C--G..... .C......A. .......... .....T.... .......G.. .......... .....A.G.. ....G..... .......... A.......T. A......... .......... ......TC.. T...---CA. ..
70MiddleTexas.......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ...CG..... .......... A.......TT A......... .......... ......T... T...---CA. ..
71MiddleTexas.......-.. .C--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
72MiddleTexas.......-.. .T.--..... .C......A. .......... .....T.... .......G.. .......... .....A.... .......... .......... A.......TT A......... .......... ......T... T...---CA. ..
73MiddleTexas.......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....-.... .......... .......... ........T. AC........ .......... ......T... T...---CA. ..
74MiddleTexas.......-.. .T--G..... .C......A. .......... .....T.... .......G.. .......... .....A.... ....G..... .......... A.......TT A......... .......... ......T... T...---CA. ..
```

Figure A-5. Continued.

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