

- Hochachka, P. W., and Mommsen, T. P.), vol. 5, pp. 175-196, Elsevier Press, Amsterdam.
- Cohen, J. E. (1994) Marine and continental food webs: three paradoxes? *Philos. Trans. R. Soc. London B* **343**, 57-69.
- Collins, J. H., and Elzinga, M. (1975) The primary structure of actin from rabbit skeletal muscle. Completion and analysis of the amino acid sequence. *J. Biol. Chem.* **250**, 5915-5920.
- Cossins, A. R., and Macdonald, A. G. (1984) Homeoviscous theory under pressure: II. the molecular order of membranes from deep-sea fish. *Biochim. Biophys. Acta* **776**, 144-150.
- Cossins, A. R., and Macdonald, A. G. (1986) Homeoviscous theory under pressure: III. the fatty acid composition of liver mitochondrial phospholipids of deep-sea fish. *Biochim. Biophys. Acta* **860**, 325-335.
- Cossins, A. R., and Macdonald, A. G. (1989) The adaptations of biological membranes to temperature and pressure: Fish from the deep and cold. *J. Bioenerg. Biomembranes* **21**, 115-135.
- Dutton, P. H., Davis, S. K., Guerra, T., and Owens, D. (1996) Molecular phylogeny for marine turtles based on sequences of the ND4-leucine tRNA and control regions of mitochondrial DNA. *Mol. Phylogenet. Evol.* **5**, 511-521.
- Endo, H., and Okamura, O. (1992) New records of the abyssal grenadiers *Coryphaenoides armatus* and *C. yaquinae* from the western North Pacific. *Japan. J. Ichthyol.* **38**, 433-437.
- Estes, J. E., Selden, L. A., Kinoshita, H. J., and Gershman, L. C. Tightly-bound divalent cation of actin. *J. Muscle Res. Cell Motil.* **13**, 272-284 (1992).
- Fabrizio, C., Luca, B., Lucilla, O., Eliana, P., Lorenzo, C., and Tomaso, P. (1996) Molecular phylogeny of grey mullets based on mitochondrial DNA sequence analysis: evidence of a differential rate of evolution at the intrafamily level. *Mol. Phylogenet. Evol.* **6**, 416-424.
- Fajen, A., and Breden, F. (1992) Mitochondrial DNA sequence variation among natural populations of the Trinidad guppy, *Poecilia reticulata*. *Evolution* **46**, 1457-1465.
- Fields, P. A., and Somero, G. N. (1998) Hot spots in cold adaptation: localized increases in conformational flexibility in lactate dehydrogenase A4 orthologs of Antarctic notothenioid fishes. *Proc. Natl. Acad. Sci. USA* **95**, 11476-11481.
- Felsenstein, J. (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. *J. Mol. Evol.* **17**, 363-376.
- Felsenstein, J. (1985) Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* **46**, 1457-1465.
- Felsenstein, J. (1995) Phylogeny inference package (PHYLIP) Version 3.57c. Department of Genetics, SK-50, University of Washington, Seattle, WA.
- Flaherty, K. M., McKay, D. B., Kabsch, W., and Holmes, K. C. (1991) Similarity of the three-dimensional structures of actin and the ATPase fragment of a 70-kDa heat shock

cognate protein. *Proc. Natl. Acad. Sci. USA* **88**, 5041-5045.

France, S. C., and Kocher, T. D. (1996) Geographic and bathymetric patterns of mitochondrial 16 S rRNA sequence divergence among deep-sea amphipods, *Eurythenes gryllus*. *Mar. Biol.* **126**, 633-643.

Gage, J. D., and Tyler, P. A. (1991) Deep-sea Biology: A Natural History of Organisms at the Deep-Sea Floor. Cambridge Univ. Press, Cambridge.

Garland, T. Jr., and Adolph, S. C. (1994) Why not to do two-species comparative studies: limitations on inferring adaptation. *Physiol. Zool.* **67**, 797-828.

Garland, T. Jr., and Carter, P. A. (1994) Evolutionary physiology. *Annu. Rev. Physiol.* **56**, 579-621.

Gekko, K., and Hasegawa, Y. (1986) Compressibility-structure relationship of globular proteins. *Biochemistry* **25**, 6563-6571.

Gibbs, A., and Somero, G.N. (1990) Pressure adaptation of teleost gill Na^+ , K^+ -adenosine triphosphatase: role of the lipid and protein moieties. *J. Comp. Physiol. B* **160**, 431-439.

Gibbs, A. (1995) Temperature, pressure and the sodium pump: the role of homeoviscous adaptation. In *Biochemistry and Molecular Biology of Fishes* (ed. by Hochachka, P. W., and Mommsen, T. P.), vol. 5, pp. 197-212, Elsevier Press.

Gibbs, A. (1997) In *Deep-Sea Fishes* (ed. by Randall, D. J. and Farrell, A. P.), pp. 239-277. Academic Press, New York.

Gutell, R. R., Weiser, R., Woese, C. R., and Noller, H. F. (1985) Comparative anatomy of 16-S-like ribosomal RNA. *Prog. Nucleic Acid Res. Mol. Biol.* **32**, 1565-216.

Gibson, Q. H., Regan, R., Elber, R., Olson, J. S., and Carver, T. E. (1992) Distal pocket residues affect picosecond ligand recombination in myoglobin. an experimental and molecular dynamics study of position 29 mutants. *J. Biol. Chem.* **267**, 22022-22034.

Hanauer, A., Levin, M., Heilig, R., Daegelen, D., Kahn, A., and Mandel, J. L. (1983) Isolation and characterization of cDNA clones for human skeletal muscle alpha actin. *Nucleic Acids Res.* **11**, 3503-3516.

Harasewych, M. G., Adamkewicz, S. L., Blake, J. A., Saudec, D., Spriggs, T., and Bult, C. J. (1997) Phylogeny and relationships of pleurotomariid gastropods (Mollusca: Gastropoda): an assessment based on partial 18 S rRNA and cytochrome c oxidase I sequences. *Mol. Mar. Biol. Biotechnol.* **6**, 1-20.

Hardewig, I., van Dijk, P. L. M., Moyes, C. D., and Portner, H. O. (1999) Temperature-dependent expression of cytochrome-c oxidase in Antarctic and temperate fish. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **277**, R508-R516.

Heremans, K. (1982) High pressure effects on proteins and other biomolecules. *Annu. Rev. Biophys. Bioeng.* **11**, 1-21.

Hirayama, Y. and Watabe, S. (1997) Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal muscle. *Eur. J. Biochem.* **246**, 380-387.

- Hochachka, P. W. and Somero, G. N. (2002) Temperature. In *Biochemical Adaptation*, pp. 290-449, Oxford Univ. Press, New York.
- Holmes, K. C., Popp, D., Gebhard, W., and Kabsch, W. (1990) Atomic model of the actin filament. *Nature* **347**, 44-49.
- Houk, W. T., and Ue, K. (1974) The measurement of actin concentration in solution: a comparison of methods. *Anal. Biochem.* **62**, 66-74.
- Hu, M. C., Sharp, S. B., and Davidson, N. (1986) The complete sequence of the mouse skeletal alpha-actin gene reveals several conserved and inverted repeat sequences outside of the protein-coding region. *Mol. Cell. Biol.* **6**, 15-25.
- Hurley, J. H. (1996) The sugar kinase/heat shock protein 70/actin superfamily: Implications of conserved structure for mechanism. *Annu. Rev. Biomol. Struct.* **25**, 137-162.
- Imamura, S., Ojima N., and Yamashita, M. (2003) Cold-inducible expression of the cell division cycle gene CDC48 and its promotion of cell proliferation during cold acclimation in zebrafish cells. *FEBS Lett.* **549**, 14-20.
- Itoi, S., Kinoshita, S., Kikuchi, K., and Watabe, S. (2003) Changes of carp F₀F₁-ATPase in association with temperature acclimation. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **284**, R153-R163.
- Ikkai, T., and Ooi, T. (1966) The effects of pressure on F-G transformation of actin. *Biochemistry* **5**, 1551-1560.
- Iwamoto, T., and Stein, D. L. (1974) A systematic review of the rattail fishes (Macrouridae: Gadiformes) from Oregon and adjacent waters. *Occ. Pap. California Acad. Sci.* **111**, 1-79.
- Iwamoto, T., and Sazonov, Y. I. (1988) A review of the southeastern Pacific *Coryphaenoides* (sensu lato) (Pisces, Gadiformes, Macrouridae). *Proc. California Acad. Sci.* **45**, 35-82.
- Jaenicke, R. (1983) Biochemical processes under high hydrostatic pressure. *Naturwissenschaften* **70**, 332-341.
- Kabsch, W., Mannherz, H. G., Suck, D., Pai, E. F., and Holmes, K. C. (1990) Atomic structure of the actin:DNase I complex. *Nature* **347**, 37-44.
- Khaitlina, S. Y., Moraczewska, J., and Strzelecka-Golaszewska, H. (1993) The actin/actin interactions involving the N-terminus of the DNase-I-binding loop are crucial for stabilization of the actin filament. *Eur. J. Biochem.* **218**, 911-20.
- Kikuchi, K., Itoi, S., and Watabe, S. (1990) Increased levels of mitochondrial ATP synthase β -subunit in fast skeletal muscle of carp acclimated to cold temperature. *Fisheries Sci.* **64**, 629-636.
- Kimura, M. (1980) A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *J. Mol. Evol.* **16**, 111-120.

- Kinosian, H. J., Selden, L. A., Estes, J. E., and Gershman, L. C. (1991) Thermodynamics of actin polymerization; influence of the tightly bound divalent cation and nucleotide. *Biochim. Biophys. Acta* **1077**, 151-158.
- Kinosian, H. J., Selden, L. A., Estes, J. E., and Gershman, L. C. (1993) Nucleotide binding to actin. Cation dependence of nucleotide dissociation and exchange rates. *J. Biol. Chem.* **268**, 8683-8691.
- Kimura, M. (1968) Evolutionary rate at the molecular level. *Nature* **217**, 624-626.
- Kocher, T. D., Thomas, W. K., Meyer, A., Edward, S. V., Paabo, S., Villablanca, F. X., and Wilson, A. C. (1989) Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. *Proc. Natl. Acad. Sci. USA* **86**, 6196-6200.
- Krajewski, C., Blacket, M., Buckley, L., and Westerman, M. (1997) A multigene assessment of phylogenetic relationships within the dasyrid marsupial subfamily *Sminthopsinae*. *Mol. Phylogenet. Evol.* **8**, 236-248.
- Kraulis, P. J. (1991) MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures. *J. Appl. Crystallogr.* **24**, 946-950.
- Kraus, F., and Miyamoto, M. M. (1991) Rapid cladogenesis among the pecoran ruminants: evidence from mitochondrial DNA sequences. *Syst. Zool.* **40**, 117-130.
- Kuznetsova, I. M., Yakusheva, T. A., and Turoverov, K. K. (1990) Contribution of separate tryptophan residues to intrinsic fluorescence of actin. Analysis of 3D structure. *FEBS Lett.* **452**, 205-10.
- Lehrer, S. S., and Kerwar, G. (1972) Intrinsic fluorescence of actin. *Biochemistry* **11**, 1211-1217.
- Levitt, M. (1978) Conformational preferences of amino acids in globular proteins. *Biochemistry* **17**, 4277-4285.
- MacLean-Fletcher, S., and Pollard, T. D. (1980) Identification of a factor in conventional muscle actin preparations which inhibits actin filament self-association. *Biochem. Biophys. Res. Commun.* **96**, 18-27.
- Marshall, N. B. (1979) *Developments in the Deep-Sea Biology*. Blandford Press, London.
- Martin, A. P., Naylor, G. J. P., and Palumbi, S. R. (1992) Rates of mitochondrial DNA evolution in sharks are slow compared with mammals. *Nature* **357**, 153-155.
- Martin, A. P., and Palumbi, S. R. (1993) Body size, metabolic rate, generation time, and the molecular clock. *Proc. Natl. Acad. Sci. USA* **90**, 4087-4091.
- Merret, N. R. (1978) On the identity and pelagic occurrence of larval and juvenile stages of rattail fishes (family Macrouridae) from 60°N, 20°W and 53°N, 20°W. *Deep Sea Res.* **25**, 147-160.
- Meyer, A., Kocher, T. D., Basasibwaki, P., and Wilson, A. C. (1990) Monophyletic origin of Victoria cichlid fishes suggested by mitochondrial DNA sequences. *Nature* **347**, 550-553.

- Meyer, A. (1992) Evolution of mitochondrial DNA in fish. In *Biochemistry and Molecular Biology of Fishes* (ed. by Hochachka, P. W., and Mommsen, T. P.), vol. 2, pp. 1-38, Elsevier Press, Amsterdam.
- Mills, E. M. (1983) Problems of deep-sea biology: an historical perspective. In *Deep-Sea Biology* (ed. by G. T. Rowe), pp. 1-80. John Wiley, New York.
- Miya, M., and Nishida, M. (1996) Molecular phylogenetic perspective on the evolution of the deep-sea fish genus *Cyclothone* (Stomiiformes: Gonostomatidae). *Ichthyol. Res.* **43**, 375-398.
- Miya, M., and Nishida, M. (1998) Molecular phylogeny and evolution of the deep-sea fish genus *Sternoptyx*. *Mol. Phylogenet. Evol.* **10**, 11-22.
- Miya, M., Kawaguchi, A., and Nishida, M. (2001) Mitogenomic exploration of higher teleostean phylogenies: a case study for moderate-scale evolutionary genomics with 38 newly-determined complete mitochondrial DNA sequences. *Mol. Biol. Evol.* **18**, 1993-2009.
- Miyamoto, M. M., and Boyle, S. M. (1989) The potential importance of mitochondrial DNA sequence data to eutherian mammal phylogeny. In *The Hierarchy of Life* (ed. by Fernholm, B., Bremer, K., Brundin, L., and Jornvall, H.), pp. 437-450, Elsevier Press, Amsterdam.
- Moraczewska, J., Wawro, B., Seguro, K., and Strzelecka-Golaszewska, H. (1999) Divalent cation-, nucleotide-, and polymerization-dependent changes in the conformation of subdomain 2 of actin. *Biophys. J.* **77**, 373-385.
- Morild, E. (1981) The theory of pressure effects on enzymes. *Adv. Protein Chem.* **34**, 93-166.
- Mozhaev, V. V., Heremans, K., Frank, J., Masson, P., and Balny, C. (1996) High pressure effects on protein structure and function. *Proteins* **24**, 81-91.
- Nakabo, T. (2000) Macrouridae. In *Fishes of Japan with Pictorial Keys to the Species* (ed. by Nakabo, T.), ed. 2, pp. 417-435, Tokai Univ. Press, Tokyo.
- Normark, B. B., McCune, A. R., and Harrison, R. G. (1991) Phylogenetic relationships of Neopterygian fishes, inferred from mitochondrial DNA sequences. *Mol. Biol. Evol.* **8**, 819-834.
- Ohno, S. (1970) *Evolution by Gene Duplication*, Springer-Verlag, Heidelberg.
- Orlova, A. and Egelman, E. H. (1993) A conformational change in the actin subunit can change the flexibility of the actin filament. *J. Mol. Biol.* **232**, 334-341.
- Otterbein, L. R., Graceffa, P., and Dominguez, R. (2001) The crystal structure of uncomplexed actin in the ADP state. *Science* **293**, 708-711.
- Palumbi, S. R. and Wilson, A. C. (1990) Mitochondrial DNA diversity in the sea urchins, *Stronglyocentrotus purpuratus* and *S.droenachiensis*. *Evolution* **44**, 403-415.
- Perutz, M.F. (1983) Species adaptation in a protein molecule. *Mol. Biol. Evol.* **1**, 1-28.

- Phleger, C. F., and Laub, R. J. (1975) Skeletal fatty acids in fish from different depths off Jamaica. *Comp. Biochem. Physiol.* **94B**, 329-334.
- Pollard, T. D. (1986) Rate constants for the reactions of ATP- and ADP-actin with the ends of actin filaments. *J. Cell Biol.* **103**, 2747-2754.
- Pollard, T. D., and Cooper, J. A. (1986) Actin and actin-binding proteins. a critical evaluation of mechanisms and functions. *Annu. Rev. Biochem.* **55**, 987-1035.
- Rand, D. M. (1994) Thermal habit, metabolic rate, and evolution of mitochondrial DNA. *Trends. Ecol. Evol.* **9**, 125-131.
- Reisler, E. (1993) Actin molecular structure and function. *Curr. Opin. Cell Biol.* **5**, 41-47.
- Ritchie, P. A., Bargelloni, L., Meyer, A., Taylor, J. A., Macdonald, J. A., and Lambert, D. M. (1996) Mitochondrial phylogeny of Trematomid fishes (Nototheniidae, Perciformes) and the evolution of Antarctic fish. *Mol. Phylogenet. Evol.* **5**, 383-390.
- Saitou, N., and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **45**, 406-425.
- Saunders, P. M., and Fofonoff, N. P. (1976) Conversion of pressure to depth in the ocean. *Deep-Sea Res.* **23**, 109-111.
- Sheterline, P., Clayton, J., and Sparrow J. (1999) *Actin* 4th ed., Oxford Univ. Press, New York.
- Siebenaller, J. F., and Somero, G. N. (1978) Pressure adaptive differences in lactate dehydrogenases of congeneric fishes living at different depths. *Science* **201**, 255-257.
- Siebenaller, J. F., and Somero, G. N. (1989) Biochemical adaptation to the deep sea. *Rev. Aquat. Sci.* **1**, 1-25.
- Siebenaller, J. F., Somero, G. N., and Haedrich, R. L. (1982) Biochemical characteristics of macrourid fishes differing in their depths of distribution. *Biol. Bull.* **163**, 240-249.
- Siebenaller, J. F. (1991) Pressure as an environmental variable: magnitude and mechanisms of perturbation. In *Biochemistry and Molecular Biology of Fishes* (ed. by Hochachka, P. W., and Mommsen, T. P.), vol. 1, pp. 323-343, Elsevier Press, Amsterdam.
- Siebenaller, J. F., and Murray, T. F. (1995) The effects of pressure on G protein-coupled signal transduction. In *Biochemistry and Molecular Biology of Fishes* (ed. by Hochachka, P. W., and Mommsen, T. P.), vol. 5, pp 147-174, Elsevier Press, Amsterdam.
- Silva, J. L., and Weber, G. (1993) Pressure stability of proteins. *Annu. Rev. Phys. Chem.* **44**, 89-113.
- Smith, K. L. Jr. (1978) Metabolism of the abyssopelagic rattail *Coryphaenoides armatus* measured *in situ*. *Nature* **274**, 362-364.
- Somero G. N. (1990) Life at low volume change: hydrostatic pressure as a selective

- factor in the aquatic environment. *Am. Zool.* **30**, 123-135.
- Somero, G.N. (1992) Adaptations to high hydrostatic pressure. *Annu. Rev. Physiol.* **54**, 557-577.
- Somero, G. N. (1995) Proteins and temperature. *Annu. Rev. Physiol.* **57**, 43-68.
- Springer, M. S., Hollar, L. J., and Burke, A. (1995) Compensatory substitutions and the evolution of the mitochondrial 12 S rRNA gene in mammals. *Mol. Biol. Evol.* **12**, 1138-1150.
- Spudich, J. A. and Watt, S. (1971) The regulation of rabbit skeletal muscle contraction. I. Biochemical studies of the interaction of the tropomyosin-troponin complex with actin and the proteolytic fragments of myosin. *J. Biol. Chem.* **246**, 4866-4871.
- Stein, D. L., and Pearcy, W. G. (1982) Aspects of reproduction, early life history, and biology of macrourid fishes off Oregon, USA. *Deep-Sea Res.* **29**, 1313-1329.
- Steinar, J., and Ingrid, B. (1996) The complete mitochondrial DNA sequence of Atlantic cod (*Gadus morhua*): relevance to taxonomic studies among codfishes. *Mol. Mar. Biol. Biotechnol.* **5**, 203-214.
- Sturmbauer, C., and Meyer, A. (1992) Genetic divergence, speciation and morphological stasis in a lineage of African cichlid fishes. *Nature* **358**, 578-581.
- Stutz, F., and Spohr, G. (1986) Isolation and characterization of sarcomeric actin genes expressed in *Xenopus laevis* embryos. *J. Mol. Biol.* **187**, 349-361.
- Swezey, R. R., and Somero, G. N. (1982) Polymerization thermodynamics and structural stabilities of skeletal muscle actins from vertebrates adapted to different temperatures and hydrostatic pressures. *Biochemistry* **21**, 4496-4503.
- Swezey, R.R., and Somero, G.N. (1985) Pressure effects on actin self-assembly: interspecific differences in the equilibrium and kinetics of the G to F transformation. *Biochemistry* **24**, 852-860.
- Swofford, D. L. (1998) Phylogenetic Analysis Using Parsimony (PAUP) 4d64 test version. Laboratory of Molecular Systematics MSC, MRC-534, Smithsonian Institution, Maryland.
- Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* **22**, 4673-4680.
- Tobacman, L. S., Brenner, S. L., and Korn, E. D. (1983) Effect of *Acanthamoeba* profilin on the pre-steady state kinetics of actin polymerization and on the concentration of F-actin at steady state. *J. Biol. Chem.* **258**, 8806-8812.
- Torigai, M., and Konno, K. (1997) Thermal stability of fish G-actin extracted from the acetone-dried myofibril-powder. *Fish. Sci.* **63**, 403-406.
- Uyeno, T. (1967) A Miocene alepisauroid fish of a new family, *Polymerichthyidae*, from Japan. *Bull. Nat. Sci. Mus. Tokyo* **10**, 383-391.

- Uyeno, T. (1980) On the rate of evolution in fishes. *Aquabiology* **9**, 242-247 (in Japanese).
- Venkatesh, B., Tay, B. H., Elgar, G., and Brenner, S. (1996) Isolation, characterization and evolution of nine pufferfish (*Fugu rubripes*) actin genes. *J. Mol. Biol.* **259**, 655-665.
- Vogler, A. P., and Welsh, A. (1997) Phylogeny of North American *Cicindela* tiger beetles inferred from multiple mitochondrial DNA sequences. *Mol. Phylogenet. Evol.* **8**, 225-235.
- Waechter, F., and Engel, J. (1975) The kinetics of the exchange of G-actin-bound 1: N6-ethenoadenosine 5'-triphosphate with ATP as followed by fluorescence. *Eur. J. Biochem.* **57**, 453-459.
- Watabe, S., Hirayama, Y., Imai, J., Kikuchi, K., and Yamashita, M. (1995) Sequences of cDNA clones encoding alpha-actin of carp and goldfish skeletal muscles. *Fish. Sci.* **61**, 998-1003.
- Watabe, S. (2002) Temperature plasticity of contractile proteins in fish muscle. *J. Exp. Biol.* **205**, 2231-2236.
- Weber, G., and Drickamer, H. G. (1983) The effect of high pressure upon proteins and other biomolecules. *Q. Rev. Biophys.* **16**, 89-112.
- Wilson, R. R. Jr., Siebenaller, J. F., and Davis, B. J. (1991) Phylogenetic analysis of species of three subgenera of *Coryphaenoides* (Teleostei:Macrouridae) by peptide mapping of homologs of LDH-A4. *Biochem. Syst. Ecol.* **18**, 565-572.
- Wilson, R. R. Jr. (1994) Interrelationships of the subgenera *Coryphaenoides* (Gadiforms: Macrouridae): Comparison of protein electrophoresis and peptide mapping. *Copeia* **1**, 42-50.
- Yamashita, M., Ojima, N., and Sakamoto, T. (1996) Molecular cloning and cold-inducible gene expression of ferritin H subunit isoforms in rainbow trout cells. *J. Biol. Chem.* **271**, 26908-26913.
- Yancey, P. H., and Siebenaller, J. F. (1999) Trimethylamine oxide stabilizes teleost and mammalian lactate dehydrogenases against inactivation by hydrostatic pressure and trypsinolysis. *J. Exp. Biol.* **202**, 3597-3603.
- Yancey, P. H., Fyfe-Johnson, A.L., Kelly, R.H., Walker, V.P., and Aunon, M.T. (2001) Trimethylamine oxide counteracts effects of hydrostatic pressure on proteins of deep-sea teleosts. *J. Exp. Zool.* **289**, 172-176.
- Yancey, P. H., Blake, W.R., and Conley, J. (2002) Unusual organic osmolytes in deep-sea animals: adaptations to hydrostatic pressure and other perturbants. *Comp. Biochem. Physiol. A Mol. Integr. Physiol.* **133**, 667-676.

Table 1-1. Species used in this study

Family / Species	Collection site and depth (m)		
Macrouridae			
(Ingroup taxa)			
<i>Coryphaenoides nasutus</i>	38° 01.76' N	142° 12.73' E	810 m
<i>C. cinereus</i>	38° 02.13' N	142° 22.05' E	997 m
<i>C. acrolepis</i>	42° 04.00' N	144° 42.80' E	1960 m
<i>C. pectoralis</i>	37° 21.35' N	142° 18.42' E	1001 m
<i>C. longifilis</i>	37° 21.35' N	142° 18.42' E	1001 m
<i>C. armatus</i>	44° 00.70' N	145° 22.20' E	3940 m
<i>C. yaquinae</i>	39° 58.10' N	154° 59.50' E	5600 m
(Outgroup taxa)			
<i>Abyssicola macrochir</i>	37° 58.81' N	141° 48.97' E	250 m
<i>Caelorinchus gilberti</i>	37° 26.28' N	142° 00.81' E	603 m

Table 1-2. Pairwise sequence estimates (above diagonal) and number of base substitutions (below diagonal) for 12S rRNA gene

	1	2	3	4	5	6	7	8	9
1. <i>C. armatus</i>		0.0073	0.0571	0.0557	0.0545	0.0570	0.0556	0.0942	0.0885
2. <i>C. yaquinae</i>	8 (1)		0.0571	0.0584	0.0545	0.0597	0.0556	0.0970	0.0913
3. <i>C. longifilis</i>	45 (7)	45 (7)		0.0049	0.0061	0.0061	0.0286	0.0916	0.0776
4. <i>C. pectoralis</i>	44 (6)	46 (6)	4 (1)		0.0061	0.0037	0.0274	0.0929	0.0789
5. <i>C. cinereus</i>	42 (6)	44 (8)	5 (2)	5 (1)		0.0073	0.0286	0.0902	0.0776
6. <i>C. acrolepis</i>	45 (6)	47 (6)	5 (1)	3 (0)	6 (1)		0.0286	0.0915	0.0775
7. <i>C. nasutus</i>	44 (4)	44 (4)	23 (7)	22 (6)	23 (7)	23 (6)		0.1024	0.0883
8. <i>C. gilberti</i> *	73 (15)	74 (14)	70 (15)	61 (14)	70 (16)	70 (14)	78 (12)		0.0350
9. <i>A. macrochir</i> *	69 (13)	70 (12)	61 (14)	62 (13)	62 (15)	61 (13)	68 (10)	28 (6)	

Above diagonals include pairwise sequence divergence estimated by the Kimura's two-parameter model. Below diagonals include the number of total base substitutions and that of transversion in parentheses. Asterisks indicate the outgroup species.

Table 1-3. Pairwise sequence estimates (above diagonal) and number of base substitutions (below diagonal) for COI gene

	1	2	3	4	5	6	7	8	9
1. <i>C. armatus</i>		0.0252	0.1519	0.1525	0.1469	0.1519	0.1488	0.2167	0.2256
2. <i>C. yaquinae</i>	11 (1)		0.1543	0.1550	0.1438	0.1543	0.1512	0.2141	0.2156
3. <i>C. longifilis</i>	60 (10)	61 (9)		0.0183	0.0442	0.0136	0.0991	0.1822	0.1715
4. <i>C. pectoralis</i>	60 (12)	91 (11)	8 (2)		0.0347	0.0091	0.0969	0.1801	0.1634
5. <i>C. cinereus</i>	58 (12)	57 (11)	19 (2)	15 (2)		0.0300	0.1099	0.1822	0.1540
6. <i>C. acrolepis</i>	60 (10)	61 (9)	6 (0)	4 (2)	13 (2)		0.0991	0.1733	0.1569
7. <i>C. nasutus</i>	59 (9)	60 (8)	41 (3)	40 (5)	45 (5)	41 (3)		0.1664	0.1763
8. <i>C. gilberti</i> *	80 (24)	79 (25)	69 (22)	68 (24)	69 (22)	66 (22)	64 (19)		0.1051
9. <i>A. macrochir</i> *	82 (29)	79 (28)	65 (25)	62 (27)	59 (25)	60 (25)	67 (22)	43 (7)	

Above diagonals include pairwise sequence divergence estimated by the Kimura's two-parameter model. Below diagonals include the number of total base substitutions and that of transversion in parentheses. Asterisks indicate the outgroup species.

Table 2-1. Comparison of the deduced amino acid sequences of actin isoforms from *Coryphaenoides* species and various species

Actin type	Position													
	2	3	54	67	88	137	155	165	228	278	299	354	358	
Actin 1	D	E	V	L	T	Q	A	V	A	A	L	S	S	
Actin 2a	S	
<i>yaq</i> actin 2b	.	.	.	P	.	K	S	
<i>arm</i> actin 2b	.	.	A	.	.	K	S	
Pufferfish 1	.	D	
Pufferfish 2	.	D	.	.	S	.	S	I	G	T	.	.	.	
Walleye pollack 1	
Walleye pollack 2	S	
Atlantic salmon	.	D	S	I	.	.	.	A	T	
Carp	.	D	T	
Zebrafish	
Medaka	
Tilapia	.	D	
Chicken	E	D	S	I	.	T	M	.	T	

A dot indicates the amino acid residue identical to that in actin 1. Numbers above the sequence indicate the residue position. *yaq* actin 2b and *arm* actin 2b are those cloned from *C. yaquinae* and *C. armatus*, respectively. The GenBank accession numbers for species lists are described in Materials and Methods in Section 2 in Chapter 2.

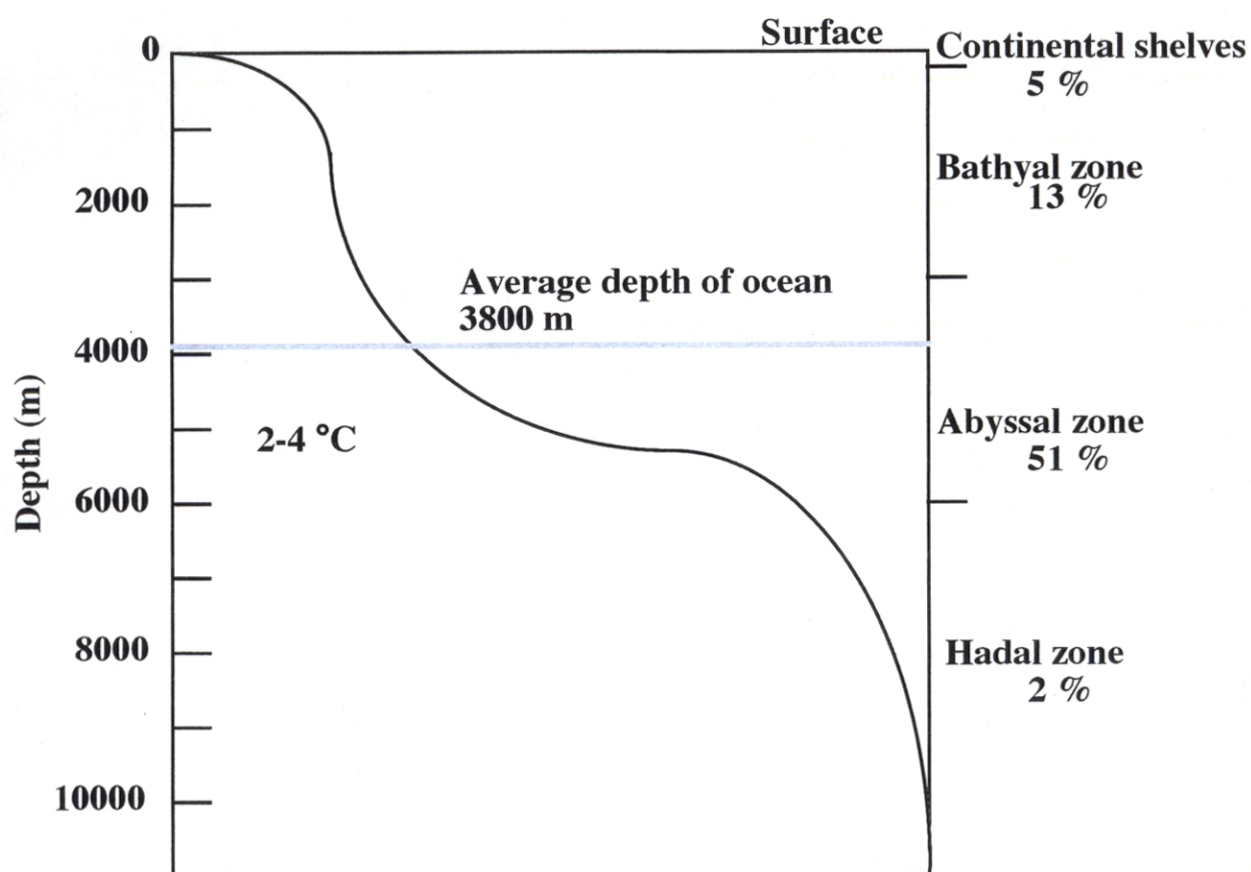


Fig. 0-1. Classification of the marine environments. The percentages refer to all Earth's surface area of the ocean floor included in each depth zone.

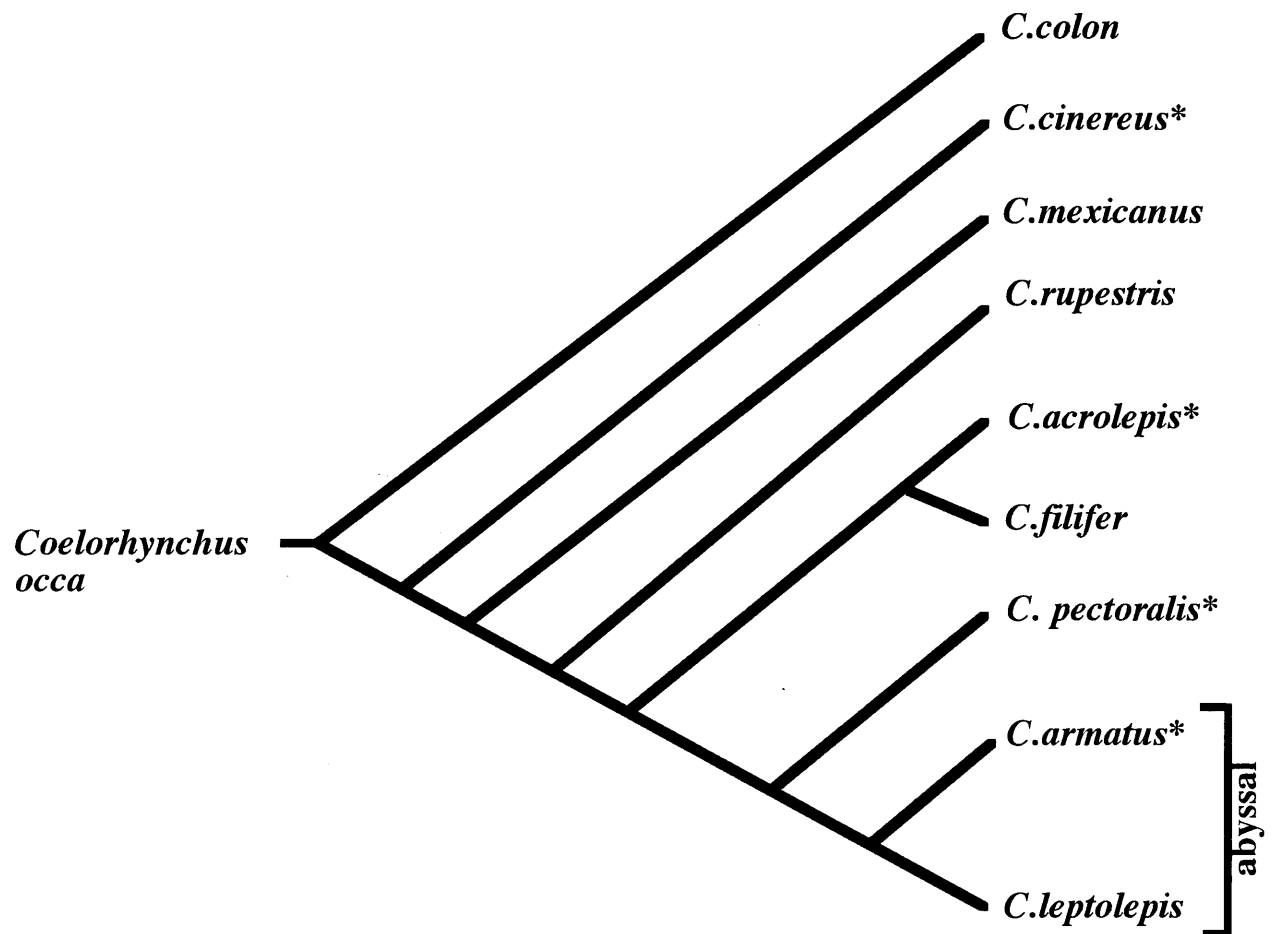


Fig. 1-1. Phylogenetic tree constructed by least-squares (Fitch-Margoliash) analysis based on peptide mapping of A₄-LDH homologs from *Coryphaenoides* species (Wilson et al., 1991). *Species used in this study.



Fig. 1-2. Deep-sea fish *Coryphaenoides yaquinae*. These fish were caught from 5600 m deep.

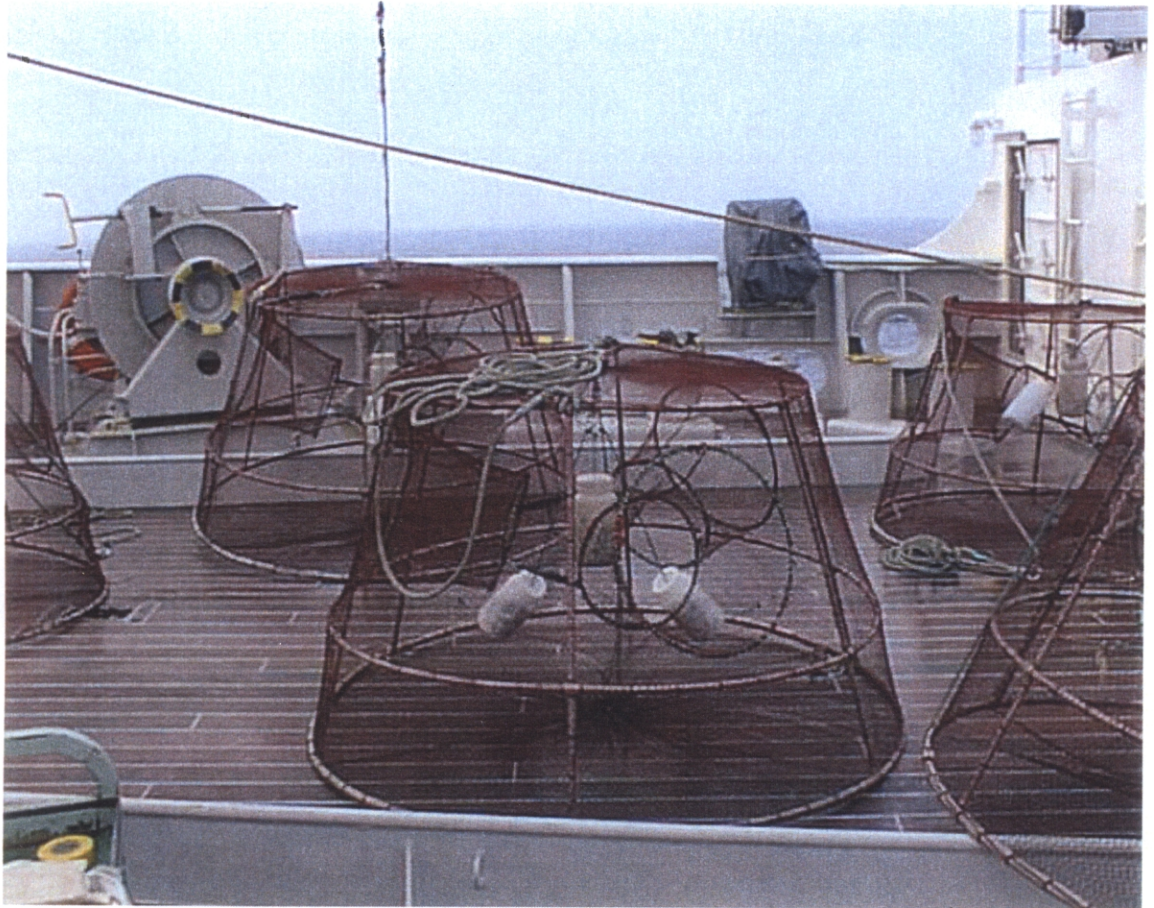


Fig. 1-3. The deep-sea pot. The bait, mostly sardine, were put into the white bottles in the pot.

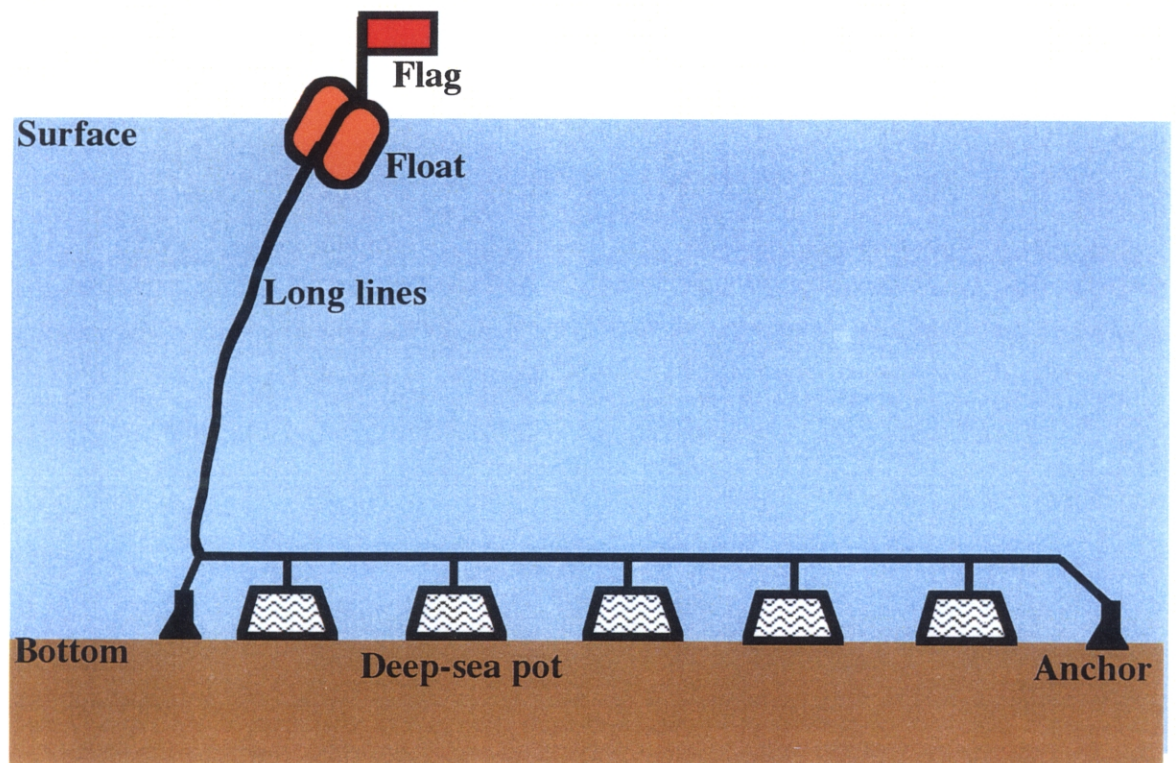


Fig.1-4. Deep-sea pots with long lines for sampling the deep-sea fish. Distance between two pots is about 100 m. The pots are set on the bottom overnight.



Fig. 1-5. The R/V Soyo-maru is a research vessel of National Research Institute of Fisheries Science. This ship has 892 gross tons.

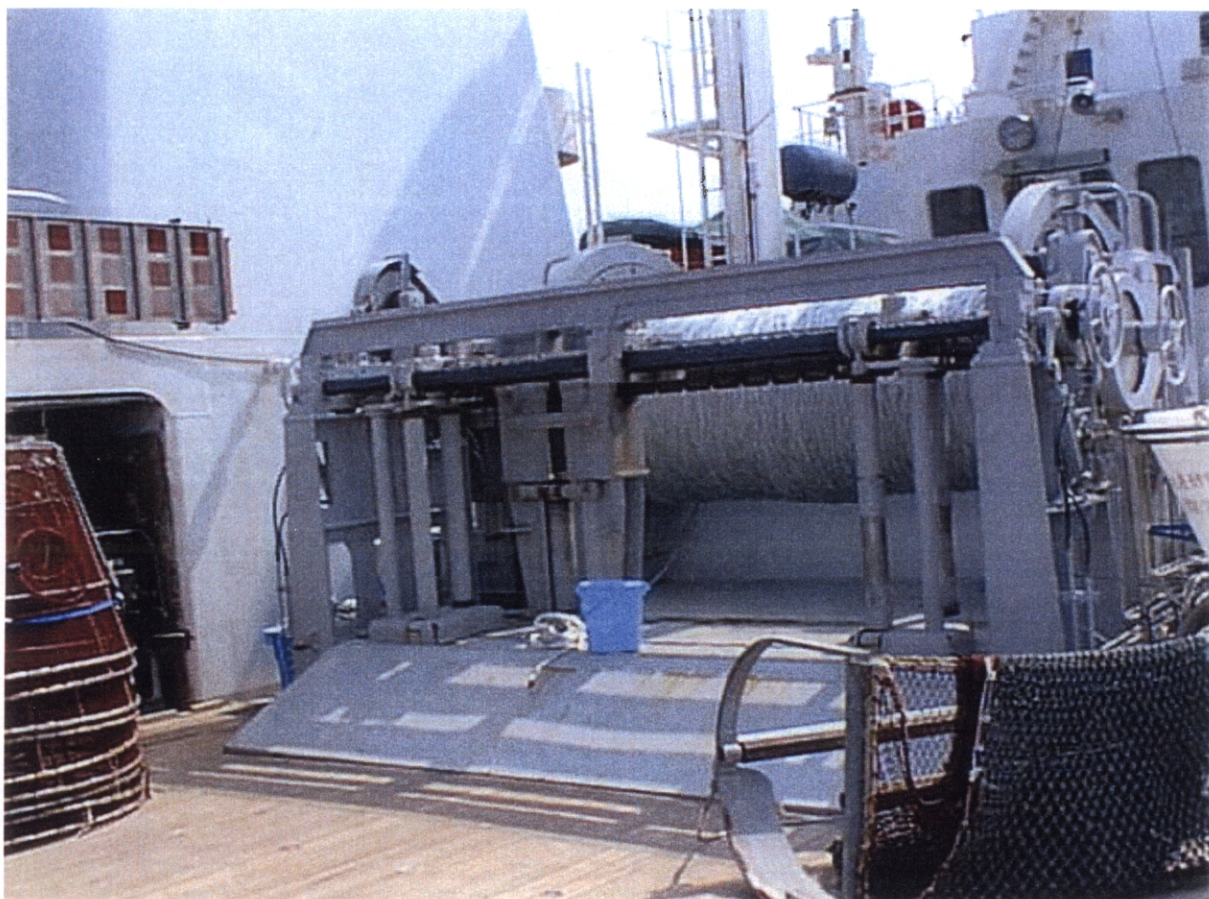


Fig.1-6. The 10000 m trawl winch used in sampling by the deep-sea pots. The trawl winch has no long lines in this condition. The volume of the blue bucket on the winch is 20 L.

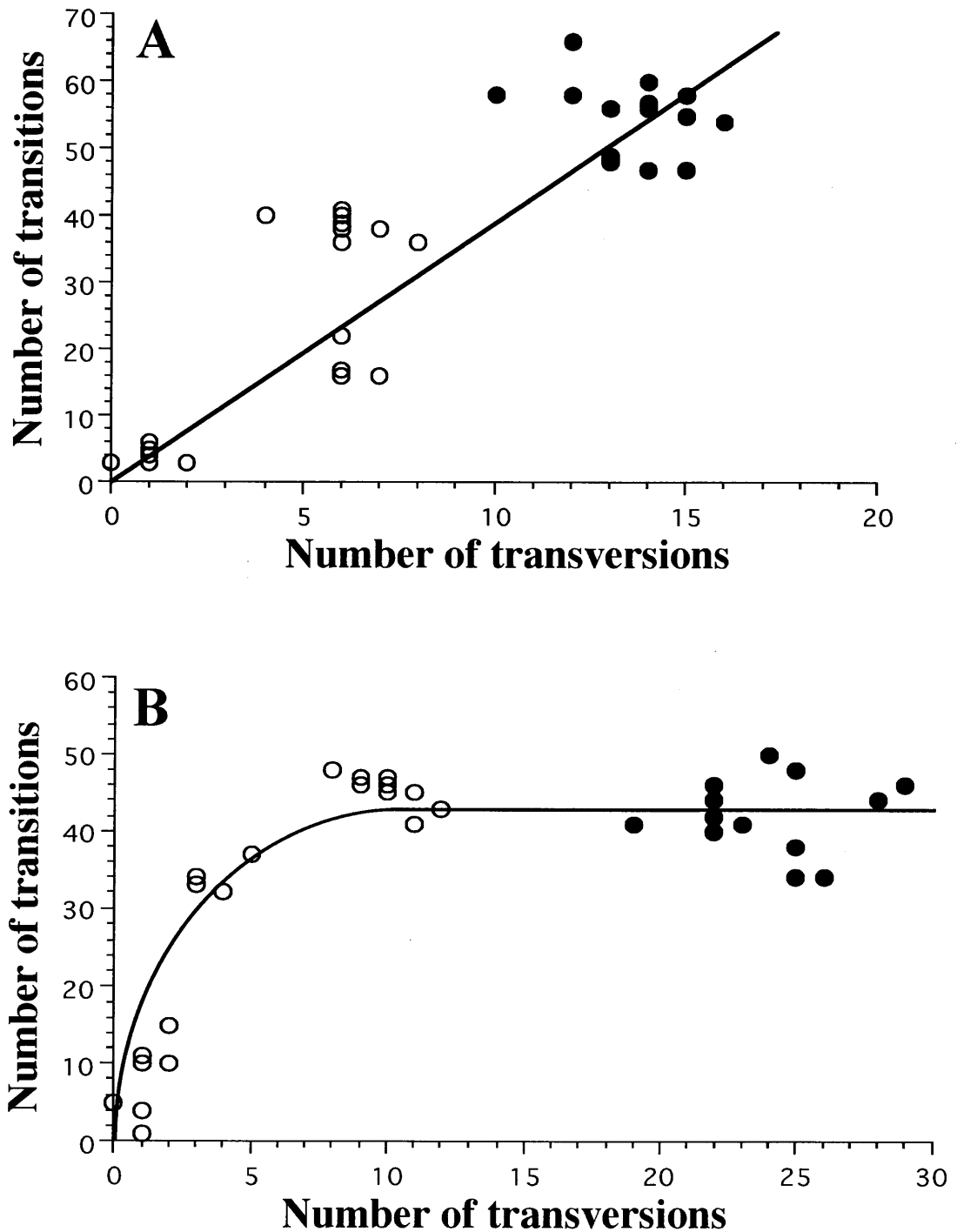


Fig.1-7. Levels of saturation for base substitutions in the 12S rRNA and COI genes among the ingroup *Coryphaenoides* species and between *Coryphaenoides* species and outgroup species. (A) 12S rRNA and (B) COI (third codon position) genes. Open symbols indicate pairwise comparisons of transition vs. transversion within the ingroup, and closed symbols indicate those between ingroup and outgroup species.

				80
<i>C. acrolepis</i>	CACAAAGGTTTGGTCCTAGC	TTTACTATCAACTCTAACCT	AATTTACACATGCAAGTCTC	CGCACTCCTGTGAGAATGCC
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----G-----	-----	-----
<i>C. nasutus</i>	-----	-----	-----	-----T-----
<i>C. armatus</i>	--T-----G--	-----	G-----	-----
<i>C. yaquinae</i>	--T-----	-----	G-----	-----
<i>A. macrochir</i>	-----	--T--G--T--G--	T-----	-----
<i>C. gilberti</i>	--T-C-----	-----G-----	T-----	-----
				160
<i>C. acrolepis</i>	CTTATTGTCCTGCCTAGGAA	CTAAGGAGCAGGTATCAGGC	ACGATC/ATCAGCCCAATAC	ACCTTGTTTGGCCACACCCC
<i>C. cinereus</i>	-----	-----	---T/-----	-----
<i>C. longifili</i>	-----	-----	/-----	-----
<i>C. pectorali</i>	-----	-----	/-----	-----
<i>C. nasutus</i>	-----	-----	/-----C--	-----
<i>C. armatus</i>	-----	-----	TTG-----C--	-----C--
<i>C. yaquinae</i>	-----	-----	TAG-----C--	-----C--
<i>A. macrochir</i>	-----	-----	TA-----C--	-----
<i>C. gilberti</i>	-----	-----	TA-----	-----
				240
<i>C. acrolepis</i>	CACGGGTAATCAGCAGTGAT	AAACTTTTAGCTATAAGTGA	AAACTTGACTTAGTTAAGGT	TAAA/AGGGCCGGTAAACCT
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	T-----	-----C-----	-----	-----
<i>C. armatus</i>	-----	-----	-----	---G/---T-----
<i>C. yaquinae</i>	-----	-G-----	-----	---G/---T-----
<i>A. macrochir</i>	-----	-----	-----C-----	---TA---T-----
<i>C. gilberti</i>	-----	-----	-----C---C-----	---/----T-----
				320
<i>C. acrolepis</i>	CGTGCCAGCCACCGCGGTTA	AACGGGAGGCCCAAGTTGAA	AGACAGCGCGCTAAAGCGTG	GTTAAGGTACTATATAAA/
<i>C. cinereus</i>	-----	-----	-----	-----A-----/
<i>C. longifili</i>	-----	-----	-----	-----/
<i>C. pectorali</i>	-----	-----	-----	-----/
<i>C. nasutus</i>	-----	-----A-----C---	---G-----	-----A---/-C---G-/
<i>C. armatus</i>	-----	-----A-T-----	-----	-----AC---/-GC---/
<i>C. yaquinae</i>	-----	-----A-T-----	-----	-----AC---/-GC---/
<i>A. macrochir</i>	-----	-----A-----T---	---A-----	-----A---/A-----A
<i>C. gilberti</i>	-----	-----A-----T---	---A-----	-----A---T-/A-----/
				400
<i>C. acrolepis</i>	TAGGGCCGAATAGTCTCAAA	GCAGTCAAATCTATTGAGA	CCACGAAGCACATCCACGAA	GGTGGCCCTAACACCCCTGA
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	-----	A-----	-----	-----T-----
<i>C. armatus</i>	-----GAC-----	A-----	-----T-----	-----TG--T-----
<i>C. yaquinae</i>	-----GAC-----	A-----	-----T-----	-----TG--T-----
<i>A. macrochir</i>	---T-A---C---T---	-----ACTA-----	---A-----T-----	A-AA---T-----
<i>C. gilberti</i>	---TTA---G-C---T---	-----ACTA---AG---	---A-----T-----	A-AA---GTT-TTA---
				480
<i>C. acrolepis</i>	CCCCACGAAAGCCATAACAC	AAACTGGGATTAGATACCCC	ACTATGTATGGCCGTCAAAA	TTGATGGTACTTCACTCGAA
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	-----	-----	-----	-----
<i>C. armatus</i>	-----	-----	-----T-----	-----
<i>C. yaquinae</i>	-----	-----	-----T-----	-----
<i>A. macrochir</i>	-----	-----	-----T---G-----	-----C-----
<i>C. gilberti</i>	-----	-----	---T-----T---T---	-----

Fig.1-8. Comparison of partial nucleotide sequences of the 12S rRNA gene of *Coryphaenoides* species. A dash indicates an identical nucleotide with that of *C. acrolepis*. The sequences correspond to positions 68-892 of the Atlantic cod homolog (Steinar and Ingrid, 1996). The sequences of *Coryphaenoides* species are available from the DDBJ/EMBL/GenBank nucleotide databases with accession numbers AB018224-AB018232.

				560
<i>C. acrolepis</i>	CCATCCGCCCCGGGACTACG	AGCCCTAGCTTAAACCCAA	AGGACCTGGCGGTGCTTTAG	ATCCCCCTAGAGGAGCCTGT
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	---T-----A	-----	-----	-----
<i>C. armatus</i>	-----A--A-T---	G---C-----	-----	-----
<i>C. yaquinae</i>	---T---A--A-T---	G---C-----	-----	-----
<i>A. macrochir</i>	-----A-----	-----C-----	-----	-----
<i>C. gilberti</i>	-----A-----	---TC-----	-----	-----
				640
<i>C. acrolepis</i>	CCTGTAACGACAAACCCCG	TTAAACCTCACCACCCCTTG	TCAATCCCGCCTATATACCA	CCGTCGTAAGCTTACCCTAT
<i>C. cinereus</i>	---A-----	-----	-----	-----
<i>C. longifili</i>	---A-----	-----	-----	-----
<i>C. pectorali</i>	---A-----	-----	-----	-----
<i>C. nasutus</i>	---A-----	-----T---	-----	-----
<i>C. armatus</i>	---A-----	---G-----	---T---T---	-----
<i>C. yaquinae</i>	---A-----	---G-----T---	---T---T---	-----
<i>A. macrochir</i>	T-A-----T---	-----	---AT-----	---C-----
<i>C. gilberti</i>	T-A-----T---	-----	---AT-----	---C-----
				720
<i>C. acrolepis</i>	TGAAGGTTCA/AAAGTAGGC	TCTAATAGTAATACTAAAGA	CGTCAGGTCGAGGTGTAGCG	TATGGGGTGGGAAGAGATGG
<i>C. cinereus</i>	-----/------	-----G---	-----	-----
<i>C. longifili</i>	---A-T/------	-----G---	-----	-----
<i>C. pectorali</i>	-----/------	-----G---	-----	-----
<i>C. nasutus</i>	-----/-A-----	A-----G---	-----	-----
<i>C. armatus</i>	-----ATA-----	C-----G---	-----	C---C-----
<i>C. yaquinae</i>	-----ATA-----	C-----G---	-----	C---C-----
<i>A. macrochir</i>	-----/-A-----A--	C-C-----	-----	---A-----A---
<i>C. gilberti</i>	-----/-A-----A--	C-C-----C---	-----	---A-----A---
				800
<i>C. acrolepis</i>	GCTACATTCCCTAATGAAGA	GAATACGAACGGTAATTGA	AAAAATTACACTGAAGGAGG	ATTAGTAGTAAGGAAGGAG
<i>C. cinereus</i>	-----	-----C-----	-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	-----T-----	-----C-----	-----	-----
<i>C. armatus</i>	-----	---C-----CG---	---C-----	---A---A-----
<i>C. yaquinae</i>	-----	-----CG---	---C-----	---A---A-----
<i>A. macrochir</i>	-----G-----	---C---T---G---	---C-----	---A---A-----
<i>C. gilberti</i>	-----G-A---G---	---C---T---G---	---C-----	---A---A-----
				829
<i>C. acrolepis</i>	CAGAGTGCCCTATTGAAGAT	GGCCCTAAT		
<i>C. cinereus</i>	-----C-----	-----		
<i>C. longifili</i>	-----C-----	-----		
<i>C. pectorali</i>	-----	-----		
<i>C. nasutus</i>	-----	-----		
<i>C. armatus</i>	-----	-----		
<i>C. yaquinae</i>	-----C-----	-----		
<i>A. macrochir</i>	T---A---T-GC-----	-----		
<i>C. gilberti</i>	T-----T-GC-----	-----		

Fig.1-8. *continued*

				80
<i>C. acrolepis</i>	GTCTATATTTTAATCTCTCC	CGGCTTCGGGAATAATCTCCC	ACATTGTAGCTTACTACTCA	GGCAAAAAGAACCATTCCG
<i>C. cinereus</i>	-----	-----	-----	-----
<i>C. longifili</i>	-----	-----	-----T-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	-----C-G--T-A--	-----T-----	-----	-----T--
<i>C. armatus</i>	-----C-T--A--	-----	-----C-G-C-----	-----
<i>C. yaquinae</i>	-----C-C--A--	-----	-----C-G-----	-----
<i>A. macrochir</i>	--G-----T-G--	T-----T-T-----A--	-----C-----	--A-----G--G-----
<i>C. gilberti</i>	--G-----G-CT-G--	T-----T-----G--	-----C-----T-----	--G--G-----G-----T--
				160
<i>C. acrolepis</i>	ACACATAGGAATAGTCTGAG	CCATGATGGCCATCGGACTT	CTAGGCTTTATTGTATGAGC	ACACCACATATTTACTGTAG
<i>C. cinereus</i>	-----G--T-----	-----	-----	-----T-----
<i>C. longifili</i>	-----	-----	-----G-----	-----C-----
<i>C. pectorali</i>	-----	-----	-----G-----	-----
<i>C. nasutus</i>	---T-----	---A--A---T-----	T-G-----G-G--	-----C-C---
<i>C. armatus</i>	---T--G--G--G--T---	T-----A-----C---	-----G-G--G--	G-----G--
<i>C. yaquinae</i>	---T--G--G--G--T---	T-----A-----C---	-----G-----	G-----G-----
<i>A. macrochir</i>	-----C-----	T--A--A--T--T--T--	-----C-----	-----T-----C---
<i>C. gilberti</i>	G-----G--C---T---	T--A--A--T--T--T--C	-----C-----	--T-----C--T--
				240
<i>C. acrolepis</i>	GAATGGATGTTGACACACGA	GCCTACTTCACATCTGCAAC	TATAATCATCGCCATCCCA	CAGGCGTTAAAGTATTTAGC
<i>C. cinereus</i>	-----	-----	-----T-----	-----T-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	-----	-----	-----	-----
<i>C. nasutus</i>	-G--A-----G-----	-----T--G---G--	-----	-----T-----
<i>C. armatus</i>	-G--A-----	-----T--T--C--C---	G---T-----	-C--T-----G---
<i>C. yaquinae</i>	-G--A-----	-----T--T--C--C---	A---T--T-----	-C--T-----G---
<i>A. macrochir</i>	-C--A---C---T---	-----C-----	-----T-----C---	-----A--A-----
<i>C. gilberti</i>	-T--A-----C---	T-----T-----C---	-----T--T-----C---	-----A-----T--
				320
<i>C. acrolepis</i>	TGACTAGCAACCCCTTCATGG	AGGCTCAATTAAATGAGACA	CCCCCCTTCTATGAGCCCTC	TGGATTTATTTTCCTCTTCA
<i>C. cinereus</i>	-----	-----	-----G-----	-----
<i>C. longifili</i>	-----	-----	-----	-----
<i>C. pectorali</i>	---T-----	-----	-----	-----
<i>C. nasutus</i>	---T-----C---	-----	T-----G-----	-----
<i>C. armatus</i>	---T--G---G---	G-----C---G---	---T--T--G--G--T---	-----C-----
<i>C. yaquinae</i>	---T--G---A---	G-----C---G---	---T--T--G--G--T---	-----C-----
<i>A. macrochir</i>	-----C-----C---	---A-----G--G---	-A--A---G-----T	-T-----G--T--
<i>C. gilberti</i>	-----C-C---	---A-----G-----	-A-----G-----T	-T-----C---A--T--
				400
<i>C. acrolepis</i>	CAGTTGGAGGCCTAACAGGG	GTAGTACTAGCCAATTCATC	CCTAGACATCGTCCTTCATG	ACACTTACTATGTAGTCGCC
<i>C. cinereus</i>	-----	-----T-----	-----T--T-----	-----C---T---
<i>C. longifili</i>	-----G-----	-----	-----C-----	-----
<i>C. pectorali</i>	-----	---A-----	-----	-----
<i>C. nasutus</i>	---C--G-----T---	-----C-----	T-----	T--C---C---T--T--
<i>C. armatus</i>	---G-----G---	---T-----C---T	T-----T--A-----	---C---T--T--
<i>C. yaquinae</i>	---G-----G---	G--T-----C---T	T-----T--T-----	---C---T--T--
<i>A. macrochir</i>	---A---T--T---C---	T--T-----C-----	-----T--T-----	---C---C---T--T--
<i>C. gilberti</i>	---A--G---T---T---	C-----C-----	-----T--A-----	---C---C---T--T--
				444
<i>C. acrolepis</i>	ATTTCCTACTATGTTTATCT	ATGGGTGCCGTATTGCCAT	TATA	
<i>C. cinereus</i>	-----G-----	---A-----	---	
<i>C. longifili</i>	-----C-----	-----	---	
<i>C. pectorali</i>	-----G-----	-----	---	
<i>C. nasutus</i>	-----T-----	---A--C--A-----	---	
<i>C. armatus</i>	-C-----CC---C---	---C--A-----	C--G	
<i>C. yaquinae</i>	-C-----CC---C---	---A--C--A-----	C--G	
<i>A. macrochir</i>	-C-----C-----	---A--A--A-----	---	
<i>C. gilberti</i>	-----T-----C-----	---C--A-----T---	---	

Fig.1- 9. Comparison of partial nucleotide sequences of the COI gene of *Coryphaenoides* species. A dash indicates an identical nucleotide with that of *C. acrolepis*. The sequences correspond to positions 6167-6611 of the Atlantic cod homolog (Steinar and Ingrid, 1996). The sequences of *Coryphaenoides* species are available from the DDBJ/EMBL/GenBank nucleotide databases with accession numbers AB018233-AB018241.

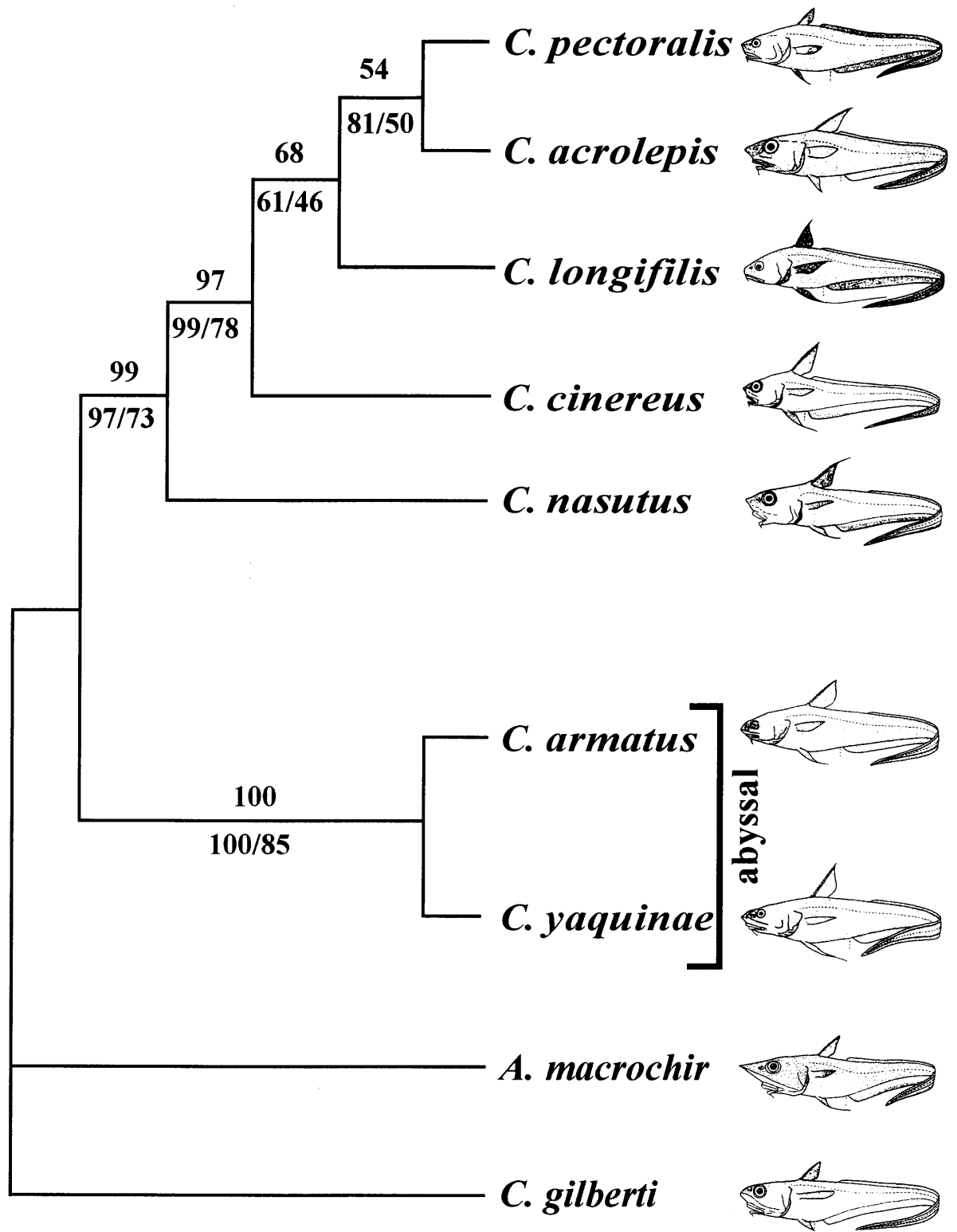


Fig.1-10. Phylogenetic tree constructed by the maximum parsimony method based on the 12S rRNA gene of *Coryphaenoides* species. Numbers denote the bootstrap percentages out of 1000 replicates, above branches for MP, left below branches for NJ and right for ML. *A. macrochir* and *C. gilberti* are used as the outgroup. Fish appearances were cited from Nakabo (2000).

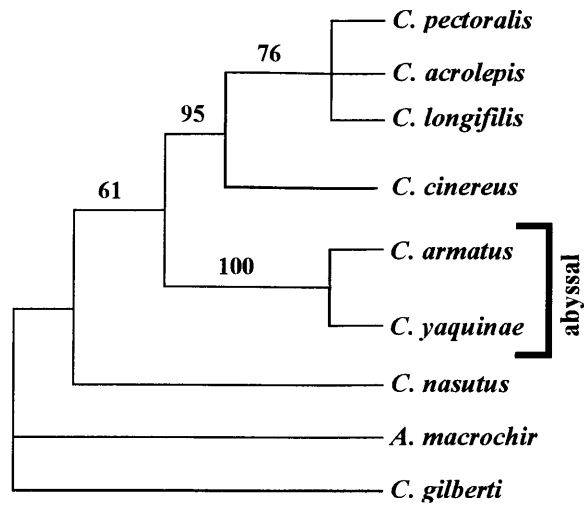
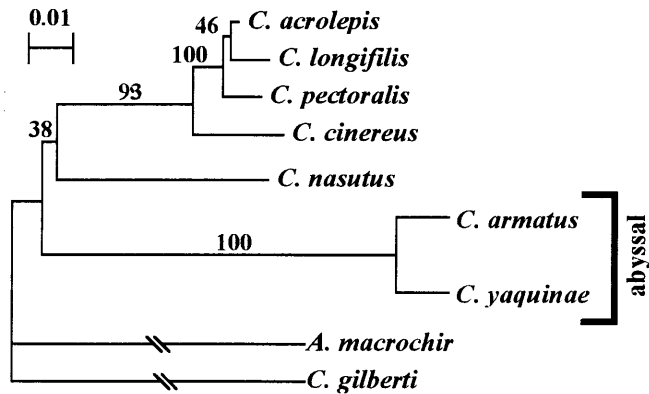
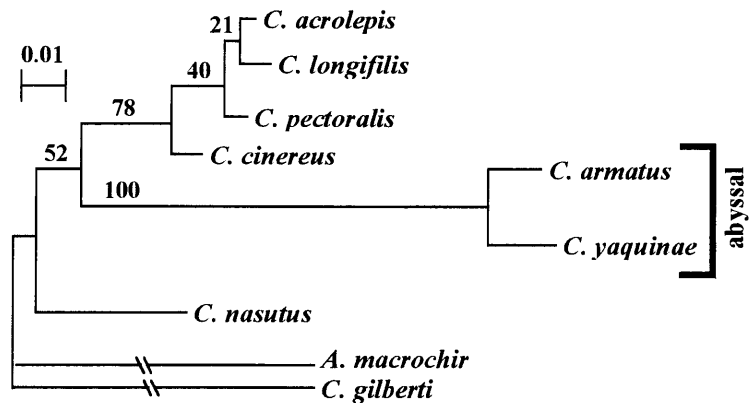
A**B****C**

Fig.1-11. Phylogenetic trees constructed by maximum parsimony method (A), neighbor joining method (B) and maximum likelihood method (C) based on the COI gene sequences of *Coryphaenoides* species. Numbers on internal branches denotes the bootstrap percentage out of 1000 replicates. Scales indicate the evolutionary distances of the base substitution per site, estimated by the Kimura's two-parameter method. *A. macrochir* and *C. gilberti* are used as the outgroup.

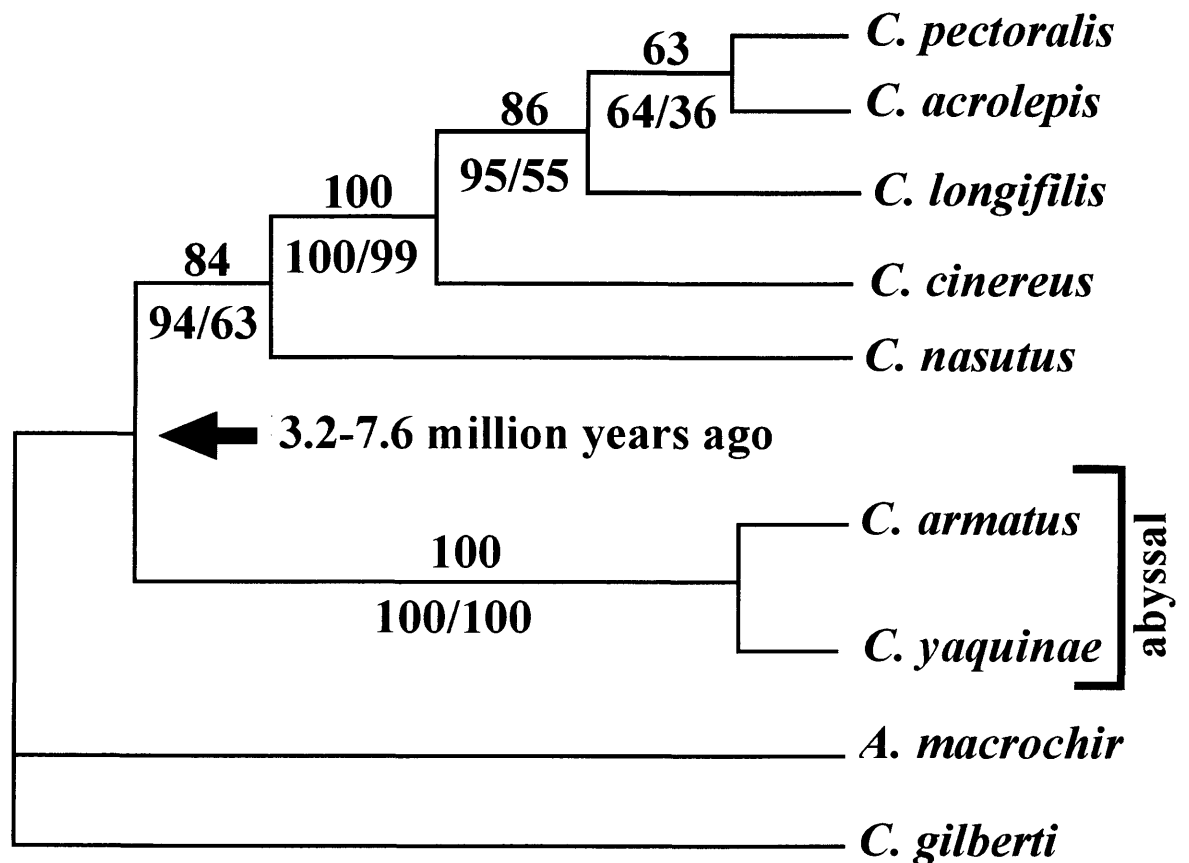


Fig.1-12. Phylogenetic tree constructed by the maximum parsimony method by combination data of the 12S rRNA and the COI genes of *Coryphaenoides* species. Numbers denote the bootstrap percentage out of 1000 replicates, above branches for MP, left below branches for NJ and right for ML. *A. macrochir* and *C. gilberti* are used as the outgroup. An arrow indicates the point of the radiation between abyssal and non-abyssal *Coryphaenoides* species, which was estimated to have occurred approximately 3.2-7.6 million years ago (see text).