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Pigment-dispersing activities and cortisol-releasing activities of melanocortins and their receptors in xanthophores and head kidneys of the goldfish *Carassius auratus*

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ABSTRACT

The five subtypes of melanocortin receptors (MCRs) mediate the functions of α-melanocyte-stimulating hormone (α-MSH) and adrenocorticotropic hormone (ACTH). In fish, these hormones are involved in pigment dispersion and cortisol release, respectively. α-MSH-related peptides exhibit ACTH-like activity in certain fishes. We recently found that multiple *Mcr* transcripts are expressed in some cell types in the barfin flounder, which is related to regulation of α-MSH activities. Similar results were also observed for the cortisol-releasing activity of α-MSH-related peptides in the head kidney. The present study was undertaken to assess relationship between the expression of multiply expressed *Mcrs* and α-MSH activities using goldfish. We also determined if α-MSH-related peptides exhibit ACTH-like activity in goldfish. The transcripts of *Mc1r*, but not those of other subtypes, were observed in xanthophores. α-MSH, which has an acetyl group at the N-terminus, was found to disperse pigment in a dose-dependent manner in xanthophores. This potency was found to be slightly greater than that of desacetyl-α-MSH. These results support our findings that MCR has a higher affinity for α-MSH when single *Mcr* subtype is expressed. On the other hand, transcripts of *Mc2r*, but not those of other subtypes, were observed in the head kidney. $ACTH_{1-24}$-stimulated cortisol release was observed in a dose-dependent manner, while α-MSH-related peptides showed no activity. It therefore appears that MC2R also acts as an ACTH-specific receptor in goldfish and that association of α-MSH-related peptides upon release of cortisol is uncommon in fishes.

1. Introduction

α-Melanocyte-stimulating hormone (α-MSH) and adrenocorticotropic hormone (ACTH) are peptide hormones liberated from a common precursor known as proopiomelanocortin (POMC) [54–56]. While POMC is biosynthesized in both the pars distalis (PD) and the neurointermediate lobe (NIL) of the pituitary in teleost fish, ACTH is mainly produced in the PD, and α-MSH in the NIL in a manner that depends upon tissue-specific proteolytic cleavage [6,21,35,39,51]. While ACTH is generally composed of 39 amino acid residues, α-MSH is identical to *N*-acetyl-$ACTH_{1-13}$-amide. ACTH, α-MSH, and their related peptides are collectively classified as melanocortins (MCs) on the basis of the presence of the common amino acid sequence—His-Phe-Arg-Trp [12].

MC receptors (MCRs) are members of the G protein-coupled receptor (GPCR) family. The members of this family have seven transmembrane domains [16,33,34]. MC system consisting of POMC and MCRs in fish have been shown to be similar to that of mammals. For example, the ACTH signal is mainly mediated by the MC2 receptor (MC2R), which is one of the five subtypes of MCRs [23,48]. While MC2R selectively binds ACTH, ACTH can bind to other MCRs in addition to MC2R [1,23,48]. Although α-MSH does not bind to MC2R, the signal of α-MSH, is mediated by other MCRs. The representative biological activities of ACTH and α-MSH (including cortisol release from interrenal cells [3,57,60] and pigment dispersion [12,14,15], respectively) are related to tissue-specific expression of different MCR subtypes [33]. However, the studies on the biological activities of the MC system using barfin flounder, *Verasper moseri*, a teleost, have shown interesting relationships between different molecular forms of α-MSH-related peptides and MCRs [25–27,56].

The barfin flounder is a large commercially important flatfish that inhabits the Pacific coast of northern Japan. We demonstrated the existence of pigment-dispersing activities of α-MSH-related peptides in skin parts [26]. Interestingly, while α-MSH modified with a monoacetyl group at N-terminus was found to mediate

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dispersion of pigments in xanthophores, this peptide exhibited negligible pigment-dispersing activities in melanophores. On the contrary, desacetyl (Des-Ac)-α-MSH, which lacks the acetyl group, has pigment-dispersing activities in both xanthophores and melanophores, while the activities in xanthophores were found to be lower than the activities caused by α-MSH. Subsequently, we identified expression of only *Mc5r* in xanthophores and concomitant expression of *Mc1r* and *Mc5r* in melanophores [27]. Similar relationships between the degree of acetylation and biological activities were also observed for *in vitro* cortisol-releasing activities in the barfin flounder. While Des-Ac-α-MSH–stimulated cortisol release from interrenal cells was observed, α-MSH showed negligible effects. Moreover, both *Mc2r* and *Mc5r* were expressed in the interrenal cells [25].

There is a growing body of evidence indicating that many GPCRs form heterodimers that may affect ligand affinity [2,5,13, 28,32,36,38,43,47]. Therefore, the concomitant expression of the different *Mcr* subtypes in melanophores and interrenal cells led to the assumption that a heterodimer consisting of MC1R and MC5R in melanophores, or MC2R and MC5R in interrenal cells, may have low binding affinity for α-MSH [25,27]. This assumption conversely suggests that expression of only one *Mcr* subtype may lead to enhancement of biological activity of α-MSH relative to that of Des-Ac-α-MSH. In fact, acetylation enhances the activities of α-MSH-related peptides via MCRs expressed in human embryonic kidney-293 cells [44–46]. The present studies were undertaken to examine these possibilities using pigment cells and head kidney tissues from goldfish, *Carassius auratus*. We also determined if the cortisol-releasing activities of α-MSH-related peptides are common to goldfish by determining whether other *Mcrs*, in addition to *Mc2r*, are expressed in goldfish head kidney.

2. Materials and methods

2.1. Fish

Immature goldfish, *C. auratus*, were obtained from a commercial dealer in Shizuoka, Japan, and all experiments were conducted according to the Guidelines for the Care and Use of Animals of Kitasato University. The fish were reared in indoor tanks with circulating freshwater under a natural photoperiod. The average body sizes of the fish used for molecular cloning and gene expression tests and pigment-dispersing activities were 4.9 cm, standard length (SL), and 3.9 g body weight (BW). For these experiments, tissue samples were collected from fish anesthetized with 0.2% 2-phenoxyethanol, and subsequently frozen in dry ice/ethanol bath. Skin samples used for measurements of pigment-dispersing activities and for cell dispersion were collected from fish (4.9 cm SL, 4.1 g BW on average) anesthetized with ice-cold water. Head kidneys used in experiments for cortisol-releasing activities were collected from fish (13.5 cm SL, 87 g BW on average) anesthetized with 0.2% 2-phenoxyethanol.

2.2. Peptides

α-MSH was purchased from the Peptide Institute (Osaka, Japan). Diacetyl (Di-Ac)-α-MSH was purchased from Sigma Chemical (St. Louis, MO, USA). Des-Ac-α-MSH and $ACTH_{1-24}$ were synthesized and purified according to the previously described methods [53]. The amino acid sequence of $ACTH_{1-24}$, which is identical to that of barfin flounder ACTH-A, salmon ACTH-A, and tuna ACTH [52], differs by one residue with respect to the sequence of goldfish ACTH at position 20 (Ile in goldfish *vs* Val in others) [11].

2.3. Molecular cloning

2.3.1. Nucleic acid preparation for sequence determination

Total RNA was extracted from brain and head kidney using Isogen (Nippon Gene, Tokyo, Japan). First-strand cDNAs were synthesized from total brain RNA for amplification of *Mc1r* and *Mc3r*, cDNA, and from head kidney RNA for *Mc2r* cDNA with the SMART RACE cDNA Amplification Kit (BD Biosciences, Palo Alto, CA, USA). Custom oligonucleotides were synthesized at Nihon Gene Research Labs, Inc. (Sendai, Japan).

2.3.2. Amplification of DNA fragments for sequence determination

Polymerase chain reaction (PCR) using a thermal cycler (MJ Mini, BIO-RAD, Hercules, CA, USA) under conventional conditions was performed to amplify the DNA fragments with HotStar Taq Master Mix (Qiagen, Hilden, Germany), or Takara LA Taq (Takara, Otsu, Japan). Amplification procedures were common for all three *Mcr* cDNAs. First, the middle segment of the cDNA of each *Mcr* was amplified from first-strand cDNA by PCR using HotStar Taq DNA polymerase with primers designed from fish *Mcr* nucleotide sequences. Then, the 3′ region of each *Mcr* cDNA was amplified from first-strand cDNA by 3′ rapid amplification of cDNA ends (3′RACE) using HotStar Taq DNA polymerase with a gene-specific primers and Universal Primer A Mix (UPM) provided in the SMART RACE cDNA Amplification Kit. The 5′ region of each *Mcr* cDNA was amplified from first-strand cDNA by 5′RACE using HotStar Taq DNA polymerase with UPM and gene-specific primers. Finally, each *Mcr* cDNA containing the full-length reading frame was amplified from first-strand cDNA by PCR using HotStar Taq DNA polymerase with gene-specific primers. Primer sequences are listed in Table 1.

2.3.3. Sequence determination and data processing

PCR-amplified DNA was purified by agarose gel electrophoresis (NuSieve GTG Agarose; Cambrex Bio Science, Rockland, ME, USA). DNA was extracted from the agarose gel using a QIAEX II Gel Extraction Kit (Qiagen), ligated into plasmid pT7 Blue T-Vector (Novagen, Madison, WI, USA) or pSTBlue-1 AccepTor Vector (Novagen) and transfected into JM109-competent cells. Recombinant plasmid DNA was prepared using the alkaline-SDS method and both strands were sequenced using a capillary DNA sequencer (3130-Avant Genetic Analyzer; Applied Biosystems, Foster City, CA, USA) using the BigDye Terminator Cycle Sequencing Ready Kit ver. 3.1. DNASIS-Pro (Hitachi Software Engineering, Yokohama, Japan) was used to process nucleotide and amino acid sequences, to calculate amino acid sequence identity, to align amino acid sequences, and to construct a phylogenetic tree by the neighbor-joining (NJ) method. Transmembrane domains were predicted using a program for the prediction of transmembrane helices in proteins "TMHMM Server v2.0" (http://www.cbs.dtu.dk/services/TMHMM-2.0/).

2.4. Reverse transcription (RT)-PCR for tissue distribution

Dorsal skin, caudal fin, and head kidney tissue were taken from three goldfish. A sample of RNA was prepared using Isogen (Nippon Gene). RNA was then treated with TURBO DNase (Ambion, Austin, TX, USA) for 4 h at 37 °C. RNA yield was estimated by spectrophotometry. For each tissue, an equal amount of total RNA (100 ng) from three individuals was combined and subjected to amplification using a One-Step RT-PCR kit (Qiagen) with primer sets shown in Table 2. *β-actin* cDNA was used as a positive control. PCR products were electrophoresed on 3% agarose gel (Agarose S, Nippon Gene) and visualized with 0.025% ethidium bromide. Photographs were taken using a Densitograph (Atto, Tokyo, Japan).

Table 1
Custom oligonucleotide primers used for PCR to amplify cDNA fragments of goldfish *Mc1r*, *2r*, and *3r*.

Primer	Target	Nucleotide sequence
MC1-fw1	MC1R	5′-ATG (TC)TA CTG A(CA)G GA(GC) CAT GG-3′
MC1-rv1	MC1R	5′-(GT)GC TGA A(AG)T AGC ACT TGC AG-3′
GSP-MC1-fw1	MC1R	5′-CGT CAC GTT TTT TGG CTT GA-3′
GSP-MC1-rv1	MC1R	5′-GGA AAC GAC GGA ACT GCA TA-3′
GSP-MC1-fw2	MC1R	5′-GTC AAA GGT GTG CTG AAG GA-3′
GSP-MC1-rv2	MC1R	5′-CAA CGC AGA TGC TCC TTA AG-3′
MC2-fw1	MC2R	5′-AC(TA) GAC TGC GCT GAG GTC CA-3′
MC2-rv1	MC2R	5′-CAC ATG CAG AGT AGA GAG TC-3
MC2-fw2	MC2R	5′-GTT GTT TAA AGA CGC CGG AC-3′
MC2-rv2	MC2R	5′-GAG TGA (AG)CG GTA GCA (TC)TC AC-3′
GSP-MC2-fw1	MC2R	5′TTG ATT GGG GTG TTT GTG GC-3′
GSP-MC2-rv1	MC2R	5′CTT GAT GTC GGC TAG GAT CA-3′
GSP-MC2-fw2	MC2R	5′CCA GAC TCA TGT CTC TGA GA-3′
GSP-MC2-rv2	MC2R	5′-GTG AAG CAT GTA TTG CTG GG-3′
MC3-fw1	MC3R	5′-TAT GTG ACG AGG TCC (AC)(AG)A T(CT)C A-3′
MC3-rv1	MC3R	5′-AG(AG) A(CT)C AGG TAT GTG (GT)TG AA(AG)-3′
GSP-MC3-fw1	MC3R	5′-CCA CCT CAT TCT GCT GGT GT-3′
GSP-MC3-rv1	MC3R	5′-CCA AGA TGA CGA GGA TGT TC-3′
GSP-MC3-fw2	MC3R	5′-CAG TCC ACC ATC TGA ATC AG-3′
GSP-MC3-rv2	MC3R	5′-ACC ACC ATG CTT TGG CAT CT-3′
UPM	MC1R, 2R,3R	5′-CTA ATA CGA CTC ACT ATA GGG CAA GCA GTG GTA TCA ACG CAG AGT -3′

Synthesis of primers was performed by Nihon Gene Research Lab. (Sendai, Japan).

Table 2
Custom oligonucleotide primers used for tissue distribution of goldfish *Mcrs*.

Primer	Target	Nucleotide sequence
MC1-TD-fw1	MC1R	5′-GCT TGT CAC GGC AAA GAT GT-3′
MC1-TD-rv1	MC1R	5′-TGG CTT GTC GGC GAC TCT TA-3′
MC2-TD-fw1	MC2R	5′-ACA CCT GAA CGG TCG TTT CG-3′
MC2-TD-rv1	MC2R	5′-CTC AAG CCA CTT TGT CTC TG-3′
MC3-TD-fw1	MC3R	5′-TGT CTG TTC TTC CCC ATC TC-3′
MC3-TD-rv1	MC3R	5′-GGC GAT TGT TTA GTA CAG CA-3′
MC4-TD-fw1	MC4R	5′-TGC CTC CGA AAC GGT AGT GA-3′
MC4-TD-rv1	MC4R	5′-GCT GAT AAG GCA GAT GAG AA-3′
MC5-TD-fw1	MC5R	5′-CTG TCA CTT TGG GCC ATC AG-3′
MC5-TD-rv1	MC5R	5′-TCT GAT GAA ATG GTC CTC CA-3′

Synthesis of primers was performed by Nihon Gene Research Lab. (Sendai, Japan).

2.5. Skin cell dispersion and RT-PCR

Skin cell dispersion was performed as described previously [26,27]. Small parts of caudal fin or dorsal skin were rinsed in Hanks' balanced salt solution (HBSS). The samples were allowed to stand for 20 min at room temperature in a dissociation medium [DM: 1 mg/mL collagenase type III (Worthington, Freehold, NJ, USA), 1×10^{-4} M epinephrine (Sigma–Aldrich, St. Louis, MO, USA), 2 mg/mL bovine serum albumin (Sigma–Aldrich), 0.1 mg/mL soybean trypsin inhibitor (Roche, Indianapolis, IN, USA), and 5 U/mL DNase I (Takara)] and then gently agitated for 10 min in the same solution. The DM was removed, and the samples were rinsed three times with HBSS. Finally, during the gentle agitation in fresh DM, dispersed single xanthophores and other nonchromatophoric dermal cells were isolated using glass capillaries under a microscope. cDNA from an isolated cell was synthesized using the Super-Script III CellsDirect cDNA Synthesis System (Invitrogen, Carlsbad, CA, USA), according to the manufacturer's instructions. The cDNA obtained from three cells was dissolved in 90 μL H_2O, and a 5-μL aliquot was analyzed using PCR to detect *Mcr* mRNAs. As a control, 2 μL was analyzed to detect *β-actin* mRNA. The primer sets for *Mcrs* and β-*actin* mRNA were the same as those used in Section 2.4. The PCR conditions programmed into the thermal cycler (MJ Mini; BIO-RAD) included reverse transcription at 50 °C for 50 min followed by amplification of the appropriate cDNA fragment with activation of the enzyme at 95 °C for 15 min followed by 40 cycles of (i) denaturation for 15 s at 94 °C, (ii) annealing for 30 s at 60 °C, and (iii) extension for 40 s at 72 °C. The PCR products were electrophoresed and visualized as described above. The series of experiments from cell dispersion to PCR was repeated three times.

2.6. Incubation of fish scales with MC peptides for measurements of pigment-dispersing activities

Scales removed from the dorsal skin were incubated in HBSS for 1 h at 20 °C. After changing HBSS, the scales were incubated under the same conditions. Subsequently, the scales were incubated in HBSS containing serially diluted MSH at final concentration of 1 nM to 1 μM for 1 h. Photographs were taken using a light microscope equipped with a digital still camera (PDMCII, Olympus, Japan), and subsequently ten randomly selected xanthophores from five skin parts were observed for each peptide concentration. The xanthophore index (XI) was calculated to evaluate the pigment-dispersing activity of each peptide by analogy with melanophore index [12]. An average XI obtained from 10 xanthophores represented XI of each skin part ($n = 5$).

2.7. Incubation of head kidney parts with MC peptides for measuring cortisol-releasing activities

L-15 medium was used for incubation. The washing and incubation temperature was 20 °C. Head kidney tissues dissected from several goldfish were diced to approximately 1 mm^3 and combined. A flask containing the diced tissue (1 g/100 mL) was incubated for 30 min with occasional shaking. This incubation for washing was repeated three times and the medium was exchanged at the end of each incubation period. Following the transfer of approximately 20 mg of the diced tissues to each well of a 48-well plate, the tissue was preincubated for 90 min in 0.5 mL medium. After changing the medium, the tissue was incubated for an additional 60 min in 0.5 mL medium containing MC peptides ($ACTH_{1-24}$, Des-Ac-α-MSH, α-MSH, or Di-Ac-α-MSH). Final concentrations ranged from 10 to 100 nM. Control experiments were carried out for the same time periods without including hormone in the medium. Each assay was performed in duplicate ($n = 5$). Preincubation and incubation media were used for the cortisol assay. Cortisol levels after incubation were expressed as percentage of the levels

present in the preincubation media. Cortisol was extracted from the medium as described previously [63]. The cortisol levels were measured using a time-resolved fluoroimmunoassay for cortisol [62].

2.8. Statistics

All data are expressed as the mean ± standard error values. The variances of the xanthophore index were tested by the Kruskal–Wallis test [50], a nonparametric test analog to one-way analysis of variance (ANOVA). When significant differences were detected, comparisons of treatments versus the control were performed with a post hoc multiple comparison test for the Kruskal–Wallis test. The amounts of cortisol in the head kidney were compared by one-way ANOVA. Significance was determined at 5% level.

3. Results

3.1. Nucleic acid sequence determination

Because *Mc4r* and *Mc5r* cDNAs have been cloned in goldfish [8,10], the nucleotide sequences of *Mc1r*, *Mc2r*, and *Mc3r* cDNAs were determined in the present study. Fig. 1 shows the assembly of cDNA fragments amplified by RT-PCR for each *Mcr* cDNA. Nucleotide sequences were determined using these fragments.

3.1.1. Nucleic acid sequence of goldfish Mc1r cDNA

The nucleotide sequence of a cDNA amplified from goldfish brain total RNA was found to encode a reading frame consisting of 321 amino acid residues (Fig. 2). Phylogenetic analysis revealed that the new sequence is localized in a clade of MC1R of various species in a phylogenetic tree for the five different MCRs (Fig. 3). This indicates that the new receptor sequence encodes MC1R of goldfish. The locations of the seven transmembrane domains were predicted as shown in Fig. 2. The DRY motif is present at a position homologous to that of MC1R of the other species [33]. There are three potential sites for *N*-linked glycosylation [4] and eight potential sites for phosphorylation by protein kinase C [61] (Fig. 2).

3.1.2. Nucleic acid sequence of goldfish Mc2r cDNA

The nucleotide sequence of a cDNA amplified from goldfish head kidney total RNA was found to encode a reading frame consisting of 302 amino acid residues (Fig. 2). Phylogenetic analysis revealed that the new sequence is grouped into a clade together

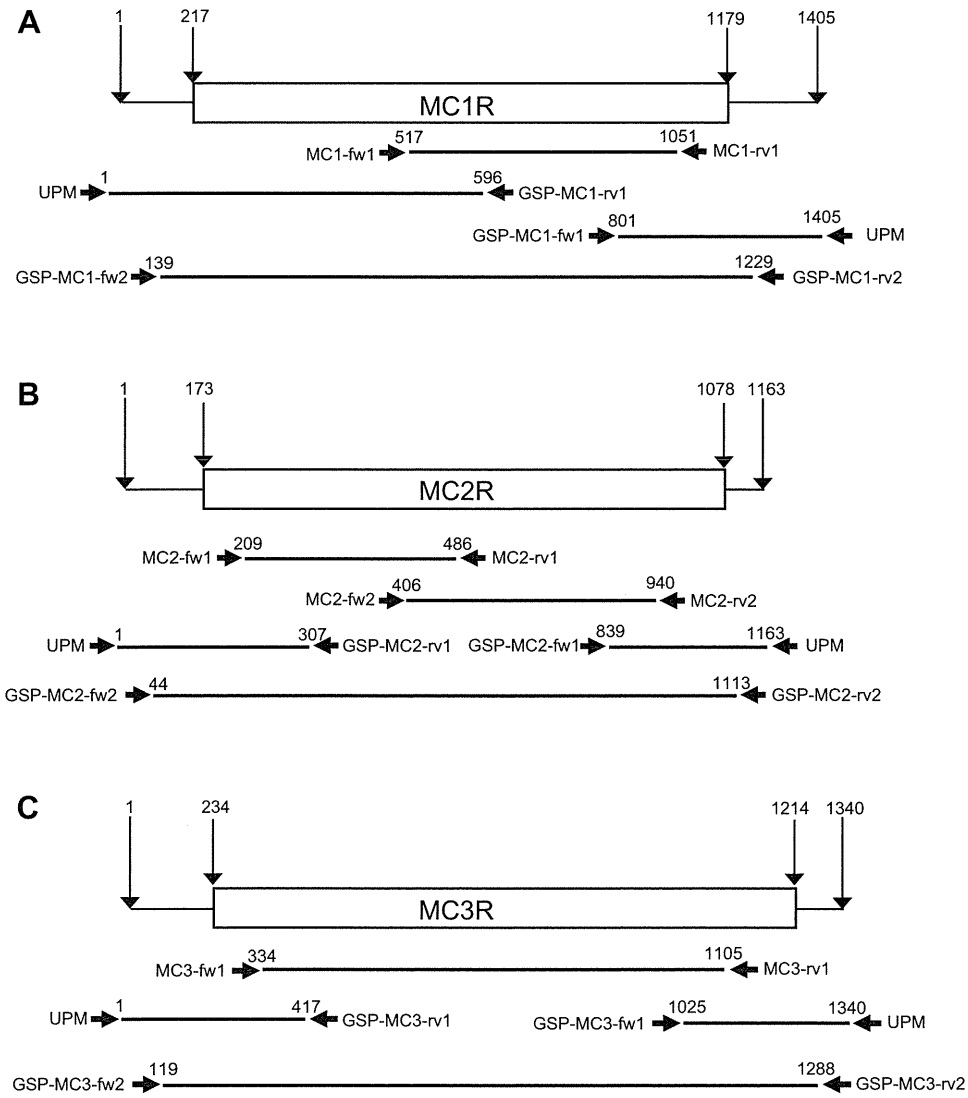

Fig. 1. Schematic representation of the relative positions of the DNA fragments of *Mc1r* (A), *Mc2r* (B), and *Mc3r* (C) in goldfish. DNA fragments were amplified from brain or head kidney cDNA. Boxes show reading frames. Horizontal arrow shows relative positions and direction of primers. The numbers show positions on each cDNA. For details regarding the nucleotide sequences, see Accession No. AB618067 for *Mc1r*, AB618068 for *Mc2r*, and AB618069 for *Mc3r*.

Fig. 2. Amino acid sequences of five subtypes of goldfish MCRs. Common amino acids with MC1R are shaded. Transmembrane domains (TM) were deduced for each MCR subtype. Italicized amino acids show potential *N*-glycosylation motifs. Lowercase letters show potential protein kinase C phosphorylation motifs. Numbers in parentheses show sequence identity with MC1R sequence. ###DRY motif.

with the remaining MC2Rs (Fig. 3). This indicates that the new receptor sequence encodes for the goldfish MC2R. The locations of the seven transmembrane domains are shown in Fig. 2. The DRY motif is present at a position homologous to that of MC2R of the other species. There is one potential site for *N*-linked glycosylation as well as three potential sites for phosphorylation by protein kinase C (Fig. 2).

3.1.3. Nucleic acid sequence of goldfish Mc3r cDNA

The nucleotide sequence of a cDNA amplified from total RNA of goldfish brain was found to encode a reading frame consisting of 327 amino acid residues (Fig. 2). Phylogenetic analysis revealed that the new sequence is related to the MC3Rs in other species (Fig. 3). This indicates that the new receptor sequence encodes a goldfish MC3R. The locations of the seven transmembrane domains were predicted as shown in Fig. 2. The DRY motif is present at a position homologous to that of MC3R of the other species. There are three potential sites for *N*-linked glycosylation and two potential sites for phosphorylation by protein kinase C (Fig. 2).

3.2. Expression of Mcrs in goldfish skin, fin and head kidney

Fig. 4 shows the detection by RT-PCR of all cloned goldfish *Mcrs* in the fin, skin and head kidney. The negative control for the expression of each *Mcr* and amplification of positive control *β-actin* are also shown. Expression of *Mc1r* was observed in skin and fin. Expression of *Mc2r* was observed in head kidney. When RT-PCR was performed for the all five goldfish *Mcrs* by using total RNA extracted from single cells of the fin and skin, a cDNA fragment of *Mc1r* was amplified from the total RNA derived from xanthophores (Fig. 5). None of the cDNA fragments of the five subtypes of *Mcr* were amplified from the total RNA derived from nonchromatophoric dermal cells. Because of the limitations of the kit used in this experiment, the absence of genomic DNA in the total RNA samples was indirectly evaluated using *β-actin* amplification. The *β-actin* fragment containing the intron was never amplified (Fig. 5).

3.3. Biological activities of α-MSH-related peptides

3.3.1. Pigment-dispersing activities

Fig. 6 shows the effects of α-MSH-related peptides on *in vitro* pigment dispersion in goldfish scales. Des-Ac-α-MSH was found to stimulate the dispersion of pigments in xanthophores in a dose-dependent manner (Fig. 6A). α-MSH and Di-Ac-α-MSH also showed similar effects on pigment dispersion (Fig. 6B and C). At a concentration of 1 nM, the effect of α-MSH was greater than that of Des-Ac-α-MSH. At a concentration of 100 nM, the effect of Di-Ac-α-MSH was greater than that of Des-Ac-α-MSH.

3.3.2. Cortisol-releasing activities

The effects of MC peptides on *in vitro* cortisol release from the head kidney of goldfish are shown in Fig. 7. $ACTH_{1-24}$ was found to stimulate cortisol release in a dose-dependent manner. However, Des-Ac-α-MSH, α-MSH, and Di-Ac-α-MSH were found to have negligible effects on cortisol release.

4. Discussion

4.1. Phylogenetic distribution of MCR and the MC system in goldfish

The presence of MCR has been demonstrated across a wide spectrum of vertebrate classes, including Cephalaspidomorphi (lampreys), Chondrichthyes (sharks), Sarcopterygii (lobe-finned fish including tetrapods), and Actinopterygii (ray-finned fish) [17,18,24,48]. While mammals and chickens possess five MCR subtypes (MC1R to MC5R), zebrafish is the only fish species in which the five subtypes were demonstrated with MC5R subdivided into MC5Ra and MC5Rb [30]. *Fugu* lacks *Mc3r*, while four *Mcr* subtypes have been identified by genomic studies [23,30]. In goldfish, the presence of *Mc4r* and *Mc5r* has been shown in our previous studies [8,10]. Therefore, the identification of *Mc1r*, *Mc2r*, and *Mc3r* cDNA provides a second line of evidence for the presence of five MCR subtypes in fish. The cypriniformes including goldfish and zebrafish are a rather primitive group of ray-finned fish when compared

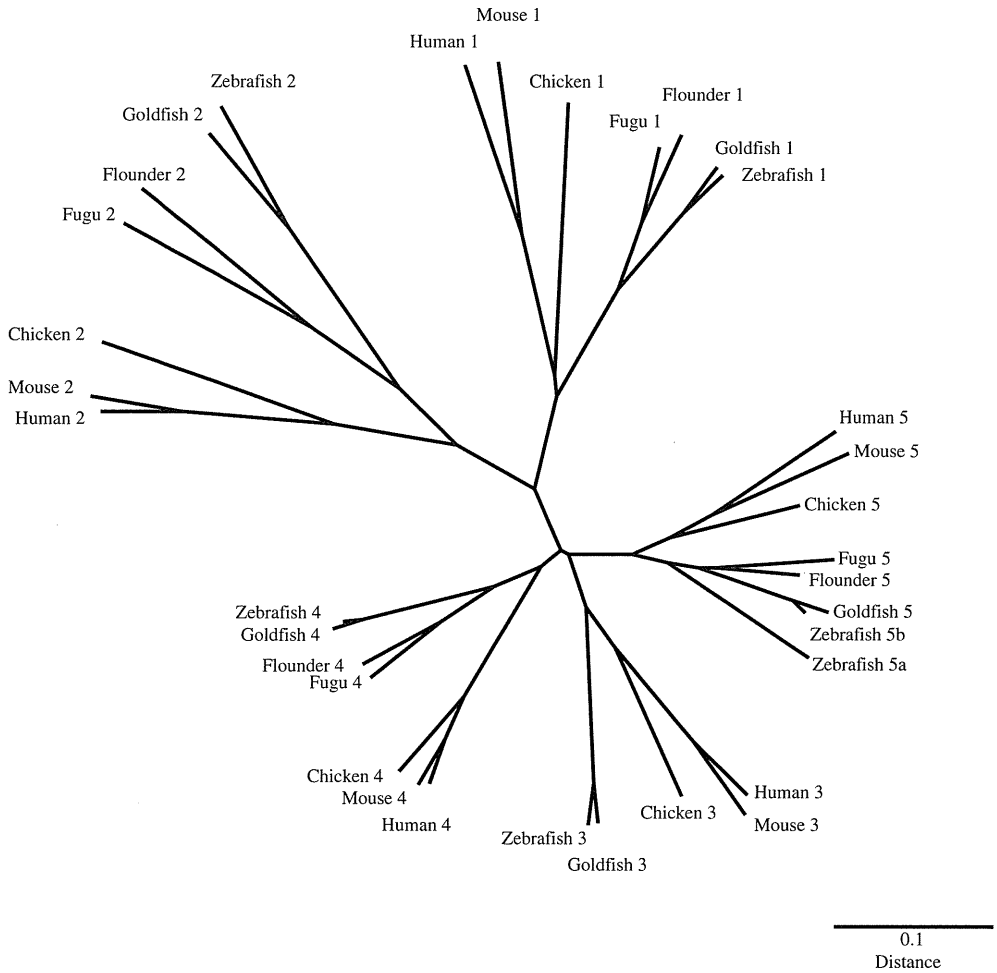

Fig. 3. Phylogenetic tree for MC receptors of fish, chickens, and mammals including 5 MCR subtypes of goldfish constructed by the NJ method. Accession Numbers of MC1R for *Fugu*: AAO65548, flounder: AB287974, goldfish: AB618067, zebrafish: NP_851301, chicken: P55167, mouse: BAD16661, and human: Q01726; MC2R for *Fugu*: AO65550, flounder: AB541411, goldfish: AB618068, zebrafish: NP_851302, chicken: BAA24002, mouse: NP_032586, and human: AAH69074; MC3R for goldfish: AB618069, zebrafish: NP_851303, chicken: BAA32555, mouse: NP_032587, and human: AAH69599; MC4R for *Fugu*: AAO65551, flounder: AB287975, goldfish: CAD58853, zebrafish: NP_775385, chicken: AAT73773, mouse: P56450, and human: AAH69172; MC5R for *Fugu*: AAO65553, flounder: AB540951, goldfish: CAE11349, zebrafish-a: NP_775386, zebrafish-b: NP_775387, chicken: BAA25640, mouse: P41149, and human: AAH69545.

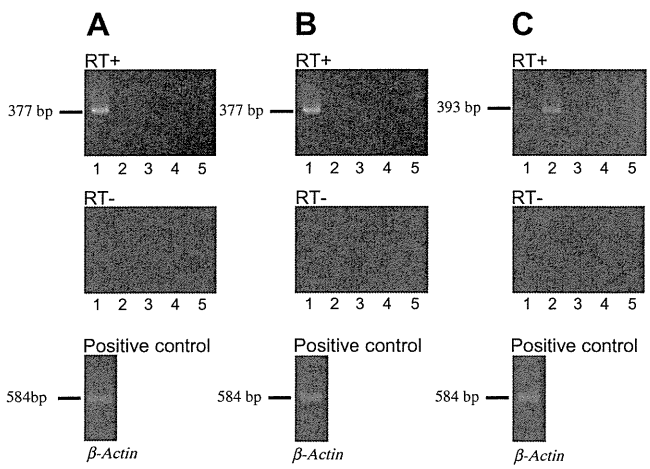

Fig. 4. Expression of *Mcrs* in caudal fin (A), dorsal skin (B), and head kidney (C). Total RNA samples prepared from these tissues were subjected to RT-PCR (RT+) using specific primers for *Mcrs* (see Table 2 for primer sequences). Numbers indicate *Mcr* subtypes. "RT−" indicates negative control (PCR for *Mcrs* in total RNA). "Positive control" shows amplification of *β-actin* fragment in each tissue.

to tetradontiformes [37]. It is therefore possible that the five subtypes of MCR may have appeared in a common ancestor of ray-finned fish and tetrapods. Subsequently, in the branch leading to derived group of ray-finned fish such as tetradontiformes, *Mc3r* may have been deleted during the course of evolution.

In goldfish, the primary structure of POMC has been reported previously [11]. MC peptides such as Des-Ac-α-MSH, α-MSH, Di-Ac-α-MSH, and some ACTH variants released from pituitary cells have been identified [58]. Moreover, primary structures of agouti-signaling protein and agouti-related protein as endogenous antagonists for α-MSH have been reported in goldfish [7,9]. Here, we demonstrated the presence of five MCR subtypes thus showing that the goldfish MC system possesses a molecular repertoire comparable to that of tetrapods.

4.2. Effects of α-MSH-related peptides on pigment dispersion

The pigment-dispersing activity of Des-Ac-α-MSH, α-MSH, and Di-Ac-α-MSH are almost equal in goldfish, but the activity of α-MSH is somewhat greater than that of Des-Ac-α-MSH. These results are similar to those observed in xanthophores of barfin flounder [26]. In both species, the xanthophores express only one

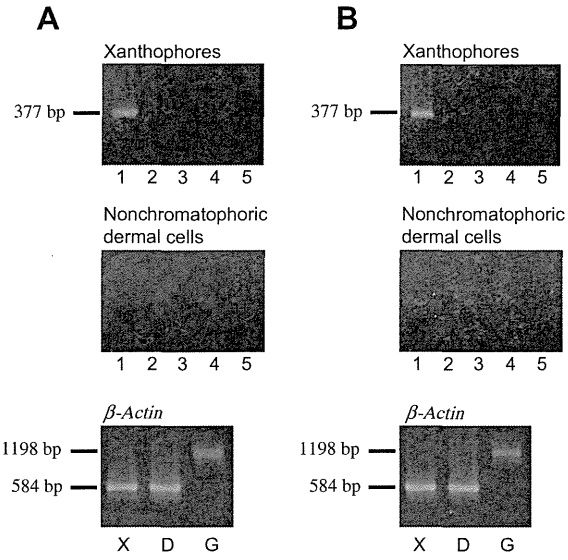

Fig. 5. Expression of *Mcrs* in cells isolated from the caudal fin (A) and dorsal skin (B). RT-PCR was performed using the total RNA extracted from xanthophores and nonchromatophoric dermal cells (see Table 2 for primer sequences). Numbers indicate *Mcr* subtypes. Total RNAs prepared from three single cells were combined. *β-Actin* was used as an internal control. Amplification of the *β-actin* fragment from xanthophores "X," and nonchromatophoric dermal cells "D" was not observed. Genomic DNA was use as a template in "G." The amplified DNA for *β-actin* contained one intron.

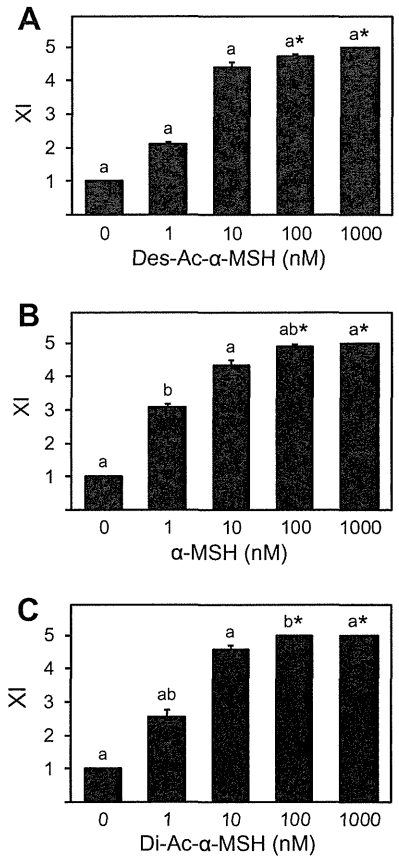

Fig. 6. Pigment-dispersing activity of synthetic Des-Ac-α-MSH, α-MSH, and Di-Ac-α-MSH on xanthophores. XI, xanthophore index analogous to the melanophore index. Asterisks show significant differences compared to the control value determined by a post hoc comparison test for the Kruskal–Wallis test at $P < 0.05$. Alphabetical letters indicate the differences in potency among the three peptides at one dose according to the results of the same test at $P < 0.05$ ($n = 5$). For example, the pigment-dispersing activity of 1 nM α-MSH was greater than that of 1 nM Des-Ac-α-MSH.

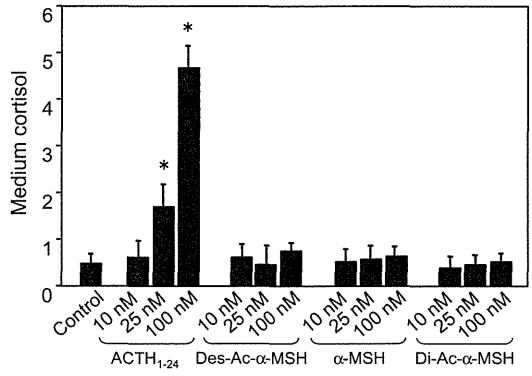

Fig. 7. Effects of MC peptides, including $ACTH_{1-24}$, Des-Ac-αMSH, α-MSH, and Di-Ac-α-MSH on *in vitro* cortisol release from the head kidney of goldfish. Head kidney tissue parts were preincubated for 1 h and then followed by incubation with each MC peptide for 1 h. The concentration of cortisol in the incubation medium was estimated relative to that of the preincubation medium. Asterisks show significant differences compared to the control value by ANOVA at $P < 0.05$ ($n = 5$).

Mcr subtype, i.e. *Mc1r* and *Mc5r* in goldfish and barfin flounder, respectively. On the other hand, the response of goldfish xanthophores to α-MSH is quite different from that of melanophores of barfin flounder in which α-MSH has negligible effects on melanin dispersion in a range from 1 nM to 1 μM. Goldfish xanthophores are also different from barfin flounder melanophores because two different subtypes of *Mcr*—*Mc1r* and *Mc5r*—are expressed in the flounder melanophores [27]. We recently observed that *Mc1r* and *Mc5r* are expressed in melanophores of Japanese flounder where α-MSH showed no effects on pigment dispersion, while Des-Ac-α-MSH is effective. Moreover, both α-MSH and Des-Ac-α-MSH are effective in xanthophores where only *Mc5r* is expressed (manuscript in preparation). Taken together, these results indicate that there is a good correlation between pigment-dispersing activities, the degree of acetylation, and the specific *Mcr* subtype(s) expressed in chromatophores. α-MSH-related peptides exhibit pigment-dispersing activities irrespective of the degree of acetylation when one type of *Mcr* is expressed and monoacetylation, which leads to generation of α-MSH, cancels the activities when two types of *Mcrs* are concomitantly expressed.

Monoacetylation of the N-terminus may contribute to an increase in pigment-dispersing activity of α-MSH-related peptides in goldfish because the activity of α-MSH was found to be slightly but significantly higher than Des-Ac-α-MSH when their effects at the concentration of 1 nM were compared. Pharmacological studies on sea bass MC1R have revealed that α-MSH is more effective than Des-Ac-α-MSH in stimulation of cellular activities [45]. Acetylation-mediated augmentation of the binding affinity of α-MSH-related peptides was also observed during pharmacological studies with human and mouse MC1R [33,49]. Taken together, these results suggest that α-MSH may have higher activity than Des-Ac-α-MSH as a result of increased affinity for an MCR when only one MC subtype (at least MC1R or MC5R) is present. Similar enhancing effects of pigment-dispersion caused by monoacetylation have also been observed in grass carp, tilapia, and frogs [12,22,59]. According to our data, it is reasonable to propose that only one *Mcr* subtype may be expressed in melanophores of these species.

The pigment-dispersing activity of α-MSH was found to be indistinguishable from that of Di-Ac-α-MSH in the goldfish xanthophores. In pharmacological studies of sea bass, α-MSH was found to have efficacy similar to that of Di-Ac-α-MSH for stimulation of cellular activities via MC1R [45]. Given that goldfish MC1R may

have similar properties to sea bass, it is likely that α-MSH and Di-Ac-α-MSH interact with goldfish MC1R with similar binding affinities.

4.3. Effects of ACTH and α-MSH-related peptides on cortisol-release

Recently, we reported on interesting relationships among molecular forms of α-MSH-related peptides with respect to N-terminal acetylation, cortisol-releasing activity, and *Mcr* subtypes expressed in interrenal cells of barfin flounder [25]. First, Di-Ac-α-MSH and Des-Ac-α-MSH were found to stimulate cortisol release, and the former showed greater activity than the latter, while the activity of α-MSH was negligible. Second, transcripts of *Mc2r* and *Mc5r* were detected in the interrenal cell. These relationships are similar to those observed for pigment-dispersing activities of α-MSH-related peptides in melanophores of this specie [26,27]. Hence, we assumed that a heterodimer consisting of MC2R and MC5R is associated with the differences in the activity of these peptides in the interrenal cells. The present study was undertaken to characterize the relationships between all the three players in the goldfish. The *Mc2r* was found to be the only *Mcr* expressed in head kidney containing interrenal cells and, supporting our hypothesis, the three α-MSH-related peptides were found to not have cortisol-releasing activities.

Among the five MCR subtypes, MC2R has been shown to be an ACTH-specific receptor because MC2R exclusively binds ACTH but not α-MSH-related peptides [1,23,48]. A classical study has shown that a central region of the ACTH molecule, which consists of basic amino acid residues, is important for binding to the receptor [19,40]. These properties have been confirmed using native and expressed ACTH-receptors (namely MC2R) [19,20,41]. In the present study, it was found that $ACTH_{1-24}$, which consists of an N-terminal region corresponding to α-MSH, a central basic region corresponding to $ACTH_{15-18}$, and a short C-terminal region corresponding to $ACTH_{19-24}$, exhibits dose-dependent cortisol releasing activity. These results confirm that ACTH is a major secretagogue of cortisol in goldfish and MC2R the main link of the pituitary-interrenal axis.

Because MC2R is a specific receptor for ACTH, the other MC peptides never interact with this receptor [23,33,48]. Therefore, the finding that there are no cDNAs for *Mcr* subtypes other than *Mc2r* cDNA is in agreement with the lack of cortisol-releasing activities of α-MSH-related peptides in goldfish head kidney tissues. Also in carp, ACTH stimulates cortisol release, but α-MSH does not [31]. The presence and absence of the MC2R and MC5R, respectively, have been shown for this species, while investigations of the other MCR subtypes have not been reported. Even though cypriniformes such as goldfish and carp generally have only the MC2R subtype in interrenal cells, two MCR subtypes may heterodimerize in tilapia, rainbow trout and barfin flounder because cortisol-releasing activities of α-MSH-related peptides have been observed in these species [25,29,42]. Interestingly, tilapia has some similarities to barfin flounder in relation to potency of cortisol-releasing activities and degrees of acetylation. Di-Ac-α-MSH has greater activity than Des-Ac-α-MSH, and α-MSH exhibits the lowest activity among the three α-MSH-related peptides. Similar results have also been observed in investigations of rainbow trout, while data are not available for Di-Ac-α-MSH.

5. Conclusions

We recently hypothesized that coexpression of different types of *Mcr* leads to the formation of heterodimers of MCRs, which decrease the pigment-dispersing activities of α-MSH. The activity of this peptide is enhanced only when one subtype of MCR is present [26,27]. In goldfish xanthophores, where only *Mc1r* was expressed, α-MSH displayed similar activity to that of Des-Ac-α-MSH and Di-Ac-α-MSH; moreover, the activity of α-MSH was greater than that of Des-Ac-α-MSH. These results support our assumption. On the other hand, $ACTH_{1-24}$, but not any α-MSH-related peptides, was found to stimulate cortisol release from goldfish head kidney where only the *Mc2r* subtype is expressed. These results indicate that MC2R is specific for ACTH and the link member in the pituitary–interrenal axis of the goldfish.

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シリーズ　新しい内分泌現象

メラトニンの新規作用：骨に対する作用とその誘導体を用いた骨疾患治療薬の開発

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1．はじめに

メラトニンは概日リズムを調節するホルモンであるが、骨に作用することが最近わかってきた。さらに筆者らのグループは、新規メラトニンの誘導体が骨芽細胞の活性を上昇させ、破骨細胞の活性を抑制することを魚のウロコを用いた*in vitro*評価系を用いて発見した。新規メラトニン誘導体の作用は、骨疾患モデル動物においても認められているので、骨疾患の治療薬として有望である。本稿では、メラトニンの骨に対する作用について述べ、次に新規メラトニン誘導体を用いた骨疾患の治療薬の開発について述べる。

2．メラトニンの生理作用

2-1．メラトニンの分布

メラトニンは、必須アミノ酸の1つであるトリプトファンからセロトニンを経て合成される分子量232のアミン(N-アセチル-5-メトキシトリプタミン：N-acetyl-5-methoxy-tryptamine)である。これまで一般的にメラトニンは、松果体に特異的なホルモンといわれてきた。しかし、近年、網膜や脳(大脳皮質、縫線核、線条体など)、脊髄、消化管(小腸、胃など)、精巣、卵巣、水晶体、蝸牛、皮膚、骨髄、リンパ球においても産生されることが明らかにされた[1)]。骨髄でメラトニンが産生することからも、メラトニンが骨に作用することを示唆しており、最近、メラトニンの骨代謝に対する作用を調べた研究が少しずつではあるが増えつつある。

2-2．松果体除去により引き起こされる脊柱変形

最初に骨形成に関する松果体の役割を指摘したのは、1959年のThillardの研究[2)]である。孵化直後のニワトリの松果体を除去すると、約6割から7割の個体に脊柱側彎変形が生じる。筆者の一人である服部が、実際にニワトリの松果体を除去すると、図1のように脊柱側彎変形を引き起こす。しかし、Thillardの報告ではメラトニンとの関係を直接証明したわけではなかった。さらにこの報告はフランス語で書かれていることもあり、その後、しばらく追試されることはなかった。

メラトニンの関与について調べた研究は、町田ら(1995年)[3)]により実施された。即ち、松果体を除去したニワトリに体重100 g当たり25 mgのメラトニンを隔日3週間腹腔内に投与すると、側彎発生率を20%にまで抑制できることが報告された。加藤と服部(1995年)[4)]も、松果体を除去したニワトリにメラトニン入りチューブを皮下に移植し、正常個体の夜間のメラトニンレベルに相当する濃度

図1　松果体除去ニワトリに多発する脊柱側彎変形

を維持するという方法を用いて、側彎発生率を約45%にまで抑制できることを見出した。さらに、椎骨や長管骨には、脳に存在するメラトニンレセプターと同様の生化学的特徴を持つレセプターが存在することを明らかにした[4]。しかし、その後の様々な研究にもかかわらず、現在でも、松果体を除去すると脊柱変形が生じるのかは不明のままである。メラトニンと骨代謝との研究のきっかけとなったが、メラトニンの間接的な影響である可能性や松果体にメラトニン以外の生理活性物質が存在していることも考えられ、不明な点が多い現象である。

2-3. メラトニンの骨芽細胞（*in vitro*）に対する作用

メラトニンの骨芽細胞に対する直接作用を最初に報告したのは、1999年のRothら[5]と中出ら[6]のグループである。前者は、マウスの骨芽前駆細胞株やラットの骨芽細胞様骨髄腫細胞株を用いて、骨芽細胞への分化が促進されることを示した。後者は、ヒトの骨芽細胞様細胞株を用いて、50 μMのメラトニンが約2倍の増殖を引き起こすことを報告している。しかしこれらの研究では、破骨細胞との共存培養ではなく、さらにメラトニンの濃度も高くないと効果がない。後述のウロコを用いて得られた結果の方が、破骨細胞との共存培養であり、マウスやラット等の哺乳類を用いた*in vivo*のデータに近い。

2-4. メラトニンの骨疾患モデル動物（*in vivo*）に対する作用

一般に骨粗鬆症は、原発性骨粗鬆症と続発性骨粗鬆症とに分けられる。前者の骨粗鬆症は、閉経に伴うエストロゲンの急激な分泌低下が主因となっており、高齢化に伴い社会的な問題になっている。骨は海綿骨と皮質骨より構成されているが、エストロゲンの低下により初期に海綿骨が、その後皮質骨も影響を受ける。閉経後骨粗鬆症の骨代謝は高回転型であり、骨密度減少の速度は急激であり、海綿骨の骨量減少は年間4〜8%にも及ぶ。この閉経後骨粗鬆症のモデルとして一般的に用いられるのが、人為的に卵巣を摘出したラットである。

卵巣を摘出した群では骨吸収マーカーの一つである尿中デオキシピリジノリン値が51%上昇するのに対して、メラトニン（25 μg/ml）を飲み水に溶解させて経口投与した群では、骨吸収が抑制され、卵巣摘出前と比べて変化しなかったという報告がある[7]。しかし彼らの実験では、骨組織（骨密度、骨量や骨面積）には、メラトニン投与群との間で大差は認められなかった。さらに、卵巣摘出ラットにエスラジオールを投与するとともに、メラトニンを追加投与することにより、各骨代謝マーカーの変化を調べた報告もある[8]。各マーカーに対する効果の現れ方には多少の違いはあったが、卵巣を摘出することにより上昇する骨吸収マーカーをエストラジオールは

抑制して、その効果をメラトニンがさらに補強するという報告である。

一方、正常な実験動物を用いた研究もある。即ち、4週齢の若いマウスを使った実験では、1ヶ月間かなり高濃度のメラトニン(5 mg あるいは50 mg/100 g体重)を与え続けると、骨密度が36%、骨量が49%上昇した。これらのメラトニン投与個体では骨形成パラメーターはほとんど変化しなかったが、骨吸収パラメーターは顕著に減少していた[9]。

したがって、*in vitro*の骨芽細胞の単独培養による結果とは矛盾して、*in vivo*においてメラトニンは、骨形成に作用するというよりも、骨吸収を抑制するように作用するという見解が有力である。

3．メラトニンの破骨細胞及び骨芽細胞に対する作用：キンギョのウロコを用いた*in vitro*評価系による解析

3-1．魚類のウロコの構造

硬骨魚のウロコは、石灰化した骨基質の上に骨芽細胞と破骨細胞が共存した構造をしており(図2)[10]、その基質は、I型コラーゲンからなる線維層とI型コラーゲンとハイドロキシアパタイトからなる骨質層の二層からなる。骨質層は骨芽細胞によって膜内骨化と同様の様式で形成される。また、ウロコに存在する破骨細胞は多くは単核であるが、多核で波状縁を持つものも観察され、そのような破骨細胞は哺乳類の破骨細胞と同様の微細構造をもち(図3)[11]、カテプシンKや酒石酸抵抗性酸フォスファターゼが発現している(図4)[12]。

3-2．魚類のウロコを用いた評価システムの開発と様々な物質に対する応答

筆者らはこのような特徴を持つウロコを培養し、生理学的活性を指標とした評価システムを開発した。ウロコの培養には炭酸ガスは不要であり、培地には血清不含のL-15(水生動物用の培地)に抗生物質を入れて用い、低温(15℃)で少なくとも1週間培養可能である。

このシステムを用いて、骨代謝に関与するホルモン等の作用を調べると、以下のことが判明した。カルシトニンが哺乳類と同様にウロコの破骨細胞の活性を抑制することを証明した[13]。カルシトニン(100 ng/ml)のウロコの破骨細胞に対する作用は、淡水産のキンギョでも海産魚のメジナでもみられ、淡水産のキンギョの方がその効果が強かった。さらにキンギョでは、雌雄共にカルシトニンの効果が認められたが、メジナでは雌のみしか効果がなかった。そこで入手・飼育も容易なキンギョを主な実験材料として用いて、これまで実験をしている。

副甲状腺ホルモン、エストロゲン、インスリン様成長因子I及び活性型ビタミンD_3の骨芽細胞に対する作用も解析済みであり、カルシトニン、副甲状腺ホルモン、エストロゲン及び活性型ビタミンD_3の受容体もウロコからクローニングしている[11, 14〜16]。

さらにウロコのシステムの感度は良く、極めて低濃度(10^{-13}M)のカドミウムにも応答

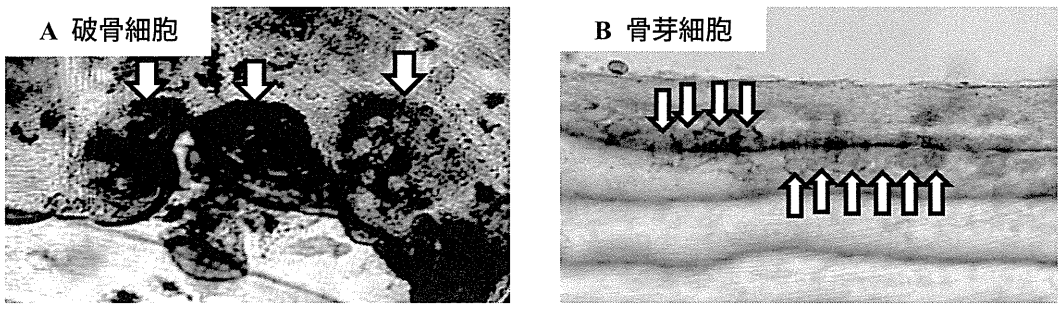

図2　キンギョのウロコに存在する破骨細胞(A)と骨芽細胞(B)(文献10より改変)
A：酒石酸抵抗性酸フォスファターゼの活性染色
B：アルカリフォスファターゼの活性染色
図中の矢印は、破骨細胞及び骨芽細胞を示す。

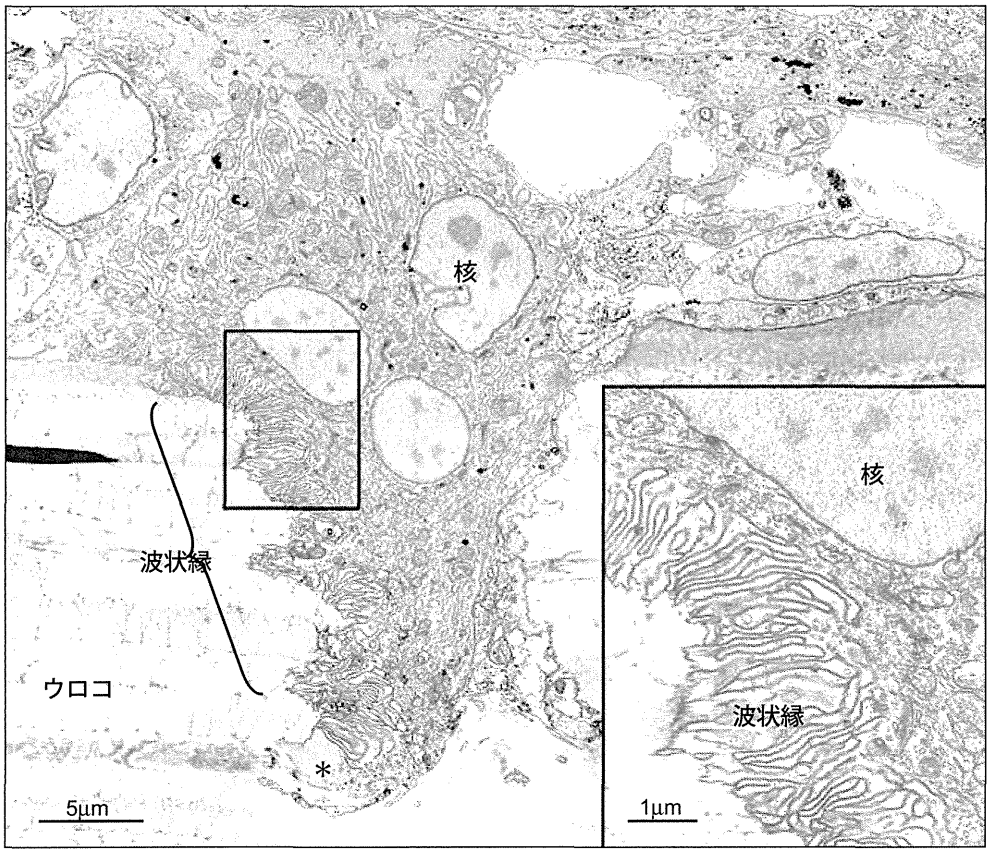

図3　副甲状腺ホルモン処理により活性化した破骨細胞の電子顕微鏡写真（文献11より改変）

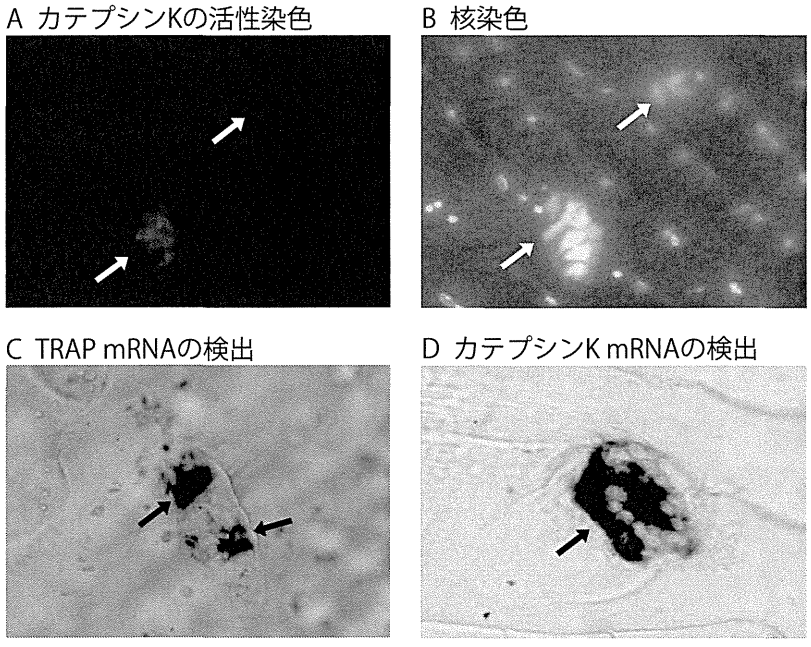

図4　キンギョのウロコに存在する破骨細胞（文献12より改変）

A：カテプシンKの活性染色
B：4',6-diamino-2-phenylindoleを用いた核染色
C：*in situ*ハイブリダイゼーション法による酒石酸抵抗性酸フォスファターゼ（TRAP）mRNAの検出
D：*in situ*ハイブリダイゼーション法によるカテプシンK mRNAの検出
図中の矢印は、破骨細胞を示す。

し[17]、内分泌攪乱化学物質であるトリブチルスズ[18]や重油に含まれる成分である多環芳香族炭化水素に対しても鋭敏に反応する[19]。

3-3. 破骨細胞及び骨芽細胞で特異的に発現しているマーカー遺伝子のクローニング

最近哺乳類において、骨芽細胞と破骨細胞の相互作用に関係する遺伝子が明らかにされた[20]。この遺伝子は骨芽細胞で特異的に発現しているReceptor Activator of NF-κB Ligand (RANKL) と破骨細胞で発現しているReceptor Activator of NF-κB (RANK) である。特に、破骨細胞を多核の活性型に誘導するには、骨芽細胞との連絡が必要であり、RANKLがリガンドとなり、破骨細胞のレセプターであるRANKと結合しなければ多核の活性型に誘導されない。これらの遺伝子は、哺乳類でしかクローニングされていなかったが、最近キンギョのウロコからcDNAの全長のクローニングに成功した。この遺伝子の発現を解析することで、骨芽細胞と破骨細胞とのクロストークを解析できる。そこで副甲状腺ホルモンの作用を解析した結果、骨芽細胞の活性は6時間培養で上昇し、培養18時間後に破骨細胞の活性が上昇するという結果が得られた[11]。その活性の変化の理由としてRANK 及びRANKLの関与を証明した。すなわち、RANK mRNAの発現が顕著に上昇し、破骨細胞の活性が上昇することを証明した[11]。

さらに前述の破骨細胞のマーカー(カテプシンKや酒石酸抵抗性酸フォスファターゼなど)に加えて、骨芽細胞で発現しているI型コラーゲン、オステオカルシン、アルカリフォスファターゼ、オステリックス、Runx 2 (runt-related transcription factor 2) も既にクローニング済みであり、これらについても解析可能である。したがって、ウロコの評価システムは骨のモデルとして遺伝子レベルからアプローチすることができる。

3-4. メラトニンの破骨細胞及び骨芽細胞に対する作用

ウロコの評価システムを用いて、メラトニンの破骨細胞と骨芽細胞に対する作用を解析した。その結果、メラトニンが、破骨細胞や骨芽細胞に対して抑制的に作用することを、脊椎動物を通して初めて明らかにした[21]。これらのメラトニンの作用は、骨芽細胞で発現しているインスリン様成長因子-I mRNAやエストロゲン受容体mRNAの発現を低下させることによって引き起こされていた。なお、ウロコにメラトニン受容体が発現していることも確認している[22]。

前述のように骨芽細胞の単独培養では、薬理的な量のメラトニンは骨芽細胞の増殖促進に作用するが、ラットを用いた*in vivo*の実験では、メラトニンを投与すると、血液中のALP活性が低下することが報告されており[8]、筆者らのウロコの評価系の方が*in vivo*の状態を再現していることを示している。

4. 骨疾患の治療薬としての新規メラトニン誘導体

4-1. 新規メラトニン誘導体のウロコの骨芽細胞及び破骨細胞に対する応答

メラトニンの骨に対する作用が明確になったので、新規メラトニン誘導体を合成して骨芽細胞及び破骨細胞に対する作用をメラトニンと比較した[23]。即ち、メラトニン、2-ブロモメラトニン、2,4,6-トリブロモメラトニン、1-アリル-2,4,6-トリブロモメラトニン、1-プロパルギル-2,4,6-トリブロモ-メラトニン、1-ベンジル-2,4,6-トリブロモメラトニン及び2,4,6,7-テトラブロモメラトニン(図5)を合成して、これら化合物の破骨細胞及び骨芽細胞に対する作用をキンギョのウロコを用いた培養系で評価した。培養時間は6時間で、濃度は10^{-8}、10^{-6}、10^{-4} Mでその作用を解析した。培養方法等の詳細は、鈴木と服部(2002)[21]の方法に従った。

次に最も効果があった化合物において、6時間及び18時間培養で、10^{-10}、10^{-9}、10^{-8}、

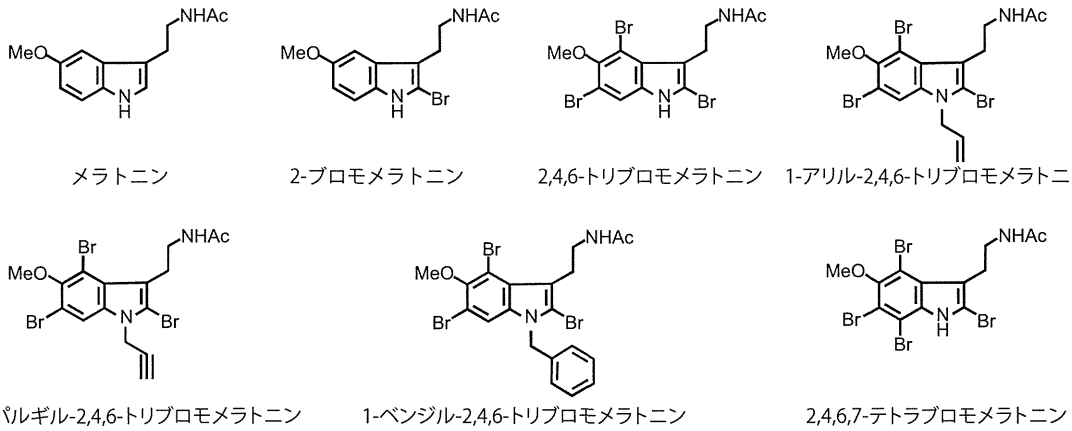

図5　メラトニンと新規メラトニン誘導体の構造式（文献10より改変）

10^{-7}及び10^{-6}Mにおいて、骨に対する作用をメラトニンと比較した。さらに、骨芽細胞で発現しているエストロゲン受容体mRNAの発現（6時間培養）に対する影響も解析した。

その結果、メラトニンは骨芽細胞の活性を低下させたが、Br原子を導入した全ての誘導体は、骨芽細胞の活性を上昇させることが判明した。一方、Br原子を3個導入した誘導体では破骨細胞の活性抑制作用は強く、メラトニンと同程度であった。しかしBr原子を1及び4個入れた誘導体では、メラトニンの方が破骨細胞の活性抑制作用は強かった。今回調べた化合物の中で、特に1-ベンジル-2,4,6-トリブロモメラトニンの骨芽細胞の活性を上昇させる作用は強く、この化合物を用いてさらに詳細に調べた。

結果を図6及び7に示す。1-ベンジル-2,4,6-トリブロモメラトニンはメラトニンと異なり、骨芽細胞の活性を上げ、その作用は18時間後でも持続しており、10^{-8} Mでも効果が認められた。また1-ベンジル-2,4,6-トリブロモメラトニンの破骨細胞の活性抑制作用は、メラトニンのそれよりも強く、6時間培養で10^{-10} Mでも効果が認められた。さらに骨芽細胞のマーカーであるエストロゲン受容体 mRNAの発現は、1-ベンジル-2,4,6-トリ

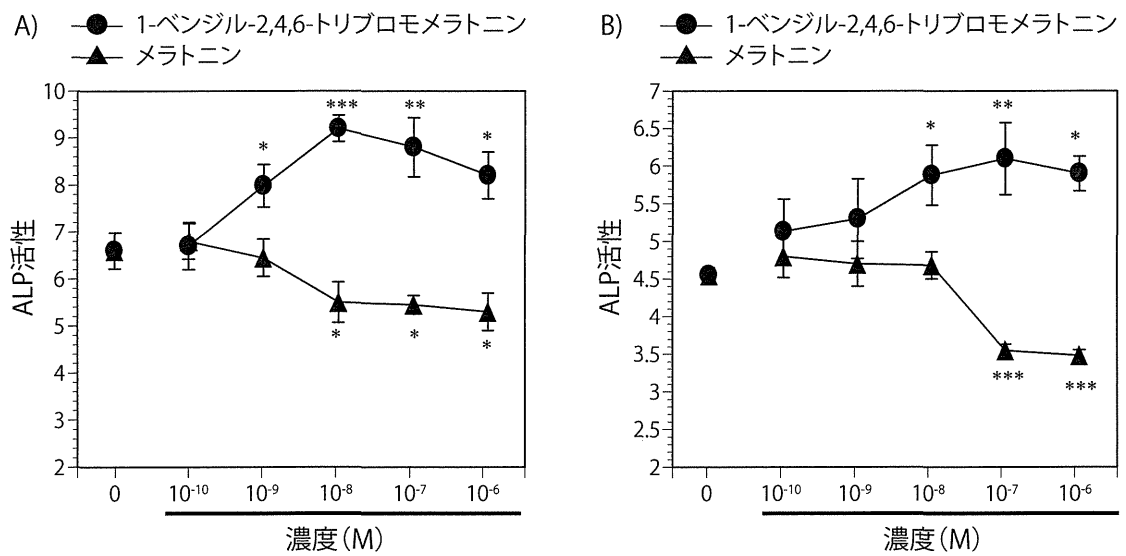

図6　新規メラトニン誘導体のキンギョのウロコの骨芽細胞に対する作用（文献23より改変）
A：6時間培養の結果　　B：18時間培養の結果
*：P＜0.05；**：P＜0.001；***：P＜0.001

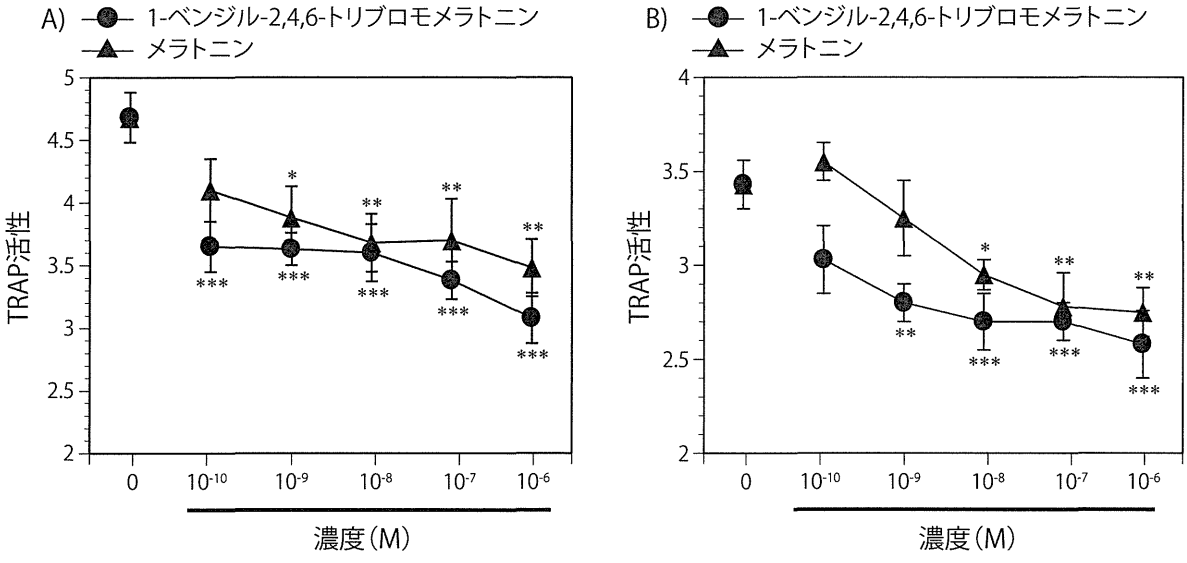

図7　新規メラトニン誘導体のキンギョのウロコの破骨細胞に対する作用（文献23より改変）
A：6時間培養の結果　　B：18時間培養の結果
*：P＜0.05；**：P＜0.001；***：P＜0.001

ブロモメラトニン処理で有意に上昇することも判明した。

4-2. 新規メラトニン誘導体の変異原性試験及び急性毒性試験

新規メラトニン誘導体を用いた骨疾患治療薬の開発の基礎として変異原性試験（エームス試験）と急性毒性試験を行った。

エームス試験は、大腸菌とサルモネラ菌を用いて、プレート（25 ml）当たり、新規メラトニン誘導体（1-ベンジル-2,4,6-トリブロモメラトニン）を8、40、200、1,000、3,000及び5,000 μg添加して、コロニー数をカウントした。その結果、化合物の添加量が変化してもコロニーの数は変化せず、ジメチルスルホキシドを添加したコントロールとほとんど同じコロニー数だった。したがって、この化合物の変異原性は認められなかった。

次にラットに新規メラトニン誘導体を2,000 mg/kgの割合で単回経口投与して、14日間観察して、急性毒性を調べた。その結果、ラットの行動及び食欲にも変化はみられず、死亡する個体もみられなかった。さらに、解剖して肝臓等の主要臓器を検査した結果、異常は認められなかった。

以上のことから、新規メラトニン誘導体には変異原性も急性毒性もみられないことが明らかになった。

4-3. 骨疾患モデル動物に対する作用

これまで骨粗鬆症の治療薬は骨吸収を抑制する薬剤（ビスフォスフォネイト）が主流であり、骨吸収を抑制してかつ骨形成を顕著に促進する薬剤は未だ開発されていない。そこで、卵巣摘出ラットを用いて新規メラトニン誘導体の実験を行った。その結果、卵巣摘出ラットの大腿骨の海綿骨の骨密度が上がり、骨強度が有意に上昇した（図8）。

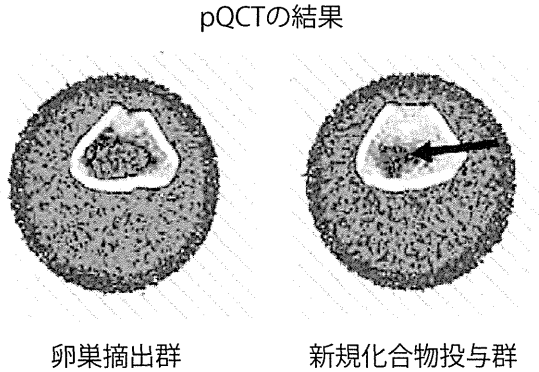

図8　新規メラトニン誘導体の卵巣摘出ラットに対する作用
矢印は、骨形成が促進された部分を示す。

さらにカルシウムの摂取量が少ない現代人の食生活から引き起こされる骨疾患モデル(低カルシウム食ラット)でも、大腿骨の海綿骨の骨密度が有意に上昇した[10]。メラトニンは、骨吸収を抑制したが、新規メラトニン誘導体は骨吸収抑制に加えて骨形成も促進している可能性がある。現在、大腿骨を外科的に切断したラット(骨折モデル動物)を用いて実験中であり、骨形成を促進する治療薬になる可能性を秘めている。

4-4. 新規メラトニン誘導体を用いた宇宙実験

骨のモデルとして魚類(キンギョ)のウロコを使用して「きぼう」の国際宇宙ステーションを用いた宇宙実験を2010年5月に実施した。本実験の目的は、①宇宙における骨量減少のしくみを探ること、②骨形成を促す物質(新規メラトニン誘導体)の効果を調べること、である。

前述のようにウロコには骨芽細胞と破骨細胞が共存していること(図2)に注目して、ウロコの培養システムを開発した。骨量維持には、骨の形成系(骨芽細胞)と骨の吸収系(破骨細胞)のバランスが保たれていなければならない。骨芽細胞は、重力の刺激をうけると活性化することが知られている。しかし宇宙空間では、重力の刺激がないため、骨量が減少する。そこで、①メカニズムを解明して、②骨量減少を抑制する薬剤の効果を調べた。

宇宙実験の概要[24]を図9に示す。筆者らが提案した宇宙実験は、野口総一宇宙飛行士により実施された。現時点での解析結果から新規メラトニン誘導体の効果は確認できており、前述の骨疾患モデル動物の結果と合わせて考えると、本物質は骨疾患治療薬として有望である。

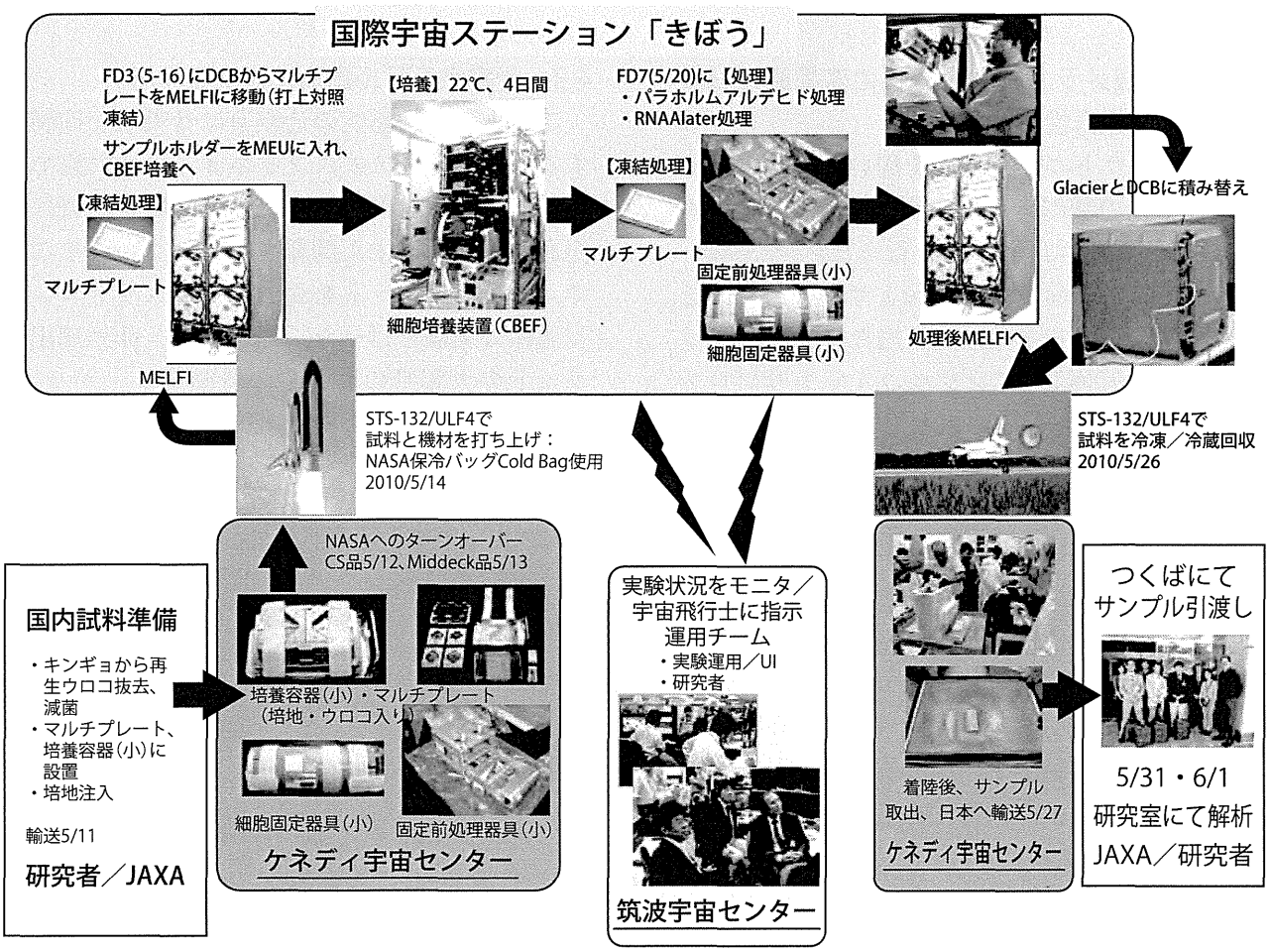

図9　宇宙実験の概要(文献24より改変)

5．おわりに

本稿では、メラトニン及びその誘導体の硬組織（骨とウロコ）に対する作用に注目した。しかしメラトニンは、植物にも含まれており、現時点では、植物においては、受容体を介した作用ではなく、ラジカル除去に作用している可能性が高い[1)]。メラトニン自身のラジカル消去作用にとどまらず、メラトニンから酵素的、酸化的に生成したN^1-acetyl-N^2-formyl-5-methoxykynuramine（N^1-アセチル-N^2-ホルミル-5-メトキシキヌラミン）などが、ラジカルを除去すると考えられている[25)]。メラトニンは元来、ヒトの体内で作られるホルモンなので、過剰摂取しても副作用がない。今後、骨に対する作用以外にも、ラジカル除去作用のあるメラトニンは、「抗加齢薬」として広まる時期が来る可能性がある。

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