A study of somatolactin actions by ectopic expression in transgenic zebrafish larvae

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Abstract

Somatolactin (SL) is a fish-specific hormone that belongs to the prolactin (PRL) and GH family. Recently, two forms of SL, SLα and SLβ, have been found in some species, and may have different actions and functions. To investigate the role of SL in fish growth and metabolism, we generated transgenic fish founders with ectopic expression of SLα and SLβ to study the physiological functions and actions of these SLs among several marker genes. We fused the cDNAs encoding the precursor SLs in frame to a zebrafish β-actin gene promoter to generate transgenic zebrafish lines that were co-injected with a green fluorescent protein (GFP) driven by the same promoter. The transgenic zebrafish were selected based on GFP expression and confirmed by genomic PCR, Southern blot analysis, and transgene expression. Investigations into the expression of marker genes in larvae on different pathways using real-time PCR have provided a general understanding of the actions of SLs. This study found that the overexpression of SLα and SLβ in vivo significantly enhanced the transcription of IGFs, insulin, leptin, sterol regulatory element binding protein 1, and fatty acid synthase, as well as the expression level of vitellogenin and proopiomelanocortin, while causing reduced levels of catalase and glutathione S-transferase in the larvae of transgenic zebrafish.

Journal of Molecular Endocrinology (2010) 45, 301–315

Introduction

Somatolactin (SL) is a recently discovered glycoprotein hormone in fish of GH/prolactin (PRL) superfamily, with significant structural homology in all fish taxa studied to date (Ono et al. 1990, Rand-Weaver et al. 1991, 1992, Chen et al. 1994). According to sequence comparisons, it is generally believed that SL and PRL evolved from a common ancestral gene related to GH with two successive rounds of gene duplication before the divergence between vertebrates and invertebrates (Chen et al. 1994, Fukamachi & Meyer 2007). However, the SL gene is not found in tetrapods and might have been lost during the evolution of early land vertebrates (Fukamachi & Meyer 2007). Fish SL is mainly expressed in the pars intermedia of the pituitary gland and distinct from proopiomelanocortin (POMC)-producing cells (Kaneko 1996); hence, it should have physiological actions different from those of GH and PRL. In addition, despite the conserved helical bundles, the number of disulfide bonds (6 or 7) is different from that found in GH and PRL (4), and the low sequence identity found between SL and GH (50–60%) also suggests that they have dissimilar functions in fish (Chen et al. 1994, Fukamachi & Meyer 2007).

Two isoforms of SL, SLα and SLβ, have been identified in zebrafish (Zhu et al. 2004) and grass carp (Jiang et al. 2008), and phylogenetic analyses suggest that they are paralogs that result from an ancient duplication of SL genes in ray-finned fish probably related to reproduction (Planas et al. 1992, Chen et al. 1994, Yang & Chen 2003). The tertiary structures of these two SLs may be different because there is an extra third cysteine in SLα, and they share only 60% sequence identity within the same species (Jiang et al. 2008). Therefore, it would be of interest to know whether the actions and functions of these two SLs differ. The main physiological function of the SL gene remains a matter of debate, but it is likely that SL is involved in multiple and even overlapping functions with other members of the GH/PRL family. Recent studies suggest that SLs are involved in steroidogenesis and reproductive maturation (Planas et al. 1992, Rand-Weaver et al. 1992, Olivereau & Rand-Weaver 1994, Johnson et al. 1997), acid–base balance (Kakizawa et al. 1996), background adaptation (Kakizawa et al. 1995, Zhu & Thomas 1995), immune function (Calduch-Giner et al. 1998), energy mobilization and stress (Rand-Weaver et al. 1993), lipid metabolism and pigmentation (Zhu & Thomas 1997, Fukamachi et al. 2004, 2005, 2009), and the regulation of chromatophores (Zhu & Thomas 1995, 1996, 1997). The recent discovery of an SL-deficient mutant in medaka (Oryzias latipes) (color interfere, ci) indicated that SL might function in the proliferation and morphogenesis of epidermal chromatophores, body color regulation, or cortisol secretion in vivo (Fukamachi et al. 2005, ...
The gene silencing of SLs in zebrafish (Danio rerio) by antisense morpholino oligonucleotides during embryonic development, however, only showed their different effects on the delay in swim bladder inflation (Zhu et al. 2007).

The presence of two distinct GH receptors (GHRs), GHR clade 1 and GHR clade 2, has been detected in several teleost species (Fukamachi et al. 2005, Jiao et al. 2006, Pierce et al. 2007, Benedet et al. 2008), and phylogenetic analyses of salmon GHRs suggest that GHR clade 1 is an SL receptor (SLR), whereas GHR clade 2 is the actual GHR (Benedet et al. 2008). A recent study showed that SL could act as a novel regulator of insulin-like growth factor (IGF) gene expression in fish (Wan et al. 2009), which suggests that SL may exert its effects indirectly by way of the GH/IGF axis. Whether the actions of the SL on the GHR or SLR remains to be investigated; however, SL and GH may have overlapping functions. Among mammals are a large number of paralogous genes (e.g. there are 26 PRL-related genes in rats and mice), and the non-classical actions of these ligands are mediated through neither the PRL nor the GHR (Ain et al. 2004, Green 2004). Therefore, it is believed that the functional study of SLs by knockdown assay in embryos has been impaired by the compensational effects of other genes because of redundant functions in the GH/PRL family. Nevertheless, the overexpression of SLs in vivo can reveal a gain of function that may be unrecognized by targeted mutational analysis because of functional redundancy.

To study the actions of two closely related SL genes by ectopic expression in transgenic zebrafish, we cloned cDNAs encoding the precursor SLs in frame to a zebrafish b-actin (bA) gene promoter that would overexpress SL genes ubiquitously to generate transgenic zebrafish lines coinjected with a green fluorescent protein (GFP) driven by the same promoter. Larvae of these transgenic fish founders were used for many experiments. The protocols for rearing and keeping zebrafish were adopted from Westerfield (1995). A local strain of zebrafish derived from India that is used for many experiments. The protocols for rearing and keeping zebrafish were adopted from Westerfield (1995).

DNA constructs

Genomic DNA samples were purified from whole zebrafish by grinding in liquid nitrogen and further digestion with proteinase K and phenol–chloroform extraction (Westerfield 1995). The zebrafish bA gene promoter (Liu et al. 1990, 1991) was amplified using the Expand High Fidelity PCR System (Roche). Purified zebrafish genomic DNA (200 ng) was mixed with 5 ml of 10× Expand High Fidelity buffer, 15 mM of MgCl2, 1·5 ll of 10 mM bA forward primer (5′-GGGTTACC AGTAAcGACGCCTGaAG-3′), 1·5 ml of 10 mM bA reverse primer (5′-TCCCCCGGGGGTGTAGGA CAAAAGCG-3′), 1 ml of 10 mM of dNTP mix, and 0·75 ml of Expand High Fidelity Enzyme Mix (Applied Biosystems, Foster City, CA, USA). Finally, distilled water was added to increase the reaction volume to 50 ml. The DNA primers were designed with enzyme sites (KpnI and SmaI) for cloning into pGL3-Basic vector (Promega) according to the zebrafish genomic sequence in the GenBank database of the National Center for Biotechnology Information (NCBI) (accession no. AL928650). PCR was performed on the TaKaRa PCR Thermal Cycler Dice with the following conditions: one cycle at 94 °C for 2 min, 30 cycles at 94 °C for 30 s, 60 °C for 30 s, and 72 °C for 3 min, followed by one cycle of 72 °C for 7 min. The gel-extracted PCR product was cloned into the pGEM-T Easy Vector System (Promega) and sent to a commercial DNA sequence service, Tech-Dragon, for nucleotide sequence determination.

The cDNA obtained by reverse transcriptase (Promega) was used as a template for zebrafish SLa, SLb, and GH gene amplification using the following specific primer sets:

\[
\begin{align*}
zLzF (5′-ATGAACACAGTTAAGTTCTCGAGG-3′) & \text{ and } zLzR (5′-CTATTAGGGCCAGGCGCTTAGTT-3′); 
zSLbF (5′-ATGAAGAAAACGGCAGA-3′) & \text{ and } zSLbR (5′-CTATTAGGGCCAGGCGCTTAGTT-3′); 
zGHF (5′-ATGCTAGCGACTGTTGC-3′) & \text{ and } zGHR (5′-CTATTACAGGGTGACAGTTGGAATCCA-3′).
\end{align*}
\]

The primers were designed according to the zebrafish database of the NCBI (accession no. NM_001037674 for SLz, NM_001037674 for SLb, and BC116501 for GH). GFP was amplified from a commercial vector, phrGFP II-1 (Stratagene, La Jolla, CA, USA).

The bA gene promoter was cloned into the pGL3-Basic vector (Promega) to study the promoter activity that drives the firefly luciferase reporter gene. The cDNAs of zebrafish SLz, SLb, GH, and humanized renilla GFP (hrGFP) were respectively replaced with luciferase reporter gene, and the hormone overexpression constructs were linearized, containing only the promoter element, hormone cDNA, and polyA signal elements, with plasmid and its antibiotic resistance gene removed (Fig. 1).
Generation of transgenic zebrafish

Adult zebrafish were reared in a closed water circulation system at 28 °C under a controlled photoperiod of 14 h light:10 h darkness cycle (Westerfield 1995). An egg collection device was placed into a tank of fish at the beginning of the light cycle. Eggs were collected ~20 min after being laid (one- to two-cell stage) and coinjected with the linearized vectors dissolved in 0.25% phenol red in 0.1 M Tris–HCl (zβAzSLα and zβAhrGFP, zβAzSLβ and zβAhrGFP, zβAzSLβ and zβAhrGFP, zβAzSLβ and zβAhrGFP, zβAzSLβ and zβAhrGFP, zβAzSLβ and zβAhrGFP, using the PV820 Pneumatic PicoPump (World Precision Instruments; Chong & Vielkind 1989, Hamada et al. 1998). Approximately, 500 pl of DNA solution represented a final number of 10⁶ copies of each transgene per injected embryo (Zhu et al. 1985). The microinjection needles were made from Narishige GD-1 glass capillaries using the MODEL P-97 microelectrode puller (Sutter Instrument Co., Novato, CA, USA;
The injected embryos were incubated at 28°C (Chong & Vielkind 1989). GFP expression was analyzed 24 h after fertilization using a Leica DM1L fluorescence microscope with a Leica filter set (excitation = 485 nm; emission = 520 nm), and pictures were taken using the Leica DFC420 digital camera system (shown in Fig. 2). Mosaicism in the first transgenic generation (G₀) was classified according to the GFP expression patterns as follows: weak, a few cells expressing GFP; moderate, <50% of the body expressing GFP; or strong, more than 50% of the body expressing GFP (Gibbs & Schmale 2000). For the generation of stable transgenic lines, the founders were raised to sexual maturity. Transgenic screening was performed by crosses with wild-type (WT) zebrafish. At least 100 embryos from each founder were examined for GFP fluorescence.

Investigation of transgenes

Genomic DNA was isolated from G₀ and G₁ transgenic fish larvae as mentioned above to confirm the positive transgenes by PCR and Southern blotting. The following primers were used for PCR analysis of the transgenes:

- zβAzSLz P1 (5’-GAATCGGCGGATTGAG-3’);
- zβAzSLz P2 (5’-TCCAGAGGACCCGACC-3’);
- zβAzSLβ P3 (5’-GAGCTCATCACCACCCCTTG-3’);
- zβAzSLβ P4 (5’-GTCGAGCAACTCGTA-3’);
- zβAzGH P5 (5’-GAATCGGCGGATTGAG-3’); and
- zβAzGH P6 (5’-AAGACGAGCCCATCTTG-3’).

PCR was carried out in a 25 µl volume containing 25 pM of each primer, 1 mM of each dNTP, and 1 unit of Expand High Fidelity Enzyme (Applied Biosystems) for 35 cycles. Each cycle included 1 min at 94°C, 30 s at 60°C, and 1 min at 72°C.

The probes for Southern blot analysis were amplified from the hormone overexpression constructs using the following primers:

- zβAzSLz F: 5’-CCCATCCAAACATCCAGA-3’;
- zβAzSLz R: 5’-ATACAGCACCGGCTCCATC-3’;
- zβAzSLβ F: 5’-GTCGACTTATCCGGATGTG-3’; and
- zβAzSLβ R: 5’-CCAGGCTCCTTCACCC-3’.

Double-stranded oligonucleotide probes, zβAzSLz-102 bp and zβAzSLβ-308 bp (Δ in the probes indicated intron in the genomic DNA of the WT fish, which is shown in Fig. 1), were end labeled with digoxigenin (DIG)-11-ddUTP using Terminal transferase (Roche). Purified genomic DNA (5 µg) was digested with EcoRI or Smal and XhoI overnight, resolved by electrophoresis in a 0.8% agarose gel, and blotted onto a nylon membrane (Immobilon-N; Millipore, Billerica, MA, USA) using an electroblotting apparatus (TE70 ECL Semi-Dry Transfer Unit, Amersham) according to the manufacturer’s instructions. The DNA was fixed onto the membrane by cross-linking it with a transilluminator, and prehybridized in a solution containing 5X SSC.
(3 M NaCl and 0.3 M trisodium citrate, pH 8.0), 1% SDS, 5× blocking reaction (Roche), 50% (v/v) formamide, and denatured salmon sperm DNA at 68°C for 4 h. The prehybridization solution was then removed, and a fresh hybridization solution (5× SSC, 1% SDS, 5× blocking reaction, and 50% (v/v) formamide) containing the denatured DIG-labeled DNA probe (about 25 ng/ml) was added and incubated at 68°C overnight. The hybridized membrane was washed first in 2× SSC, 1% SDS at 25°C with constant agitation for 5 min, and 0.5× SSC, 0.1% SDS at 68°C under constant agitation for 15 min. After the immunological detection of the DIG-11-ddUTP, positive signals were detected using FUJI X-ray film for autoradiography.

Table 1 Nucleotide sequences of gene-specific primers for real-time PCR in zebrafish

<table>
<thead>
<tr>
<th>Genes</th>
<th>Forward primer (5′–3′)</th>
<th>Reverse primer (5′–3′)</th>
<th>Amplicon size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>βA</td>
<td>CGACGAGGAGATGGGAACC</td>
<td>CAACGAAAAAGCTCATTGC</td>
<td>102</td>
</tr>
<tr>
<td>SLα</td>
<td>CAACAGGCGTGGAAACACC</td>
<td>GGTCCATCCACGACTGAA</td>
<td>129</td>
</tr>
<tr>
<td>SLβ</td>
<td>GATGCGGTTGGCTGCTTAA</td>
<td>CTCTCCGCTGAGATTGTC</td>
<td>102</td>
</tr>
<tr>
<td>GH</td>
<td>GACATCCGCGTCTGCAATCA</td>
<td>CCTAGGTCAGTGAATACTC</td>
<td>101</td>
</tr>
<tr>
<td>PRL</td>
<td>ATCTCACGACTCTACCAA</td>
<td>GCTGATCTCCCGGACTT</td>
<td>147</td>
</tr>
<tr>
<td>IF1G</td>
<td>TGTGAGAGAGCACCAGGAG</td>
<td>TTGGTCAGTGATGAAACTCA</td>
<td>211</td>
</tr>
<tr>
<td>IF2Gα</td>
<td>CTCGGCCAGAGAGGAGA</td>
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<td>229</td>
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<tr>
<td>IF2Gβ</td>
<td>TTGGGGATTGGGAGGAGG</td>
<td>CGCAAGATGGCCAGGAT</td>
<td>243</td>
</tr>
<tr>
<td>IF3G</td>
<td>AGAAGTGGCGGCTGTGAT</td>
<td>TGAGGGTGTTGCTGGTC</td>
<td>194</td>
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<tr>
<td>LEP</td>
<td>TCCAGGACCTATCCAGAG</td>
<td>TCCAGGTAACCAAGAAT</td>
<td>159</td>
</tr>
<tr>
<td>SREBP1</td>
<td>GCCGCCGAGGCAAGCAAAG</td>
<td>GCCGCGGTGCTTACAAG</td>
<td>108</td>
</tr>
<tr>
<td>SREBP2</td>
<td>CAGACAGGCGGATGACGCT</td>
<td>TCCAGGCGGCTTACGAG</td>
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<tr>
<td>FAS</td>
<td>TGACGCCGACGGTATGAG</td>
<td>CAACGCAGTCGGTAAAG</td>
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<tr>
<td>ACC2</td>
<td>GCGGCTACCTCTCATC</td>
<td>CGACTACCGTATCGATC</td>
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<td>VTG</td>
<td>TCTGGAGTTGGCCATCGATA</td>
<td>GATGAAACCTTGGCTGTA</td>
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<tr>
<td>POMC</td>
<td>CACCCGCGGAGTGGAGGAG</td>
<td>CACGCGGAAATGCGGTA</td>
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<tr>
<td>PEPCK</td>
<td>GACCGGCGGGCGAGATGTT</td>
<td>AAAGCAGGACGAGCAAGA</td>
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<tr>
<td>INS</td>
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<td>CACGCTCAGCCATGCAGT</td>
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<tr>
<td>CAT</td>
<td>TGAGGCTGCGGCGCACTAAGTA</td>
<td>AAAGCATGCGGACAGAAGC</td>
<td>138</td>
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<tr>
<td>GST</td>
<td>CTGAGACATCTGGGTCGAAA</td>
<td>AGATCTTCAACTCCGTCTTG</td>
<td>92</td>
</tr>
</tbody>
</table>

Quantification of mRNA levels using real-time PCR

Using ABI Primer Express software (Applied Biosystems), specific primers (Table 1) for zebrafish βA (AF057040), SLα (AY376857), SLβ (AJ867249), GH (AJ937858), PRL (NM_181437), IGF1 (NM_181425), IGF2a (NM_131433), IGF2b (NM_001001815), IGF3 (EU272146), leptin (LEP, NM_001128576), sterol regulatory element binding protein 1 (SREBP1, DQ836065), SREBP2 (ENSDARG00000063438), fatty acid synthase (FAS, XM_682295), acetyl-CoA carboxylase 2 (ACC2, XM_678989), vitellogenin (VTG, NM_001044897), POMC (NM_181438), phosphoenolpyruvate carboxykinase (PEPCK, NM_214751), insulin (INS, NM_131056), catalase (CAT, AF170069), and glutathione S-transferase (GST, AB194127) were designed to span two exons at the intron–exon junction to prevent the primers from binding to the genomic DNA sequences amplifying the contaminated DNA in the samples, and hence minimize genomic contamination in reverse transcription-PCR (Table 1).

Rearing of larvae and growth analysis

Transgenic and non-transgenic fish were reared until 6 months of age in a closed circulation water system composed of 15-l tanks. Triplicate samples were collected from each genetic group (SLα-transgenic G0, SLβ-transgenic G0, and GH-transgenic G0), with twenty fish each. Water quality was monitored once a day, and temperature, pH, nitrogenous compounds, and photoperiod were maintained according to zebrafish requirements (Chong & Vielkind 1989, Westerfield 1995, Gibbs & Schmale 2000). The fish were fed a high-quality commercial fish diet (ZM Systems, Winchester, UK): all fry were fed with infusoria grade ZM-000 (30–50 μm, 52% protein) at week 1, ZM-100 (80–200 μm, 55% protein) at week 2, ZM-200 (150–300 μm, 60% protein) at weeks 3–5, and Mediquafood Guppy Food (300–500 μm, 48% protein, Japan) together with freshly hatched brine shrimp (Brine Shrimp Direct, Ogden, UT, USA) from week 6 on. In all situations, the food was completely consumed within 10 min. After the first month, the fish were anesthetized (Tricaine, 0.1 mg/ml) and weighed every 2 weeks to maintain the percentage of food by biomass in each tank. At the end of the experiment, the mean weight was compared among the three test groups. In addition, the total length of individual fish was measured, and the condition factor (K) was calculated using the formula K = (W/L^3) × 10^3, where W is the mass in milligrams and L is the total length in millimeters.
Transgenic larvae and non-transgenic larvae (N=6) at week 5 were sampled to grind in liquid nitrogen. TRIzol reagent (Invitrogen) was used for total RNA extraction. Then, DNase treatment was performed with RNase-free DNase (Takara, Kyoto, Japan). Reverse Transcriptase (Promega) was used for cDNA synthesis. To perform real-time PCR, a reaction mixture was set up in a 0.2 ml clear thin-walled, optical-grade PCR tube that contained 12.5 ml Brilliant SYBR Green QPCR master mix (Applied Biosystems), 0.5 ml of forward primer (10 μM), 0.5 ml of reverse primer (10 μM), 2 μl cDNA template, and 9.5 μl nuclease-free water for a final volume of 25 μl.

Real-time quantitative PCR was carried out on the ABI 7700 detection system (Applied Biosystems). The PCR cycles were 1 cycle at 95 °C for 10 min, 40 cycles at 95 °C for 30 s, 58 °C for 30 s, and 72 °C for 1 min. All PCR assays were performed in triplicate. The fold inductions of candidate genes were determined by dividing the relative mRNA levels of transgenic samples by those of the control samples, all normalized with the level of βA. All of the data were analyzed using one-way ANOVA and Tukey’s multiple comparison tests with a 95% confidence level on GraphPad Prism 5.

Results

Production of SL-transgenic fish

From a local strain of zebrafish, a 2-2 kb region of zebrafish βA gene promoter was isolated using genomic PCR. Potential transcription factor binding sites that may be involved in regulating the βA gene promoter were found (Fig. 1a). SLα-transgenic and SLβ-transgenic zebrafish were produced by the coinjection of the transgenes zβAzSLα and zβAhrGFP, and zβAzSLβ and zβAhrGFP respectively in an equimolar ratio (1:1), using one-cell embryos (Fig. 1).

At the time of assessment by fluorescence microscopy (Fig. 2), which was 1 week after fertilization, the survival rate of the untreated fish embryos was observed and recorded as 786 out of 1120 (70.2%), whereas the survival rate of the microinjected embryos was 352 out of 1100 (32%) for the SLα-transgenic ones and 343 out of 1300 (26.4%) for the SLβ-transgenic ones respectively. Among the 352 SLα-transgenic embryos, 118 (33.5%) were classified as GFP negative (no expression), 111 (31.5%) as weakly GFP positive, 89 (25-3%) as moderately GFP positive, and 34 (9-7%) as strongly GFP positive. Among the 343 SLβ-transgenic embryos, 127 (37%) were classified as GFP negative (no expression), 135 (39-4%) as weak GFP positive, 62 (18-1%) as moderately GFP positive, and 19 (5.5%) as strongly GFP positive. GH-transgenic zebrafish were used as positive controls by coinjecting the transgenes zβAζGH and zβAhrGFP. The strongly GFP-positive samples were collected and used for further analysis.

Identification of transgenic zebrafish by genomic DNA PCR and Southern blot

Genomic DNA was extracted from the samples of 5-week-old transgenic fish with strong GFP expression to determine the presence of the zβAζSLα, zβAζSLβ, and zβAζGH transgenes. In the PCR analysis, a 299 bp fragment was generated from SLα-transgenic G0 zebrafish #14 and #28 using primers P1 and P2, and a 298 bp fragment was generated from SLβ-transgenic G0 zebrafish #5 and #11 using primers P3 and P4 (Fig. 3a).

![Figure 3](https://example.com/figure3.png)

**Figure 3** Identification of transgenic fish by genomic DNA PCR. (a) Positive transgenic fish were identified using primers P1 and P2 for SLα (299 bp) and primers P3 and P4 for SLβ (298 bp). Lane 1, 1 kb Plus DNA Ladder (Invitrogen); lanes 2 and 3, SLα-transgenic samples #14 and #28; lanes 6 and 7, SLβ-transgenic samples #5 and #11; lanes 4 and 5 and lanes 8 and 9, non-transgenic samples. (b) Positive transgenic fish were identified using primers P5 and P6 for GH (673 bp). Lane 1, 1 kb Plus DNA Ladder (Invitrogen); lanes 2 and 3, GH-transgenic samples #25 and #26; lanes 4 and 5, non-transgenic samples.
samples (GH-transgenic $G_0$ zebrafish #25 and #26) using primers P5 and P6 (Fig. 3b). Southern blot analysis revealed that three bands were present separately in SL$\alpha$-transgenic $G_0$ zebrafish #14 and #28 (Fig. 4a), one band in SL$\beta$-transgenic $G_0$ zebrafish #5 and two bands in SL$x$-transgenic $G_0$ zebrafish #11 in the digestion of EcoRI (Fig. 4b). It is suggested that the transgene $zB\alpha xSL\alpha x$ was integrated into three different sites in the genome of SL$x$-transgenic $G_0$ zebrafish #14 and #28, and the transgene $zB\alpha xSL\beta x$ was integrated into only one site in SL$\beta$-transgenic $G_0$ zebrafish #5 and two sites in SL$\beta$-transgenic $G_0$ zebrafish #11. Simultaneously, in the digestion of SmaI and XhoI, which cut through the whole length of SL$x$ and SL$\beta$ cDNA in the transgenes, a 700 bp band was found as expected and detected in both the SL-transgenic $G_0$ and $G_1$ samples (Fig. 4c and d). All of these data suggest that the transgenes $zB\alpha xSL\alpha x$, $zB\alpha xSL\beta x$, and $zB\alpha xGH$ were integrated into the host genome, consistent with hrGFP expression.

**Growth analysis of SL-transgenic $G_0$ founders**

The SL-transgenic $G_0$ founders did not grow faster or bigger than the non-transgenic fish; however, a special stripe phenotype was found in the SL$\alpha$-transgenic $G_0$ line (Fig. 5). At the end of the growth experiment, the SL$\alpha$-transgenic $G_0$ zebrafish reached a final average body weight of $421.1 \pm 78.3$ mg; their SL$\beta$-transgenic $G_0$ siblings reached a final average body weight of $443.4 \pm 82.6$ mg; and their GH-transgenic $G_0$ siblings reached a final average body weight of $542.9 \pm 103.7$ mg. The transgenic fish all show higher body mass in comparison with their non-transgenic siblings (328.6 $\pm$ 68.2 mg; Fig. 6a). The SL subtypes had a similar growth enhancement effect, which was less than that of GH. The condition factors calculated for all transgenic and non-transgenic zebrafish used in this experiment are shown in Fig. 6b. However, the $K$ values of the transgenic and the non-transgenic fish show no significant difference.

**Assessment of the physiological effects of SL among SL-transgenic $G_0$ founders**

To find out whether the overexpression of hormones would affect the expression of their family members, the endogenous mRNA levels of SL$,\alpha$, SL$,\beta$, and GH genes in 5-week-old transgenic zebrafish were investigated (Fig. 7). The results show a 24.3-fold induction of SL$\alpha$ in the SL$\alpha$-transgenic fish without obvious up-or down-regulation of other members in the GH family.
Figure 6 Body weight (a) and calculation of condition factor K (b) in 6-month-old zebrafish (Danio rerio) of transgenic zebrafish. WT, wild-type, non-transgenic fish; SLα, SLα-transgenic G0 fish; SLβ, SLβ-transgenic G0 fish; GH, GH-transgenic G0 fish. Different letters indicate significant differences (P<0.05) among the fish groups; N=10.

A similar result is found for the SLβ-transgenic fish, with a 14-5-fold induction of SLβ; however, only a 9-81-fold induction of GH is found in the GH-transgenic fish. The results indicate the successful overexpression of hormones in vivo, as anticipated.

Three types of IGF have been identified in zebrafish so far: IGF1, IGF2, and IGF3, with two subtypes of IGF2: IGF2a and IGF2b. Figure 8 shows the gene expression levels (fold induction over non-transgenic control) of IGFs in transgenic fish. The level of IGF1 was up-regulated by 5·46- and 6·77-fold in the SLα-transgenic and the SLβ-transgenic fish respectively, whereas there was a sharp induction of 88·34-fold in SLb-transgenic (0·57-fold in the SLb-transgenic, GH-transgenic fish (Fig. 14).

Regarding energy metabolism, key marker genes, such as LEP, insulin (INS), PEPCK, SREBP, FAS, and ACC, were selected to understand the effect of SL on glucose synthesis and lipid metabolism. The two types of SREBP in zebrafish, SREBP1 and SREBP2, and only ACC2 were considered in this experiment. The expression levels of leptin, insulin, and PEPCK were found to demonstrate a 2·58-, 2·96-, and 1·32-fold increase in the SLα-transgenic fish, a 2·14-, 1·92-, and 1·14-fold increase in the SLβ-transgenic fish, and a 1·89-, 1·95-, and 5·42-fold increase in the GH-transgenic fish as positive controls (Fig. 9). It is interesting to discover that the expression level of SREBP1 was up-regulated 1·51- and 1·40-fold and that of SREBP2 was down-regulated 0·51- and 0·53-fold in the SLα-transgenic and SLβ-transgenic lines respectively. GH-transgenic fish demonstrated a 2·13-fold increase in SREBP1 expression and a 1·35-fold increase in SREBP2 expression. FAS expression increased 5·10- and 2·81-fold, whereas ACC2 expression decreased 0·66- and 0·76-fold in the SLα-transgenic and SLβ-transgenic lines respectively. GH-transgenic fish demonstrated a 4·82-fold increase in FAS mRNA level and a 3·41-fold increase in ACC2 mRNA level by comparison (Fig. 10).

VTG was selected to analyze the possible role of SLs in reproduction. It was found that VTG mRNA was up-regulated in the SLα-transgenic and SLβ-transgenic fish with a 5·94- and 6·02-fold increase respectively over the control, and VTG mRNA was up-regulated in the GH-transgenic fish with a 2·04-fold increase (Fig. 11). POMC was chosen to understand the role of SLs in pigmentation, and a moderate increase of 2·55- and 2·26-fold was found in the SLα-transgenic and SLβ-transgenic fish respectively, but only 1·45-fold in the GH-transgenic fish (Fig. 12).

CAT and GST mRNA levels were used to investigate the effect of redundant SLs on the antioxidant defense system. CAT gene expression was found to decrease slightly in both the SLα-transgenic (0·75-fold) and the SLβ-transgenic (0·82-fold) fish, but it was found to increase a little in the positive GH-transgenic fish (1·27-fold; Fig. 13). A moderate reduction in GST gene expression was observed in the SLα-transgenic (0·55-fold) and the SLβ-transgenic (0·46-fold) fish, whereas almost no change was observed in the GH-transgenic fish (Fig. 14).

Discussion

It is generally assumed that the direct microinjection of gene constructs into the pronucleus or nucleus of a fertilized egg before the onset of cleavage is the most effective way to incorporate new genetic material into...
the genome of injected embryos (Zhu et al. 1985, Ozato et al. 1986, Culp et al. 1991, Chen et al. 1993, Morales et al. 2001); however, the exact time of gene integration after microinjection is not guaranteed (Hamada et al. 1998, Figueiredo et al. 2007). Recently, the use of reporter genes that allow the evaluation of the degree of in vivo mosaicism in transgenic fish has facilitated the identification of probable germ line founders (Rahman et al. 1997, 1998, Hamada et al. 1998, Ju et al. 1999, Liu et al. 2003), and the coinjection of a reporter transgene along with the gene construct of interest represents a considerable reduction in the effort needed to establish transgenic germ lines (Rahman et al. 1997, 1998). The analysis of the GFP expression patterns permitted the selection of possible germ line founders in the G0 generation. One week after microinjection, 66.5% (SLα) and 63% (SLβ) of the fish embryos expressed GFP, indicating highly efficient transgenic fish production. However, part of this observed expression may be attributed to transitory expression due to the transcription of unintegrated transgenes (Chong & Vielkind 1989, Therms et al. 2002). However, as the DNA injected contained no plasmid DNA, the chance of DNA replication following embryogenesis was reduced. We found that 9.7% (SLα) and 5.5% (SLβ) of the fish that we analyzed showed strong GFP reporter gene expression, similar to 5% of the fish with strong GFP expression reported by Gibbs & Schmale (2000) for G0-transgenic zebrafish and >3% of the fish with strong GFP expression reported by Gibbs & Schmale (2000) and Therms et al. (2002) for G0-transgenic medaka. Our conditions were similar to those of Gibbs & Schmale (2000) and Therms et al. (2002), who also used linearized transgenes in which GFP gene expression was under the control of ubiquitous promoters (α- or βA).

In addition to genomic PCR confirmation, Southern blot analysis was used to reconfirm the GFP-positive transgenic fish. The probes designed in SL gene cDNA contained several introns in WT genomic DNA to avoid a false positive signal. After digestion with EcoRI, three different bands were detected in SLα-transgenic G0 sample #116 and #117, whereas only one band and two bands appeared in SLβ-transgenic G0 sample #103 and #104 respectively. We used Smal and XhoI to digest the whole genomic DNA to see whether the transgenes of total SL cDNA would be released, and the results showed only one band, as expected, but with different copies in the genomic DNA.

Measurement of the mRNA expression of SLs using real-time PCR revealed that the ααSLαα and αβSLβ

Figure 8 Insulin-like growth factor (IGF1, IGF2a, IGF2b, and IGF3) gene expression in the non-transgenic and different transgenic lines. Both SLs and GH induced different levels of IGFs in vivo. Each value represents the mean ± s.d. of the three replicates. Different letters indicate significant differences (P<0.05) from each other (one-way ANOVA).

Figure 9 Leptin (LEP), insulin (INS), and phosphoenolpyruvate carboxykinase (PEPCK) gene expression in the non-transgenic and different transgenic lines. Both SLs and GH regulated the expression of LEP, INS, and PEPCK in different ways in vivo. Each value represents the mean ± s.d. of the three replicates. Different letters indicate significant differences (P<0.05) from each other (one-way ANOVA).

Figure 10 Sterol regulatory element binding protein (SREBP1 and SREBP2), fatty acid synthase (FAS), and acetyl-CoA carboxylase 2 (ACC2) gene expression in the non-transgenic and different transgenic lines. Both SLs and GH regulated the expression of SREBP, FAS, and ACC in different ways in vivo. Each value represents the mean ± s.d. of the three replicates. Different letters indicate significant differences (P<0.05) from each other (one-way ANOVA).
transgenes produced high levels of ubiquitous active hormone mRNAs, with an increase of 24·3-fold for SLα and 14·5-fold for SLβ, compared with the non-transgenic controls, but without any increase in the GH mRNA level. A primary function of GH is to promote somatic growth in fish; however, this function is accomplished indirectly through the GH/IGF1/IGF2 axis. This axis has been shown to play important roles in fish growth and development. After GH binds to the GHR in the target tissue and activates it, a tyrosine kinase called janus kinase (JAK) is activated to transduce the GH signal in the target tissue to release IGF1 or IGF2 (Carter-Su & Smit 1998). To find out whether SLs affect fish growth and development as GHs are mediated by IGFs, the expression level of IGFs in SL-transgenic fish was investigated. In mammals, IGF1 plays an important role in both embryonic and postnatal growth (Baker et al. 1993), primarily through its stimulatory effects on cell proliferation and inhibition of cell death (apoptosis). Mice carrying null mutations in the IGF1 gene are born small and grow very poorly postnatally (Baker et al. 1993, Powell-Braxton et al. 1993, Liu et al. 1998). IGF2 is thought to be a primary growth factor required for early development, whereas IGF1 expression is required for achieving maximal growth (O’Dell & Day 1998). In our in vivo study, a significant increase in IGF1 (5·46- and 6·77-fold), IGF2a (4·38- and 4·35-fold), and IGF2b (2·83- and 3·94-fold) in the SLα-transgenic and the SLβ-transgenic zebrafish larvae respectively brought about a moderate enhancement of zebrafish growth, with a respective 1·28- and 1·35-fold increase in body weight gain, by comparison with a 1·65-fold increase in the GH-transgenic zebrafish.

Our data agree with those of the transfer and overexpression of GH transgenes from other groups, including salmonid (2–6-fold; Du et al. 1992), common carp (1·2–1·8-fold; Chen et al. 1993), zebrafish (2·6-fold; Figueiredo et al. 2007), and tilapia (3·5–4-fold; Rahman et al. 1998). SLα and SLβ could act on growth development to some extent as GH does – through IGF signaling. Recently, IGFs have been found to be expressed in teleosts in a wide range of tissues throughout life, which suggests that the autocrine/paracrine role of this hormone may be of particular physiological importance in bony fish (Schlueter et al. 2007, Sang et al. 2008, Wang et al. 2008). For example, gonad-specific IGF3 was found to be present only in the fish genome (Sang et al. 2008), which suggests its potential function in gonad development and
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reproduction in teleosts. IGFs have also been found to be required for primordial germ cell migration and survival (Mommsen & Plisetskaya 1991, Papasani et al. 2006). However, SLs did not appear to enhance IGF3 gene expression in this study.

Glucose is stored as glycogen in the liver and muscle (Wang et al. 1994, Elo et al. 2007). PEPCK is an indicator of blood glucose levels for the examination of glucose metabolism, which catalyzes a rate-limiting step in gluconeogenesis, and is transcriptionally regulated by glucagon and insulin (Brown & Goldstein 1997). Our study showed that the overexpression of GST, whereas GH had no effect on it. Each value represents the mean ± S.D. of the three replicates. Different letters indicate significant differences (P<0.05) from each other (one-way ANOVA).

A similar result was also found in European sea bass (Johnson et al. 1997). Leptin plays a key role in regulating energy intake and energy expenditure, including appetite and metabolism (Mayer et al. 1998). A moderate induction (2.58- and 2.14-fold) of LEP in SLβ-transgenic and SLβ-transgenic fish helps to execute anti-obesity effects.

However, studies of seasonal changes in SL mRNA showed the gradual stimulation of SL synthesis and release during sexual maturation, and spawning females tend to have more SL cells than equivalent males, indicating that SL may play a role in the control of some steps of reproduction (Planas et al. 1992, Rand-Weaver et al. 1992, Oliverau & Rand-Weaver 1994). Plasma SL concentrations were found to remain relatively constant throughout gonad development but were found to drop during or following ovulation in sole and halibut (Schneider 1996). SL was found to stimulate gonad steroidogenesis produced by testicular fragments and ovarian follicles in vitro in coho salmon; however, this steroidogenic activity was considerably less than that of GH (Planas et al. 1992). SL synthesis and release were found to be inhibited by gonadectomy (Specker & Sullivan 1994). VTG is an egg yolk precursor protein crucial for reproductive success, such as oocyte growth, oocyte maturation, early embryogenesis, and later, larval development (Nguyen et al. 2006). Our study showed that the ectopic expression of SLβ and SLβ in vivo significantly induced the mRNA expression of VTG, indicating that SLs play a role in vitellogenesis. The stimulation and secretion of VTG might pass through the granulose and thecal cell layers, bind to specific receptors on the oocyte surface, and are sequestered via receptor-mediated endocytosis (Schallreuter et al. 2008).

SL has also been found to be related to pigmentation, melanosome aggregation, chromatophore proliferation, and morphogenesis. A medaka (O. latipes) ci mutant in which the proliferation and morphogenesis of chromatophore pigment cells are deficient was recently found to have SL gene mutation (Fukamachi et al. 2006). An increased number and more dendritically shaped leucophores were observed, and fewer xanthophores were visible in the mutant, so the body of the WT was darker than that of the ci mutant (Fukamachi et al. 2006). The effect of SL on melanosome aggregation was studied in red drum (Zhu & Thomas 1997) and zebrafish (Castrucci et al. 1997) in a dose-dependent manner. A ci-/lf double mutant (ci and lacking leucophores) was used to investigate the role of SL in the regulation of body color, and the results showed that the lf gene played an indispensable role in leucophore development of epistatic to SL signaling (Fukamachi et al. 2006). In the present study, the POMC gene was used to study the effect of SL on pigmentation. A twofold induction of POMC was found in both the

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**Figure 14** Glutathione S-transferase (GST) gene expression in the non-transgenic and different transgenic lines. SLs reduced the expression of GST; whereas GH had no effect on it. Each value represents the mean ± S.D. of the three replicates. Different letters indicate significant differences (P<0.05) from each other (one-way ANOVA).

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SLα-transgenic and the SLβ-transgenic zebrafish larvae, indicating the role of SL in body color and background adaptation. POMC (expressing melanocyte-stimulating hormone) can stimulate the production and release of melanin (melanogenesis) by melanocytes in the skin (Brown-Borg & Rakoczy 2005, Brown-Borg et al. 2005). An interesting disrupted stripe phenotype was found only in the SLα-transgenic fish (Fig. 5). The molecular mechanism of SLα in stripe morphogenesis in fish remains to be investigated.

GH is a key player in the physiological mechanisms of altered stress resistance, such as the alteration in the activity of multiple enzymatic components of methionine and glutathione metabolism in Ames dwarf mice (Brown-Borg et al. 2009). Studies show that Ames dwarf mice live significantly longer than their WT siblings and exhibit elevated antioxidative defences and reduced oxidative damage, perhaps leading to their extended longevity (Chelikani et al. 2004, Leggatt et al. 2007). Research into GH-transgenic salmon shows the up-regulation of the components of the glutathione antioxidant system to combat potentially higher reactive oxygen species production, based on the accelerated growth and increased metabolic rates. We, however, found slight reductions in the expression of the catalase (CAT) gene and GST gene in both the SLα-transgenic and the SLβ-transgenic fish. Catalase is a common central enzyme involved in reactive oxygen species (ROS) scavenging through the degradation of hydrogen peroxide into oxygen and water (Chelikani et al. 2004). GSTs involved in xenobiotic metabolism are cytosolic proteins that catalyze the conjugation of glutathione with a substrate bearing an electrophilic atom. Free reactive electrophilic intermediates of xenobiotics can produce damage to important cellular constituents. The decreases in these two key enzymes in the antioxidant defence system in the SL-transgenic fish suggest a reduction in the capability to deal with an oxidative stress situation (Leggatt et al. 2003). An increased growth rate in transgenic zebrafish was found to be associated with an increased metabolic rate (Rosa et al. 2008). It is expected that the antioxidant system in GH-transgenic fish might be up-regulated to cope with increased ROS production based on the high metabolic demand due to accelerated growth rate in these transgenic fish. The glutathione antioxidant system was found to be enhanced in GH-transgenic coho salmon (Leggatt et al. 2003); however, a resistance effect to excess GH caused a decrease in the catalytic subunit expression of glutamate-cysteine ligase, an enzyme responsible for glutathione synthesis, in GH-transgenic zebrafish (Rosa et al. 2008). The reduction in the efficiency of the antioxidant defence system due to the overexpression of SLs may result in the greater susceptibility of SL-overexpressing fish to oxidative stress, and such altered stress capacity may affect their health and life span.

In summary, we have successfully generated transgenic zebrafish with the ectopic expression of SLα and SLβ of zebrafish in vivo using the coinjection strategy. The data obtained here indicate that the overexpression of SLs can induce IGFs, but that the level of induction is well below that of GH; however, overexpressing SLs could affect growth, development, glucose synthesis, lipid metabolism, reproduction, pigmentation, and the antioxidant defence system. Whether these observed effects were mediated via GHRs or SLR remain to be investigated. To find out the full pictures of the actions of SLs on growth and metabolisms, adult transgenic fish should be employed for further investigations.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Funding
This research did not receive any specific grant from any funding agency in the public, commercial, or not-for-profit sector, all equipments used are already available in the Department of Biochemistry, and consumables were paid by research allowance from the Department of Biochemistry, Chinese University.

Acknowledgements
The authors thank the graduate division of Biochemistry (Science) for the provision of a post-graduate studentship to GW and the Department of Biochemistry for its support of this research with a high degree of academic freedom.

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Received in final form 4 August 2010
Accepted 26 August 2010
Made available online as an Accepted Preprint 26 August 2010