Cloning of a novel insulin-regulated ghrelin transcript in prostate cancer

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Abstract

Ghrelin is a multifunctional hormone, with roles in stimulating appetite and regulating energy balance, insulin secretion and glucose homoeostasis. The ghrelin gene locus (GHRL) is highly complex and gives rise to a range of novel transcripts derived from alternative first exons and internally spliced exons. The wild-type transcript encodes a 117 amino acid preprohormone that is processed to yield the 28 amino acid peptide ghrelin. Here, we identified insulin-responsive transcription corresponding to cryptic exons in intron 2 of the human ghrelin gene. A transcript, termed in2c-ghrelin (intron 2-cryptic), was cloned from the testis and the LNCaP prostate cancer cell line. This transcript may encode an 83 amino acid preproghrelin isoform that codes for ghrelin, but not obestatin. It is expressed in a limited number of normal tissues and in tumours of the prostate, testis, breast and ovary. Finally, we confirmed that in2c-ghrelin transcript expression, as well as the recently described in1-ghrelin transcript, is significantly upregulated by insulin in cultured prostate cancer cells. Metabolic syndrome and hyperinsulinaemia have been associated with prostate cancer risk and progression. This may be particularly significant after androgen deprivation therapy for prostate cancer, which induces hyperinsulinaemia, and this could contribute to castrate-resistant prostate cancer growth. We have previously demonstrated that ghrelin stimulates prostate cancer cell line proliferation in vitro. This study is the first description of insulin regulation of a ghrelin transcript in cancer and should provide further impetus for studies into the expression, regulation and function of ghrelin gene products.

Key Words
- ghrelin
- cryptic exon
- splicing
- testis
- prostate
- cancer
- insulin

Introduction

The 28 amino acid hormone ghrelin has emerged as a multifunctional peptide hormone with actions beyond its roles in GH secretion, appetite regulation and energy balance (Kojima et al. 1999, Wren et al. 2000, Nakazato et al. 2001, Lim et al. 2011). In addition to its role in normal physiology, ghrelin has been associated with a number of disease processes, including obesity (Scerif et al. 2011, Yi et al. 2011), type 2 diabetes mellitus and hyperinsulinaemia (Ukkola 2011), gastrointestinal disease (Jeffery et al. 2011), cardiovascular disease (Isgaard & Granata 2011), reproductive disorders (Repaci et al. 2011), mental health (Steiger et al. 2011) and cancer (Chopin et al. 2011, Deboer 2011). Ghrelin may play a role in prostate cancer progression, and we have previously demonstrated that ghrelin mRNA and protein is expressed in prostate cancer cell lines and tissues and that ghrelin...
stimulates cell proliferation in prostate cancer cell lines (Jeffery et al. 2002, Yeh et al. 2005).

The ghrelin gene consists of four preproghrelin-coding exons (exons 1–4) that give rise to a 117 amino acid preproghrelin peptide (Kojima et al. 1999, Seim et al. 2011b). The first 23 amino acids are encoded by exon 1 and harbour a secretory signal peptide, while the remainder of exon 1 and part of exon 2 encode the 28 amino acid ghrelin peptide. Exon 3 encodes obestatin, a recently discovered 23 amino acid peptide hormone with a range of novel functions, including regulation of adipogenesis, insulin secretion and pancreatic homeostasis and cancer cell progression (Zhang et al. 2005, Seim et al. 2011b).

Following cleavage of the signal peptide, the 94 amino acid proghrelin peptide is post-translationally modified in the endoplasmic reticulum where an octanoyl fatty acid group (acyl group) is added to the third residue of ghrelin, a serine, by the recently discovered enzyme ghrelin O-acyl transferase (GOAT; Gutierrez et al. 2008, Yang et al. 2008). Although both ghrelin and desacyl ghrelin circulate in the blood, the levels of desacyl ghrelin are significantly higher (Date et al. 2000, Patterson et al. 2005, Holmes et al. 2009). This may be the result of the rapid conversion of ghrelin to desacyl ghrelin by esterases in the circulation (Beaumont et al. 2003, De Vriese et al. 2004, Satou et al. 2010, Eubanks et al. 2011). Alternatively, desacyl ghrelin may be produced from proghrelin in the absence of GOAT expression or when the fatty acid substrates for GOAT are unavailable (Takahashi et al. 2009). Only the acylated form of ghrelin is able to bind the cognate receptor, the GH secretagogue receptor type 1a (GHSR1a; Howard et al. 1996, Kojima et al. 1999), although alternative receptors for both acylated and desacyl ghrelin must also exist (Seim et al. 2011a). It has been demonstrated that GOAT and ghrelin play a crucial role in glucose balance, particularly in response to caloric restriction (Zhao et al. 2010); however, this finding has not been replicated in a number of mouse models (Yi et al. 2012). While the role of the ghrelin axis in insulin and glucose balance is currently unclear, ghrelin and GOAT may be useful therapeutic targets for treating insulin resistance (Kirchner et al. 2010, Romero et al. 2010, Lim et al. 2011). Insulin resistance is also common in prostate cancer patients after androgen deprivation therapy (Aggarwal et al. 2011).

It is now well established that the majority of genes generate alternative splice forms, many of which have novel functions (Nilsen & Graveley 2010). This is particularly true for preprohormones, which frequently harbour a range of bioactive peptides. The ghrelin gene (GHRL) is no exception, and it is now realised that the ghrelin locus encodes multiple bioactive molecules derived by alternative transcriptional splicing, proteolytic cleavage of larger precursor peptides and by other post-translational modifications (Seim et al. 2009, 2011a).

Here, we report a novel preproghrelin splice variant termed in2c-ghrelin (intron 2-cryptic) that contains a novel exon sequence derived from intron 2 of the ghrelin gene and investigate its expression in cancer. We demonstrate that this novel transcript, as well as the recently described in1-ghrelin transcript (Kineman et al. 2007, Gahete et al. 2010, 2011), is upregulated in response to insulin treatment in the 22Rv1 and lymph node carcinoma of the prostate (LNCaP) prostate cancer cell lines and, therefore, they may have a role in prostate cancer progression, particularly in cases of hyperinsulinaemia.

Materials and methods

Cell culture

Cell lines were originally obtained from the American Type Culture Collection (ATCC; Rockville, MD, USA). The PC3 (ATCC CRL-1435), DU145 (ATCC HTB-81), LNCaP (ATCC CRL-1740) and 22Rv1 (ATCC CRL-2505) prostate cancer cell lines were maintained in RPMI 1640 medium (Invitrogen) with 10% New Zealand Cosmic Calf Serum (FCS, HyClone, South Logan, UT, USA) supplemented with 100 U/ml penicillin G and 100 μg/ml streptomycin (Invitrogen). All cell lines were passaged at 2- to 3-day intervals at 70% confluency using 0.25% trypsin/EDTA (380 mg/ml or 0.913 mM EDTA and 2500 mg/ml or 0.105 mM trypsin; Invitrogen). Cell morphology and viability was monitored by microscopic observation and regular testing was performed by PCR (Universal Mycoplasma Detection Kit, ATCC) to ensure that cells were not contaminated with Mycoplasma.

Microarray profiling of insulin-treated LNCaP prostate cancer cell line

To identify RNAs expressed in the prostate that could be developed as disease-specific targets for prostate cancer treatment, we employed a custom-designed microarray from the Vancouver Prostate Centre (VPC). The microarray, an Agilent custom 2X105K array (Agilent Technologies, Wilmington, DE, USA), combines the probes from the Agilent 44K (v1) human gene expression set with probes targeting alternative protein isoforms and
non-coding RNAs. All probes on the microarray were classified based on their relationship to the RNAs in the NCBI RefSeq database (http://www.ncbi.nlm.nih.gov/RefSeq; December 2010).

LNCaP prostate cancer cells were seeded on 10 cm tissue culture flasks (Nunc International, Penfield, NY, USA) in phenol red-free RPMI 1640 medium with 5% FCS (Invitrogen) and left overnight to attach. The following day, serum was replaced with 5% charcoal-stripped serum (Invitrogen) for 48 h, followed by a 24-h incubation in serum-free medium and treatment with 10 nM insulin (Sigma–Aldrich) or an equal volume of vehicle (70% ethanol) for 10 h. All treatments were performed in triplicate. Total RNA was isolated using TRIzol (Invitrogen); one-colour gene expression analysis was performed following Agilent labelling (Quick Amp Labeling Kit), hybridisation and scanning (Agilent Feature Extraction version 10.5.1) protocols using the custom Agilent 2×105K microarray. Data were normalised using the quantile normalisation method in Linear Models for Microarray Data (LIMMA), an open-source R-based Software package for the analysis of gene expression data (Smyth 2005). Differential gene expression was determined using LIMMA linear models with a false discovery rate (FDR)-adjusted P value ≤0.05 and fold change ≥1.5.

In silico and RT-PCR verification of putative ghrelin exons identified by microarray analysis
To investigate whether novel exons identified by microarray analysis correspond to splice variants of the preproghrelin gene (GHRL), and to determine the open reading frame of any resulting full-length transcript, we performed BLAST queries (Johnson et al. 2008), UCSC Genome Browser multigenome alignments (specifically, the 17-way conservation track; Fujita et al. 2011) and RT-PCR with primers spanning the putative exons (In2c-ghrelin-ORF–F/R, Table 1). Briefly, for RT-PCR analyses, 2 μg total RNA from human testis and pancreas (FirstChoice, Ambion, Austin, TX, USA), and from the LNCaP prostate cancer cell line, were subjected to DNaseI digestion (amplification grade, Invitrogen) and cDNA synthesis with SuperScript III and oligo(dT)18 primers (Invitrogen) according to the manufacturer’s instructions. RT-PCR was performed in a total reaction volume of 50 μl containing 1×PCR buffer, 0.2 mM deoxynucleotide triphosphates, 1.5 mM MgCl2, 0.2 μM primers (in2c-ghrelin-ORF–F/R, Table 1), 1 μl cDNA and 1 unit of Platinum Taq DNA Polymerase (Invitrogen) on a PTC-200 thermal cycler (MJ Research, Watertown, MA, USA) according to the manufacturer’s instructions. Negative, no-template controls were performed.

Quantitative real-time RT-PCR of cultured cells and tissues
Unless otherwise noted, total RNA was harvested from cultured cells using QIAshredder and RNEasy Plus Mini Kits (Qiagen), according to the manufacturer’s instructions, and stored frozen at −80°C. RNA concentration and purity were measured using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific, Scoresby, Victoria, Australia) to ensure adequate RNA quality. Contaminating genomic DNA was removed by DNaseI digestion (amplification grade, Invitrogen), and 2 μg total RNA were reverse transcribed with oligo(dT)18 primers using SuperScript III (Invitrogen). The prostate cancer cell lines described earlier, as well as RNA previously isolated from cell lines derived from normal lung (Beas-2B, ATCC CRL-9609),

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Primer sequence</th>
<th>Ta (ºC)</th>
<th>Expected size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>In2c-ghrelin-ORF</td>
<td>F: CTTCCTGAGCCCTGAAACCC</td>
<td>64</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>R: TCACCGTCAGGCTCAATGGGA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>In2c-real</td>
<td>F: AGAGGCAATTAGCGAATGTC</td>
<td>64</td>
<td>131</td>
</tr>
<tr>
<td></td>
<td>R: GTGCTCTGGAAGAATGTC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>In1-real</td>
<td>F: TCTGGGGTTTCTGCTTCC</td>
<td>60</td>
<td>215</td>
</tr>
<tr>
<td></td>
<td>R: GTTCATCTGCTGCTTCTCTCTCT</td>
<td></td>
<td></td>
</tr>
<tr>
<td>wt-real</td>
<td>F: TCACGGGAGTTGACACGCA</td>
<td>60</td>
<td>158</td>
</tr>
<tr>
<td></td>
<td>R: CAACGGAAAGGCGAGTGAC</td>
<td></td>
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</tr>
<tr>
<td>RPL32</td>
<td>F: CCCCCGTGAGGCGAGGAGA</td>
<td>60</td>
<td>59</td>
</tr>
<tr>
<td></td>
<td>R: GACCTGTTCCGATCCAGCTC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18S</td>
<td>F: TTCGGAACTGAGGGAGAT</td>
<td>60</td>
<td>151</td>
</tr>
<tr>
<td></td>
<td>R: CGAACCCTCCAGCTTCTCC</td>
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non-small-cell lung cancer (A549, ATCC CCL-185 and NCI-H1299, ATCC CRL-5803), normal ovary (hOSE17.1), ovarian cancer (SKOV-3, ATCC HTB77) and breast cancer (MDA-MB231, ATCC HTB-26), were examined. Quantitative real-time RT-PCR was performed using primers in2c-real–F/R (Table 1) with 2×SYBR green master mix (Applied Biosystems) on a PRISM 7000 Sequence Detection System (Applied Biosystems). Data were analysed using the comparative $2^{-\Delta\Delta Ct}$ method (Livak & Schmittgen 2001). Expression in different samples is shown as fold change (relative values) compared with a calibrator sample (value denoted as 1) after normalisation to the 18S ribosomal RNA housekeeping gene. Primers are shown in Table 1.

Normal human tissue (HMRT102) and cancer (CSRT103) cDNA panels were purchased from OriGene (Rockville, MD, USA). HMRT102 consists of 48 normal tissues (adrenal gland, bone marrow, brain, breast, cervix, colon, duodenum, epididymis, fat, heart, small intestine, intracranial artery, kidney, liver, lung, lymph node, peripheral blood leucocytes, muscle, nasal mucosa, oesophagus, optic nerve, ovary, oviduct, pancreas, penis, pericardium, pituitary, placenta, prostate, rectum, retina, seminal vesicles, skin, spinal cord, spleen, stomach, testis, thymus, thyroid, tongue, tonsil, trachea, urethra, urinary bladder, uterus, uvula, vagina and vena cava), while CSRT103 consists of two to six normal and ~20 tumour samples from a range of tissues. In2c-ghrelin was interrogated as detailed earlier using the AB PRISM 7000 Sequence Detection System in a total reaction volume of 20 μl using 2×SYBR green master mix (Applied Biosystems) on separate, identical array plates, which were loaded with equal amounts of cDNA per well.

Quantitative real-time RT-PCR analysis of the effect of insulin on in2c-ghrelin and in1-ghrelin expression in cultured prostate cancer cells

In order to verify the microarray data, which indicated that the novel in2c-ghrelin transcript is upregulated by insulin, we performed qRT-PCR on RNA extracted from the LNCaP prostate cancer cell line, human testis and pancreas (with a forward primer in exon 1 of ghrelin and a reverse primer in the open reading frame of these transcripts, RT-PCRs were performed as outlined earlier. In1-ghrelin (in1-real–F/R, Table 1) and wild-type ghrelin (wt-real–F/R, Table 1) were detected using primer sequences published by Gahete et al. (2010, 2011). All treatments were performed in triplicate.

Data were analysed using the comparative $2^{-\Delta\Delta Ct}$ method (Livak & Schmittgen 2001). Ribosomal protein, L32 (RPL32F/R, Table 1), which is particularly suitable for cultured prostate cancer cells (Lubik et al. 2011), was employed as a housekeeping gene for qRT-PCRs.

RT-PCR product purification and sequencing

All RT-PCR products were, unless noted, purified using a MinElute (Qiagen) PCR Purification Kit, cloned into pGEM-T Easy (Promega), transformed into One Shot MAX Efficiency DH5a-TIR chemically competent cells (Invitrogen) and sequenced at the Australian Genome Research Facility (AGRF, Brisbane, Queensland, Australia) using BigDye III (Applied Biosystems).

Statistical analyses

Data are expressed as mean±s.d. Statistical significance was determined using Student’s t-test using GraphPad Prism (La Jolla, CA, USA) or Microsoft Excel Software with a P value <0.05 considered to be statistically significant.

Results

Identification and cloning of novel, cryptic exons of the ghrelin gene (GHRL)

Using human exon-junction microarray probes, novel exons (named I and II) located in intron 2 of GHRL were found to be upregulated 3.9-fold by treatment with 10 nM insulin in the LNCaP prostate cancer cell line (Fig. 1). These exons match four GenBank entries (EF139854-57) that partially overlap the ghrelin coding exons and contain novel exon sequence in intron 2 (Fig. 2). Interestingly, the GenBank entries are previously unpublished RT-PCR validations of testis-specific exons, which were identified in a large-scale study by Clark et al. (2007). Their study employed exon arrays to locate tissue-specific exons in 16 normal tissues, but focused on novel, brain-enriched exons in the published manuscript (Clark et al. 2007). To verify whether the novel exons correspond to splice variants of the ghrelin gene and to determine the open reading frame of these transcripts, RT-PCRs were performed (using cDNA reverse transcribed with oligo(dT)18 primers) using RNA from the LNCaP prostate cancer cell line, human testis and pancreas (with a forward primer in exon 1 of ghrelin and a reverse primer in the novel exon II, which is common to all of the testis-derived GenBank entries). A single, major amplicon was obtained.
in the testis and LNCaP cell line, representing exons 1, 2 and II of GHRL (Fig. 1; Supplementary Figure 1, see section on supplementary data given at the end of this article; GenBank: JN243773). We have termed the identified full-length splice variant in2c-ghrelin (intron 2 cryptic-ghrelin). The exons for in2c-ghrelin have canonical GT/AG splice junctions, with the exception of the intron flanking a 5′ truncated exon II, exon IIb, which harbours a rare GT/AC junction (Burset et al. 2000; Fig. 2). The cryptic exons in the human gene are not conserved in the mouse or rat, which would, therefore, be unlikely to express the in2c-ghrelin isoform (data not shown). These analyses demonstrate that the human GHRL gene contains additional exons within intron 2 that are bona fide internal exons of preproghrelin splice variants that harbour exons 1–4.

The novel in2c-ghrelin isoform includes cryptic exons that lead to a frameshift in the translation of preproghrelin. The 83 amino acid in2c-ghrelin isoform harbours the coding region for the 28 amino acid mature ghrelin peptide (Fig. 3). While the C-terminal (C-ghrelin) region of wild-type ghrelin encodes a 66 amino acid peptide, the open reading frame of in2c-ghrelin encodes the first 24 amino acids of the C-ghrelin sequence and eight unique C-terminal residues, before the introduction of a stop codon. As a result of the frameshift, it lacks the coding sequence for obestatin (Fig. 3). The 3′ untranslated region of the mRNA is otherwise identical to wild-type ghrelin and has the same polyadenylation signal.

Quantification of in2c-ghrelin in normal tissues

To selectively amplify the in2c-variant and to avoid co-amplification of ghrelin pre-mRNA or genomic DNA, we designed a reverse qRT-PCR primer that spans the exon II–exon 3 junction (Supplementary Figure 2, see section on supplementary data given at the end of this article). Quantitative real-time RT-PCR analyses of 48 tissues show that in2c-ghrelin mRNA, in contrast to...
the wild-type ghrelin transcript (Gnanapavan et al. 2002, Ueberberg et al. 2009), is expressed in a small number of tissues, including the stomach, lymph node, peripheral blood leucocytes, testis, epididymis, skin and adrenal gland (Fig. 4).

Quantification of in2c-ghrelin in cell lines

Next, we examined the expression of in2c-ghrelin in cultured cells using qRT-PCR. In2c-ghrelin was highly expressed in the PC3, LNCaP and 22Rv1 prostate cancer cell lines, while the DU145 prostate cancer cell line did not express this transcript (Fig. 5). In2c-ghrelin expression was low in the lung, ovarian and breast cell lines examined. Interestingly, in2c-ghrelin is expressed in the SKOV-3 ovarian cancer cell line but not in the hOSE1.7 normal ovarian cell line (Fig. 5).

In2c-ghrelin expression in normal vs tumour samples

To further explore the role of in2c-ghrelin in cancer, we analysed the expression of the variant using commercial cDNA arrays from OriGene. In the testis cDNA tissue panel, in2c-ghrelin was expressed in normal testicular tissue but is absent or present at low levels in testicular tumour samples (Fig. 6A). Conversely, prostate tumours exhibited high levels of in2c-ghrelin compared with normal prostate tissue (with 9/19 expressing higher levels than normal tissue and 14/19 prostate tumours expressing the variant; Fig. 6B). Finally, normal breast (Fig. 6C) and ovary (Fig. 6D) samples did not express in2c-ghrelin, while the transcript was expressed in 13/20 breast tumours and 7/21 ovarian tumours examined. Together, these results demonstrate that in2c-ghrelin is expressed at high levels in prostate cancer cell lines and prostate tumour tissue. It is expressed in all normal testis samples examined, while its expression is low or absent in testicular tumours, and it is expressed in breast and ovarian tumour, but not normal tissue.

In2c-ghrelin expression is regulated by insulin in prostate cancer cells

The microarray experiment revealed that in2c-ghrelin was regulated by insulin in LNCaP prostate cancer cells; therefore, we confirmed that this transcript is insulin regulated using quantitative RT-PCR of the LNCaP and 22Rv1 prostate cancer cell lines. As shown in Fig. 7A, treatment with 10 nM insulin significantly increased the expression of in2c-ghrelin in the LNCaP (1.3-fold, P<0.05) and 22Rv1 (4.4-fold, P<0.05) prostate cancer cell lines. Interestingly, insulin also significantly upregulated the expression of a recently reported intron 1-retained transcript, in1-ghrelin (Kineman et al. 2007, Gahete et al. 2010, 2011). A 2.2-fold increase in expression was observed in LNCaP cells and a 2.8-fold increase in 22Rv1 cells (Fig. 7B).

Discussion

We have demonstrated a new ghrelin isoform that is regulated by insulin treatment in prostate cancer cell lines. Cryptic exon sequence in the in2c-ghrelin variant leads to a frameshift in the translation of preproghrelin

Figure 4
Relative expression of in2c-ghrelin in human tissues by quantitative real-time RT-PCR. Data were normalised to β-actin and are represented as fold changes relative to the expression in the adrenal gland (1.0).
and leads to an open reading frame that would encode an 83 amino acid preproghrelin peptide, which is considerably shorter than the 117 amino acid wild-type form. This isoform contains the 28 amino acid ghrelin but lacks an 83 amino acid preproghrelin peptide, which is conserved to normal prostate tissue, which may indicate that the variant could be a useful diagnostic or prognostic marker for this cancer. A recent in vitro binding study using a fluorescein-labelled ghrelin-derived probe (consisting of the first 18 amino acids of ghrelin) has demonstrated that ghrelin may have potential as a diagnostic or prognostic marker for prostate cancer (Lu et al. 2012). Ghrelin binding was significantly higher in clinical samples of prostate cancer compared with normal tissue and samples of benign prostate hyperplasia in a study with 13 patients undergoing radical prostatectomy (Lu et al. 2012). If this probe is effective in vivo, it could be combined with positron emission tomography scanning and be useful for discriminating between benign disease and cancer and possibly for detecting micrometastases (Lu et al. 2012).

Treatment with acylated ghrelin stimulates cell proliferation through the ERK1/2 pathway in the PC3 and LNCaP prostate cancer cell lines (Jeffery et al. 2002, Yeh et al. 2005). Ghrelin may stimulate cell proliferation by acting through the GHSR1a, which is expressed in prostate cancer cell lines (Jeffery et al. 2002, Yeh et al. 2005), although it is also possible that ghrelin may act through the unidentified, widely hypothesised alternative ghrelin receptor (Chopin et al. 2012). We have demonstrated that GOAT is expressed in prostate cancer cell lines (I Seim, P Jeffery, I Amorim, A Herington & L Chopin 2012, unpublished observation), indicating that ghrelin may be acylated in these cells. The role of ghrelin in prostate cancer growth remains uncertain, however. A similar increase in cell proliferation in response to ghrelin treatment was seen in the PC3 cell line in another study using lower concentrations of ghrelin, while supraphysiologi- cal levels (1000 nM) inhibited proliferation in this study (Cassoni et al. 2004). Recently, a third laboratory demonstrated that ghrelin decreases proliferation and promotes apoptosis of PC3 cells (Diaz-Lezama et al. 2010). In this study, however, the investigators measured tritiated thymidine incorporation (DNA synthesis) in the last 6 h of a 72-h ghrelin treatment, and it is unlikely that ghrelin would have been intact at this point of the experiment. Ghrelin is unstable in culture, with a short half-life, with the octanoyl group (acylation) being rapidly lost and the peptide rapidly cleaved (De Vriese et al. 2004, Hosoda et al. 2004). Contrasting observations have also

Figure 5
Relative expression of in2c-ghrelin in human cell lines using quantitative real-time RT-PCR. Data are represented as mean and ± S.E.M. from two technical replicates of two independent replicate experiments (n = 2). The housekeeping gene, 18S ribosomal RNA, was used as a reference for normalisation. Data are represented as fold changes relative to expression of transcripts in the Beas-2B normal lung cell line (set at 1).
been observed for the LNCaP and DU145 cell lines (Cassoni et al. 2004, Yeh et al. 2005). We propose that the observed discrepancies may arise from the use of different forms of the cell lines, the different types of assays used and the handling and stability of the acylated ghrelin peptide.

In2c-ghrelin is expressed in all normal testis samples examined, while it is expressed in a small number of testicular tumours. This correlates well with previous studies, which have shown that the ghrelin peptide is present in normal human testis (Gaytan et al. 2004, Ishikawa et al. 2007) and in a subset of testicular tumours (Gaytan et al. 2004). Employing a small number of normal samples, we also demonstrate that in2c-ghrelin is expressed in breast and ovarian tumours but not in normal breast or ovary. The SKOV-3 ovarian cancer cell line expresses the in2c-ghrelin variant, but no expression was detected in the hOSE17.1 normal ovary-derived cell line. Ghrelin has previously been shown to be expressed in breast cancer and, as is the case for prostate cancer, studies from other laboratories report different responses in cell proliferation assays when cell lines are treated with exogenous ghrelin peptide (Cassoni et al. 2001, Jeffery et al. 2005).

The in2c-ghrelin isoform is expressed in a limited number of normal tissues (including the testis) and at higher levels in many tumours. In normal tissues, in2c-ghrelin expression was most abundantly expressed in lymph node tissue. Interestingly, the LNCaP cell line, which demonstrated very high levels of in2c-ghrelin, is derived from a lymph node metastasis (Yu et al. 2009). Furthermore, in2c-ghrelin is expressed in peripheral blood leukocytes, indicating that it may play a role in immune regulation. Indeed, the ghrelin peptide has been shown to play an immunoregulatory role (Baatar et al. 2011).

Figure 6
Relative expression of in2c-ghrelin in cancer determined using real-time quantitative RT-PCR. The labels in X-axis indicate the clinical status of the subjects (N denotes normal, Roman numerals indicate disease stages). Data represented as fold changes relative to the expression in a normal tissue sample (set at 1.0) or in the absence of expression in a normal tissue a tumour sample. (A) Testis, (B) prostate, (C) breast and (D) ovary.
A number of other ghrelin isoforms have also been described previously (Seim et al. 2009, 2011a), including exon 3-deleted preproghrelin (Jeffery et al. 2005, Yeh et al. 2005) and the intron 1-retained transcript (originally termed in2-ghrelin but renamed in1-ghrelin using the current ghrelin gene nomenclature; Kineman et al. 2007, Gahete et al. 2010, 2011). In1-ghrelin would encode a 117 amino acid polypeptide that includes the signal peptide of preproghrelin, the first 12 amino acids of the 28 amino acid ghrelin peptide sequence and a novel 81 amino acid C-terminal peptide, but not obestatin (Gahete et al. 2007). In1-ghrelin is regulated in response to metabolic stress in mice (Kineman et al. 2007) and is down-regulated in particular brain regions in Alzheimer’s disease in humans (Gahete et al. 2010) and upregulated in breast cancer (Gahete et al. 2011).

We speculate that the in2c-ghrelin variant is another example that illustrates an emerging theme where mRNA transcripts encode ghrelin but not obestatin, as is the case for exon 3-deleted ghrelin and in1-ghrelin. Indeed, evidence is emerging that obestatin, the peptide derived from exon 3 of preproghrelin, may be a growth factor that could promote or inhibit cancer progression, depending on the cancer type (Pazos et al. 2007, 2009, Volante et al. 2009). Similarly, putative obestatin-coding transcripts that lack the ghrelin coding region are also expressed in prostate cancer cell lines (Seim et al. 2007). These studies suggest that cells can regulate the production of ghrelin gene-derived peptides independently by means of alternative splicing and this could partly explain the observed lack of correlation between plasma ghrelin and obestatin (or C-ghrelin) peptide levels (Bang et al. 2007, Pemberton et al. 2003). One small study has reported that the ratio of acylated ghrelin to total ghrelin (acyl and desacyl ghrelin combined) in the circulation was higher in prostate cancer patients compared with subjects with benign prostatic hyperplasia (Malendowicz et al. 2009). By contrast, obestatin was not elevated in these patients (Malendowicz et al. 2009).

Insulin regulates a large number of genes (O’Brien & Granner 1996, Rome et al. 2003, Hartmann et al. 2009), and in this study, we have demonstrated that insulin increases the expression of in2c-ghrelin and in1-ghrelin in the LNCaP and 22Rv1 prostate cancer cell lines. Insulin treatment also up-regulates ghrelin expression in mouse stomach oxyntic glands (which are the major site of ghrelin expression; Toshinai et al. 2001) and in adipocytes (Gurriaran-Rodriguez et al. 2011). Conversely, insulin down-regulates the expression of wild-type and in1-ghrelin mRNA in the mouse hypothalamus, where it has an effect on appetite regulation (Kineman et al. 2007, Fick et al. 2009). The regulation of ghrelin in cancer has yet to be established, and this is the first study to demonstrate regulation of ghrelin transcripts by insulin in cancer.

Although in2c-ghrelin is insulin regulated in the prostate, we failed to detect the in2c-ghrelin isoform in the pancreas itself, despite the fact that the wild-type ghrelin transcript and the ghrelin peptide are abundantly expressed in the endocrine pancreas and ghrelin appears to play an important role in glucose homoeostasis and insulin regulation (Granata et al. 2010). The importance of the ghrelin axis in the regulation of blood glucose was recently illustrated in a study of the ghrelin acylation
enzyme, GOAT, knockout mouse, which is unable to produce acylated ghrelin. Under severe caloric restriction (60%), GOAT knockout mice are unable to maintain glucose homeostasis and die; however, animals can be rescued with the administration of acylated ghrelin or GH (Zhao et al. 2010). This finding has been contradicted, however, by a comprehensive study using a range of mouse models, suggesting that the ghrelin axis may not play an important role in insulin regulation in response to caloric restriction (Yi et al. 2012).

Ghrelin has been linked directly with obesity given its clear role in appetite, energy balance and metabolic regulation, and ghrelin and GOAT are important targets for the treatment of obesity (Lim et al. 2011). In addition to being a risk factor for cancer, obesity is associated with metabolic syndrome, which is also typified by hyperinsulinaemia (Hammarsten & Peeker 2011). There is mounting evidence that elevated circulating insulin levels are positively associated with increased cancer risk and particularly with breast and prostate cancer (Amling 2005, Hammarsten & Hogstedt 2005, Buschemeyer & Freedland 2007, Ma et al. 2008, Gunter et al. 2009, Hammarsten et al. 2010, Healy et al. 2010, LeRoith 2010, Bao et al. 2011, Hammarsten & Peekler 2011, Suissa et al. 2011, Wilson 2011). Although there have been few studies at the cellular level, insulin appears to play a role in the progression of prostate cancer. Insulin stimulates cell proliferation in cultured breast and prostate cancer cell lines (Lann & LeRoith 2008, Pollak 2008) and promotes tumour progression by stimulating de novo steroidogenesis in prostate cancer (Lubik et al. 2011). Interestingly, diet-induced hyperinsulinaemia results in increased cell proliferation of LNCaP prostate cancer cell xenografts in mice (Venkateswaran et al. 2007). We show that in2c-ghrelin is expressed in the PC3 prostate cancer cell line, which is derived from a bone metastasis (Yu et al. 2009). Men with hyperinsulinaemia are more likely to develop bone metastases and progress faster to terminal, castrate-resistant prostate cancer (Amling 2005, Hammarsten & Hogstedt 2005, Buschemeyer & Freedland 2007, Ma et al. 2008, Gunter et al. 2009, Hammarsten et al. 2010, Healy et al. 2010, LeRoith 2010, Bao et al. 2011, Hammarsten & Peekler 2011, Suissa et al. 2011, Wilson 2011). Although there have been few studies at the cellular level, insulin appears to play a role in the progression of prostate cancer. Insulin stimulates cell proliferation in cultured breast and prostate cancer cell lines (Lann & LeRoith 2008, Pollak 2008) and promotes tumour progression by stimulating de novo steroidogenesis in prostate cancer (Lubik et al. 2011). While hyperinsulinaemia has been associated with prostate cancer progression, androgen deprivation therapy, the standard treatment for advanced prostate cancer, frequently gives rise to metabolic syndrome and insulin resistance, with hyperinsulinaemia, elevated fasting blood glucose and elevated C-reactive peptide (Aggarwal et al. 2011). As insulin treatment leads to increased ghrelin expression in the LNCaP prostate cancer cell line, this may also increase cell proliferation in prostate cancer.

In conclusion, in this study, we have identified bona fide exons within intron 2 of the ghrelin gene locus (GHRL) and described a novel ghrelin isoform that, together with the recently described in1-ghrelin isoform, is upregulated by insulin in prostate cancer cell lines. In2c-ghrelin includes cryptic exon sequence and would result in the translation of an 83 amino acid preproghrelin isoform that encodes ghrelin but not obestatin. In2c-ghrelin is expressed in a range of tumour samples derived from the prostate, breast and ovary, but in a limited number of normal tissues, including lymph nodes, stomach and testis. Further studies are warranted to elucidate the role of ghrelin gene products in normal physiology and in conditions associated with hyperinsulinaemia and in cancer.

Supplementary data
This is linked to the online version of the paper at http://dx.doi.org/10.1530/JME-12-0150.

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.

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References


Chopin LK, Seim I, Walpole CM & Herlinton AC 2012 The ghrelin axis—does it have an appetite for cancer progression? *Endocrine Reviews* **33** 849–891. (doi:10.1210/er.2011-00107)


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