

## Distribution and Regional Stressor-Induced Regulation of Corticotrophin-Releasing Factor Binding Protein in Rainbow Trout (*Oncorhynchus mykiss*)

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The corticotrophin-releasing factor (CRF) system plays a key role in the co-ordination of the physiological response to stress in vertebrates. Although the binding protein (BP) for CRF-related peptides, CRF-BP, is an important player in the many functions of the CRF system, the distribution of CRF-BP and the impact of stressors on its expression in fish are poorly understood. In the present study, we describe the distribution of CRF-BP in the brain and peripheral tissues of rainbow trout (*Oncorhynchus mykiss*) using a combination of real-time reverse transcriptase-polymerase chain reaction, *in situ* hybridisation and immunohistochemistry. Our results indicate a widespread and highly localised distribution of CRF-BP in the central nervous system, but do not support a significant peripheral production of the protein. Major expression sites in the brain include the area ventralis telencephali, nucleus preopticus, anterior and lateral tuberal nuclei, and the posterior region of the pituitary pars distalis. We further characterise changes in CRF-BP gene expression in three discrete brain regions after exposure to 8 h and 24 h of social stress or hypoxia. The plasma cortisol concentration in subordinate fish was much higher than in dominant fish and controls, and was indicative of a relatively severe stressor. By contrast, the increase in plasma cortisol concentration in fish exposed to hypoxia was characteristic of the response to a mild stressor. Changes in CRF-BP gene expression were only observed after 24 h of either stressor, and were region-specific. CRF-BP mRNA in the telencephalon increased in both subordinate fish and fish exposed to hypoxia, but CRF-BP in the preoptic area only increased after 24 h of hypoxia exposure. In the hypothalamus, CRF-BP mRNA levels decreased in dominant fish relative to controls after 24 h. Taken together, our results support a diverse role for CRF-BP in the central actions of the fish CRF system, but a negligible role in the peripheral functions of circulating CRF-related peptides. Furthermore, the differential changes in fore-brain CRF-BP mRNA appear to occur independently of the hypothalamic-pituitary-inter-renal axis.

**Key words:** CRF, CRF-BP, gene expression, *in situ* hybridisation, stress.

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Corticotrophin-releasing factor (CRF) belongs to a family of related neuropeptides that regulate a variety of physiological processes associated with the maintenance of homeostasis during stress (1). In fish, other members of the CRF family include urotensin-I (UI; orthologue to tetrapod urocortin, UCN), and homologous peptides to mammalian UCN-2 and -3 (2). CRF is perhaps best known as the apex hormone of the hypothalamic-pituitary-inter-renal (HPI) axis that controls circulating levels of glucocorticoids; however,

CRF-related peptides play a diverse role in mediating an animal's response to stress (3), including cardiovascular modulation (4) and altered food intake (5). CRF-related peptides signal through a common family of receptors (6,7) and are further modulated by a shared binding protein (CRF-BP) (8).

CRF-BP is a highly conserved 37-kDa protein originally isolated from human plasma (9) and is present in all vertebrate classes (8). With a high-affinity for all CRF-related peptides (10) and a broad

distribution in the brain (11, 12), CRF-BP is likely to be an important player in the many functions of the vertebrate CRF system. Central distribution of CRF-BP in the zebrafish (12) is widespread and shares some homologous expression sites with mammals (11). Conversely, peripheral distribution varies tremendously among vertebrates. For example, most primates have a circulating CRF-BP (13) that is produced in the liver (14) and intrauterine tissues (15). *Xenopus laevis* tadpoles express CRF-BP in the tail (16) and *Cyprinus carpio* contain CRF-BP immunopositive cells in the gills and skin (17).

The first functions described for CRF-BP were to inhibit CRF signalling at its receptors. For example, CRF-BP reduced CRF-induced release of adrenocorticotrophic hormone (ACTH) in rat pituitary cultures (14), and the high levels of circulating CRF during the third trimester are attenuated by parallel high levels of CRF-BP in humans (18). More recently, high levels of CRF-BP in tadpole tails have been shown to protect the cells from the apoptotic signalling of CRF (19). Contrary to these inhibitory functions, CRF-BP is obligate for CRF signalling in certain dopaminergic neuronal populations in rats (20); thus, its functional role is likely distribution-dependent (21). Furthermore, regulation of CRF-BP by glucocorticoids and/or CRF in the brain (22, 23), plasma (24, 25), and in cultured nerve cells (26–28) implies a role for CRF-BP in the stress-induced functions of the CRF system.

Fish present an opportunity to study both conserved and unique attributes of the vertebrate CRF system. Although stressor-induced activation of the HPI-axis and changes in CRF-related peptide expression have been well studied, the impact of stress on CRF-BP expression in fish is poorly understood. Both UI and CRF circulate in fish (29, 30), and the concentrations of plasma CRF reached in stressed fish greatly exceeds any reported in mammals (30). Conversely, CRF-BP does not appear to circulate in fish (30), suggesting that it may be involved in local and tissue-specific peripheral regulation of CRF-related peptides. The extent of CRF-BP production outside the central nervous system (CNS) remains largely unknown. The present study aimed to characterise CRF-BP distribution in rainbow trout (*Oncorhynchus mykiss*) using a combination of gene and protein expression tools, and to assess its regulation during two different stress regimes in three brain regions. We measured the relative mRNA levels using real-time reverse transcriptase-polymerase chain reaction (RT-PCR) in ten regions of the CNS, twelve peripheral tissues, and in the brains of fish in dominant-subordinate pairs or exposed to hypoxia at two time points. CRF-BP location in the brain was further characterised using *in situ* hybridisation and immunohistochemistry. This research supports an important functional role for CRF-BP in the fish CRF system based on its broad central distribution and region- and time-specific responses to stressors.

## Materials and methods

### Animals

Juvenile rainbow trout (*O. mykiss*) of mixed sex were obtained from Rainbow Springs Trout Farm (Thamesford, ON, Canada) and housed in 650-l fibreglass

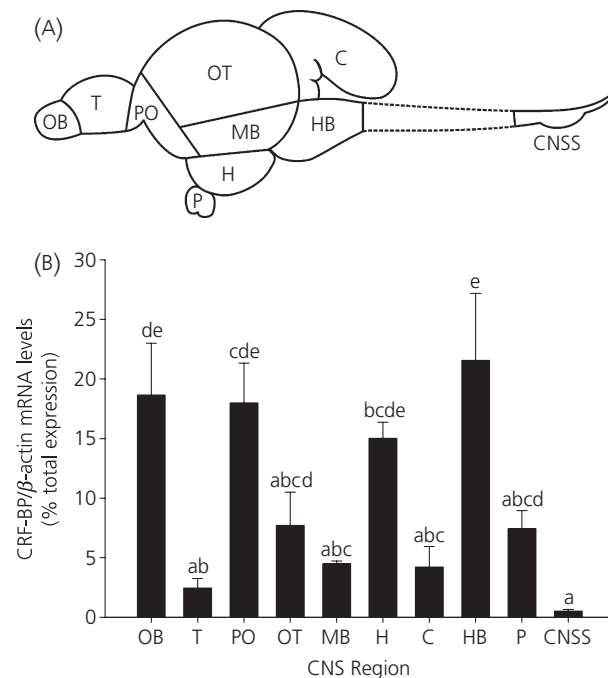
tanks in the Hagen Aqualab Facility at the University of Guelph (Guelph, ON, Canada). Tanks were supplied with aerated local well water maintained at 14 °C. Fish were exposed to a 12 : 12 h light/dark cycle and fed *ad lib* once daily with commercial trout pellets (4pt Classic Sinking fish pellets; Martin Mills, Elmira, ON, Canada). The University of Guelph Animal Care Committee approved care and use of the animals, as per the principles of the Canadian Council for Animal Care.

### Tissue survey of CRF-BP gene expression

Fish of either sex weighing approximately 200 g ( $n = 6-8$ ) were terminally anaesthetised in 2 ml/l 2-phenoxyethanol (Sigma-Aldrich, St Louis, MO, USA) and placed on ice. The CNS was regionally dissected into ten parts: the caudal neurosecretory system (CNSS), and eight brain regions plus the pituitary after (31) (Fig. 1A). The following twelve peripheral tissues were also collected: whole blood, gill, heart, stomach, intestine, liver, spleen, head kidney, posterior kidney, adipose, skin, and skeletal muscle. All tissues were snap frozen in liquid nitrogen and stored at  $-80$  °C until total RNA extraction.

### Social stress experiment

Twenty-one pairs of juvenile trout ( $101.0 \pm 1.9$  g) were size-matched according to weight. The average difference within a pair was  $1.5 \pm 0.2$  g,



**Fig. 1.** Evidence for broad distribution of CRF-binding protein (CRF-BP) mRNA in the central nervous system (CNS) of rainbow trout. (A) Schematic of the trout CNS showing the ten regions assayed for CRF-BP mRNA. (B) Real-time reverse transcriptase-polymerase chain reaction amplification of CRF-BP normalised to  $\beta$ -actin gene expression in the CNS regions outlined in (A), expressed as per cent total expression. Bars that do not share a common letter are significantly different, as assessed with a one-way ANOVA and Tukey's test ( $n = 6-7$ ;  $P < 0.05$ ). C, cerebellum; CNSS, caudal neurosecretory system; H, hypothalamus; HB, hindbrain; MB, midbrain; OB, olfactory bulb; OT, optic tectum; P, pituitary (hypophysis); PO, preoptic area; T, telencephalon.

with a maximal difference of 4.4 g. Each fish in a pair was placed in 30-l aquaria on either side of an opaque divider supplied with constant system water. Fish were fed daily during a 72-h acclimation period, at the end of which the divider was removed and fish were allowed to interact for 8 h or 24 h. During the first 3 h of interaction, social behaviour was indirectly observed for three 5-min periods through an angled mirror. Points were assigned for aggressive attacks, position in the tank, and food acquisition as previously described (31) such that the dominant fish in each pair would have a higher score. In all but one pair, the score of the dominant fish was three- to 50-fold higher than the subordinate; the pair without a clear difference in behavioural score was removed from further analysis. After 8 h or 24 h of interaction, each pair was quickly and terminally anaesthetised as above. Blood was collected via caudal puncture, separated by centrifugation, and the plasma stored at  $-80^{\circ}\text{C}$ . The telencephalon, preoptic area, and hypothalamus from each fish were collected and snap frozen for subsequent RNA extraction. Additionally, six fish ( $162.4 \pm 10.6$  g) were quickly netted from the original stock tank that had not been disturbed for at least 2 weeks prior. These fish were sampled as above and served as a control group.

### Hypoxia stress experiment

Fish were divided into three 125-l tanks ( $n = 10-11$ ;  $120.2 \pm 3.2$  g) and acclimated for 3 weeks during which they were fed daily. At the end of the acclimation period, fish were exposed to normoxic water (85%  $\text{O}_2$  saturation;  $8.8 \text{ mgO}_2/\text{l}$ ; control) or hypoxic water (30%  $\text{O}_2$  saturation;  $3.1 \text{ mgO}_2/\text{l}$ ) for 8 h or 24 h. The oxygen was stripped from a header tank by bubbling nitrogen through the water column, and this water was used to supply the hypoxia treatment groups. At the end of the exposure, fish were terminally anaesthetised and sampled as in the social stress experiment.

### Total RNA extraction and first strand cDNA synthesis

All tissues were mechanically homogenised and total RNA was extracted using TRIzol Reagent according to manufacturer's instructions (Invitrogen Life Technologies, Carlsbad, CA, USA). One microgram of total RNA was treated with DNase I and reverse transcribed to cDNA using SuperScript II RNase H<sup>-</sup> reverse transcriptase according to manufacturer's instructions (Invitrogen). Nonreverse transcribed (no-RT controls) representatives from each tissue were included during cDNA synthesis to monitor genomic contamination.

### Real-time RT-PCR analysis of gene expression

Triplicates of each cDNA sample were amplified by real-time RT-PCR using an ABI Prism 7000 sequence detection system (Applied Biosystems, Foster City, CA, USA). The 20- $\mu\text{l}$  reactions contained 10  $\mu\text{l}$  2X SYBR Green PCR Master Mix (Applied Biosystems), 5  $\mu\text{l}$  five-fold diluted first strand cDNA template or no-RT controls, and 2.5  $\mu\text{l}$  each of forward and reverse primers (0.4  $\mu\text{M}$ ). Manufacturer's settings were used for PCR: 10 min initial denaturation at  $95^{\circ}\text{C}$ , followed by 40 cycles of 15 s denaturation at  $94^{\circ}\text{C}$  and 1 min of annealing/extension at  $60^{\circ}\text{C}$ . To verify that the amplification signal resulted from a single PCR product, a dissociation cycle from  $60-90^{\circ}\text{C}$  was performed following the 40th cycle, and only samples with a unimodal dissociation curve and predicted melting temperature were used. No template controls were used to monitor background amplification and were consistently free of contamination. Primer pairs for real-time RT-PCR were designed using Primer Express 2.0 (Applied Biosystems) based on the complete coding sequence for rainbow trout  $\beta$ -actin (GenBank accession number: AJ438158) and CRF-BP (GenBank accession number: AY363677). An

exon-exon boundary, identified by homology alignments of known genomic sequences ( $\beta$ -actin) or the rainbow trout partial genomic sequence (CRF-BP; GenBank accession number: AY686703) was positioned in either the forward or reverse primer, respectively, to prevent co-amplification of genomic DNA. Primer pairs are listed in Table 1. No-RT controls did not amplify genomic DNA, thus confirming the efficiency of DNase I treatment and primer design. As the level of  $\beta$ -actin mRNA can be affected by exposure to cortisol (S. Alderman, unpublished observation), elongation factor-1 $\alpha$  (EF-1 $\alpha$ ; GenBank accession number: AF498320) was used for normalisation in both stress experiments.

An initial survey of peripheral tissues suggested a low and inconsistent expression of CRF-BP. To ensure that the signal obtained was not a result of nonspecific PCR products, these samples were additionally analysed with the more specific TaqMan assay. Samples ( $n = 6$  per tissue) were run in duplicate and two no-RT controls were included for each tissue. Each reaction contained 12.5  $\mu\text{l}$  of TaqMan Universal PCR Master Mix (Applied Biosystems), 2.5  $\mu\text{l}$  each of forward and reverse primers (9  $\mu\text{M}$ ), 2.5  $\mu\text{l}$  of probe (2.5  $\mu\text{M}$ ), and 5  $\mu\text{l}$  of five-fold diluted first strand cDNA template or no-RT control. With the exception of the dissociation curve, PCR conditions were as described above. Primers and probe were designed against the reverse complement of the tCRF-BP coding sequence and were generously provided by Applied Biosystems (Table 1). The probe was labelled at the 5' end with a FAM fluorescent reporter dye, and at the 3' end with the nonfluorescent quencher minor groove binder.

To account for differences in amplification efficiency, a standard curve was constructed for each target gene using known dilutions of pituitary or hypothalamus cDNA. Input values were obtained by fitting the average threshold cycle ( $C_T$ ) value to the antilog of the standard curve. To correct for minor variations in template input and transcriptional efficiency, these input values were then normalised to the housekeeping gene  $\beta$ -actin (distribution survey) or EF-1 $\alpha$  (stress experiments). To account for regional differences in  $\beta$ -actin expression levels, all input values were corrected to the mean input of the hypothalamus (arbitrarily chosen). All data are expressed as mean  $\pm$  SEM.

**Table 1.** Sequences of Primer Pairs and Probe Used to Amplify  $\beta$ -Actin, Elongation Factor-1 $\alpha$  and Corticotrophin-Releasing Factor Binding-Protein (CRF-BP) in Two Real-Time Reverse Transcriptase-Polymerase Chain Reaction Assays and for Synthesising the CRF-BP Riboprobe Used for *In Situ* Hybridisation.

	Sequence (5' to 3')
SYBR Green assay	
$\beta$ -actin	F: GCC CCC CTC AAC CCC R: GAA GGT CTC AAA CAT AAT CTG GGT C
EF-1 $\alpha$	F: GGG CAA GGG CTC TTT CAA GT R: CGC AAT CAG CCT GAG AGG T
CRF-BP	F: GGA GGA GAC TTC ATC AAG GTG TT R: CTT CTC TCC CTT CAT CAC CCA G
TaqMan assay	
CRF-BP	F: GAG TAT GAC AGC GTT GAC ATC GA R: CAT CAC CCA GCC ATC AAA CAC P: TTG ATG AAG TCT CCT CCC CT
Riboprobe synthesis	
CRF-BP	F: GCT GGA CCC GAC CAG GTC AT R: CAG CTC CAC AAA GTC CCC TG

F, Forward primer; R, reverse primer; P, probe; EF-1 $\alpha$ , elongation factor-1 $\alpha$ .

## Plasma cortisol measurements

The cortisol content of plasma samples was determined using a radioimmunoassay. Each 600  $\mu$ l reaction contained equal volumes of plasma or standards,  $^3$ H-cortisol (7500 cpm; 73.0 Ci/mmol; Amersham Biosciences, Piscataway, NJ, USA) and rabbit anti-cortisol antibody (cat no. F3-314; Esoterix Endocrinology, Calabasas Hills, CA, USA), all appropriately diluted in assay buffer (21.4 mM  $\text{Na}_2\text{HPO}_4 \cdot 7 \text{H}_2\text{O}$ ; 9.3 mM  $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ ; pH 7.6; 0.1% gelatin; 0.01% thimerosal; Sigma). Following overnight incubation at 4 °C, reactions were cooled on ice for 10 min then incubated a further 10 min in the presence of 200  $\mu$ l dextran-coated charcoal (0.5% activated charcoal and 0.05% dextran in assay buffer; Sigma). Bound cortisol was pelleted by centrifugation and the supernatant was combined with 5 ml scintillation cocktail [667 ml toluene, 333 ml Triton X-100, 4 g 2,5-diphenyloxazole, and 0.2 g 1,4-bis(5-phenyl-2-oxazolyl)benzene; 2,2'-*p*-phenylene-bis(5-phenyloxazole); Sigma] and counted on a multi-purpose scintillation counter (LS 6500; Beckman, Fullerton, CA, USA). The antibody concentration used was adjusted to yield 35–45% binding in the absence of cold competitor, and the assay was validated with serial dilutions of trout plasma that ran parallel to the standard curve. Samples were diluted to fall within the 20–80% range of the standard curve (ten- and 100-fold for unstressed and stressed fish, respectively). Determination of plasma cortisol concentration was achieved by a three-parameter sigmoidal curve regression equation fitted to the standard curve (SigmaPlot 10.0; SPSS, Chicago, IL, USA).

## In situ hybridisation

Juvenile trout of either sex weighing 80–120 g ( $n = 5$ ) were terminally anaesthetised in 2 ml/l 2-phenoxyethanol then injected with 100 IU heparin in 0.9% NaCl by caudal puncture. Fish were transcardially perfused with 0.9% NaCl for 10 min, followed by 25 min with 4% paraformaldehyde (PFA) in phosphate-buffered saline (PBS) at 2 ml/min using a Miniplus 3 peristaltic pump (Gilson Inc, Middleton, WI, USA). Brains were removed intact to 4% PFA in PBS and processed for cryosectioning as previously described (12). Serial transverse 12  $\mu$ m cryosections were collected every 150  $\mu$ m throughout the brain. Sense and antisense digoxigenin (DIG)-labelled riboprobes were generated using a 479-bp cloned fragment of tCRF-BP and were hybridised to adjacent sections as previously described (12) (for primers, see Table 1). Identification of positively stained nuclei was performed as previously described (32).

## Immunohistochemistry

Two fish were terminally anaesthetised and the hypothalamus quickly removed for overnight fixation in Bouin's fixative. Following dehydration and embedding in paraffin, serial sagittal sections (7  $\mu$ m) were collected and immunostained for CRF-BP, as previously described (33), using the Vectastain ABC method (Vector Laboratories, Burlingame, CA, USA). Briefly, sections were deparaffinised in xylene and rehydrated through a graded ethanol series. Endogenous peroxidase activity was blocked in 1%  $\text{H}_2\text{O}_2$  in methanol, and nonspecific binding sites were blocked in 5% goat serum. Rabbit anti-human CRF-BP (generously donated by W. Vale) was applied at 1 : 2000 for 1 h at room temperature, followed by goat anti-rabbit IgG-biotin (1 : 200) for 30 min. After 30 min of incubation in an avidin-biotin horseradish peroxidase (HRP) complex (Vectastain ABC reagent; Vector Laboratories), HRP was visualised using freshly prepared 0.1% 3,3'-diaminobenzidine tetrachloride in 0.1 M Tris buffer (pH 7.2) containing 0.02%  $\text{H}_2\text{O}_2$ . Controls on serial sections for endogenous protein-bound biotin and cross-reactivity of the primary and secondary antibodies were all negative. Pre-adsorption controls on serial sections were also included to confirm positive immunostaining results. Briefly, the undiluted primary antibody was incubated with recombi-

nant hCRF-BP (kindly provided by W. Vale) at a ratio of 1 : 10 (v/w) overnight at 4 °C and centrifuged for 25 min at 17 000 g. The supernatant was diluted to the working dilution of 1 : 2000 in PBS and used in place of the primary antibody in the procedure above.

## Imaging

Photomicrographs were captured on a digital camera using OpenLab software (Improvision Incorporated, Lexington, KT, USA). Minor adjustments in brightness and contrast were made in Adobe Photoshop 6.0 (Adobe Systems Inc., San Jose, CA, USA) to improve the quality of presentation without changing or enhancing positive staining. Line drawings were created from original photomicrographs using CorelDRAW X3 (Corel Corporation, Ottawa, Canada).

## Statistical analysis

For the tissue survey of gene expression, four outliers from the CNS, one from each of olfactory bulbs, telencephalon, pituitary, and midbrain, were determined as being greater than or less than 2.0 $\times$  inter-quartile range from the upper quartile or lower quartile, respectively, and were subsequently removed. A one-way ANOVA followed by Tukey's test for multiple comparisons was used to determine differences in gene expression between regions in the CNS ( $n = 6$ –7) or between treatment groups ( $n = 6$ –11), and to assess changes in plasma cortisol between treatment groups ( $n = 6$ –11). Data that did not meet the assumption of normality was log-transformed prior to analysis (Social Stress: telencephalon and hypothalamus gene expression; Hypoxia: telencephalon and preoptic area gene expression). If the transformed data still did not conform to the assumptions of ANOVA, a Kruskal-Wallis one-way ANOVA on ranks followed by a Dunn's test for multiple comparisons was performed (Social Stress: hypothalamus gene expression; Hypoxia: plasma cortisol). All analyses were performed using SigmaStat 3.0 (SPSS Inc., Chicago, IL, USA).  $P < 0.05$  was considered statistically significant.

## Results

### Distribution of CRF-BP in the trout central nervous system

Overall, there was a broad distribution of CRF-BP gene expression in the trout CNS (Fig. 1), with four of the ten regions accounting for over 70% of total expression (Fig. 1b). Moving caudally, these areas of highest expression were the olfactory bulbs (18.7%), preoptic area (18%), hypothalamus (15%), and hindbrain (21.5%). CRF-BP gene expression was lowest in the CNSS, which represented only 0.5% of the total CRF-BP gene expression in the CNS. Although the level of expression in the CNSS did not differ significantly from other areas of low expression ( $P > 0.05$ ), it was at least five-fold lower than any other region in the CNS. The remaining five regions combined (telencephalon, optic tectum, midbrain, cerebellum, and pituitary) accounted for less than 30% of total CRF-BP gene expression, with none of the regions individually representing more than 10% of total expression.

Trout brain sections successfully hybridised the antisense DIG-labelled CRF-BP riboprobe, whereas sections applied with the sense riboprobe were consistently clear of staining. Although no CRF-BP mRNA was labelled in the olfactory bulbs, the telencephalon showed positive staining in the pars ventralis (Vv; Fig. 2A) and

pars supracommisuralis (Vs; not shown) of the area ventralis telencephali.

CRF-BP mRNA was observed in both the parvocellular and magnocellular divisions of the nucleus preopticus, with the majority of expression occurring in the pars anterior of the parvocellular division (PPa; Fig. 2b). In the optic tectum, CRF-BP mRNA was circumferentially scattered around the ventriculus mesencephali in the first proximal layer of the tecti mesencephali (stratum periventriculare; SPV; Fig. 2c). Staining of the SPV occurred from the rostral tip of the tectum through to the caudal end (Fig. 3c–f). Expression of CRF-BP in the pituitary gland occurred in both the proximal pars distalis (PPD) and the pars intermedia (PI; Fig. 2d), but was absent in the rostral pars distalis. Hypothalamic expression of CRF-BP was extensive, including the lateral and anterior divisions of the tuberal nucleus (nlt and nat, respectively; Fig. 2e, f), the nucleus lateralis recessus (nrl) and the nucleus magnocellularis hypothalami (nmh; Fig. 2f). CRF-BP-like immunoreactive (ir) nerve fibres were also prominent in the hypothalamus (Fig. 4a). In the tuberal hypothalamus, vertically oriented parallel fibre tracts were observed in the anterior region (Fig. 4b). Ventral to the recessus lateralis, darkly stained granular fibres were densely packed (Fig. 4c), reflecting the abundant CRF-BP mRNA in this region (Fig. 2f). Several granular CRF-BP-like-immunoreactive fibres were also found ventral to the recessus posterior (Fig. 4d). Preabsorption of the primary antibody with hrCRF-BP completely absolved the signal on serial sections (Fig. 4e).

In the cerebellum, diffuse expression of CRF-BP was observed in the stratum granulare (not shown). In the hindbrain, the raphe nucleus showed extensive expression in the superior division (ras;

Fig. 2g) and a few cells in the intermediate division (not shown). Hybridisation of CRF-BP mRNA in the hindbrain was also evident in the nucleus motorius nervi trigemini (not shown).

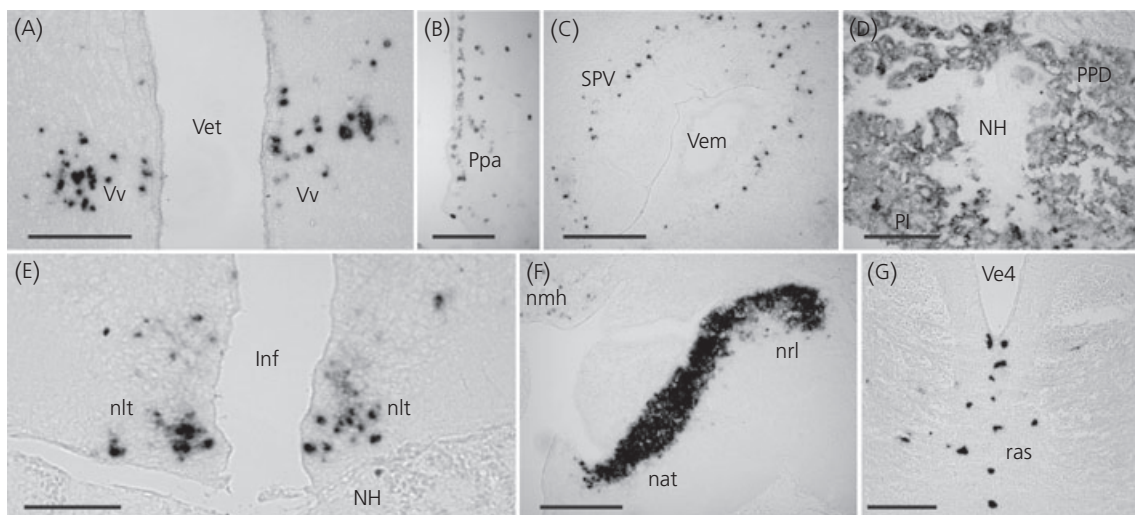
The distribution of CRF-BP mRNA in the trout brain is summarised in Fig. 3, with the level and plane of each section depicted in Fig. 3(A).

### Expression of CRF-BP mRNA in peripheral tissues

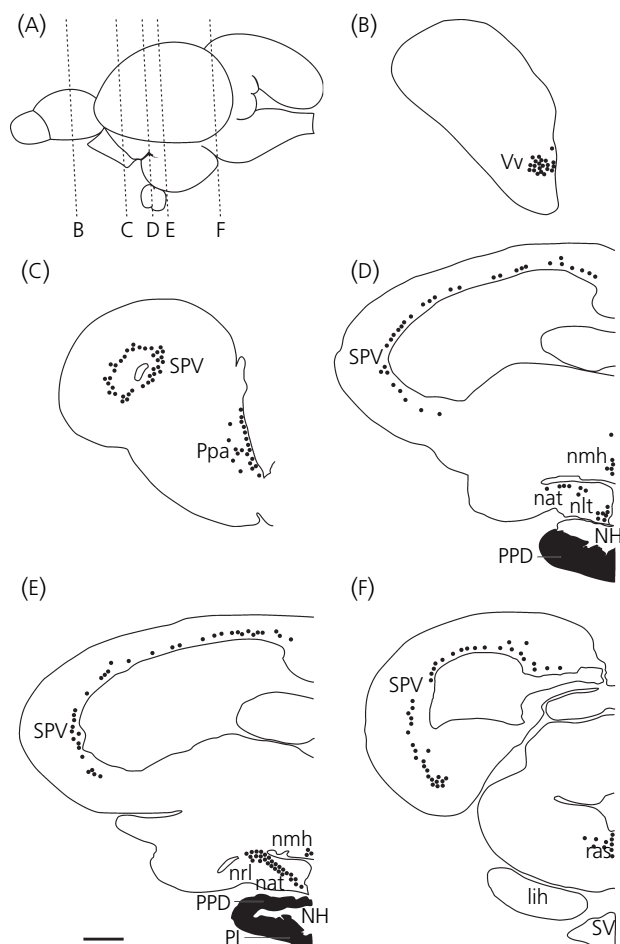
Real-time RT-PCR of CRF-BP in trout peripheral tissues using the SYBR Green assay suggested a very low or negligible level of template cDNA was present in these samples. We therefore employed a more specific technique, the TaqMan assay, to better detect any low level of peripheral expression. Of the 72 tissue samples assayed, only six detected CRF-BP: three gills, and one each of heart, spleen, and skin. Due to this variable and inconsistent amplification, we did not pursue further characterisation of peripheral expression.

### Effect of stress on CRF-BP expression

Size-matched juvenile rainbow trout quickly and irreversibly established a dominant-subordinate ranking in all but one pair. The twenty dominant fish aggressively controlled resources whereas the twenty subordinate fish were restricted to a corner of the aquarium by the frequent aggressive attacks of the dominant fish. The plasma cortisol concentration of the subordinate fish 8 h and 24 h after social stress ( $405.3 \pm 74.7$  ng/ml and  $153.7 \pm 19.3$  ng/ml, respectively) was significantly higher than the control ( $2.9 \pm 0.6$  ng/ml), 8-h post-stress dominant ( $13.7 \pm 6.9$  ng/ml)



**Fig. 2.** CRF-binding protein (CRF-BP) mRNA localisation in the rainbow trout brain as determined by *in situ* hybridisation. (A) The pars ventralis (Vv) shows symmetrical staining on either side of the telencephalic ventricle (Vet). (B) Positively stained nuclei of the anterior parvocellular division of the nucleus preopticus (Ppa) line the third ventricle. (C) CRF-BP expression in the rostral tip of the optic tectum is circumferentially scattered around the ventriculus mesencephalon (Vem) in the stratum periventriculare (SPV). (D) Extensive staining of the pituitary occurred in both the proximal pars distalis (PPD) and pars intermedia (PI), but is obviously absent in the neurohypophysis (NH). (E) CRF-BP is expressed in the lateral tuberal nucleus (nlt) on either side of the infundibulum (Inf). (F) The most prominent staining occurred in the anterior tuberal nucleus (nat) and nucleus lateralis recessus (nrl). Several cells in the magnocellular nucleus of the hypothalamus (nmh) are also positive for CRF-BP mRNA. (G) CRF-BP expression in the superior raphe nucleus (ras) just below the fourth ventricle (Ve4). Scale bars = 300  $\mu$ m, except in (E) where it equals 150  $\mu$ m.



**Fig. 3.** Line drawings through five planes of the trout brain depicting CRF-binding protein (CRF-BP) mRNA expression (black circles). (A) Schematic of the trout brain, sagittal view, showing the sectioning level of the hemisections in (B–F). The drawings correspond approximately to the following figures in the atlas of the trout brain (32): (B) fig. 15.25, (C) fig. 15.22, (D) fig. 15.19, (E) fig. 15.18, (F) fig. 15.16. Scale bar = 600  $\mu\text{m}$ . lih, lateral inferior hypothalamus; nat, anterior tuberal nucleus; NH, neurohypophysis; nlt, lateral tuberal nucleus; nmh, magnocellular nucleus of the hypothalamus; nrl, nucleus lateralis recessus; PI, pars intermedia; Ppa, anterior parvocellular division of the nucleus preopticus; PPD, proximal pars distalis; ras, superior raphe nucleus; SPV, stratum periventriculare; SV, saccus vasculosus; Vv, pars ventralis.

and 24 h-post-stress dominant ( $10.3 \pm 1.9$  ng/ml) fish groups ( $P < 0.001$ ; Fig. 5A). Intra-pair differences between dominant and subordinate fish ranged from four- to over 200-fold. After 8 h of social stress, there was no difference in CRF-BP gene expression associated with social rank in any of the brain regions assessed (Fig. 5B–D). After 24 h of social stress, however, there were clear regional changes in CRF-BP mRNA levels associated with social rank. In the telencephalon, subordinate fish had nearly four-fold higher CRF-BP gene expression than any other group (Fig. 5B;  $P < 0.05$ ). In the preoptic area, there was still no difference in CRF-BP mRNA levels (Fig. 5C;  $P > 0.05$ ) whereas, in the hypothalamus of dominant fish, there was a significant decrease in CRF-BP

mRNA relative to control fish (Fig. 5D;  $P < 0.05$ ) but not their subordinate counterparts ( $P > 0.05$ ).

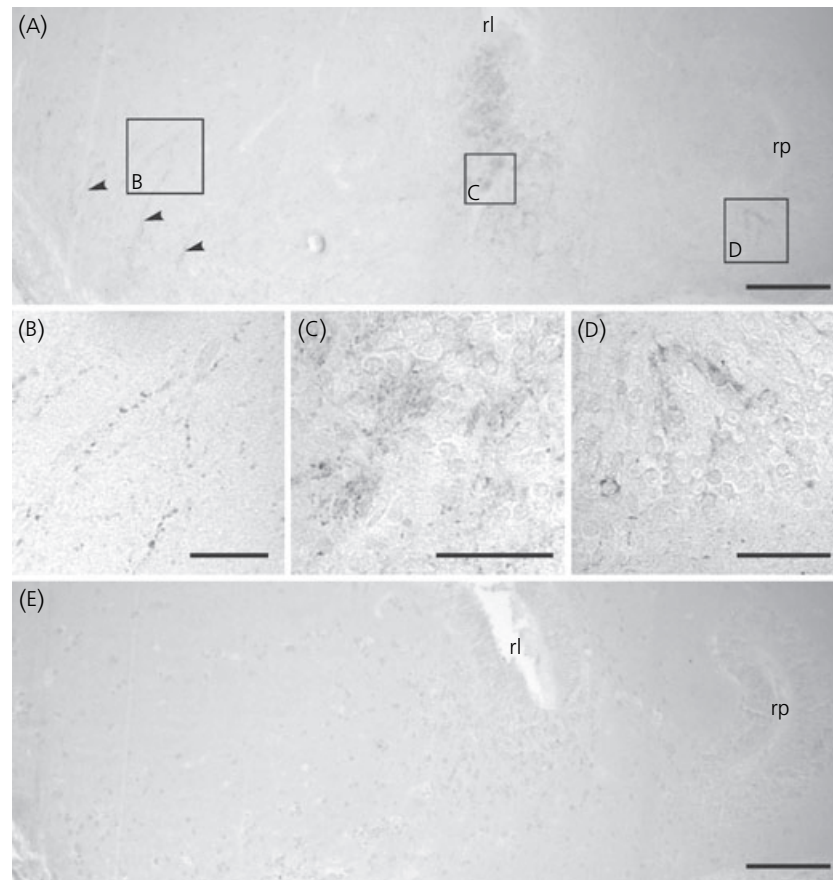
For hypoxia exposure, the desired  $\text{O}_2$  level was achieved gradually over a 1-h period and maintained at  $28 \pm 2\%$  saturation for the duration of the exposure. Although control fish kept to the bottom of the tanks and were comparatively active, fish exposed to hypoxia were found at the surface of the water and tended to remain very still. The plasma cortisol concentration in fish exposed to hypoxia for 8 h ( $7.8 \pm 2.3$  ng/ml) was significantly higher than control fish ( $4.4 \pm 1.8$  ng/ml;  $P < 0.05$ ) but not the 24-h hypoxia-exposed fish ( $8.5 \pm 3.5$  ng/ml), and there was no significant difference between control and 24-h hypoxia-exposed fish (Fig. 6A). After 8 h of exposure to 30% hypoxia, there was no difference in CRF-BP expression relative to control fish in any of the three brain regions (Fig. 6B). After 24 h, CRF-BP mRNA in the telencephalon and preoptic area was significantly higher than the control and 8 h expression levels ( $P < 0.05$ ), but remained basal in the hypothalamus (Fig. 6B). Finally, there was no effect of treatment on the gene expression levels of EF-1 $\alpha$  in either experiment.

## Discussion

The present study provides a thorough analysis of CRF-BP distribution in a teleost fish, including a survey of CRF-BP mRNA expression across the CNS and peripheral tissues. By utilising a combination of molecular techniques, we were able to detail the widespread but highly localised expression pattern of CRF-BP in the CNS of rainbow trout. Our results are supported by other studies of CRF-BP distribution (11, 12) and are in line with the known distribution and many functions of the CRF system. We further show regional- and time-dependent changes in CRF-BP gene expression in response to two unique stressors, suggesting stressor-specific responses by different CRF-BP expressing neuronal populations. Taken together, these results make a significant contribution towards understanding the distribution and function of CRF-BP in lower vertebrates.

As suggested for mammals (34), the broad distribution pattern of CRF-BP in the brain of trout is likely indicative of a role for this protein in the various endocrine and neurotransmitter functions of the equally widespread CRF-related peptides. The mechanism by which CRF-BP interacts with CRF-related peptides is likely to be reflected by its distribution. In rats, for example, the ability of CRF-BP to inhibit CRF-stimulated ACTH release (14) is reflected in the localisation of CRF-BP to corticotrophs (11), whereas the requirement of CRF-BP for CRF-stimulated firing of dopaminergic neurones in the ventral tegmental area (20) predicts a co-localisation of CRF and its binding protein in afferent fibres to this region. Indeed, throughout the rat brain, CRF and its binding protein show varying degrees of co-localisation (34), which may prescribe different functional roles for CRF-BP in different regions, as suggested by its differential subcellular localisation across the brain (35). Additionally, CRF-BP may associate with the CRF-related peptides, UCN (mammals) or UI (fish), in regions where it is not colocalised with CRF. In zebrafish, CRF-BP shows pronounced regional co-expression with CRF and comparatively little UI co-expression (12).





**Fig. 4.** Immunohistochemical localisation of CRF-binding protein (CRF-BP) in the hypothalamus. (A) Low power photomicrograph of CRF-BP-like immunoreactive nerve fibres in the hypothalamus. Image is in sagittal plane, oriented rostral-caudal. (B) Higher magnification of box B in (A) showing positively stained nerve fibres in the anterior tuberal region. (C) Higher magnification of box C in (A) showing positively stained nerve fibres in the area ventral to the recessus lateralis (rl). (D) Higher magnification of box D in (A) showing prominent CRF-BP-like immunoreactivity in the area ventral to the recessus posterior (rp). (E) Pre-absorption of the primary antibody with hrCRF-BP applied to a serial section completely absolved positive staining in the regions described above. (A, E) Scale bar = 200  $\mu\text{m}$ ; (B–D) scale bar = 50  $\mu\text{m}$ .

## CRF-BP localisation in the rainbow trout brain

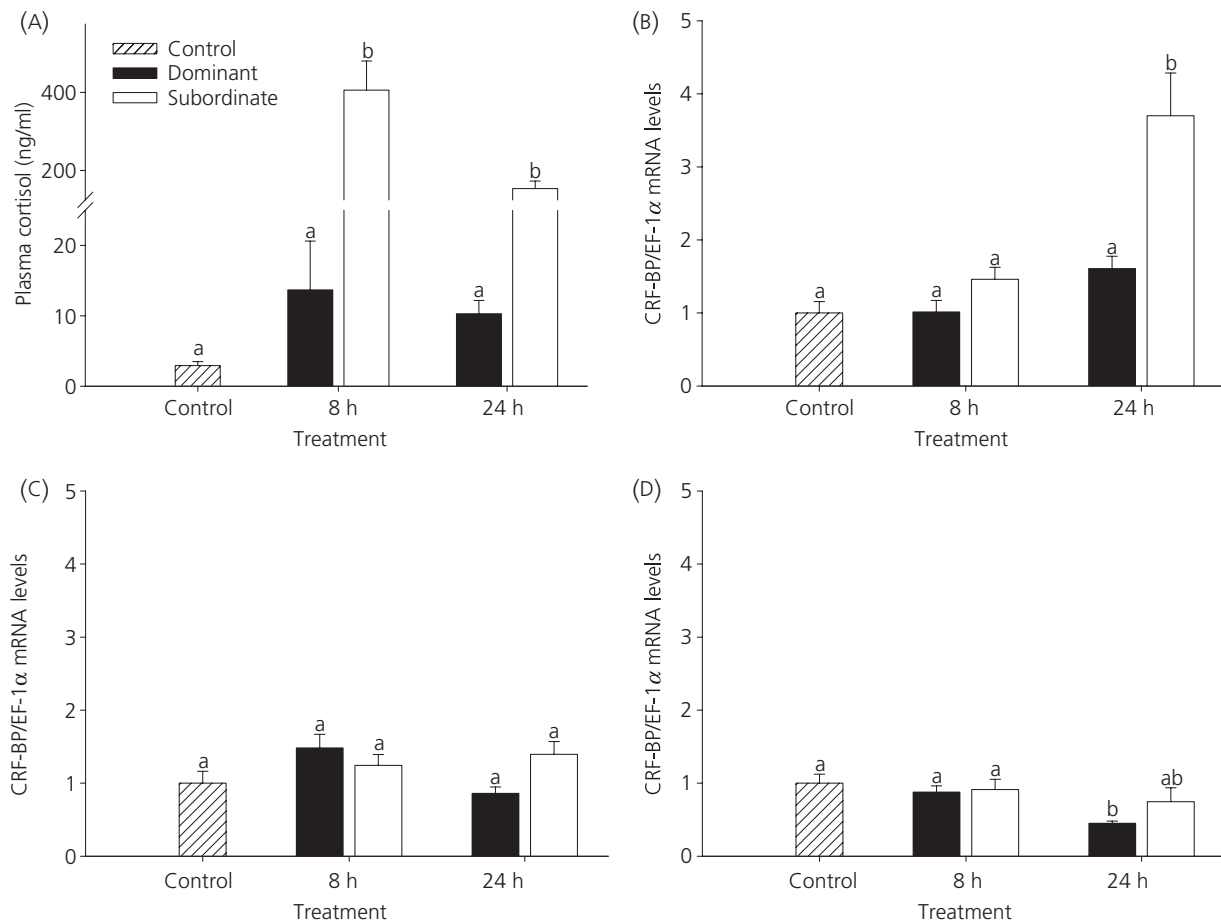
### Olfactory bulbs

The olfactory bulbs in rats are known to contain CRF-BP (11); however, it has yet to be localised to this region in fish. We describe the olfactory bulbs as one of four regions of highest expression in the CNS using real-time RT-PCR, however we were unable to localise the expression by *in situ* hybridisation. Indeed, this apparent discrepancy underlines the importance of complementing these two techniques for studying unknown peptide distribution, especially when comparing expression patterns in tissues with varying signal-to-volume ratios. Assuming that CRF-BP is only expressed in a subset of the diffusely arranged neurones of the olfactory bulbs, two explanations can be provided for these inconsistent results. First, weak or scattered expression might not be detected well by our chromogenic technique and may require the additional sensitivity of fluorescent *in situ* hybridisation in order to be visualised. Second, our sectioning regime yielded less than ten cryosections through the olfactory

bulbs. If CRF-BP expression is localised to a very discrete portion of the olfactory bulbs, these neurones may not have been included in the tissue sections we stained.

### Telencephalon

Expression of CRF-BP in the telencephalon of rainbow trout was restricted to the area ventralis, as was true in zebrafish (12). In rats, telencephalic CRF-BP is predominantly in the amygdala (11). Due to partial eversion of the telencephalon during teleostean development, the amygdala homologue in fish is likely the medial zone of the dorsal telencephalon, which is further supported by the distribution of several neurotransmitters (36). The presence of CRF-BP in the area ventralis and absence in the area dorsalis of fish may indicate novel functions not yet described in vertebrates. CRF-related peptides have also been located in the fish telencephalon (12, 37–39), and their ability to induce anxiety and fear-related behaviours in the mammalian limbic system (40, 41) implicates the telencephalon as an important extra-hypothalamic branch of the CRF system.



**Fig. 5.** Effects of social stress on (A) plasma cortisol, and CRF-binding protein (CRF-BP) mRNA expression in the (b) telencephalon, (c) preoptic area, and (d) hypothalamus of rainbow trout. Fish ( $n = 7-10$ ) were size-matched according to weight and allowed to interact for 8 h or 24 h. Dominance was assigned using behavioural scoring such that dominant fish had a higher score. A control group ( $n = 6$ ) was sampled at random from a stock tank for comparison. CRF-BP mRNA levels were normalised to EF-1 $\alpha$ . Differences between control (hatched bar), dominant (black bars) and subordinate (white bars) fish were determined by a one-way ANOVA and Tukey's post-hoc test (A-C), or a Kruskal-Wallis one-way ANOVA on ranks and Dunn's post-hoc test (D;  $n = 6-10$ ;  $P < 0.05$ ). Bars that do not share a common letter within a given brain region are significantly different.

### Preoptic area

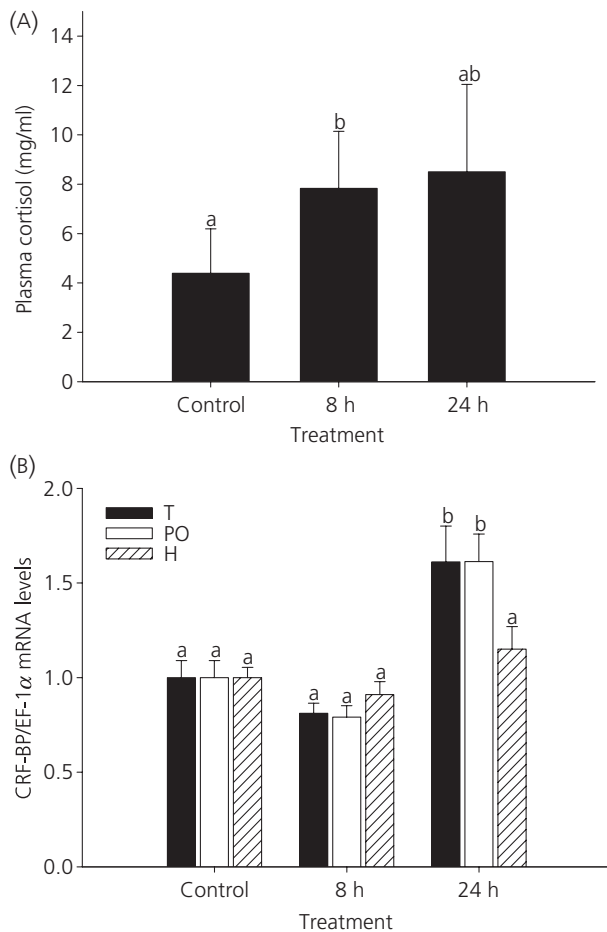
The principal nucleus contained within the preoptic area is the nucleus preopticus (NPO), homologous to the paraventricular nucleus of other vertebrates. This major site of CRF production is where regulation of pituitary ACTH secretion and thus glucocorticoid regulation is initiated. We found abundant expression of CRF-BP in the preoptic area of *O. mykiss*. Although mainly localised to the PPa lining the third ventricle, some expression was found in all major divisions of the NPO. Results of CRF-BP distribution in other fish suggest possible interspecies differences in preoptic area expression. In zebrafish, for example, CRF-BP mRNA was mostly found in the PPa, occasionally in the posterior parvocellular division (PPp) and never in the magnocellular division (PM) (12). At the protein level, only a few CRF-BP-immunoreactive perikarya were observed in the NPO of the common carp (42). It should be noted, however, that all of the histological evidence for CRF-BP distribution in the NPO has been gained from unstressed fish; thus, the potential for CRF-BP expression in the various divisions of the NPO remains to be determined.

### Hypothalamus

The hypothalamus proper is arguably among the most important regions of CRF-BP production in trout, and suggests a functional role for this protein in the CRF system and the neuroendocrine and autonomic control of homeostasis. Real-time RT-PCR analysis grouped the hypothalamus among those regions of highest gene expression, and *in situ* hybridisation highlighted several distinct populations of CRF-BP expression, namely nmh, nat, nlt, and nrl. CRF-BP-like-immunoreactive nerve tracts extending from the tuberal and lateral recessus nuclei reinforced the mRNA expression profile in this area, and the absence of signal in preadsorption controls implies specificity of at least some epitopes for trout CRF-BP. Huising *et al.* (42) also reported a high level of mRNA and little immunoreactivity for CRF-BP in the hypothalamus of *C. carpio*.

Several functions of the CRF-system can be attributed to hypothalamic expression. In fish, CRF-related peptides produced in the nlt are responsible for stimulating the production of ACTH in





**Fig. 6.** Effect of hypoxia on (A) plasma cortisol, and (B) CRF-binding protein (CRF-BP) mRNA expression in the telencephalon (T), preoptic area (PO), and hypothalamus (H) of rainbow trout after 8 h and 24 h of exposure. Differences in plasma cortisol were determined by a Kruskal–Wallis one-way ANOVA on ranks and Dunn's post-hoc test ( $n = 10\text{--}11$ ;  $P < 0.05$ ). CRF-BP mRNA levels were normalised to EF-1 $\alpha$ , and differences between treatments were determined by a one-way ANOVA and Tukey's test ( $n = 9\text{--}11$ ;  $P < 0.05$ ). Bars that do not share a common letter within a given brain region are significantly different.

pituitary corticotrophs (43). The additional presence of CRF-BP in this nucleus (12; present study) lends support to a functional role for CRF-BP in regulating the neuroendocrine activities of the CRF-system. Stress-induced anorexia is another documented role for CRF-related peptides in the hypothalamus (5). Intracerebroventricular injections of CRF, UI, or CRF-receptor antagonists (44, 45) implicate the CRF-system in the central control of food intake in goldfish. Mammalian studies further suggest a functional role for CRF-BP in the neural control of feeding (46–48).

### Optic tectum

Expression of CRF-BP occurs throughout the optic tectum in the first proximal layer, or SPV. Zebrafish also express CRF, UI, and CRF-BP in

the proximal optic tectum (12). In general, the optic tectum is responsible for processing visual input and integrating it with other sensory information. The SPV itself harbours the most numerous population of tectal neurones (32). A functional role for the CRF system in the optic tectum has been well described in amphibians, where CRF-producing neurones in the tectum are part of a circuit activated in response to a predator-like visual stimulus (49).

### Hindbrain

CRF-BP expression in the hindbrain was relatively high, and transcripts were mainly concentrated in the superior and intermediate divisions of the raphe nucleus. Some CRF-BP expression in the hindbrain can also be attributed to the nucleus motorius nervi trigemini. This expression pattern mimics that observed in zebrafish (12) and rats (11), suggesting a strong evolutionary conservation for CRF-BP functions in the brainstem. Indeed, the CRF system has been implicated in locomotor activity stemming from serotonergic neurone activation in the raphe nucleus of fish (50), amphibians (51), and mammals (52, 53). In mammals, the CRF system in the raphe nucleus also affects the activity of forebrain projecting serotonergic neurones that contribute to various non-ambulatory stress-related behaviours (54). Current perspectives on the involvement of the brainstem CRF system in ambulatory and non-ambulatory stress-induced behaviours are provided elsewhere (55).

### Pituitary

There are several reports of CRF-BP mRNA and protein isolated to rat corticotrophs (11, 35), where it inhibits CRF-induced release of ACTH (14, 56). By contrast, we found no evidence of CRF-BP in the rostral pars distalis of rainbow trout. This pituitary region in fish contains the corticotrophs which, as in all vertebrates, are responsive to CRF-related peptide signalling (57,58). In the present study, CRF-BP mRNA was only detected in the proximal pars distalis and pars intermedia. Interestingly, the proximal pars distalis in fish secretes thyrotrophin (TSH) and the pars intermedia secretes melanotrophin ( $\alpha$ -MSH) in response to CRF and UI (57, 58). In carp, the majority of pituitary CRF-BP mRNA was located in the pars intermedia (42). Doyon *et al.* (59) observed a stress-induced increase in pituitary CRF-BP expression; however, Huising *et al.* (42) found no change in the level of mRNA in the carp pars distalis. Unlike other vertebrates, in fish, the hypothalamic-releasing factors that influence pituitary secretions are released directly on the pituitary cells rather than into a portal system (1); thus, involvement of CRF-BP in the ACTH-releasing actions of the CRF system could stem from co-synaptic or parasynaptic release from NPO neurones onto corticotrophs. Indeed, CRF-BP is localised with CRF and UI in the zebrafish PPa (12), and stress increases expression in the preoptic area of CRF-BP in fish (42; present study). Conversely, CRF-stimulated TSH release from the proximal pars distalis and  $\alpha$ -MSH release from the pars intermedia could be modulated by locally produced CRF-BP.

### Peripheral expression

Recently, Pepels *et al.* (30) showed a rapid and massive increase in circulating CRF following stress in tilapia, likely originating from the lateral nucleus of the area ventralis telencephali. Another source of circulating CRF and UI in fish is the CNSS (60). Despite high circulating levels of its ligands, CRF-BP is believed not to circulate in fish (30). This is in sharp contrast to the situation in primates, where elevated circulating CRF during late gestation is attenuated with parallel high plasma levels of CRF-BP produced by intrauterine tissues (61). Instead, CRF-BP may serve a paracrine modulatory role in peripheral targets of CRF-related peptides in nonmammalian species, as suggested by studies in *Xenopus* (19) and carp (17, 62). Although we were unable to conclude that CRF-BP is constitutively produced in any of the trout peripheral tissues that we assessed, we cannot exclude local production by specific cell types in some tissues. However, our results support the brain and pituitary as phylogenetically conserved expression sites of CRF-BP (63), whereas the variation in peripheral expression sites among vertebrate taxa (64) suggests a more recent incorporation of CRF-BP outside the CNS. Consequently, the functions of CRF-BP within the CNS are likely more conserved, whereas peripheral functions may be more specialised.

### Regulation of CRF-BP during stress

The stress regimes used in this study were chosen for two reasons. First, they offered two extremes of HPI-axis activation to help ascertain how CRF-BP fits into our current understanding of the CRF system in fish. We have shown previously that social subordination elicits a pronounced and robust cortisol response that contrasts the slight increase observed during hypoxia exposure, and that both stressors elicit a concomitant increase in CRF-related peptide mRNA in the preoptic area (65). Second, given the nature of each stressor, their perception and integration at the level of the brain is likely to be quite different, therefore helping to elucidate any regional differences in CRF-BP functions. In rats, for example, CRF-BP mRNA increased after acute stress in the basolateral but not the central amygdalar nucleus (22).

There is currently no direct evidence to support involvement of CRF-BP in CRF-related peptide signalling activities of fish; however, the changes in CRF-BP gene expression observed in the present study and previously (59) suggest a stress-induced response by the CRF-BP gene. Of particular interest in the present study are the differing responses observed between brain regions during the same stressor, and within brain regions during different stressors. Although CRF-BP expression in the telencephalon increased after 24 h of both social and hypoxic stress, preoptic area expression only increased after 24 h of hypoxic stress, and hypothalamic expression actually decreased in dominant fish after 24 h while remaining at control levels in subordinate fish. Interestingly, increased gene expression was observed with hypoxia exposure despite only a very small increase in plasma cortisol, and preoptic area CRF-BP remained at control

levels in subordinate fish despite a very large increase in plasma cortisol, suggesting that CRF-BP can be regulated independently of the HPI-axis.

The mechanism of CRF-BP gene activation remains poorly understood, and only a partial promoter has been sequenced to date (66). Although *in vitro* studies suggest CRF-BP is modulated in neuronal tissue by numerous factors including CRF and the synthetic glucocorticoid dexamethasone (28), results obtained *in vivo* confirm CRF activation but fail to show a response to corticosterone in the rat amygdala (23). Because CRF mRNA in the preoptic area of *O. mykiss* increases over a similar time course (65) to that of telencephalic CRF-BP in the present study in response to the same stressors, and NPO neurones project to the Vv and Vs (67, 68), CRF may also regulate CRF-BP in fish. Furthermore, the distribution of glucocorticoid receptors in the brain of *O. mykiss* (69) parallel many of the key CRF-BP expressing regions we observed (e.g. Vv, NPO, nlt, nrl), thus providing an opportunity for feedback regulation by cortisol.

### General conclusions

In short, CRF-BP is abundantly and broadly expressed in the CNS of rainbow trout, and its distribution suggests involvement in the many functions of the CRF system. By contrast, despite the presence of circulating CRF-related peptides in fish, the peripheral expression of CRF-BP appears to be negligible and any peripheral function of CRF-BP is likely to be highly localised. The increased expression of CRF-BP in fish under social and hypoxic stress suggests an involvement of this peptide in mediating the physiological response to various stressors; however, the increased gene expression observed in the absence of a clear cortisol response in hypoxia-exposed fish suggests that CRF-BP can be regulated independently of the HPI-axis. Further investigations into the connectivity of CRF-BP expressing neurones will enhance our understanding of the neural circuitry controlling stress physiology. Promoter sequencing combined with *in vitro* and *in vivo* studies of CRF-BP gene regulation will help clarify the activation and feedback regulating mechanisms of the CRF-system.

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