Steroidogenic factor 1-DNA binding: a kinetic analysis using surface plasmon resonance

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ABSTRACT

Basal expression of the glycoprotein hormone α-subunit gene in pituitary gonadotrophs is partially dependent on a gonadotroph specific element (GSE) which binds the nuclear receptor, steroidogenic factor-1 (SF-1). We have used surface plasmon resonance (SPR) to determine the association ($k_{ass}$), dissociation ($k_{diss}$) and affinity ($K_A$) constants of SF-1 binding to immobilized oligonucleotides containing either the GSE consensus motif or a GSE mutant with a 2 bp substitution in the GSE site (GSE$_{\text{MUT}}$).

In vitro translated SF-1 protein bound the consensus GSE with a threefold increase in affinity constant ($P<0.01$) compared with the GSE$_{\text{MUT}}$. This was due primarily to a significant increase ($P<0.05$) in the $k_{ass}$ for SF-1 to the GSE and a slower $k_{diss}$ ($P<0.05$). The binding interaction was specific and could be significantly inhibited ($P<0.001$) by either anti-SF-1 antibody or excess non-biotinylated GSE. The addition of 14 bp wild-type flanking sequences significantly reduced the affinity of SF-1 to both the GSE ($P<0.05$) and the GSE$_{\text{MUT}}$ ($P<0.01$). This was due to a significant ($P<0.01$) decrease in $k_{ass}$ for the wild-type and mutant long oligonucleotides compared with the short GSE. Nuclear extracts from αT3–1 gonadotroph cells also bound the GSE and GSE$_{\text{MUT}}$, giving $k_{diss}$ values which were two- to threefold slower than those obtained with in vitro translated SF-1.

Thus, SPR is a powerful technique for examining kinetic interaction between SF-1 and its binding site, and is able to demonstrate the effects of mutations and flanking sequences on that interaction.

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INTRODUCTION

Steroidogenic factor (SF-1) is one of two proteins expressed from the mouse homologue of the Drosophila fushi tarazu-factor 1 (Ftz-F1) gene (Lala et al. 1992). SF-1 is also known as adrenal-4-binding protein (Ad4bP) and gonadotroph-specific element binding protein 1 (GSE-B1) (Morohashi et al. 1992, Horn et al. 1992). It was revealed by cloning to be highly homologous to members of the nuclear receptor family, especially in the zinc-finger DNA-binding domain (Laudet et al. 1992, Wong et al. 1996). Expression of SF-1 occurs in a cell-selective manner, and has been shown to be necessary for the expression of steroid enzymes in the adrenal cortex and gonad (Parker & Schimmer 1996). Until recently, putative ligands for SF-1 had not been identified but selective endogenous oxysterols have now been shown to be transcriptional activators of SF-1 activity in vitro and this data suggest that SF-1 may be a ligand-activated receptor (Lala et al. 1997). Whether oxysterols bind SF-1 directly or indirectly remains unknown, as do the mechanisms involved and the biological significance of the interaction.

Although little is known about the molecular mechanisms involved in the control of SF-1 cell-specific expression, various studies have shown that SF-1 is an essential determinant of adrenal and gonadal development, male sexual differentiation and formation of the ventromedial hypothalamic nucleus (Parker & Schimmer 1996). In the adult mouse, SF-1 is constitutively expressed in the hypothalamus, adrenal cortex, pituitary gonadotroph, testis and the thecal and granulosa cells of the ovary (Barnhart & Mellon 1994). In addition to these observations, SF-1 has been shown to regulate a number of genes including the luteinizing hormone β-subunit gene and the glycoprotein hormone α-subunit (α-SU) gene in pituitary...

During the development of the anterior pituitary, five endocrine cell types are produced: gonadotrophs, thyrotrophs, corticotrophs, somatotrophs and lactotrophs, each producing specific hormones. Gonadotrophs produce luteinizing hormone (LH) and follicle-stimulating hormone (FSH), whilst thyrotrophs produce thyroid-stimulating hormone (TSH). These three hormones are heterodimers made up of the glycoprotein (gp) hormone α-subunit non-covalently associated with the distinct β-subunits. The gp α-SU gene is the common element in this family of glycoprotein hormones and is the earliest of the hormone genes to be expressed in the developing mouse pituitary (Simmons et al. 1990, Japon et al. 1994). Expression of the α-subunit gene in pituitary gonadotrophs involves a gonadotroph specific element (GSE), conserved in all mammalian α-subunit genes, which has been shown to bind to SF-1 in αT3–1 cells (a mouse clonal gonadotroph cell line) (Horn et al. 1992, Barnhart & Mellon 1994). However relatively little is known about the molecular mechanisms involved in the control and expression of the SF-1 gene in the gonadotroph or of the regulation by SF-1 of gonadotroph-specific genes.

In order to understand the role of SF-1 in the regulation of endocrine differentiation and function, several areas need to be addressed, including the interaction of SF-1 with other transcription factors and various binding motifs. In this investigation, the interaction between SF-1, the mouse GSE consensus motif TGTCCCTTG and a GSE mutant (GSEmut) have been studied using surface plasmon resonance technology. Biosensor technology exemplified by the BIAcore allows analysis in real time of molecular interaction, for example protein–protein or DNA–protein interactions (Bondeson et al. 1993, Johne et al. 1993, Malmborg et al. 1995). Studies of protein–DNA interactions have shown that this technique permits reproducible measurements of binding kinetics which are not feasible using other methods (Bondeson et al. 1993, Malmborg et al. 1995). The interactions between two macromolecules, one immobilized, is analyzed and quantitated in terms of their association and dissociation rates and hence affinity for each other. The results presented here demonstrate differences between the interaction of SF-1 with its putative binding site, the GSE and a GSEmut.

**MATERIALS AND METHODS**

**Instrumentation and reagents**

The BIAcore sensorchip CM5, Tween-20 surfactant (P20) and amine coupling kit containing N-hydroxysuccinimide (NHS), N-ethyl-N-(3-diethylaminopropyl) carbodiimide (EDC) and ethanolamine hydrochloride were obtained from BIAcore (Uppsala, Sweden). Immunopure neutrAvidin was obtained from Pierce and Warriner (Rockford, Illinois, USA). Rabbit polyclonal antibody to SF-1 was obtained from Upstate Biotechnology (Lake Placid, New York, USA).

**Oligonucleotides**

Oligonucleotides (Table 1) representing the mouse alpha subunit (α-SU) gene gonadotroph specific element (GSE) - the wild type SF-1 binding site, a mutant with a 2 bp substitution in the GSE site (GSEmut), and a negative control oligonucleotide, the human α-SU cyclic AMP response element (CRE) (Deutsch et al. 1987) were synthesized and purified by HPLC (R and D Systems Ltd, Abingdon, Oxon, UK). Oligonucleotides were synthesized with and without a 5′ biotin group for the wild-type SF-1 binding site (GSE), and the 15 bp mutant described (GSEmut). In addition, two longer oligonucleotides (30 bp) containing flanking sequences, GSE-L and GSEMUT-L were synthesized. As a control for non-specific binding, a 35-base pair oligonucleotide (NFIL6) was synthesized (Table 1). This sequence represents the binding site for the unrelated transcription factor

<table>
<thead>
<tr>
<th>Oligonucleotide</th>
<th>Length (bp)</th>
<th>Mismatch</th>
<th>Sequence (5′ to 3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GSE</td>
<td>15</td>
<td>WT</td>
<td>GCTGTCCCTTGAGGTC</td>
</tr>
<tr>
<td>GSEmut</td>
<td>15</td>
<td>2 bp</td>
<td>GCTGTTTTTGAGGTC</td>
</tr>
<tr>
<td>CRE</td>
<td>19</td>
<td>WT</td>
<td>AAAATTGACGTATGGTAA</td>
</tr>
<tr>
<td>GSE-L</td>
<td>30</td>
<td>WT</td>
<td>CTCCTTCATAAAGCTGTCCCTTGAGGTCACCAC</td>
</tr>
<tr>
<td>GSEmut-L</td>
<td>30</td>
<td>2 bp</td>
<td>CTCCTTCATAAAGCTGTCCCTTGAGGTCACCAC</td>
</tr>
<tr>
<td>NFIL6</td>
<td>35</td>
<td>WT</td>
<td>TAAAGGACGTGACATTGCAACAACTTTAAATAGGTT</td>
</tr>
</tbody>
</table>

WT, wild-type.
NFIL6, a member of the CCAAT/enhancer-binding protein family (Akira et al. 1990). Each biotinylated oligonucleotide and its non-biotinylated complementary sequence were diluted to 70 pM (1:1 ratio) in 10 mM Hepes, 150 mM NaCl, 3·4 mM EDTA and 0·5 g/l surfactant P20 (Hepes buffered saline (HBS)) pH 7·4 (all supplied by Aldrich, Poole, Dorset, UK). Oligonucleotides were heated to 70 °C and allowed to anneal by cooling slowly to room temperature.

Protein expression
The expression vector pGex-1 lambda T was obtained from Pharmacia Biotech (Uppsala, Sweden). The procedure used to obtain the glutathione S transferase (GST)-SF-1 fusion protein was as previously described (Malim & Cullen 1991). Briefly, SF-1 full length cDNA (kindly donated by K Parker, Duke University, North Carolina, USA), was excised from blue script (pBS+) using EcoRI and sub-cloned into the expression vector pGex-1 lambda T. The recombination-deficient E. coli strain DH5α obtained from Clon’Tech (Palo Alto, CA, USA) was used for all subsequent transformations. A single colony shown by restriction endonuclease digestion to contain SF-1 DNA, was used to inoculate 10 ml Luria-Bertani (LB) medium (Life Technologies, Paisley, Strathclyde, UK) and the culture was grown for 12–18 h at 37 °C with shaking. A 1:10 dilution of the overnight culture was then used to inoculate fresh prewarmed medium and the culture grown until the optical density at 600 nm (O.D600) was between 0·6 and 1·0. Isopropylthiogalactopyranoside (100 mM) (Life Technologies) was added to a final concentration of 0·1 mM and the incubation continued for a further 2 h, after which time the culture was pelleted by centrifugation at 8340 g for 5 min to lyse the cells. The homogenate was pelleted and the lysate was sedimented using a block magnet and the supernatant was then neutralized with an equal volume of 0·1 M sodium phosphate (Aldrich) pH 7·0, filtered, then stored at −20 °C until required.

Cell culture
The α-SU expressing gonadotroph cell line αT3–1, an adherent line (Dr P Mellon, University of California, San Diego, CA, USA), was cultured using standard procedures. Briefly, cells were grown in Dulbecco’s modified Eagle’s medium (DMEM) containing 10% fetal bovine serum, 1 × 10⁵ U/l penicillin and 100 mg/l streptomycin (Life Technologies) at 37 °C in a humidified 5% CO₂ incubator and subcultured every 3–5 days.

Extraction of nuclear protein
Nuclear extract was prepared from αT3–1 cells in their exponential growth phase. Cells were washed twice with ice-cold phosphate buffered saline (PBS), before being scraped and pelleted by centrifugation at 8340 g. Cells were resuspended in ice-cold PBS, pelleted a second time and resuspended in 5 packed cell volumes of buffer A (10 mM KCl, 1·5 mM MgCl₂, 10 mM Hepes pH 7·9, 0·5 mM dithiothreitol (DTT), 0·5 mM phenylmethylsulphonyl fluoride (PMSF), 0·1 mM EGTA, 0·1 mM EDTA, 100 mg/l aprotilin) (all supplied by Aldrich). Cells were left to swell on ice for 15 min before Nonidet P-40 (NP40) was added to a final concentration of 1 g/l, vortexed vigorously and left for a further 5 min to lyse the cells. The homogenate was pelleted for 20 seconds at 4 °C and the supernatant which represented the cytoplasmic fraction discarded. The nuclei were resuspended in 1 packed cell volume of buffer B (20 mM Hepes pH 7·9, 1·5 mM MgCl₂, 2·5 g/l glycerol, 420 mM NaCl, 1 mM EDTA, 1 mM EGTA, 0·5 mM DTT, 1 mM PMSF, 100 mg/l aprotilin) and extracted for 1 h at 4 °C with occasional mixing. The supernatant containing nuclear proteins was aliquoted and stored at −70 °C until required.
Surface plasmon resonance (SPR)

The BIAcore Upgrade was used in all experiments at a temperature of 25°C with a flow rate of 10 µl/min, with HBS used as both the dilution and flow buffer unless otherwise stated. Each new sensorchip was preconditioned before use by treating with two pulses of 50 mM sodium hydroxide. The capturing of DNA to the surface of the sensorchip relies on derivatizing the carboxylated dextran matrix of the chip and subsequent conjugation via an amine to neutrAvidin and then the biotinylated oligonucleotide.

The surface of the sensorchip was activated using standard procedures. Briefly, after equilibration of the sensorchip surface with HBS, equal volumes (35 µl) of NHS and EDC were mixed in equal proportions using an automated program, and 35 µl were injected across the surface to activate the carboxymethylated dextran layer. Thirty-five microlitres neutrAvidin (200 µg/l in 10 mM sodium acetate (Aldrich) pH 4.5) were injected across the flowcell. Excess reactive NHS esters were deactivated by injecting 35 µl 1 M ethanolamine pH 8:5 across the flowcell. The sensing surface was washed (regenerated) by injecting 30 µl 0.5 g/l SDS and 3.4 mM EDTA (Aldrich). Typically, between 5000–7000 response units (RU) of neutrAvidin were immobilized on the chip. Target oligonucleotides (Table 1) were immobilized on the chip by injecting 35 µl biotinylated double-stranded oligonucleotide (70 pM). Non-covalently bound ligand was removed from the surface by injecting 30 µl of the regeneration solution (0.5 g/l SDS, 3.4 mM EDTA) twice. Specificity was tested by passing various concentrations of either bovine serum albumin or SF-1/GST fusion protein across a sensorchip with an unrelated ligand (alkaline phosphatase antibody) immobilized or where the sensorchip was activated but no ligand immobilized. Both the association (k<sub>ass</sub>) rate, and the dissociation (k<sub>diss</sub>) rate constants were determined from the binding rate of the protein to the sensorchip.

Kinetic analysis

The determination of kinetic rate constants on the BIAcore has been described previously (Karlsson 1994). The association rate equation that applies under the BIAcore experimental conditions is shown below.

\[ R = \frac{k_{ass} C R_{max}}{k_{ass} C + k_{diss}} \quad [1 - e^{- (k_{ass} C + k_{diss})t}] \]

where R=response (RU), k<sub>ass</sub>=association rate constant, k<sub>diss</sub>=dissociation rate constant, C=concentration of free analyte, R<sub>max</sub>=maximal response and t=time.

Assuming a model reaction of A+B ↔ AB, a plot of dR/dt vs t from the association part of the reaction has a slope=k<sub>ass</sub>. k<sub>ass</sub> is calculated using a single exponential fit to the experimental data. Plotting k<sub>ass</sub> against C and using linear regression analysis, the slope of this secondary plot gives the k<sub>ass</sub>.

k<sub>diss</sub> is determined from the dissociation phase of the interaction by plotting, Ln (R<sub>o</sub>/R) vs t where R<sub>o</sub>=initial response, and R=response at time t. This plot should be linear with a slope=k<sub>diss</sub>.

The goodness of fit of the experimental data to both association and dissociation models is assessed by Chi squared analysis. The affinity constant, K<sub>A</sub> is calculated using the relationship K<sub>A</sub>=k<sub>ass</sub>/k<sub>diss</sub> M<sup>-1</sup>.

Statistical analysis

Analysis of variance was determined using StatView ANOVA statistics, as the model can detect complex relationships between the independent and dependent variables. In this investigation, multiple comparisons were made using Fisher's protected least significant difference at the 5% significance level.

RESULTS

Use of BIAcore to study SF-1-DNA interaction

In order to investigate the interaction between the putative GSE and SF-1, biospecific interaction analysis using BIAcore biosensor technology was employed. To study the binding characteristics, biotinylated GSE oligonucleotide, a 2 bp mutant GSE oligonucleotide and a negative control CRE oligonucleotide (Table 1) were immobilized on a neutrAvidin-coated sensorchip. Full length purified SF-1 protein translated in vitro as described above bound in a concentration-dependent manner (Fig. 1a) to the immobilized GSE oligonucleotide. The concentration of neutrAvidin (200 µg/l) used to capture the biotinylated oligonucleotides has been described previously and results in saturated binding (Yang et al. 1995).

Optimization of system

A third concern, mass transport which can alter the binding progress curve and hence affect the kinetics of ligand association and dissociation was also addressed. Intrinsic reaction rate is flow
independent, therefore with the oligonucleotide GSE kept constant, the amount of protein bound was compared at different flow rates. Binding of SF-1 at a flow rate of 10 µl/min (170 RU) was greater than at 5 µl/min (93 RU), but with no further significant increase at 15 or 20 µl/min, thus a flow rate of 10 µl/min was used in all analyses.

Specificity of binding was examined first by observing the effect of a non-specific protein (in vitro translated GST), which gave negligible background values (data not shown), and secondly, by demonstrating significant inhibition of binding using rabbit polyclonal immunoglobulin G anti-SF-1. This antibody has previously been shown to block the ability of SF-1 to bind to the promoter element of a number of genes including the gp α-subunit (Barnhart & Mellon 1994). Incubation of in vitro translated SF-1 protein with this SF-1 specific antiserum significantly decreased the binding of SF-1 in terms of relative RU to the immobilized GSE oligonucleotide after background subtraction of the bulk shift effect (Fig. 2), (SF-1: 60·7 ± 7·5 RU, SF-1 plus antibody: 23·6 ± 0·6 RU, P<0·001), while the addition of control antiserum had no effect. Additional experiments to assess the specificity of binding included the use of an unrelated oligonucleotide, NFIL6 (Table 1) or the addition of non-biotinylated GSE oligonucleotide to the SF-1 protein prior to injection. When biotinylated NFIL6 oligonucleotide was immobilized on the sensorchip and increasing concentrations of in vitro translated SF-1 protein (0·125 to 0·625 µM) were injected, concentration-dependent binding was not observed and the mean binding seen across the range of concentrations was 12 ± 3 RU reflecting background or non-specific binding to a component of the stationary phase. Pre-incubation of in vitro translated SF-1 protein (0·625 µM) with 1 µM non-biotinylated GSE oligonucleotide prior to injection eliminated binding of the SF-1 protein to the GSE oligonucleotide on the sensorchip (SF-1: 52·1 ± 7·5 RU, SF-1 plus GSE: 3 ± 1·0 RU, P<0·001). The results from these experiments confirm that the GSE of the mouse α-subunit gene promoter is bound in a specific and concentration-dependent fashion by in vitro translated SF-1 protein.

As shown in Fig. 1, binding occurred in a concentration-dependent manner for the GSE oligonucleotide and, indeed, similar concentration-dependent binding was seen with all oligonucleotides (data not shown). As expected, binding of SF-1 to the CRE oligonucleotide was greatly reduced compared with the GSE and GSE MUT oligonucleotides at all concentrations used.

**SF-1 shows differences in reaction rate constants for immobilized wild type GSE compared with the mutant GSE oligonucleotide**

Kinetic rate constants were obtained by measuring the interaction of the SF-1 protein at several different concentrations with each oligonucleotide. The association and dissociation rate constants for the SF-1 fusion protein were then calculated using the BIAcore kinetic evaluation 2·1 program. In all cases, the $k_{\text{ass}}$ and $k_{\text{diss}}$ were observed to be monophasic. Having controlled for all the different non-specific interactions that might interfere with the analysis, for example immobilizing the same.
molar concentration of each oligonucleotide on the sensorchip, the association/dissociation and affinity constants were determined for SF-1 (Table 2). When the dissociation constants were compared for the GSE, GSE\textsubscript{MUT} and CRE (negative control) short oligonucleotides, it was observed that there was an increase in the $k_{\text{diss}}$ value, 42% and 76% for the GSE\textsubscript{MUT} ($P<0.05$) and the CRE (not significant) respectively compared with the GSE. Moreover, when comparing results for the $k_{\text{ass}}$, a twofold (100%) difference was observed for the GSE oligonucleotide compared with the GSE\textsubscript{MUT} ($P<0.01$). This resulted in a threefold difference in the affinity $K_A$ constant for the GSE compared with the GSE\textsubscript{MUT} ($P<0.01$).

The data generated from the above experiments was also analyzed by the BIAcore binding isotherm analysis program, an equilibrium binding analysis method. The $k_{\text{eq}}$ obtained from analysis of this data was very similar to that obtained by kinetic analysis (see Table 2). In particular, the threefold significant difference between the GSE and GSE\textsubscript{MUT} was still apparent ($P<0.01$).

### Oligonucleotide flanking sequences modify SF-1 reaction rate constants

Further to establish the role of flanking sequences in the interaction of SF-1 with its consensus binding site, the GSE and GSE\textsubscript{MUT} oligonucleotides were synthesized such that an additional 7 bp were added either side of the original oligonucleotides used (Table 1). Using these long oligonucleotides, there now appeared to be little difference between the dissociation constant for the GSE-L compared with the GSE\textsubscript{MUT}-L (Table 2). Differences were, however, still seen for the association ($k_{\text{ass}}$) constants, $k_{\text{ass}}$ for the GSE-L showing an increase of 59% (not

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**Figure 2.** Superimposed sensorgrams of the interactions between *in vitro* translated SF-1 protein with the consensus GSE oligonucleotide incubated in the absence (top line) or presence (bottom line) of SF-1 specific antiserum.

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**Table 2.** Kinetic parameters, affinity constants and equilibrium constants ($k_{\text{eq}}$ calculated by binding isotherm analysis) for the interaction of *in vitro* translated SF-1 protein and immobilized oligonucleotides. Results are presented as the means ± S.E.M. of at least six determinations for each kinetic parameter.

<table>
<thead>
<tr>
<th>Oligonucleotide</th>
<th>$k_{\text{ass}}$ (M$^{-1}$s$^{-1}$)</th>
<th>$k_{\text{diss}}$ (s$^{-1}$)</th>
<th>$K_A$ (M$^{-1}$)</th>
<th>$k_{\text{eq}}$ (M$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GSE</td>
<td>$5.1 \pm 0.9 \times 10^4$</td>
<td>$3.8 \pm 0.2 \times 10^{-3}$</td>
<td>$1.3 \pm 0.2 \times 10^7$</td>
<td>$5.7 \pm 1.5 \times 10^6$</td>
</tr>
<tr>
<td>GSE\textsubscript{MUT}</td>
<td>$2.5 \pm 0.9 \times 10^4$*</td>
<td>$5.4 \pm 0.5 \times 10^{-3}$*</td>
<td>$4.6 \pm 1.0 \times 10^6$**</td>
<td>$1.4 \pm 0.2 \times 10^6$**</td>
</tr>
<tr>
<td>GSE-L</td>
<td>$2.1 \pm 0.3 \times 10^4$**</td>
<td>$3.4 \pm 0.2 \times 10^{-3}$*</td>
<td>$6.9 \pm 1.4 \times 10^6$*</td>
<td>$6.6 \pm 1.8 \times 10^6$*</td>
</tr>
<tr>
<td>GSE\textsubscript{MUT}-L</td>
<td>$1.3 \pm 0.2 \times 10^4$**</td>
<td>$3.5 \pm 0.1 \times 10^{-3}$**</td>
<td>$3.8 \pm 0.2 \times 10^6$**</td>
<td>$2.9 \pm 0.4 \times 10^6$**</td>
</tr>
<tr>
<td>CRE</td>
<td>$2.9 \pm 0.4 \times 10^4$*</td>
<td>$4.4 \pm 0.1 \times 10^{-3}$*</td>
<td>$6.0 \pm 0.6 \times 10^6$*</td>
<td>N.D.</td>
</tr>
</tbody>
</table>

* $P<0.05$ and ** $P<0.01$ compared with the GSE for each column. N.D., not determined.

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Thus in both cases, flanking sequences appeared to reduce the affinity for SF-1 protein.

Analysis of oligonucleotide interactions using αT3–1 nuclear extracts

Nuclear extract prepared from the α-subunit secreting gonadotroph cell line αT3–1 was used as a crude source of SF-1 protein. The extract was used to study SF-1-DNA interaction in a more complex setting. The binding that occurred when increasing amounts of αT3–1 nuclear protein extract was allowed to interact with the GSE, GSEmut and CRE is shown in Fig. 3. As before, binding occurred in a concentration-dependent manner for all oligonucleotides. As the precise amount of SF-1 protein in the heterogeneous nuclear protein extract was unknown, it was not possible to investigate association rates, and hence affinity constants. However, as the dissociation rate constant is not concentration dependent, it was possible to study the dissociation phase. Dissociation of SF-1 from the GSE, GSEmut and CRE oligonucleotides showed a monophasic pattern, with no significant differences observed between the different oligonucleotides. SF-1 was calculated to have a $k_{\text{diss}}$ of $1.5 \times 10^{-3}\text{s}^{-1}$ for the GSE and $k_{\text{diss}}$ of $2.0 \times 10^{-3}\text{s}^{-1}$ for the GSEmut, which indicates that SF-1 dissociates from the GSE oligonucleotide at a rate 30% slower compared with GSEmut (Table 3). No differences are observed for the $k_{\text{diss}}$ of the CRE oligonucleotide which was found to have a value of $2.1 \times 10^{-3}\text{s}^{-1}$ similar to that seen for the GSEmut. However, when the dissociation rate constants are compared for in vitro translated SF-1 and crude nuclear extract derived SF-1, approximately threefold differences were observed (Table 2 vs Table 3). Dissociation of SF-1 from all oligonucleotides used in the investigation occurred 62%, 63% and 69% slower for the GSE, GSEmut and CRE respectively than when using purified SF-1 protein suggesting that the presence of other proteins in the cell extract may affect SF-1-DNA interaction.

DISCUSSION

Numerous studies have established an essential role for SF-1 in endocrine development and function and as an important transcriptional regulator of a number of genes including key products of pituitary gonadotrophs (Barnhart & Mellon 1994, Halvorson et al. 1996). However, the precise mechanisms involved in the regulation and expression of target genes by SF-1 remains obscure. To gain insight into the interactions that occur between SF-1 and its target DNA, we have used the technique of surface plasmon resonance to investigate the kinetics of interaction between SF-1 and its putative binding site in the α-subunit promoter.

Using the BIAcore, we were able to monitor the binding of SF-1 protein to DNA and hence determine the association, dissociation and affinity constants for defined oligonucleotide sequences, including the consensus motif. By comparing the results obtained with consensus and mutant oligonucleotides, insights into the mechanisms involved in protein–DNA interaction were obtained. Using in vitro translated mouse SF-1 protein and oligonucleotides for the mouse GSE and mouse GSEmut, we demonstrated concentration-dependent binding.
to both sequences, with apparently reduced binding occurring to the sequence containing a 2 bp mutant. Binding to the mouse GSE was shown to be specific since it could be reduced significantly in the presence of antibody to mouse SF-1 and excess non-biotinylated GSE.

It has been reported previously that the introduction of two C to T mutations in the mouse GSE oligonucleotide (termed GSE\textsubscript{MUT}) eliminates the binding of SF-1 in both South Western blotting and gel retardation experiments (Horn \textit{et al.} 1992, Barnhart \& Mellon 1994). These studies were performed using the GSE of the human \(\alpha\)-subunit promoter and nuclear extracts from \(\alpha\)T3–1 cells. To our knowledge no such experiments have been performed with the murine promoter and \textit{in vitro} translated SF-1 protein, although Wilson \textit{et al.} (1993) have described single nucleotide changes in the SF-1 binding site that either diminish or enhance SF-1 binding in gel mobility shift assays. It is of interest to note that the introduction of a similar 2 bp C to T mutation within the human LHß GSE sequence, although blunting the ability of SF-1 to bind to this promoter, still allowed partial SF-1 responsiveness of the mutant construct in transfection assays (Halvorson \textit{et al.} 1996), suggesting that some interaction still occurred. Using SPR we were able to show that a threefold reduction in the affinity constant occurred with this 2 bp mutation and that this was due to both a reduction in the \(k_{\text{ass}}\) and an increase in the \(k_{\text{dis}}\). It is tempting to speculate that this reduction in affinity is sufficient to blunt the ability of SF-1 to bind to this sequence under the conditions used in gel mobility shift assays. Other authors have also used SPR to demonstrate alterations in affinity constants following the introduction of point mutations in binding sequences (Malmborg \textit{et al.} 1995).

The major advantage of SPR is that the protein–DNA interactions are monitored in real time and this allows detailed calculations of kinetic parameters, giving additional quantitative information to that obtained from gel shift assays. It has been reported that gel shift assays can be used in kinetic analysis (Hoopes \textit{et al.} 1992) but are hampered by the need for recording a rapid reaction with a small number of data points—a technical difficulty being the lag time from the loading of the sample onto the gel to the separation of bound and free reactants. When relative rate determinations have been attempted using this technique, it has been reported to produce inconsistent results (Yang \textit{et al.} 1995). Thus in contrast to SPR, gel shift assays do not provide a real time picture of the association events, although they are of benefit in binding specificity studies.

Previous data have suggested that the GSE consensus sequence alone cannot be sufficient for protein–DNA binding specificity and that flanking sequences may be involved (Wilson \textit{et al.} 1993). We examined the effect of introducing 7 bp wild-type flanking regions either side of the sequences for the GSE and GSE\textsubscript{MUT}. Interestingly, introduction of flanking sequences reduced the affinity constant for SF-1, predominantly due to a reduction in the association rate constant. The observed differences in the affinity constant could be the result of secondary structural changes resulting in steric hindrance but this seems unlikely with such a short flanking sequence. Other SPR studies of transcription factor–DNA interaction have also suggested that flanking sequences can reduce protein binding and in some cases these flanking elements have been shown to compensate for observed differences between wild-type and mutant core motifs (Malmborg \textit{et al.} 1995). Our data would also suggest that the addition of wild-type flanking sequences had more marked effects on the kinetic constants of the GSE compared with the GSE\textsubscript{MUT}, although the functional consequences of such changes remain to be determined.

Using crude nuclear extracts from \(\alpha\)T3–1 cells we were also able to show a specific interaction with both the GSE and the GSE\textsubscript{MUT}. Again, the calculated \(k_{\text{dis}}\) for the GSE was slower than that for the GSE\textsubscript{MUT}. However, in both cases the \(k_{\text{dis}}\) values were two- to threefold slower than those obtained with \textit{in vitro} translated SF-1 protein, suggesting that secondary protein interactions might be occurring to account for these changes. Thus SPR may prove to be a useful tool in the kinetic analysis of transcription factor complex formation.

In conclusion, we have shown that the technique of SPR can be used to provide detailed kinetic parameters of the interaction between SF-1 and its consensus motif and in addition it can demonstrate the effects of mutations and flanking sequences on that interaction. Since, as described above, naturally occurring variants of the consensus GSE sequence are found both between species and in different target genes (Horn \textit{et al.} 1992, Barnhart \& Mellon 1994, Halvorson \textit{et al.} 1996, Parker \& Schimmer 1996) it would appear that SPR is a powerful technique for revealing differences in kinetic interactions between these sequences and their binding protein, SF-1.

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