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Effect of H bond removal and changes in the position of the iron–sulphur head domain on the spin–lattice relaxation properties of the $[2Fe–2S]^{2+}$ Rieske cluster in cytochrome bc_1†

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Here, comparative electron spin–lattice relaxation studies of the 2Fe–2S iron–sulphur (Fe–S) cluster embedded in a large membrane protein complex – cytochrome bc_1 – are reported. Structural modifications of the local environment alone (mutations S158A and Y160W removing specific H bonds between Fe–S and amino acid side chains) or in combination with changes in global protein conformation (mutations/inhibitors changing the position of the Fe–S binding domain within the protein complex) resulted in different redox potentials as well as ***g***-, ***g***-strain and the relaxation rates (T_1^{-1}) for the Fe–S cluster. The relaxation rates for $T < 25$ K were measured directly by inversion recovery, while for $T > 60$ K they were deduced from simulation of continuous wave EPR spectra of the cluster using a model that included anisotropy of Lorentzian broadening. In all cases, the relaxation rate involved contributions from direct, second-order Raman and Orbach processes, each dominating over different temperature ranges. The analysis of T_1^{-1} (T) over the range 5–120 K yielded the values of the Orbach energy (E_{Orb}), Debye temperature θ_D and Raman process efficiency C_{Ram} for each variant of the protein. As the Orbach energy was generally higher for mutants S158A and Y160W, compared to wild-type protein (WT), it is suggested that H bond removal influences the geometry leading to increased strength of antiferromagnetic coupling between two Fe ions of the cluster. While θ_D was similar for all variants (~107 K), the efficiency of the Raman process generally depends on the spin–orbit coupling that is lower for S158A and Y160W mutants, when compared to the WT. However, in several cases C_{Ram} did not only correlate with spin–orbit coupling but was also influenced by other factors – possibly the modification of protein rigidity and therefore the vibrational modes around the Fe–S cluster that change upon the movement of the iron–sulphur head domain.

Introduction

Iron–sulphur proteins are common elements of many bioenergetic systems in which they play the role of electron carriers or constitute catalytic sites of enzymes involved in energy conversion.[1] The active sites of these proteins bind a compact inorganic cluster that usually contains two, three or four iron ions bridged by sulphur ions.[2,3] These clusters are chelated by proteins through either cysteine or, in the case of Rieske clusters, by cysteine and histidine side chains. A characteristic feature of the iron–sulphur clusters is the presence of strong antiferromagnetic coupling between high-spin iron ions that, depending on the redox state, leads to the formation of the diamagnetic ($S = 0$) or paramagnetic state ($S = 1/2$) in the centre with average ***g***-tensor values lower than $g_e = 2.0023$.[4,5] Electron paramagnetic resonance spectroscopy (EPR) is widely recognised as the main experimental tool to investigate the properties of paramagnetic iron–sulphur proteins.[2,6]

The family of 2-iron-2-sulphur proteins is divided into two classes according to the average value of ***g***-tensor principal components (g_{av}): ferredoxins with $g_{av} \sim 1.96$, and Rieske clusters with $g_{av} \sim 1.91$.[7] The EPR spectra of clusters reveal a clear rhombic or close to axial symmetry. Variations in g values observed for the Rieske clusters have been explained on the basis of a ligand-field model of antiferromagnetically coupled iron ions.[8]

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† Electronic supplementary information (ESI) available: Fig. S1: results of equilibrium redox titration of the Fe–S cluster for different forms of cytochrome bc_1; Fig. S2: selected results of simulations of X-band CW EPR spectra of the Rieske cluster recorded at 25 K using a single-component model; Fig. S3: temperature dependence of the spin–lattice relaxation rate ($1/T_1$) of the Rieske cluster for the tds-inhibited WT in linearized form for Raman and Orbach processes; Table S1: values of ***g*** and ***g***-strain components determined from fitting the two-component model to X-band CW EPR spectra (25 K) for different forms of cytochrome bc_1. See DOI: 10.1039/c5cp02815a

Modifications of g values are particularly associated with subtle changes in the ligand field around the Fe^{2+} ion which is coordinated by histidines. Additionally, the microheterogeneity of the protein environment around the cluster is a source of spread in the ligand field which is manifested as a g-strain effect in the EPR spectra of the clusters in frozen glassy solutions. A statistical theory for the $\boldsymbol{g}$-strain tensor has been developed to describe asymmetry in the line shapes of the iron–sulphur cluster spectra linking the g-strain with rigidity of the protein core that binds the cluster.[9,10]

The spin–lattice relaxation rate (T_1^{-1}) quantitatively describes how fast the energy absorbed by the spin is transferred to the phonons' bath and its value depends on the coupling strength of the relaxing paramagnet to the surrounding environment as well as on the vibrational modes of the lattice. Commonly, the vibrational characteristics of the glassy frozen protein solution, constituting the lattice is described by the Debye model.[11] Temperature dependence of T_1^{-1} of proteins containing the [2Fe–2S] cluster has revealed the existence of direct (one-phonon), second-order Raman and Orbach relaxation processes.[12–14] The second-order Raman process is recognised as a ubiquitous relaxation mechanism for all paramagnetic centres and its efficiency depends on several factors including the extent of spin–orbit coupling and rigidity of the protein that influences the vibrational modes of a paramagnetic centre.[15,16] In general, the larger the spin–orbit coupling (reflected as a deviation of the g-value from g_e) and the less rigid the structure, the higher the efficiency of the Raman process.[17] The Orbach mechanism requires the existence of a low-lying excited state which, in the case of iron–sulphur clusters, originates from antiferromagnetic coupling between high-spin iron ions.[12,18]

The relaxation rates of iron–sulphur clusters have so far mainly been measured for small proteins such as ferredoxins. In these cases, assigning changes in parameters of relaxation to specific structural details of proteins has generally been complicated due to the fact that the comparison involves different proteins coming from different organisms. In this study, we analysed T_1^{-1} of a reduced Rieske cluster $[2Fe–2S]^{2+}$ (Fe–S) of a large membrane protein complex – cytochrome bc_1 (Fig. 1A).[19–21] This protein provides a convenient model to compare T_1^{-1} of the same metalloprotein exposed to a variety of structural changes associated with modifications of both the local environment of the cluster and the global environment at the level of the whole protein. By the term "local modifications", here we understand the changes in the structure of hydrogen bonds formed with the cluster or its ligands, while by "global modifications" we understand the changes in the position of the whole iron–sulphur protein head domain (ISP-HD) in relation to other subunits of cytochrome bc_1.

The Fe–S cluster in cytochrome bc_1 is embedded in a water-exposed extrinsic domain (ISP-HD) that naturally undergoes a large-scale movement, inherent in the catalytic cycle of the enzyme. The movement allows the cluster to transfer electrons between the catalytic Q_o site in cytochrome b and heme c_1 on the cytochrome c_1 subunit.[22–26] At one extreme

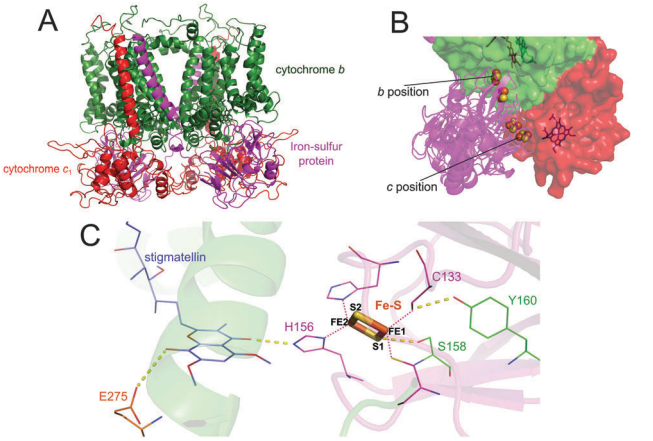

Fig. 1 Crystal structure of cytochrome bc_1 and structural details of the ISP. (A) A ribbon model of a native cytochrome bc_1 dimer from *Rhodobacter capsulatus* (PDB ID: 1ZRT[20]) containing three catalytic subunits: cytochrome b – green, cytochrome c_1 – red, and ISP – magenta. (B) A model of one monomer of cytochrome bc_1 with overlaid different positions of the ISP-HD. The Fe–S cluster is shown in b-, c- and intermediate positions as yellow-red spheres. The sticks represent hemes c_1, b_L and the inhibitor stigmatellin. The positions of the ISP-HD were taken from the structures in the PDB database: 1BCC,[22] 1BE3,[64] 1BGY[64] and 1ZRT.[20] (C) The local environment of the Fe–S cluster at the b position in the presence of stigmatellin that forms the hydrogen bond with cluster-liganding H156. Yellow dashed lines indicate the H bonds and magenta dotted lines represent the bonds between cluster ligands and iron ions of the cluster. Green and magenta ribbons represent cytochrome b and ISP subunits.

(the so-called "b position"), the ISP-HD is in close contact with the Q_o site and the Rieske cluster interacts with the substrate bound at the site, while at the other extreme (the so-called "c position") the ISP-HD is close to heme c_1 (Fig. 1B). It has been shown in previous studies that the redox potential of the cluster varies significantly between these two positions – it is generally more than 100 mV higher at the b position, compared to the c position.[25,27]

In isolated non-inhibited wild-type (WT) cytochrome bc_1, the ISP-HD is distributed between b and c position.[26] However, the average position of the ISP-HD can be modified by introducing specific mutations that affect the motion and also by addition of specific inhibitors of cytochrome bc_1.[26,28,29] Therefore, the properties of the Fe–S cluster of cytochrome bc_1 can be studied under a variety of conditions in which the position of the cluster can be controlled.

Here, we performed a detailed analysis of the spin–lattice relaxation rate of the Rieske cluster of cytochrome bc_1 isolated from *Rhodobacter capsulatus* under a variety of conditions to determine the basic parameters of the mechanisms that govern the relaxation between 5 K and 120 K particularly, the Orbach energy and Debye temperature. We compared the effect of point mutations S158A and Y160W that remove the specific H bonds in the proximity of the cluster. We also investigated the effect on the efficiency of the Raman process of changes in the global distribution of positions of the ISP-HD modified by using specific inhibitors and mutations.

Materials and methods

Bacterial strains, plasmids, and general molecular genetic techniques

Rb. capsulatus strains and *E. coli* (HB101) were grown in MPYE (mineral–peptone–yeast extract) and LB media, respectively, supplemented with appropriate antibiotics as needed.[30] Photosynthetic growth of *Rb. capsulatus* strains was tested on MPYE plates using anaerobic jars (GasPak System, BD) at 30 °C under continuous light. *Rb. capsulatus* strains with mutated cytochrome bc_1 were generated as described previously,[31] using the genetic system developed by Dr F. Daldal (University of Pennsylvania, Philadelphia, USA). The templates containing the desired mutations were obtained using the QuikChange® protocol (Stratagene). Changes in the *petA* gene (coding for the ISP subunit) resulting in the mutations S158A or Y160W were introduced by PCR using DNA as a template: pPET1 (for construction of single mutants S158A or Y160W), pPET1 containing mutations for +1Ala or +2Ala insertions[23] (for construction of double mutants S158A +1Ala or S158A +2Ala, respectively). The 1 kb *BstX*I/*Xma*I fragments containing the desired mutations (and no other mutations, as confirmed by DNA sequence analysis) were exchanged with their wild-type counterparts in pMTS1 to construct mutated variants of pMTS1. These were used as expression vectors in *Rb. capsulatus* cells. They were introduced into the MT-RBC1 strain (*pet*ABC-operon deletion background) *via* triparental crosses as described in ref. 31. In each case, the presence of engineered mutations was confirmed by sequencing the plasmid DNA isolated from the mutated *Rb. capsulatus* strains.

Biochemical procedures

The cytochrome bc_1 complex was isolated from purple bacteria *Rb. capsulatus* grown under semiaerobic conditions, according to the procedure described previously in ref. 32. The concentration of the isolated protein (per cytochrome c_1 content) was determined spectrophotometrically using ascorbate-reduced minus ferricyanide-oxidised differential spectra and an extinction coefficient $\varepsilon_{552\text{–}542\text{nm}}$ = 20 mM^{-1}. All forms of cytochrome bc_1 were dialysed against buffer containing 50 mM bicine pH 8, 100 mM KCl, 1 mM EDTA, 20% (v/v) glycerol and 0.01% dodecyl maltoside. Inhibitors tridecyl stigmatellin (tds), myxothiazol (myx), famoxadone (fam), atovaquone (ato) and antimycin (ant) were added from DMSO stock solution to obtain a molar excess over the protein. The inhibitors were purchased from Sigma-Aldrich, except for tds, which was a generous gift from Dr N. Fisher. All forms of cytochrome bc_1 bind inhibitors with similar affinities as inferred from enzymatic turnover assays and light-induced electron transfer measurements (data not shown).

The measurements of the enzymatic activity of the different forms of cytochrome bc_1 were performed as described in ref. 33 using 20 μM horse cytochrome *c*, 20 μM decylubihydroquinone and 10–100 nM of the enzyme.

Equilibrium redox titrations of the Fe–S cluster were performed on the isolated protein at pH 8. To minimise the pH shift upon freezing the bicine buffer was used.[34] The following redox mediators were applied: tetrachlorohydroquinone, diaminodurol, 1,2-naphtoquinone-4-sulfonate, phenazine methosulphate, phenazine ethosulphate, 1,2-naphtoquinone. Ambient redox potential was adjusted by addition of small aliquots of potasium ferricyanide or sodium dithionite solutions. For each point of ambient potential a small portion of the sample was anaerobically transferred to an EPR tube and frozen in liquid nitrogen. Spectra of the titrated protein were subsequently measured by CW EPR at 20 K and the redox potential was determined by fitting the Nernst equation to the data points (Fig. S1, ESI†).

Prior to EPR measurements, all samples of cytochrome bc_1, except for those prepared for redox titration, were reduced with sodium dithionite to keep all the protein cofactors in reduced state. After reduction, samples were frozen and stored in liquid nitrogen until used.

EPR measurements

EPR spectroscopy was performed on a Bruker Elexsys E580 spectrometer operating at X- and Q-bands using similar equipment and settings as described previously in ref. 26 and 35. CW spectra were recorded at the X-band over the temperature range 20–120 K using a non-saturating microwave power.

Inversion recovery measurements at 5–25 K

Pulse EPR experiments were carried out in a Bruker Q-band resonator ER5107D2. Inversion recovery (IR) measurements were performed at 5–25 K using a pulse sequence: π–t_d–$\pi/2$–t–π with a constant t = 160 ns. The initial t_d = 160 ns was incremented to cover the whole recovery curve after the inverting π pulse. Such a sequence of pulses yields an overall dead time of IR measurement of ~500 ns. Within the considered temperature range the relationship: $T_1 \gg T_2$ is valid, therefore transverse relaxation does not affect the measured IR curves.[26] The lengths of microwave pulses π/2 and π were set to 20 and 40 ns, respectively and the microwave pulse power was adjusted to obtain the maximum amplitude of the spin echo. Above 25 K the relaxation becomes very fast and most of the recovery takes place within the experimental dead time, therefore only residual slow-relaxing components of the recovery can be detected. Above 30 K the spin-echo signal becomes virtually undetectable.

The measured IR curves were non-exponential, indicating the distribution of relaxation rates or spectral diffusion. To evaluate the possible effect of spectral diffusion on the recorded IR trace we performed measurements in which the first inverting π pulse was replaced with a saturating picket-fence of microwave pulses, or with a single saturating long-pulse. However, in all cases the shape of recovery curves remained unchanged. The experimental IR curves were mathematically modelled using a stretched exponent function:

$$Y(t) = a \cdot \exp\left[-\left(\frac{t}{\tau}\right)^{\beta}\right] + y_0$$

where τ and β represent the time constant of the process and the stretching parameter, respectively.

The average spin–lattice relaxation rate was then calculated using the equation:

$$\frac{1}{T_1} = \left[\Gamma\left(\beta^{-1}\right)\frac{\tau}{\beta}\right]^{-1}$$

where Γ is the gamma function.[36]

For tds-treated WT, S158A and Y160W and non-inhibited S158A, WT, Y160W, and +2Ala, S158A +1Ala IR curves were measured at g_z, g_y and g_x transitions. In all cases the obtained T_1 values depended on their position in the Fe–S spectrum, proving the anisotropic character of the relaxation. In the presence of tds, the spin–lattice relaxation rate increased in the order: $(1/T_1)g_x < (1/T_1)g_y < (1/T_1)g_z$, while for non-inhibited enzymes a different relationship occurred: $(1/T_1)g_y < (1/T_1)g_x < (1/T_1)g_z$. The origin of these changes in the relaxation anisotropy upon addition of tds is not known but probably it could be associated with the formation of the hydrogen bond between the inhibitor and the cluster liganding histidine 156. In further analyses only T_1 determined at g_y transition was considered.

Analysis of CW EPR spectra and determination of T_1 for temperatures above 80 K

At temperatures higher than 40 K, T_1 shortens and drives transverse relaxation ($T_2 = T_1$). As temperature increases, the homogeneous broadening of the individual resonance lines increases with ${T_1}^{-1}$, affecting the CW EPR powder spectrum. Estimation of $\boldsymbol{g}$ and $\boldsymbol{g}$-strain tensors, as well as the temperature-dependent Lorentzian broadening for a particular variant of cytochrome bc_1 results from the fitting of the simulated EPR spectrum to experimentally measured traces.

A model of "powder" EPR spectrum simulation, adequate for frozen solutions of metalloproteins (with S = 1/2) was developed by Hagen.[37] In our simulations we implemented the basic foundations of Hagen's algorithm: the $\boldsymbol{g}$-strain tensor was defined in the g-values space, and its components (up to six) determined an orientation-dependent Gaussian linewidth $\gamma_G(\theta,\varphi)$ of the resonance transition at $g_{eff} = g(\theta,\varphi)$. In addition, the tensor $\boldsymbol{L}$ (expressed in terms of g-values space) was incorporated into the model to account for the presence of anisotropic homogeneous broadening. The principal values of the $\boldsymbol{L}$ tensor were used to calculate the effective value of the Lorentzian linewidth $\gamma_L(\theta,\varphi)$ using an expression analogical to that used for the Gaussian linewidth $\gamma_G(\theta,\varphi)$. The subsequent lineshape for a given resonance line resulted from convolution of the Gaussian and Lorentzian broadening mechanisms which for practical reasons was approximated by the pseudo-Voigt profile.[38,39] The simulated EPR spectrum was created as a superposition of all the calculated signals originating from particular centres that were randomly oriented with respect to the applied magnetic field. This was performed as an orientation-weighted sum over a sphere represented by a SOPHE grid,[40,41] which typically consisted of 1000 orientations. Each spectrum was transformed from the g-value domain to the magnetic field domain using proper renormalization formulas. All numerical simulations of the EPR spectra were implemented in a Matlab environment, using the original procedures (available upon request). The values of $\boldsymbol{g}$, $\boldsymbol{g}$-strain and $\boldsymbol{L}$ were determined for all examined cytochrome bc_1 samples as the "best fit" parameters. Initially, the simulated spectra were fitted using the Simplex method and then further optimised using the Levenberg–Marquardt algorithm (LMA). For temperatures where $T_2 = T_1$, based on the fitted values of the $\boldsymbol{L}$ tensor, the spin–lattice relaxation rates for each line $i = x, y, z$ were calculated using the formula:

$$\frac{1}{T_{1i}} = 2\pi\nu\frac{L_i}{g_i}$$

where ν is the microwave frequency, L_i denotes the principal value of the $\boldsymbol{L}$ tensor (full width at half maximum (FWHM) of the Lorentzian line in the g-value domain) and g_i is the principal value of the $\boldsymbol{g}$-tensor.

In the case of multicomponent spectra the average relaxation rate was calculated as the weighted mean value of relaxation rates obtained from the $\boldsymbol{L}$ tensor for each spectral component.

Analysis of temperature dependence of the relaxation rate of the Rieske cluster

Spin–lattice relaxation rates of different forms of cytochrome bc_1, determined for the whole temperature range 5–120 K, were fitted using LMA as the sum of three mechanisms: direct, Raman and Orbach:

$$\frac{1}{T_1} = C_{dir}T + C_{Ram}\left(\frac{T}{\theta_D}\right)^9 J_8\left(\frac{\theta_D}{T}\right) + C_{Orb} \cdot {E_{Orb}}^3\left[\exp\left(E_{Orb}T^{-1}\right) - 1\right]^{-1}$$

In this equation, C_{dir}, C_{Ram} and C_{Orb} are the efficiencies of direct, Raman and Orbach processes, respectively. θ_D and E_{Orb} denote the Debye temperature and Orbach energy, respectively. The transport integral J_8 was substituted with an analytical approximation, as described in ref. 42 which allowed us to fit θ_D as an independent parameter. The uncertainty levels of the determined "best-fit" parameters were obtained from square roots of diagonal elements of the covariance matrix, calculated by LMA. To compare C_{Ram} for different samples we performed additional fitting of the data obtained in the temperature range 10–25 K with the θ_D value fixed at 107 K, which is the average Debye temperature determined for all samples.

To compare spectral anisotropy between different samples we introduced a phenomenological parameter A, that provides the average (over the whole EPR spectrum) measure of spin–orbit coupling. A is defined as:

$$A = \sqrt{\sum_i^n \left[(g_e - g_i)^2 \cdot f(g_i) \cdot \Delta g\right]}$$

where i is a consecutive point of a simulated spectrum in the g-value domain, n is the total number of points of the digitised spectrum, $f(g_i)$ is the amplitude of the absorption spectrum at g_i position, g_e is the g-value of the free electron, g_i is the consecutive g-value and Δg is the resolution. The value of "A", calculated on the basis of the EPR spectrum for a disordered sample, is sensitive not only to the deviation of the adequate $\boldsymbol{g}$-tensor from g_e, but also to the sample-specific distribution $f(g_i)$. Thus, the proposed formula more reliably reflects the effective strength of spin–orbit coupling and can differentiate the samples with similar $\boldsymbol{g}$-tensors but different EPR spectrum shapes.

Table 1 Relative equilibrium redox midpoint potentials of the Fe–S cluster in the WT and mutants of cytochrome bc_1, the ability of the enzyme to support photosynthetic growth of *Rhodobacter capsulatus* cells and enzymatic activity of the enzyme

Form	$\Delta E_{m,pH8}$ [mV]	Photosynthetic growth	Turnover rate of cytochrome *c* reduction [s^{-1}] ± st. error
WT	0	+++	140 ± 5
+1Ala	+13	+++	144 ± 7
+2Ala	+89	−	4.2 ± 0.2
S158A	−133	+	18.1 ± 0.6
Y160W	−103	++	11.9 ± 0.2

Results and discussion

Effect of mutations and inhibitors on the position of the ISP-HD and redox properties of the Fe–S cluster

We analysed the properties of the ISP in the presence of various mutations and/or inhibitors of quinone catalytic sites. All these factors introduced structural changes in the local environment of the Fe–S cluster and some of them also influenced the average distribution of ISP-HD positions. The mutations affecting the motion included insertions of one or two Ala residues in position 46[23,24] (+1Ala or +2Ala) leading to a shift of various degrees of the population of the ISP-HD towards the cytochrome *b* subunit (to the *b* position) (Fig. 1B). In +1Ala, the ISP-HD is arrested at the *b* position for at least several milliseconds which leads to only a slight decrease in the enzymatic activity of cytochrome bc_1.[27,29,43,44] In +2Ala the ISP-HD is arrested at this position for hundreds of milliseconds, which relegates the electron transfer between Q_o and heme c_1 at the time scale of seconds severely inhibiting the enzymatic activity. The mutations in the local environment of the Fe–S cluster included replacement of either S158 to Ala or Y160 to Trp (Fig. 1C). S158A removes the hydrogen bond between the –OH group of serine and the S1 sulphur of the cluster, whereas changing Y160 to Trp not only removes the hydrogen bond between the –OH group of tyrosine and the sulphur atom of the cluster liganding C133, but also slightly shifts the positions of amino acid side chains around the cluster shell to accommodate a relatively large tryptophane residue.[45–48] S158A was tested alone (single mutant S158A) or in combination with +1Ala and +2Ala (double mutants S158A +1Ala and S158A +2Ala, respectively).

As shown in Table 1, S158A and Y160W decreased E_m by ~133 and ~100 mV, respectively. This is reflected in the lower enzymatic activity and the slower growth rate of bacterial cells under photosynthetic conditions.‡ The changes in the E_m of S158A and Y160W are associated with the removal of hydrogen bonds in the vicinity of the cluster as anticipated from inspection of the crystal structure of analogous mutants in *Rhodobacter sphaeroides* and biochemical studies of the mutated ISP from other organisms.[46–49]

Table 1 shows that +1Ala and +2Ala also influence the E_m, as reported earlier.[27] When the ISP-HD is in the *b* position, the redox potential of Fe–S is higher compared to the potential of Fe–S in other positions:[27] thus, in +2Ala, in which almost the entire population is in the *b* position, the redox potential is elevated by ~90 mV, while in +1Ala, in which the population at the *b* position is larger than in the WT but less than is the case for +2Ala, the potential is elevated by ~20 mV. The increase in the redox potential upon shifting the ISP-HD to the *b* position (+1Ala or +2Ala) appears to be independent from the effect of hydrogen bonding as it is also observed for mutants with the shifted ISP-HD and lacking specific H bonds (see example S158A *vs.* S158A +1Ala in Fig. S1, ESI†). The origin of the change in redox potential of Fe–S related to the change in position of the ISP-HD is still not clear,[25,50] but it is likely related to distortions of the active site upon binding the ISP-HD to the Q_o site that modifies the ionisation potential of the cluster.[4,51]

Inhibitors of the Q_o catalytic site included tds, ato, fam and myx.[52,53] The first three inhibitors (tds, ato, and fam) fix the ISP-HD at the *b* position, which can occur with (tds and ato) or without (fam) formation of a hydrogen bond between the inhibitor and cluster-liganding H156 residue. Myxothiazol has the opposite effect; it shifts the domains out of the *b* position.[54]

Inversion recovery rates of the Rieske cluster at 12 K

Fig. 2A shows inversion recovery curves measured at 12 K at the g_y transition of the Fe–S cluster for samples in which the distribution of positions of the ISP-HD was modified by +1Ala mutation or by using inhibitors tds or myx. The recovery rate increases in the order WT + tds < +1Ala < WT < WT + myx (11.3×10^3, 12.1×10^3, 15.2×10^3, and 18.3×10^3 s^{-1}, respectively, at 12 K) and appears to correlate with the shift of the ISP-HD out of the *b* position: the domains that are closer to the *b* position exhibit slower recovery rates.

The effect of point mutations S158A and Y160W on T_1 was initially tested in the presence of tds to eliminate the possible influence from changes in the distribution of ISP-HD positions on T_1. The relaxation rate for these samples increased in the order of S158A + tds < Y160W + tds < WT + tds (4.5×10^3, 6.1×10^3 and 11.3×10^3 s^{-1}, at 12 K respectively) (Fig. 2B). This effect must result from modifications in the local protein structure near the Fe–S cluster binding site, in particular the lack of specific hydrogen bonds in the mutants.

Analysis of CW EPR spectra of the Fe–S cluster at low temperature

The modification of the cytochrome bc_1 structure caused by mutations and/or inhibitors affected the features of CW EPR spectra of the Rieske cluster in particular samples; however, the general rhombic shape was preserved in all cases (see examples in Fig. 3).

Simulation of CW EPR spectra at 25 K allowed us to estimate the principal $\boldsymbol{g}$ tensor and *g*-strain values that define the inhomogeneous line broadening and the number of components in the particular CW spectrum (see Table S1 in the ESI†). Introducing off-diagonal elements of the $\boldsymbol{g}$-strain tensors did not improve the fits thus in all cases only principal *g*-strain values were considered.

‡ *Rb. capsulatus* obligatorily requires functional cytochrome bc_1 to support photosynthetic growth of the bacteria in the absence of oxygen; therefore growth under these conditions reflects the general activity of the enzyme.

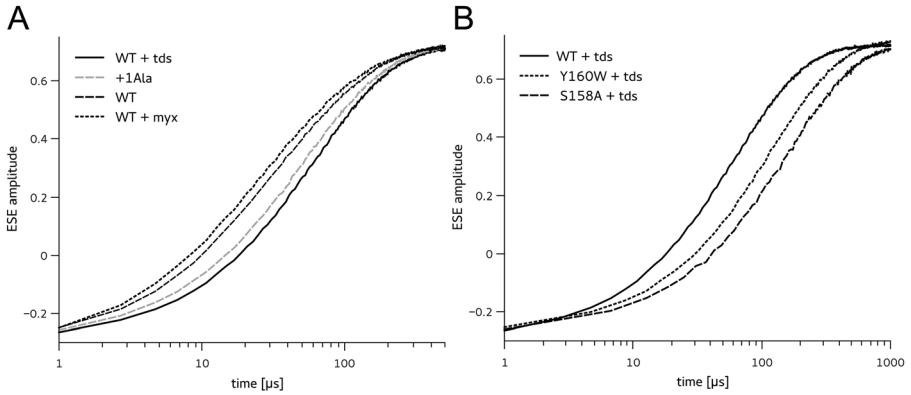

Fig. 2 Semi-log plot of inversion recovery curves measured at the g_y transition of the Fe–S cluster at 12 K. Comparison of recovery curves for cytochrome bc_1 with different average positions of the ISP-HD in the absence of point mutations (A) and for S158A or Y160W mutants with the ISP-HD arrested at the *b* position by treatment with tds (B).

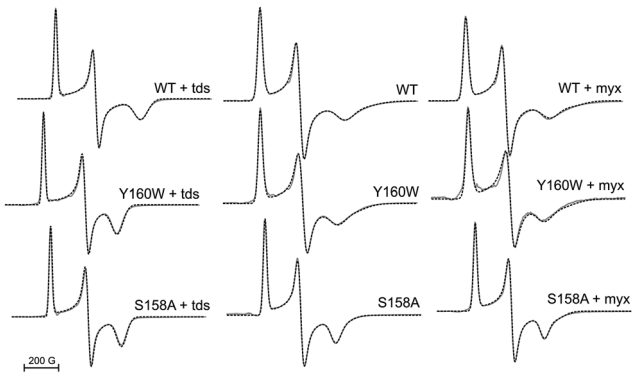

Fig. 3 Simulation of X-band CW EPR spectra measured at 25 K of the Fe–S cluster for WT, S158A and Y160W mutants. Spectra from left to right correspond to the forms in which the average distance of the Fe–S cluster from the *b* position increases. Solid grey and dashed black lines show experimental and simulated spectra, respectively.

The use of one spectral component was sufficient to simulate spectra only for samples in which the ISP-HD was fixed at the *b* position due to the presence of mutation (+2Ala, S158A +2Ala) or inhibitor tds (WT + tds, S158A + tds, Y160W + tds). This observation suggests that tds and +2Ala mutants arrest the ISP-HD at the *b* position in such a way that the population of the Fe–S clusters is uniform and single-component. Other inhibitors that also restrict the motion of the ISP-HD (ato, fam) required the introduction of two components, with clearly different ***g***-tensors, to reproduce the experimental spectra. In the presence of ato, addition of $\sim$18% of the second component was needed, while in the presence of fam, the two components contributed almost equally. The difference in the number of components between tds and ato or fam can be explained by the fact that ato and fam are not as strong inhibitors as stigmatellin and that the hydrogen bond between the inhibitor and ISP-HD is weaker (ato)[55–57] or not formed at all (fam).[52,58,59] The remaining spectra also required more than one component to obtain good fits but generally two components were sufficient to reproduce all experimental spectra. Fig. S2 (ESI†) shows the inadequacy of selected single-component fits.

Point mutations S158A and Y160W led to an increase in ***g*** values and a decrease in both average spectral anisotropy and *g*-strain values of the Fe–S cluster, when compared to WT. This effect is associated with the changes in the electronic configuration due to modifications of hydrogen bonds around the Fe–S cluster. The addition of myx to the samples led to only small changes in *g* values and *g* strain. The representative results of spectral simulations for the WT, S158A and Y160W, in combination with tds and myx are shown in Fig. 3.

Spin–lattice relaxation rate obtained from simulation of CW spectra at higher temperature

For simulations of spectra registered in the temperature range 80–120 K only homogeneous broadening was considered to change upon increase in the temperature. The other parameters (*e.g.* *g* values, *g* strain, number of components, *etc.*) were fixed at values established from simulations of the respective spectra at 25 K. This assumption was justified by the fact that temperatures below 120 K are still low enough to keep the protein structure unchanged in comparison to the structures at 25 K.

In several cases, the fitting of the CW spectra using a model with isotropic Lorentzian broadening led to unacceptably poor fits (see examples for WT and WT + myx shown in Fig. 4). Given that, and also taking into account the anisotropy of IR rates, we concluded that the broadening of the lines must be described by the anisotropic Lorentzian linewidth. Indeed, the anisotropic model of Lorentzian broadening significantly improved the fits (Fig. 4). Clearly, at higher temperatures the relaxation follows the anisotropic trend observed at low temperatures and this anisotropy is even more pronounced.

Mechanisms of spin–lattice relaxation of the Fe–S cluster

A physical explanation of the spin–lattice relaxation process must refer to the electronic states of the exchange-coupled diiron cluster and the vibrational properties of the lattice. When modifications of the structure surrounding the paramagnetic centre affect the protein vibrational modes, the measured T_1 values differ between variants of cytochrome bc_1. Within the investigated temperature range (5–120 K) we consider the

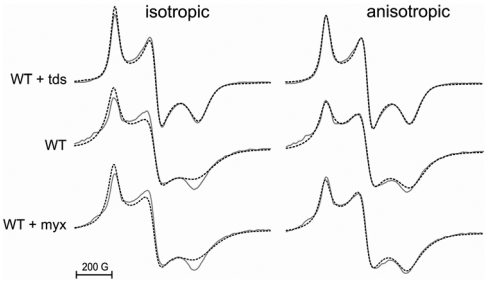

Fig. 4 CW EPR spectra of the Fe–S cluster measured at 100 K for non-inhibited WT cytochrome bc_1, treated with tridecyl-stigmatellin (tds) and myxothiazol (myx). Solid grey and dashed black lines show experimental and simulated spectra, respectively. Left and right columns show the results of fitting the same experimental data with a model assuming isotropic and anisotropic Lorentzian broadening of the lines, respectively.

existence of three relaxation mechanisms: direct, Orbach, and second-order Raman processes, as inferred from the characteristic temperature dependence of $1/T_1$ (see Fig. S3 (ESI†) for a linear representation of the relaxation rate typical for Raman or Orbach processes).

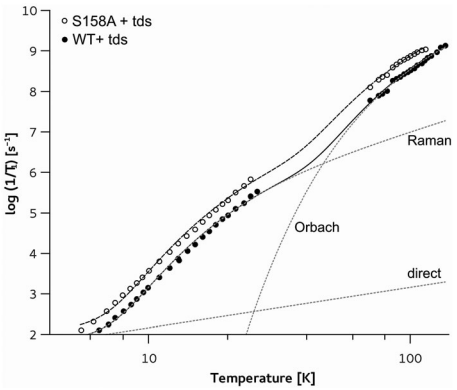

Fig. 5 Log–log plot of temperature dependence of the spin–lattice relaxation rate of the Fe–S cluster obtained for tds-treated WT and S158A (open and closed symbols, respectively). The solid line shows the fit of direct, Raman and Orbach processes to experimental data. Dashed lines show the contribution from these three processes to the relaxation of Fe–S in the mutant S158A in the presence of tds.

In Fig. 5, two representative curves of the relaxation rate as a function of temperature 5–120 K are shown. In the range 10–25 K, $1/T_1$ increases with approximately a sixth power of temperature, indicating domination of the second-order Raman process. Above 80 K this dependence is exponential, suggesting the contribution from the Orbach process, which starts to dominate upon an increase in temperature. At the lowest temperatures (below 10 K), a contribution from the direct process can be recognised from the observation that IR curves are frequency-dependent (the relaxation rates measured at the Q band are higher than those measured at the X band). This frequency-dependence becomes undetectable upon an increase in the temperature as other mechanisms prevail (data not shown). Fig. 5 also shows representative fits of the sum of these three mechanisms to the experimental data points yielding parameters shown in Table 2. For all forms of cytochrome bc_1 investigated here, the Debye temperature falls within the range 100–120 K (with an average value of 107 K), which is in agreement with values reported for frozen glassy solutions of proteins.[15] The Orbach energy falls within the range ~350–550 K with an average value of ~450 K (~300 cm^{-1}), which also is in the same order as previously reported values for ferredoxins.[14,60]

Comparison of the WT with S158A and Y160W indicates that the Orbach energy increases in these mutants (353 K for WT *vs.* 447 and 554 K in S158A and Y160W, respectively), suggesting an increased antiferromagnetic coupling between Fe ions in the cluster. This effect is likely to be related to subtle changes in the geometry of the Fe–S cluster particularly in terms of the Fe–S distance and/or Fe–S–Fe angle.[61] Inhibitors and mutations affecting the motion of the ISP-HD also influence the Orbach energy, but at this point it is difficult to find a clear tendency for these changes (Table 2).

Efficiency of Raman relaxation in different forms of cytochrome bc_1

Parameters describing the efficiency of Raman relaxation and Debye temperature are correlated.[62] This means that changes

Table 2 Parameters of spin–lattice relaxation for different forms of the Rieske cluster

Group	Sample	C_{Dir} [s^{-1} K^{-1}]	C_{Ram} [s^{-1} K^{-9}] × 10^{-10}	θ_D [K]	C_{orb} [s^{-1} K^{-3}]	Δ_{orb} [K]
A	WT	24.0 ± 3.2	1.59 ± 0.16	108 ± 4	966 ± 130	353 ± 29
	WT + tds	24.8 ± 2.9	1.24 ± 0.11	103 ± 3	612 ± 59	398 ± 25
	WT + myx	33.9 ± 5.7	1.86 ± 0.22	109 ± 5	1052 ± 225	406 ± 46
	WT + ato	40.3 ± 9.4	0.91 ± 0.17	111 ± 6	nd	nd
	WT + fam	23.0 ± 2.3	0.98 ± 0.07	104 ± 3	nd	nd
	WT + ant + myx	22.7 ± 6.8	1.96 ± 0.24	110 ± 5	nd	nd
	+1Ala	27.1 ± 2.9	1.39 ± 0.12	102 ± 3	907 ± 144	505 ± 28
	+2Ala	31.8 ± 4.0	0.913 ± 0.090	108 ± 3	444 ± 43	410 ± 25
B	S158A	14.3 ± 2.4	0.441 ± 0.066	118 ± 5	234 ± 49	447 ± 48
	S158A + tds	14.8 ± 1.2	0.411 ± 0.031	109 ± 3	364 ± 24	465 ± 16
	S158A + myx	16.0 ± 1.8	0.77 ± 0.08	101 ± 3	nd	nd
	S158A +1Ala	17.1 ± 2.0	0.71 ± 0.06	99 ± 3	345 ± 26	523 ± 16
	S158A +2Ala	21.5 ± 2.3	0.455 ± 0.046	108 ± 3	222 ± 22	470 ± 30
C	Y160W	20.6 ± 3.3	1.09 ± 0.13	108 ± 4	4290 ± 1077	554 ± 64
	Y160W + tds	14.4 ± 1.2	0.599 ± 0.041	107 ± 3	469 ± 34	425 ± 18
	Y160W + myx	23.1 ± 4.0	1.15 ± 0.13	104 ± 4	nd	nd

in C_{Ram} can be compensated by changes in θ_D. Therefore, to compare C_{Ram} for different samples, θ_D was kept constant at 107 K and only Raman efficiency was fitted yielding C_{Ram}' values.

The point mutation around the Fe–S cluster (S158A or Y160W) has a dominant effect on the relaxation rates thus, the influence of other factors differentiating the samples was further examined within 3 groups: A – encompassing WT variants with the presence or absence of different inhibitors and +1Ala, +2Ala insertions; B – S158A variants with or without inhibitors or +1Ala, +2Ala insertions; and C – Y160W variants with or without inhibitors. The values of C_{Ram}' were compared within each of these groups.

Such analysis revealed the following regularities. When the ISP-HD is fixed at the *b* position due to the presence of tds, ato, fam or mutation +2Ala, the efficiency of the Raman process decreases. On the other hand, the inhibitors that shift the ISP-HD distribution out of the *b* position (myx, and myx + ant) cause the C_{Ram}' to increase in comparison to non-inhibited enzymes. These results suggest that the relaxation efficiency of the Raman process for the Fe–S cluster in cytochrome bc_1 generally correlates with an increase in the average distance of the ISP-HD from the *b* position.

The efficiency of Raman relaxation generally increases with an increase in spin–orbit coupling, which is proportional to the difference between *g*-values and g_e = 2.0023. It is also known that for paramagnetic centres with comparable spin–orbit coupling the efficiency is smaller for structures that are more rigid. Therefore, to estimate possible contributions from spin–orbit coupling and protein rigidity, we analysed the dependence of C_{Ram}' on the average spectral anisotropy *A* (Fig. 6).

The experimental data, depicted in Fig. 6, confirmed the expected general tendency for an increase in C_{Ram}' with growing spin–orbit coupling. However, close inspection of the data in Fig. 6 reveals several cases for which an increase in spectral anisotropy does not lead to an increase in C_{Ram}' (for example C_{Ram}' in S158A +1Ala = S158A = Y160W + tds, S158A +2Ala = S158A + tds or +2Ala = WT + fam = WT + ato) or an increase in C_{Ram}' is not associated only with a change in spectral anisotropy (for example, C_{Ram}' in S158A + tds < S158A < S158A + myx, WT < WT + myx < WT + ant + myx). There is even a case for which C_{Ram}' decreases while spectral anisotropy increases (compare C_{Ram}' in a series +1Ala > Y160W + myx > WT + tds > Y160W > WT + ato).

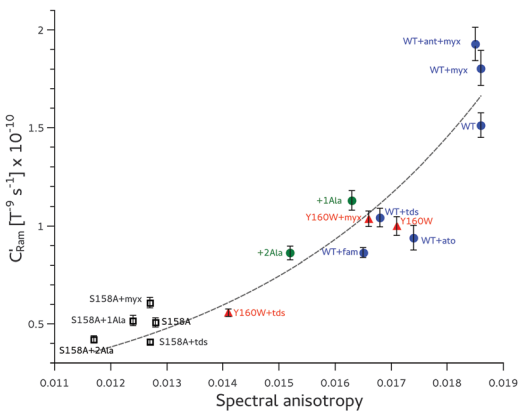

Fig. 6 Efficiency of the Raman process (C_{Ram}') plotted as a function of spectral anisotropy determined for the WT (blue) and mutants +1Ala and +2Ala (green), Y160W (red) and S158A (black) in combination with different inhibitors that influence the average position of the ISP-HD. The black dotted line represents the exponential growth fit to guide eye.

Considering the black points in Fig. 6 (all describing different forms of S158A), one can predict that of the two forms of the Fe–S cluster with the ISP-HD arrested at the *b* position (S158A +2Ala and S158A + tds) the one, with the inhibitor tds, is probably more rigid. On the other hand, the Fe–S core becomes less rigid as the population of the cluster is shifted out of the *b* position (C_{Ram}' in S158A + tds < S158A < S158A + myx). A similar trend can be observed when the ISP-HD in the WT is shifted out of the *b* position (compare C_{Ram}' for WT < WT + myx < WT + ant + myx – blue points in Fig. 6). This suggests that the rigidity of the Fe–S cluster changes depending on its position, and it is generally larger when Fe–S is in contact with the catalytic Q_o site (*b* position). In addition, in the *b* position the rigidity appears to be modified by the presence and the type of inhibitor that occupies the site (compare for example: +2Ala, WT + fam and WT + ato). This is probably related to the capability of an inhibitor to create a hydrogen bond with cluster-liganding H156.

Interestingly, Fig. 6 shows examples of C_{Ram}' values that are negatively correlated with spectral anisotropy. This is best seen for the series +1Ala, Y160W + myx, WT + tds, Y160W and WT + ato. To explain this result, we propose that the effect of an increase in spin–orbit coupling is compensated or even dominated by the progressive increase in the rigidity of the protein.

Effect of changes in hydrogen bonding on the Raman relaxation of the Fe–S cluster

The series of samples studied here allowed us to evaluate the effect of two types of hydrogen bonds on the efficiency of Raman relaxation. The first type involved intramolecular H bond located within the core of the Fe–S cluster (between the OH group of S158 and S1 of the cluster or the OH group of Y160 with the S atom of cluster-liganding C133), while the second type involved the intermolecular bond between the inhibitor occupying the catalytic Q_o site within the cytochrome *b* subunit and cluster-liganding H156 on the ISP-HD.

Removing the intramolecular H bond in S158A or Y160W leads to a decrease in C_{Ram}' which may result from changes in vibrational modes and/or spin–orbit coupling. While at this stage separating contributions from these two factors is difficult, one can expect that, if the effect of changes in vibrational modes is significant, then the intramolecular H bond provides an additional channel to transfer vibrations from the surroundings to the paramagnetic centre (Fe–S). On the other hand, an addition of the intermolecular H bond in the presence of the inhibitor may lead to an increase in the rigidity of the Fe–S binding core, probably due to the introduction of an additional constraint to the motion when two subunits of cytochrome bc_1 (cytochrome *b* and ISP) are in close contact and are additionally stabilised by interactions with the bound inhibitor. However this

interpretation should be treated with caution, as at this level we have no data on the vibrational modes of the lattice for the different variants of the cytochrome bc_1.

Concluding remarks

In this study, we examined changes in T_1 of the Rieske cluster in cytochrome bc_1 induced by several structural factors. Removal of H bonds in S158A or Y160W significantly increases T_1 of the Fe–S cluster. A somewhat weaker but similar effect was observed when the distribution of the positions of the ISP-HD (induced by mutations +1Ala, +2Ala or inhibitors) was shifted to the *b* position (to catalytic Q_o site) and this effect was independent of changes in H bonding. Therefore, the measurement of T_1 offers a way to monitor the general position of the ISP-HD with a reduced Fe–S cluster, irrespective of the redox state of the remaining cofactors of cytochrome bc_1. This is provided that mutants with the same intramolecular H bonding pattern are compared. This means that this is complementary to the previously described method of monitoring the ISP-HD distribution that was based on the measurement of the phase-relaxation-enhancement of the Fe–S cluster induced by the relaxation of heme b_L. The latter method obligatorily required the presence of oxidised heme b_L that can interact with the Rieske cluster *via* dipolar interaction.[26]

The spin–lattice relaxation rate of the Fe–S cluster revealed the existence of significant anisotropy, which becomes more pronounced as temperature increases. Above 80 K, it is so large that simulation of the CW EPR spectra of the cluster must include the anisotropic $\boldsymbol{L}$ tensor which defines different magnitude of Lorentzian broadening for the g_z, g_y, and g_x transitions.

The temperature dependence of the relaxation rates can be explained by assuming the presence of direct (below 5 K), Raman (dominating between ~10–25 K) and Orbach (dominating above ~80 K) processes. The presence of these mechanisms in the Rieske cluster of cytochrome bc_1 is in agreement with mechanisms described for spin–lattice relaxation of other iron–sulphur clusters in small proteins such as ferredoxins.[18,63]

The average Orbach energy reflecting antiferromagnetic coupling of the Rieske cluster in cytochrome bc_1 was approximately 450 K (~300 cm^{-1}) which is similar to other iron–sulphur proteins. We found that eliminating specific H bonds between the protein and sulphur atom of the cluster or sulphur atom of the cluster-liganding C133 leads to the general increase in the Orbach energy and may suggest that distances or angles between cluster atoms undergo modifications resulting in stronger spin–spin exchange coupling between Fe^{3+} and Fe^{2+} ions of the Fe–S cluster.

The efficiency of the Raman process (C_{Ram}) generally increased exponentially with an increase in spectral anisotropy *A* (related to the spin–orbit coupling). Nevertheless, for some samples characterised by rather large spectral anisotropy, the expected increase of C_{Ram}' was not observed. This lack of correlation can be interpreted as a reflection of changes in the rigidity of the protein that leads to modification of vibrational modes of the Fe–S cluster, that overlays with the effects of changes in spin–orbit coupling. This suggests that upon formation or breaking of inter- or intramolecular hydrogen bonds and/or modification of interactions of the ISP-HD with other subunits of cytochrome bc_1 the flexibility of the surroundings for the vibrational motions of the Fe–S cluster changes. It can be speculated that these changes contribute to the overall settings of the electrochemical properties of the cluster and may influence electron transfer between Fe–S and its redox partners during the reactions catalysed by cytochrome bc_1.

Abbreviations

EPR	Electron paramagnetic resonance
Fe–S	Iron–sulphur
ISP	Iron–sulphur protein subunit
ISP-HD	Movable head domain of iron–sulphur protein subunit
tds	Tridecyl-stigmatellin
ato	Atovaquone
fam	Famoxadone
myx	Myxothiazol
ant	Antimycin
E_m	Redox midpoint potential
IR	Inversion recovery
CW	Continuous wave
θ_D	Debye temperature
LMA	Levenberg–Marquardt algorithm

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