A highly processive topoisomerase I: studies at the single-molecule level

Marcin Jan Szafran¹,*, Terence Strick²,*, Agnieszka Strzałka¹, Jolanta Zakrzewska-Czerwińska¹,³ and Dagmara Jakimowicz¹,³

¹Faculty of Biotechnology, University of Wrocław, Joliot-Curie 14A, 50-383 Wrocław, Poland, ²Institut Jacques Monod, CNRS UMR 7592, University Paris Diderot, Sorbonne Paris Cité, F-75205 Paris, France and ³Ludwik Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Weigla 12, Wrocław, 53-114, Poland

Received February 14, 2014; Revised May 16, 2014; Accepted May 16, 2014

ABSTRACT

Amongst enzymes which relieve torsional strain and maintain chromosome supercoiling, type IA topoisomerases share a strand-passage mechanism that involves transient nicking and re-joining of a single deoxyribonucleic acid (DNA) strand. In contrast to many bacterial species that possess two type IA topoisomerases (TopA and TopB), Actinobacteria possess only TopA, and unlike its homologues this topoisomerase has a unique C-terminal domain that lacks the Zn-finger motifs characteristic of type IA enzymes. To better understand how this unique C-terminal domain affects the enzyme’s activity, we have examined DNA relaxation by actinobacterial TopA from Streptomyces coelicolor (ScTopA) using real-time single-molecule experiments. These studies reveal extremely high processivity of ScTopA not described previously for any other topoisomerase of type I. Moreover, we also demonstrate that enzyme processivity varies in a torque-dependent manner. Based on the analysis of the C-terminally truncated ScTopA mutants, we propose that high processivity of the enzyme is associated with the presence of a stretch of positively charged amino acids in its C-terminal region.

INTRODUCTION

In prokaryotes, and similarly in eukaryotes, deoxyribonucleic acid (DNA) needs to be highly compacted to fit the space limited by the cell size (1–4). Although the chromosome is highly condensed within a cell, it also has to be accessible for dynamic processes such as replication, transcription, recombination and segregation, the proper execution of which is dependent on spatial DNA structure. Local chromosome organization is exerted by nucleoid-associated proteins and histones in prokaryotes and eukaryotes, respectively, whilst global compaction is induced by condensins (SMC) (5–7). However, in most cases negative supercoiling is the first step of DNA compaction which within the cell is maintained by enzymes called topoisomerases.

Topoisomerases act by removing or introducing supercoils into the DNA molecule. The two evolutionarily and functionally distinct types—type I and type II (8,9)—exhibit different reaction mechanisms. Whilst type II topoisomerases (e.g. gyrase) catalyze cleavage and religation of both DNA strands, type I topoisomerases cut a single strand. Formation of an intermediate covalently linked to either strand is followed by rotation of the intact strand and religation (10). 

Type I topoisomerases are further divided into subtypes IA, IB and IC, according to the origin of the enzyme. Type IA topoisomerases are present in eukaryotes, poxviruses and a few bacteria species [their presence in bacteria may be the effect of horizontal gene transfer (10)], topoisomerases of type IC are present in eukaryotes, poxviruses and a few bacteria species [their presence in bacteria may be the effect of horizontal gene transfer (10)]. Topoisomerases of type IA and IC are characteristic of prokaryotes and archaea. Topoisomerases IB and IC form linkage with the 5′-end of DNA and remove several positive or negative supercoils (Lk, linking number; the number by which one DNA helix contacts with the second one and which cannot be altered without strand breakage) per cleavage/religation cycle using a constrained swiveling mechanism, whilst topoisomerases IA (TopA and TopB) form a 5′-phosphotyrosine intermediate and can relax only one negative supercoil per cleavage/religation event using an enzyme-bridged strand passage mechanism (11–13).

The similarity between TopA and TopB proteins manifests itself mostly in the conserved N-terminal region, containing a TOPRIM (topoisomerase-primase) domain.
and the catalytic tyrosine residue required for the trans-
esterification reaction (14,15). Although TopA and TopB share the same overall mechanism of supercoil removal, they differ in details at both the structural and mechanistic levels. TopA homologues contain a long C-terminal domain with zinc-finger motifs that are absolutely required for DNA binding and relaxation, whilst TopB homologues possess a short C-terminal domain lacking those structures. The difference in the structure of TopA and TopB reflects their cellular function and the mechanism by which they relax supercoiled DNA. Whilst *Escherichia coli* TopA removes negative supercoils efficiently and plays a major role in maintaining the appropriate superhelical density of the chromosome, TopB relaxes negatively supercoiled DNA more slowly and pauses between each relaxation burst (16). However, TopB is more efficient in decatenating single-stranded DNA rings due to the presence of a structural motif named the decatenation loop (17,18). Thus, in vivo TopB may be involved in several types of DNA transactions, but its cellular role remains still unclear.

Although many bacterial species, in particular rapidly growing ones, possess genes encoding both type IA topoisomerases, the linear chromosome of mycelial, multigenomic and sporulating bacteria, *Streptomyces coelicolor* contains only one gene encoding topoisomerase of type I (ScTopA) (19) that is essential for cell viability (20,21). In contrast to other TopA homologues, the enzyme identified in *S. coelicolor* (20), as in other *Actinobacteria* ([22,23] and Supplementary Figure S1), contains a very long C-terminal domain lacking zinc fingers but encompassing the stretch of positively charged amino acids. Thus, it exhibits poor homology to either TopA or TopB families and seemingly be-

**MATERIALS AND METHODS**

**In silico analysis**

All similarity analyses were performed using Basic Local Alignment Search Tool. Amino acid sequences of bacte-
rial topoisomerases type IA were retrieved from UniPro-
tKB Protein Knowledgebase (www.uniprot.org). Phyloge-
netic analysis of bacterial topoisomerases was prepared us-

ing MEGA5.1 software and MUSCLE algorithm for mul-
tiple sequence alignment. The guide tree was calculated us-

ing the neighbour-joining Method. Secondary structures of ScTopA and EcTopA, respectively, were predicted using GOR, HNN and SOPMA algorithms (www.expasy.org/tools).

**Protein overexpression and purification**

Topoisomerase I (ScTopA) was overproduced using the construct pET(ScTopA), and purified as described earlier (21).

To overproduce the truncated versions of ScTopA protein, the construct pET(ScTopA) was modified by λRed-mediated recombinamation with the use of the apramycin resistant cassette amplified using oligonucleotides topA_delC_FW and topA_delC_RV (for ScTopAΔC carrying 343-aa C-
terminal deletion) and topA881_FW and topA_delC_RV (for ScTopA881 carrying 71-aa C-terminal deletion) yielding pET(ScTopAΔC) and pET(ScTopA881), respectively. Both ScTopA-truncated versions were subsequently overexpressed in *E. coli* BL21 strain, purified and tested for nuclease contamination; 250 ng of the purified protein was incubated 24 h in 37°C with 200 ng of supercoiled pUC19 plasmid in 25-mM NaH2PO4 pH 8.1, 150-mM NaCl, 5% glycerol, 10-mM MgCl2 and supplemented with 1-mg/ml bovine serum albumin (BSA). After this time DNA was extracted using phenol:chlorophorm:isoamyl alcohol (25:24:1). DNA was analysed by standard gel electrophoresis in 1% agarose in 1x Tris-borate-EDTA (TBE) buffer to confirm no nicking occurred.

**Topoisomerase relaxation assay**

A 20-μl mixture containing 200 ng of negatively supercoiled plasmid, 10-mM MgSO4, 1-mg/ml BSA, 50-mM NaH2PO4 pH 8.1, 150-mM NaCl, 5% glycerol and increasing concentration of ScTopA protein (0–500 nM) was incubated in 37°C for the time indicated. To compare the activity of ScTopA and ScTopA881 proteins, we incubated 200 ng of pUC19 plasmid in the presence of 100-nM enzyme for up to 60 min. The reaction was stopped by addition of 1.5 μl of 0.5-M ethylenediaminetetraacetic acid (EDTA). DNA was subsequently extracted by vortexing with 1 volume of phe-

nol:chlorophorm:isoamyl alcohol (25:24:1). DNA was re-
solved in 1% agarose in Tris-acetate-EDTA (TAE) buffer for 14–16 h at low voltage (2 V/cm). Topoisomers distributions were visualized by staining in ethidium bromide/TAE solution at room temperature for 30 min. Band intensities and relaxation profiles were analysed on Typhoon 8600 Im-

ager using software provided by the producer. To estimate the kinetic parameters (*Km* and *Vmax*), 10 ng of ScTopA (5 nM) or 150 ng of ScTopA881 mutant truncated in positively charged C-terminus (75 nM) was incubated with increasing amount of pUC19 plasmid (100–2500 ng) carrying in each DNA molecule 8–10 supercoils that are the substrate for ScTopA. The *Vmax* parameters were subsequently lin-

early extrapolated to the same enzyme concentration allowing their comparison. The reaction was stopped at different stages (30–120 s), plasmid was resolved and visualized as described above. To estimate the initial velocity (*V0*), the in-

tensity of the band corresponding to the supercoiled form was measured using ImageJ2x Software and compared with non-relaxed plasmid −*R* value (after time 0 s) according to the protocol described by Xu and Leng (25). *V0* was
calculated from linear decrease of supercoiled form: \( V_0 = [scDNA] \times (1 - R) \times 1/t \), where \( t \) is the reaction time. Obtained values were fitted to the Michaelis–Menten model using R Software and drc package.

Single-molecule experiments: sample preparation, magnetic trap calibration and data analysis

Topoisomerase I activity can be assayed in real time on mechanically supercoiled, extended DNA as an increase in DNA extension resulting from topological relaxation of plectonemic supercoils. Controlling the extending force on negatively supercoiled DNA makes it possible to alter the balance between plectonemic and denatured states, making the appearance of denatured states more frequent by increasing the force. The analysis of ScTopA relaxation mechanism was performed for a broad range of DNA substrates (2–51 kb) in Hepes buffer (25-mM Hepes-KOH pH 8.0, 150-mM NaCl, 10-mM MgSO\(_4\), 1-mg/mL BSA 0.1% Tween), in which the same activity of ScTopA was observed as in bulk experiment. For single-molecule experiments, DNA fragments to be nanomanipulated were cut with XbaI and SacI, gel purified and subsequently ligated with purified 1-kb DNA labels XbaI-biotin and SacI-digoxigenin, respectively. One-kilobase DNA labels were prepared by polymerase chain reaction-based incorporation of either 2’-deoxyuridine-5’triphosphate-biotin (dUTP-biotin) or dUTP-digoxigenin into 1-kb fragments bearing an appropriate restriction site according to the protocol described previously by Revyakin et al. (26). The 11-kb DNA built in this manner is based on the Chromid 9–11-kb DNA; 2-kb DNA is a fragment of the S. coelicolor chromosome (oriC proximal region). The 17-kb DNA is pFX357 (a kind gift from Dr François-Xavier Barre), and 51-bp molecules are occasional trimers of pFX357 observed in the magnetic trap to be \( \sim 16 \mu m \) in length. These longer molecules were prepared by ligating AatII/XhoI-digested pFX357 to 1-kb DNA fragments bearing an AatII or XhoI site and labelled with multiple biotin or digoxigenin groups, respectively, as above.

Subsequently, labelled DNA fragments were attached first to streptavidin-coated magnetic beads (Dynal MyOne, Life Technologies), then to an antidigoxigenin-coated glass flow cell and placed on a home-built magnetic trap running the PicoTwist software suite. Preparation of flow cells for all micromanipulation experiments and measurement of stretching force were performed according to the procedure described in (26). The flow cell was placed on a magnetic trap instrument based on an inverted microscope. Here the magnetic beads were acted upon by a magnetic field gradient generated by a pair of rare earth magnets located above the sample. The gradient generated a vertical stretching force on the bead. The stretching force could be increased by moving the magnets closer to the sample, and rotation of the magnets caused the bead to rotate in lock-step register (Figure 1A). The DNA extension was measured in real time (30 Hz) by analysing the position of the bead above the surface using nm-resolution particle tracking algorithms.

To make certain whether the bead was tethered to the surface via a single, intact DNA molecule, the DNA was extended at a low force (\( F = 0.3 \) pN) and subsequently supercoils were introduced by rotating the magnet on the tweezers. In these conditions, the extension of a single supercoiled DNA molecule should decrease with the number of magnet rotations at a rate of \( \sim 50-55 \) nm/turn. Nicked molecules that did not show this characteristic correlation between DNA length and the number of rotations were omitted from subsequent analysis. Similarly, beads attached to more than one DNA molecule could also be omitted from subsequent analysis based on characteristically peaked extension versus supercoiling curves (27).

The analysis of the influence of supercoiling on a DNA molecule attached to a magnetic bead has shown that DNA can be extended by low forces and negatively supercoiled by several percent without provoking extensive DNA denaturation. At low stretching force (\( F \sim 0.3 \) pN in the salt conditions used here) negatively supercoiled DNA adopts a stable, plectonemic form. When such DNA is stretched with higher force (\( F \sim 0.5-1 \) pN in the salt conditions used here), the equilibrium between plectonemic and denatured states is shifted towards denatured states and locally single-stranded regions appear (28). On the other hand, for equally positively supercoiled DNA and within the force range discussed here, plectonemic supercoiling dominates throughout and denatured states are repressed. Unless stated otherwise, experiments were carried out at \( F = 0.3 \) pN.

RESULTS

ScTopA relaxes only negatively supercoiled DNA in a force- and torque-dependent manner

Comparison of ScTopA with its homologues from other bacteria revealed the unusual presence of a long C-terminal domain lacking zinc fingers but terminated with a stretch of positively charged amino acids (Supplementary Figure S1A–C), thus suggesting possible differences in the DNA binding and relaxation activity of ScTopA in comparison to, for instance, the enzyme from E. coli (EcTopA). The sequence analysis and the bulk assays of ScTopA activity, which suggested rapid supercoil removal [(21) and see also Figure 7A] prompted us to analyse the properties of ScTopA in single-molecule experiments using magnetic tweezers. In these experiments, the DNA substrates are tethered between a glass surface and a 1-\( \mu m \) magnetic bead and manipulated as described in the Materials and Methods section (see Figure 1A and B).

We first analysed the relaxation of positively and negatively supercoiled 2-kb DNA in the presence of ScTopA (5 nM) at two stretching forces (low force \( F = 0.3 \) pN, medium force \( F = 0.5 \) pN). When positive supercoils were introduced into the DNA molecule, no DNA relaxation by ScTopA was observed either at low or at medium extending forces (Figure 1C and Supplementary Figure S2). On the other hand, when the DNA molecule was negatively supercoiled its relaxation in the presence of ScTopA could be detected (Figure 1C).

Next, we analysed the kinetics of onset of supercoil relaxation using two related parameters: the initial time lag (ITL), defined as the time between mechanical introduction of supercoils into DNA and the first relaxation event caused by ScTopA activity, and the number of molecules for which no relaxation has been observed after 800 s (the maximal
Figure 1. Single-molecule assay for analysis of ScTopA relaxation activity. (A) The scheme of the experiment. (B) Extension versus supercoiling curve for 2-kb dsDNA extended by a force $F = 0.3$ pN. (C) Time-trace of ScTopA activity acting on 2-kb dsDNA for positive (+SC) and negative (−SC) supercoiling.

ScTopA removes several supercoils independently of enzyme concentration

Although in experiments at the single-molecule level ScTopA exhibited substrate preference characteristic of the TopA family, we also observed the atypical occurrence of full relaxation of DNA molecules in a single relaxation burst (i.e. the relaxation event consists in a continuous increase in DNA extension until nearly maximal extension). The relaxation of DNA molecules by removal of several supercoils in a rapid burst may result from the concurrent action of several enzyme molecules, although this is statistically unlikely given the long ITLs observed earlier. To further rule this possibility out, we analysed the relaxation of 2-kb DNA at different ScTopA concentrations and plotted the correlation between initial supercoiling (IS, the length by which the molecule is shortened as a result of magnet rotation) and initial relaxation (IR, the length by which DNA extension increases as a result of ScTopA activity during the first burst of relaxation). Similar values of IS and IR parameters (IS $\sim$ IR; Figure 3, marked with a dotted line)
force and concentration dependence of the rate at which ScTopA initiates DNA relaxation. (A) The initial time lag (ITL) for ScTopA activity displays a single-exponential distribution and decreases with increasing extending force. Histograms show the distribution of ITL values measured for 5-nM ScTopA and DNA extended by a force \( F = 0.5 \) pN (main panel) compared to ITL values measured at low extending force (inset, \( F = 0.3 \) pN). The lower extending force resulted in a near abolition of DNA relaxation events and a dramatic elevation of the number of unrelaxed molecules (grey bars in both panels). The number of molecules analysed (\( n \)) is shown at the top of each panel. The line corresponds to a single-exponential fit to the data obtained at 5 nM and for which unrelaxed molecules are proportionally very infrequent, giving a mean ITL = 29 s. Dashed vertical bars indicate the fraction of molecules relaxed within 100 s and 800 s, respectively.

(B) ScTopA activity initiates more rapidly as concentration increases. The rate of initiation 1/ITL is obtained at each concentration by fitting a single-exponential decay to the cumulative probability distribution of individual ITLs. The cumulative probability distribution allows one to include in the analysis the unrelaxed DNA molecules (which become more frequent at lower concentrations), and by fitting at short timescales the characteristic decay time of the distribution is obtained. For 0.5 nM, \( n = 43 \) of which 15 are molecules unrelaxed after 800 s; for 1 nM, \( n = 39 \) of which 12 are unrelaxed molecules; for 10 nM, \( n = 59 \) of which four are unrelaxed molecules; statistics for 5 nM are given in (A); and for 10 nM, \( n = 42 \) of which one is an unrelaxed molecule. Error bars represent SEM obtained from the single-exponential fit.

mean nearly complete DNA relaxation in a single relaxation burst, whilst IR < IS and IR = 0 correspond to relaxation in more than one burst and no relaxation at all, respectively. We noticed that ScTopA at a high concentration (2.5–5.0 nM) relaxed a large fraction of molecules in one burst (63.3% and 67.9%, respectively). Interestingly, decreasing the concentration of ScTopA did not lead to an increase in the fraction of molecules in the IR<IS category, corresponding to relaxation of DNA supercoils in multiple bursts. Instead, using lower ScTopA concentrations (0.5–1.0 nM) resulted in an increase of the fraction of molecules which remained supercoiled, although there was still a significant fraction of molecules that were relaxed in a single burst (41.2% and 44.1%, respectively). Thus, the removal of many supercoils in one relaxation event even at low enzyme concentration is most likely carried out by a single ScTopA molecule or its active multimer, rather than several ScTopA molecules/complexes acting independently.

We next estimated the rate of onset of supercoil relaxation by considering both the ITL and the number of molecules that have not been relaxed at the end of the experiment. We thus considered an initial population consisting of all of the initially supercoiled DNA molecules and calculated its decay over 800 s to a final state where only the unrelaxed molecules remain. We fit this decay to a single-exponential distribution and obtain the rate as the inverse of the decay time and plot the rate as a function of concentration (Figure 2B and Supplementary Figure S3). The rate of onset of supercoil relaxation increased linearly with topoisomerase I concentration, suggesting that diffusion is limiting in this concentration range and reinforcing the idea that these relaxation events result from the activity of a single topoisomerase I molecule/complex. From these measurements, we estimated an apparent first-order binding rate for the 2-kb DNA of about \( 2 \times 10^6 \)M/s, consistent with diffusion-limited activity.

To summarize, the magnetic trap experiments indicate that DNA subjected to ScTopA action remains supercoiled until the enzyme removes nearly all supercoils in a single burst of activity. This explains the apparent bimodal distribution of topoisomers observed in gel-based measurements of ScTopA activity. Although increasing ScTopA concentration shortened the initial time necessary for enzyme activity to be observed, it did not affect enzyme activity itself.

ScTopA preferentially relaxes DNA in a single relaxation burst

Our observation that ScTopA activity can remove nearly all DNA supercoils in a single burst of activity prompted us to check if this was still the case for longer DNA fragments that can accommodate more extensive supercoiling. Thus, we measured the number of relaxation bursts required to remove nearly all supercoils from the DNA substrates in the 2–51-kb range. For the 2-kb DNA substrate, the vast majority of molecules were relaxed in a single burst of ScTopA activity (\( \sim 63\% \)). For the remaining third of DNA molecules relaxation occurred in multiple bursts separated by long pauses (Figure 4B, inset); 26% and 11% of all relaxation time-traces showed one and two pauses, respectively, corresponding to two or three relaxation bursts (Figure 4A).

Interestingly, when we used longer DNA fragments—11 kb and 17 kb—in the magnetic trapping experiments, the fraction of molecules relaxed in a single burst remained similar to that calculated for 2-kb fragments (51% and 58%, respectively; Figure 4A). Even when the length of the DNA molecule was 51 kb (which allowed us to introduce up to 150 supercoils per molecule) in 49% of relaxation events nearly all supercoils were removed in a single burst, whilst for 51% of molecules we observed one or more pauses separating...
Figure 3. ScTopA concentrations do not influence enzyme processivity. The enzyme processivity as expressed by the ratio between initial supercoiling (IS) and initial relaxation (IR). Each circle represents a single DNA relaxation event; circles accumulated near the dotted line correspond to nearly full relaxation of supercoiled DNA in single relaxation event (IS = IR), circles marked with a ellipse represent the fraction of DNA molecules remaining supercoiled (IR < 0 within the 800-s recording time); circles located in between correspond to molecules relaxed in more than one burst (IS > IR). Percentage of molecules belonging to each population are shown on each diagram in brackets.

Figure 4. Relaxation bursts and pausing by ScTopA. (A) The number of relaxation bursts required to remove negative supercoils from DNA is not dependent on the length of DNA substrates. Histograms show the fractions of 2–51-kb DNA molecules relaxed in the specified number of bursts (1–5). (B) Example of a pause between two successive relaxation bursts and distribution of pause lifetimes.

Each burst. The pause duration between two bursts was calculated to be 10-fold shorter than the time necessary for reaction initiation (Figure 4B).

Independently of the length of the DNA substrate ScTopA removes all negative supercoils from it in the first relaxation burst. However, we observed that occasionally the enzyme pauses during a relaxation burst and requires some time to start the next relaxation burst. Moreover, comparison of the ITLs and the pause duration suggests that during relaxation cycle ScTopA does not dissociate form DNA, since the pause time is remarkably shorter than ITLs calculated for the same enzyme concentration.

ScTopA exhibits higher processivity and velocity than other TopA homologues

Originally all type IA (29,30) topoisomerases were demonstrated to use a strand-passage mechanism to decrease gradually the superhelical density ($\Delta L_k = -1$) of negatively supercoiled DNA resulting in a distributive pattern of relax-
ation products. However, differences in the mechanism of relaxation of negatively supercoiled DNA between TopA and TopB (both belonging to the subtype IA) have recently been described (16–18). The ability of ScTopA to remove a large number of supercoils in a single burst independently of enzyme concentration and substrate length prompted us to further explore its properties, in particular its reaction rate and processivity, using a long DNA fragment as substrate.

Reaction rates, given in µm/s, correspond to the speed at which the DNA extension increases as supercoils are removed by ScTopA (Figure 5A), and the distribution of reaction rates is given in Figure 5B. The velocity distribution appears to be Gaussian, with a mean reaction rate of 0.45 µm/s. The reaction rate in units of supercoils ($L_k$) removed per second is obtained by dividing the reaction rate given in µm/s by the size of a single supercoil (∼60 nm/supercoil in the experimental conditions used here), giving a mean on the order of 8–10 $L_k$/s (Figure 5B).

To estimate the processivity of the enzyme, we determined the number of supercoils ($L_k$) removed only in the first burst of ScTopA activity; a plot of the resulting probability distribution is shown in Figure 5C. The distribution is characterized by a weak decay at small values as well as a ‘brick wall’ at 7.0 µm corresponding to relaxation events that are substrate-limited. Clearly the very high processivity of ScTopA makes it difficult to quantify as even the longest single-molecule DNA substrate is too short for the processivity of most events to be determined. Although a significant number of events were observed for which the change in DNA extension was less than 7.5 µm and frequency of shorter bursts was constant (5–7% per 1 µm) suggesting the stochastic pause of relaxation process (Figure 5C), the most likely events corresponded to those for which nearly all supercoils were removed in the first burst of ScTopA activity. We note that some measurements show more than 150 turns removed in one burst, which is presumably due to the fact that individual molecules can occasionally be only partially relaxed during a prior relaxation run. When supercoiled by an additional 150 negative turns, the population of molecules obtained thus includes some individuals with more negative supercoiling than the 150 added turns yet which can still be removed in a single burst of catalysis.

Three parameters (ITL, processivity and velocity) influence the overall reaction velocity. Based on the collected data, we calculated the average total relaxation rate (TRR) for two DNA substrates: 2-kb DNA and pUC19 (∼2.7 kb) in single molecule and bulk experiments, respectively (Supplementary Figure S4A and B). TRR is defined by the time lapse between the mechanically introduced negative supercoils on DNA molecule to the point at which the bead returns to the starting position (as the result of enzyme activity). The TRR parameter calculated for 2 kb was similar (the values for most of them were not higher than 0.3 $L_k$/s) to the TRR$_{bulk}$ calculated for pUC19 plasmid based on the Michaelis–Menten equation (0.2 $L_k$/s) (Supplementary Figure S4C). The comparison of relaxation patterns of two negatively supercoiled plasmids differing in length and linking number ($L_k$) shows that the ScTopA relaxes both substrates with the same high processivity if the molar ratio of enzyme:plasmid is retained (Supplementary Figure S7). Thus, our results suggest that the overall relaxation velocity is the intrinsic property of the enzyme and is not dependent on the substrate type.

In summary, ScTopA differs from its TopA homologue from E. coli in terms of both burst velocity of supercoil removal and processivity. Comparing with E. coli TopA, for which average velocity and processivity were estimated as
3.3 \( L_k \)/s and 20 \( L_k \)/run, respectively (16). \( \text{ScTopA} \) is about 3-fold faster (10 \( L_k \)/s) and almost 10-fold more processive (150 \( L_k \)/burst). However, the waiting time preceding the supercoils removal by \( \text{ScTopA} \) makes the overall enzyme less effective than if calculated only based on the burst velocity and processivity.

\( \text{ScTopA} \) switches between processive and distributive DNA relaxation in a torque-dependent manner

To determine how efficient \( \text{ScTopA} \) was at completely removing all supercoils, we measured the number of residual supercoils left unremoved by \( \text{ScTopA} \) activity. This was done by initially supercoiling the DNA by a fixed number of turns, denoted by \( n \), and determining the resulting extension of the molecule, denoted by \( l_1 \). After \( \text{ScTopA} \) has been allowed to act on the DNA for a fixed amount of time, it is supercoiled anew by the same number of turns, \( n \), and the resulting extension \( l_2 \) is recorded. This extension \( l_2 \) is systematically smaller than \( l_1 \) (Figure 6A), indicating that there remained non-zero residual supercoiling after \( \text{ScTopA} \) action. The difference in extensions \( l_2-l_1 \) is thus related to the number of residual, unrelaxed supercoils, \( n_{\text{res}} \), according to \( n_{\text{res}} = (l_2-l_1)/\delta \), where \( \delta \) is the change in DNA extension associated with one supercoil.

We first determined the distribution of \( n_{\text{res}} \) for 17-kb substrate DNA supercoiled by \(-50 \) turns and allowed to react with \( \text{ScTopA} \) for 250 s at a low extending force (\( F \approx 0.3 \) pN). In this timeframe, all molecules are nearly completely relaxed by one or more bursts of \( \text{ScTopA} \) activity, however, as shown in Figure 6A, there remains on average 15 supercoils in the DNA. We next determined the distribution of \( n_{\text{res}} \) for the same DNA and the same IS, but allowing \( \text{ScTopA} \) to react for 1000 s (Figure 6B). The latter distribution shows that allowing the enzyme to act for longer leads to a slightly smaller number of residual supercoils but comparing the two distributions indicates that the enzyme has lost nearly all of its processivity and is only able to remove a small number of supercoils at a time. We next repeated this experiment using 51-kb substrate DNA supercoiled by \(-150 \) turns and allowed to react for 250 s; the distribution of residual supercoiling is shown in Figure 6C. Comparing the data obtained with the shorter and longer DNA molecules shows that \( n_{\text{res}} \) is proportional to the length of the substrate DNA, as would be expected for a topoisomerase with torque-dependent processivity. In agreement with this, we found that when the first experiment in this series was repeated but for an increased extending force (\( F = 1 \) pN), the distribution of \( n_{\text{res}} \) became centred about \( n_{\text{res}} = 0 \) (Figure 6B, inset).

We also calculated the superhelical densities of 17-kb and 51-kb DNA at the point at which the \( \text{ScTopA} \) processivity dropped as \( \sigma_{17} \approx -0.008 \pm 0.001 \) and \( \sigma_{51} \approx 0.009 \pm 0.001 \), respectively (Figure 6B and C). These results suggest that decreasing the absolute density below \(-0.01 \) inhibits enzyme processivity. From extension versus supercoiling curves (Supplementary Figure S7) we note that this supercoiling density corresponds to the buckling transition for DNA extended at this low force (\( F = 0.3 \) pN), and at this force the buckling transition occurs at a torque on the order of 4 pN-nm (or \( 1 k_B T \)) (31). This value is close to the denaturation torque for DNA, suggesting that the existence of denatured regions may be crucial to maintaining a high degree of processivity for \( \text{ScTopA} \).

To conclude, these data indicate that \( \text{ScTopA} \) removes supercoils in a highly processive fashion as long as the torque acting on the DNA is high enough, but at low torques displays distributive activity.

Processivity of \( \text{ScTopA} \) protein is provided by the positively charged C-terminus

\( \text{ScTopA} \) processivity was also analysed by resolving the relaxation intermediates in agarose gel electrophoresis. In this assay, a broad range of enzyme concentrations (0–150 nM) was used in reactions with negatively supercoiled pUC19 plasmid. \( \text{ScTopA} \)-mediated plasmid relaxation led to appearance of low-density topoisomers even when supercoiled plasmid or its partially relaxed topoisomers were still noticeable (Figure 7A) confirming the processive behaviour of \( \text{ScTopA} \) and underscoring the difference in relaxation mechanism between \( \text{ScTopA} \) protein and its homologue from \( E. coli \). The presence of positively charged amino acids at the C-terminal end of \( \text{ScTopA} \) prompted us to analyse the DNA relaxation properties of mutants lacking either the whole C-terminal domain (343 aa; \( \text{ScTopA}\Delta C \)) or the stretch of basic amino acids at the C-terminus (71 aa; \( \text{ScTopA}881 \)). Interestingly, removal of the whole C-terminal domain almost completely abolished enzyme activity (Figure 7D), whilst the pattern of \( \text{ScTopA}881 \) relaxation products was distributive (Figure 7B, left panel) instead of processive as observed for the wild-type protein (Figure 7B, right panel). By titrating the pUC19 reaction substrate from 10 to 70 nM, we measured the reaction velocities for \( \text{ScTopA} \) and \( \text{ScTopA}881 \) within their linear range and fitted the reaction kinetics to the Michaelis–Menten model (see the Materials and Methods section). Based on differential equation of the model, the maximal enzymatic rates \( v_{\text{max}} \) were calculated to be 6.5 nM/min for S-nM \( \text{ScTopA} \) and Michaelis–Menten constant \( K_m \) 5.1 nM and 0.62 nM/min and 20.7 nM, respectively, for the mutant \( \text{ScTopA}881 \) (Figure 7C).

In summary, these bulk experiments confirm the high processivity of \( \text{ScTopA} \) and demonstrate that complete removal of the C-terminal domain abolishes enzyme activity whilst truncation of its positively charged C-terminus affects affinity for substrate and processivity.

**DISCUSSION**

Many bacteria, especially rapidly growing species (\( E. coli \), \( Bacillus subtilis \)), possess two topoisomerases of type IA—topoisomerase I (TopA) and topoisomerase III (TopB). In contrast, \( Actinobacteria \) possess only one gene encoding a type IA topoisomerase, TopA. Although in \( E. coli \) both proteins TopA and TopB are closely related and share the same catalytic mechanism, they relax DNA with different efficiencies and processivities and play key roles in different cellular processes (16,32–34). Sequence and structure alignments suggest that \( S. coelicolor \) TopA (\( \text{ScTopA} \)), similar to homologous \( M. smegmatis \) TopA (\( \text{MsTopA} \)), possesses a unique C-terminal domain that terminates with a
...activity of substrates (36). Recently, Ahmed et al. (37) have shown that the C-terminal domain of MsTopA protein may play a role in strand-passage and suggested that the presence of a positively charged C-terminus may provide an additional binding site, ensuring efficient DNA relaxation. Our calculation of $K_{\text{m}}$ for the wild-type and truncated ScTopA protein (5.1 and 20.7 nM, respectively) corroborates with this notion. It was earlier reported that *M. smegmatis* MsTopA binds both single- and double-stranded DNA oligomers with similar affinity, and Mg$^{2+}$ ions are not necessary for DNA binding and cleavage (24), however their concentration affected processivity of the enzyme (23). We also found that, although ScTopA requires the presence of single-stranded regions in a substrate for relaxation, it effectively binds to double-stranded DNA (dsDNA) (Supplementary Figure S5).

Our results show that ScTopA is able to remove up to 150 supercoils per relaxation burst and that the enzyme is characterized by a torque-dependent processivity which leads to more distributive and/or lower activity at low torque when most of the DNA supercoiling has been relaxed. The apparent processivity of ScTopA could be the result of either simultaneous action of many protein molecules on DNA...
or the ability of a single ScTopA molecule or multimeric complex to remove several supercoils each time it binds to DNA. Analysis of the concentration dependence of the reaction rules out the possibility that apparent processivity is due to multiple active complexes acting independently as processive activity was observed at all concentrations tested. The formation of a multimeric complex composed of many ScTopA molecules acting and removing supercoils cooperatively could explain the long ITL observed for low ScTopA concentration (conditions in which a long ITL could be due to shifting the complex-assembly equilibrium towards an inactive monomeric state). It has been reported earlier that vaccinia virus topoisomerase IB is able to form a filament spreading along dsDNA forming synapses between distinct DNA fragments in a highly cooperative fashion (38). Detailed analysis of enzyme activity supports the idea that a single ScTopA molecule is able to act processively, although the hypothesis of multimer assembly cannot be excluded. The burst rate of supercoil removal by ScTopA was determined to be $8\, L_k/s$, comparable to $E.\, coli$ TopA ($3.3\, L_k/s$) but significantly lower than that of $E.\, coli$ TopB ($129\, L_k/s$) or human type IB topoisomerase ($6.7\, \mu m/s$; which corresponds to $134\, L_k/s$) (12,16). Nevertheless, the overall relaxation velocity results from the combination of the burst rate and the processivity related to affinity to substrate. Our single-molecule studies show that efficient DNA relaxation by ScTopA is the result of extremely high processivity ($150\, L_k/burst$), much higher than reported for $E.\, coli$
TopB (28 \( L_\alpha /\text{burst} \)) and human TopIB (50 \( L_\alpha /\text{burst} \)) estimated at similar extending force (12,16). \( E.\ coli \) TopB acts more processively than \( E.\ coli \) TopA presumably thanks to the creation of a stable enzyme-DNA complex (17,39) (Table 1). The high processivity of \( E.\ coli \) TopB was linked to the presence of the positively charged region known as the decatenation loop in its N-terminal domain (17). Disruption of the decatenation loop resulted in inhibition of the enzyme via an apparent reduction in processivity. Sc\( \text{TopA} \) does not possess a bona fide decatenation loop, although some homologous amino acids are present in its N-terminal domain (Supplementary Figure S1D). Thus, increased enzyme processivity is presumably linked to the C-terminal stretch of basic amino acids as indicated by Ahmed et al. (37). Predictions of secondary structure suggest that the C-terminus of Sc\( \text{TopA} \) forms an\( \alpha \)-helix with basic amino acids precisely oriented in a helical fashion on the surface of the\( \alpha \)-helix and which may constitute the domain interacting with the highly compacted supercoiled DNA, providing higher affinity to substrate. This could confer the ability of a single Sc\( \text{TopA} \) molecule to remove several supercoils each time it binds to DNA and leading to processive removal of supercoils. Thus, our most favoured hypothesis explaining rapid removal of several supercoils is the formation of a stable and processive Sc\( \text{TopA} \)-DNA complex, perhaps thanks to the presence of denatured regions in the DNA.

In summary, we suggest that in \( \text{Streptomyces} \), which lacks a copy of the top\( B \) gene encoding for topoisomerase III, Sc\( \text{TopA} \) exhibits some of the properties of TopA and TopB proteins. Although the portfolio of topology-modifying enzymes in \( S.\ coelicolor \) is simplified in comparison with other species, the topological problems it encounters during replication and segregation of a large number of long, linear chromosomes are presumably non-trivial. This could lead to the requirement for a highly processive topoisomerase, and indeed such features have been observed in \( \text{in vitro} \) using bulk and single molecule techniques. The unusually high processivity of Sc\( \text{TopA} \) combined with its previously demonstrated telomerase activity (20) and its ability to resolve topological problems during chromosome segregation (21) suggests specific adaptation of the only type I topoisomerase in \( S.\ coelicolor \) to efficiently fulfil multiple functions.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

**ACKNOWLEDGEMENTS**

The authors acknowledge financial support from the Parent Bridge Programme of Foundation for Polish Science, co-financed by European Union, Regional Development Fund, and from EURYI. Authors Contributions: M.J.S. contributed substantially to conception and design, acquisition of data, analysis and interpretation of data and drafting the article. T.S. contributed substantially to conception and design, acquisition of data, or analysis and interpretation of data and revising the manuscript critically for important intellectual content. A.S. contributed to acquisition of data. J.Z.C. contributed to revising the manuscript critically for important intellectual content. D.J. contributed substantially to conception and design, drafting the article and final approval of the version to be published.

**FUNDING** Parent Bridge Programme of Foundation for Polish Science; co-financed by European Union, Regional Development Fund; EURYI [to T.S.]. Funding for open access charge: Parent Bridge Programme of Foundation for Polish Science (POMOST/2010-2/5).

**Conflict of interest statement.** None declared.

**REFERENCES**


