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Sortase-catalyzed transformations that improve the properties of cytokines

Maximilian W. Poppa<sup>b</sup>, Stephanie K. Dougan<sup>a</sup>, Tzu-Ying Chuang<sup>a</sup>, Eric Spooner<sup>a</sup>, and Hidde L. Ploegh<sup>a</sup><sup>,b</sup>,<sup>1</sup>

<sup>a</sup>Whitehead Institute for Biomedical Research, 9 Cambridge Center, Cambridge, MA 02142; and <sup>b</sup>Department of Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02142

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Recombinant protein therapeutics often suffer from short circulating half-life and poor stability, necessitating multiple injections and resulting in limited shelf-life. Conjugation to polyethylene glycol chains (PEG) extends the circulatory half-life of many proteins, but the methods for attachment often lack specificity, resulting in loss of biological activity. Using four-helix bundle cytokines as an example, we present a general platform that uses sortase-mediated transpeptidation to facilitate site-specific attachment of PEG to extend cytokine half-life with full retention of biological activity. Covalently joining the N and C termini of proteins to obtain circular polypeptides, again executed using sortase, increases thermal stability. We combined both PEGylation and circularization by exploiting two distinct sortase enzymes and the use of a molecular suture that allows both site-specific PEGylation and covalent closure. The method developed is general, uses a set of easily accessible reagents, and should be applicable to a wide variety of proteins, provided that their termini are not involved in receptor binding or function.

Many clinically relevant cytokines share a four-helix bundle structure, typified by IFNα, Granulocyte colony-stimulating factor 3 (GCSF-3), Erythropoietin (EPO), IL-2, IL-4, IL-7, IL-9, and IL-15. Co-crystal structures of cytokines with receptor fragments and biochemical studies that map residues critical for interaction of a cytokine with its receptor show that the receptor contacts the sides of the helical bundles (1). This mode of interaction positions the N and C termini of the cytokine away from the receptor.

Polyethylene glycol chains attached to therapeutically important proteins increase circulatory half-life, reduce clearance by kidney filtration, reduce proteolysis, and reduce the generation of neutralizing antibodies (2–4). The attachment of PEG commonly employs standard chemistries that target reactive amino acid side chains (e.g., cysteine and lysine). This strategy often generates a heterogeneous mixture in which multiple amino acids in the target are modified with a PEG chain, necessitating cumbersome separations and characterization (5). Such PEGylated molecules often show decreased biological activity, likely due to attachment of a PEG chain to a residue important for interaction with the receptor (6)—this problem may be overcome by site-specific PEGylation. Although engineering of a carefully placed unpaired cysteine residue allows site-specific PEGylation (7, 8), this method must be tailored to the specific protein target.

Sortase A from <i>Staphylococcus aureus</i> (SrtA<sub>Staph</sub>) is a thiol-containing transpeptidase that recognizes an LPXTG motif in multiple structurally unrelated substrates (9). SrtA<sub>Staph</sub> cleaves the peptide bond between the threonine and glycine residues with concomitant formation of a thioacyl enzyme intermediate that involves the catalytic cysteine and the substrate threonine. This acyl-enzyme is resolved by nucleophilic attack of the N terminus of an oligoglycine peptide, resulting in formation of an amide acyl-enzyme is resolved by nucleophilic attack by the N terminus involving the catalytic cysteine and the substrate threonine. This concomitant formation of a thioacyl enzyme intermediate that involves the catalytic cysteine and the substrate threonine.

**Conflict of interest statement:** The authors have applied for a patent based on the technology used in the paper.

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<sup>1</sup>To whom correspondence should be addressed. E-mail: ploegh@wi.mit.edu.

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lently joining the N and C termini of these proteins (15). We present a general method for combining both site-specific PEGylation and improved thermal stability in a single molecule by using a molecular suture produced in two successive rounds of sortase-catalyzed transeptidation (Fig. 1).

**Results**

**Modification of IFNα2.** We first applied the sortase reaction to human interferon alpha (IFNα2), a four-helix bundle cytokine where chemical PEGylation results in multiple positional isomers and a ~90% decrease in biological potency (16). We expressed in *Escherichia coli* two versions of IFNα2, both with an LPETG sortase motif immediately followed by a hexahistidine tag for ease of purification. At the amino terminus, one of the two proteins possesses a diglycine motif for cyclization. This material can either be cycled or PEGylated at the C terminus (Fig. 2A). IFNα2 with an N-terminal diglycine motif and a C-terminal LPETG was successfully cyclized by incubation with SrtA*Staph* and purified to homogeneity by ion-exchange chromatography. The mass of the circularized product in a crude sortase reaction differs from a linear hydrolysis product by ~18 Da, consistent with an intramolecular transeptidation reaction (Fig. 2B). We identified the unique junction peptide that arises from intramolecular cyclization by tandem mass spectrometry (MS/MS) analysis of tryptic digests (Fig. 2C). Site-specific PEGylation of the IFNα2 variant that lacks the N-terminal diglycine motif (and thus unable to undergo intramolecular cyclization) was achieved by incubation with sortase and a GGGK peptide to which a 10 kDa PEG moiety was affixed via the lysine ε-amine (Probe 1, Fig. 2A and Fig. S1A). We confirmed equipotent biological activity of all four interferon alpha variants in a Daudi cell proliferation inhibition assay when compared to a commercially available, non-PEGylated preparation (Fig. 2D and Table S1). Addition of a protein-sized PEG module to the C terminus of IFNα2 does not appreciably perturb receptor binding and biological potency. We hypothesized that the circular IFNα2 would be more resistant to thermal denaturation, because the termini are clamped shut and thus should not “fray” (15, 17). We measured thermal denaturation with a Thermofluor assay, using the commercially available Sypro Orange dye (18). Indeed, the circular form of IFNα2 had a significantly elevated melting temperature ($T_m$) compared to the other three variants, all of which exhibited nearly identical $T_m$’s (Fig. 2E, Table S1, and Fig. S2A). Finally, we injected mice with either the linear IFNα2 variant used to construct the PEGylated form, or the IFNα2 variant bearing a 10 kDa PEG chain (Probe 1) at its C terminus and measured the serum levels over time by ELISA. The PEGylated form decayed with slower kinetics than its non-PEGylated counterpart (Fig. 2F and Table S1).

**Modification of a Single Protein Preparation by Multiple Nucleophiles.** The sortase platform offers the ability to install nearly any chemical or biological modification at the C terminus of a protein. Here we demonstrate the ability to site-specifically conjugate multiple molecules to a single protein preparation. We hypothesized that combining PEGylation and thermal stabilization would confer both biological properties. We first applied the sortase reaction to two versions of IFNα2, both with an LPETG diglycine motif immediately followed by a hexahistidine tag for ease of purification and measurement. Site-specific PEGylation of IFNα2 by using a molecular suture produced in two successive rounds of PEGylation and improved thermal stability in a single molecule by using a molecular suture produced in two successive rounds of sortase-catalyzed transeptidation (Fig. 1).
nongenetically encoded entity onto the C terminus of a single preparation of recombinant protein. We demonstrate this ability by synthesizing a nucleophile that bears a 20 kDa PEG moiety (Prote 2 and Fig. S1A), as well as the previously described 10 kDa PEG probe (Prote 1), and appended them to the identical preparation of IFNα2 (Fig. 3A). Both conjugates were tested for biological activity (Fig. 3B) and are highly potent (Table S2).

**Superior Properties Endowed upon Sortase Substrates Are Applicable to Multiple Proteins.** Sortase allows the installation of the same nonnatural group onto different proteins, unrelated in sequence or amino acid composition. Accordingly, we applied the sortase reaction to a different four-helix bundle cytokine, GCSF-3, with similar results. We first made the linear precursor GCSF variants and then cyclized or PEGylated them with probe 1 using sortase (Fig. 4A). All variants possess equal or superior in vitro bioactivity relative to a commercial non-PEGylated preparation, as assessed by a standard cell proliferation assay with the NFS-60 murine myeoblastic cell line (19) (Fig. 4B and Table S3). Like cyclic IFNα2, cyclic GCSF-3 shows increased thermostability (Fig. 4C, Fig. S2B, and Table S3) and PEGylated GCSF-3 has a significantly extended circulatory half-life relative to its non-PEGylated precursor (Fig. 4D and Table S3) upon injection into mice. PEGylated GCSF-3 also led to a more robust and prolonged proliferation of granulocytes in injected mice than its non-PEGylated analog (Fig. 4E).

**Modification of Glycoproteins.** Many important therapeutics are glycosylated proteins that traverse the secretory pathway and are produced in mammalian cell culture. Are such proteins equally amenable to engineering using sortase-mediated transpeptidation reaction? We chose human erythropoietin (EPO) because ~40% of its mass is composed of bulky, charged N-linked glycans, and cyclization provides a stringent test of the sortase method, as it requires (minimal) modifications at both termini. We replaced the endogenous EPO signal sequence with the murine H-2Kb signal sequence, followed by two glycine residues. This signal peptide is cleaved in mammalian cells with concomitant exposure of an N-terminal glycine residue. We added the requisite sortase motif followed by a hexahistidine tag at the C terminus of EPO for ease of purification. Human embryonic kidney (HEK)-293T cell lines stably transduced with this construct yielded preparations that were 50% pure after a single round of Nickel-nitrilotriacetic acid immobilized metal affinity chromatography (Ni-NTA IMAC) of conditioned medium. Material from such preparations can be cyclized successfully upon incubation with sortase (Fig. 5A). Again, we identified the unique junction peptide that arises from covalent ligation of the N and C termini by MS/MS analysis of cyclized EPO, shorn of all glycans by incubation with peptide: N-glycosidase F (PNGaseF), and digested with trypsin (Fig. 5B). Both the linear preparations as well as the sortase reaction containing cyclic EPO were tested in a cell proliferation assay with Ba/F3 cells that stably express the erythropoietin receptor (20) and these compared favorably with commercial EPO preparations. Most importantly, the cyclic form is as potent as its linear counterpart (Fig. 5C and Table S4), indicating that modification of the EPO termini does not affect its biological activity.

**Two-Step Transacylation Allows Combination of Enhanced Properties.** Having shown for multiple examples that sortase-mediated site-specific modification of the C terminus with PEG increases circulatory half-life with nearly no loss of biological activity, and that covalent closure of the N and C termini yield proteins stabilized against thermal denaturation, we executed a scheme that combines these desirable properties (Fig. 1). In the first step, we exploit a previously described sortase from Streptococcus pyogenes (13, 14) that accepts alanine-based nucleophiles to affix a peptide containing a nonnatural amino acid containing an amino oxy group at the place of suture. Next, the amino acid sequence is used in a bioorthogonal oxime ligation reaction (21–23) with commercially available methoxy-capped PEG-propionaldehyde (Fig. S1B). We recombinantly expressed IFNα2 bearing two glycines at the N terminus, and at the C terminus the SrtAStrep cleavage site, followed by a hexahistidine tag. The purified protein was subjected to the two-step transacylation procedure to yield circular IFNα2 bearing the amino acid group. After ion exchange chromatography, this material was PEGylated and purified by cation exchange chromatography (Fig. 6A). Without optimization, the final yield of circular PEGylated protein was ~10%, because of the multiple separate chromatography and protein concentration steps involved in production and PEGylation. The mass of the material before oxime ligation was consistent with its cyclization (Fig. S3). Digestion with AspN and MS/MS analysis revealed the unique peptide that arises as a consequence of backbone cyclization consisting of the molecular suture probe stitched between the C and N termini of IFNα2 (Fig. 6B). All three variants yielded virtually indistinguishable IC50 values in an inhibition of cell proliferation assay (Fig. 6C and Table S5) and the circular versions were stabilized against thermal denaturation (Fig. 6D, Table S5, and Fig. S2C). The circular versions remained biologically potent after boiling when given the opportunity to refold, whereas we were unable to extract an IC50 value for the boiled linear preparation over the concentration range assayed (Fig. 6E and Table S6). We injected the linear and the circular, PEGylated preparations of IFNα2 into the tail vein of mice and measured half life by ELISA. The circular, PEGylated species was
cleared significantly more slowly than the linear form (Fig. 6F and Table S5).

Discussion

The sortase transpeptidase reaction allows facile site-specific PEGylation of multiple distinct proteins. In all cases tested, the site-specific C-terminal PEGylation proceeds efficiently (Fig. S3B) and yields adducts of known stoichiometry that are biologically equipotent to the non-PEGylated versions, but retain the increase in circulatory half life associated with PEG modification. We attribute these properties to the fact that all enzymatic transformations are performed on native proteins, procedures that should not affect overall conformation or exposure of functionally important side chains. Because our approach to PEGylation is site specific, all preparations are also homogenous and easily purified (5). Although we limit our examples to four-helix bundle proteins, this platform should be readily extended to structurally distinct therapeutic proteins, with the singular requirement that the C terminus is not involved in receptor binding. A sortase-based approach requires the genetic fusion of a very small (five amino acid) tag to the protein of interest and all transformations occur under native conditions. The additional amino acids that result from fusion to the sortase recognition motif are close to the site of PEG attachment. Immunogenicity of this site is very likely reduced by the PEG moiety shielding this area (3). We and others have labeled proteins with an exposed N-terminal glycine using sortase (14, 24). This approach should therefore be readily extended to site-specific PEGylation at the N terminus as well.

Cyclization of the backbone of protein-based therapeutics also proceeds efficiently (Fig. S3B) and yields preparations that are more resistant to thermal denaturation. Cyclic proteins are also resistant to exoproteolytic attack (25, 26), a feature that may enhance utility of any therapeutic proteins exposed to exoproteases, for example upon receptor mediated internalization. In addition, cyclization of proteins and peptides has been shown to improve potency, stability, and oral bioavailability (27–30).

Finally, we have inserted a nontemplate encoded entity in what is topologically internal to a circular protein, a feat that cannot be accomplished genetically by intein-based methods or by any other currently known means. More generally, this dual transacylation scheme can be used to insert nonnatural groups between fully native proteins expressed separately, or between protein domains. We suspect that this approach will find application in the protein engineering field and so further extend the utility of sortases as tools.

Experimental Procedures

Sortase Reactions. Sortase reactions with SrtA<sub>Staph</sub> were performed as described previously (11). For either cyclization or PEGylation, reactions containing 50 μM substrate, 50 μM SrtA<sub>Staph</sub> and 1 mM probe (for PEGylation) were incubated overnight at 25 °C without agitation. Reactions were purified by cation exchange chromatography on a Mono-S (GE Healthcare). For IFNa2a and IFNa2b, reactions containing 50 μM substrate, 50 μM SrtA<sub>Staph</sub> and 1 mM probe were incubated overnight at 25 °C without agitation. Reactions were purified by cation exchange chromatography on a Mono-S (GE Healthcare). For IFNa2a, continuous gradient chromatography was performed with 20 mM 2-(N-morpholino) ethane sulfonic acid (MES) pH 5.0 and 20 mM MES, 1 M NaCl pH 5.0, as eluent. For GCSF re-actions, continuous gradient chromatography was performed
imidazole, and buffer exchanged into SrtAStaph buffer (50 mM Tris, 150 mM NaCl, 500 mM propionaldehyde, and 100 mM aniline (JT Baker) and incubated at 30 °C for 3 h without agitation. This reaction mixture was then supplemented with 10 mM imidazole and subjected to Ni-NTA chromatography (Qiagen) to remove prematurely cyclized material. Protein was eluted with 50 mM Tris, 150 mM NaCl, and 10 mM CaCl₂ with a PD10 desalting column (GE Healthcare). For cyclization, this material was incubated overnight with 50 

μM SrtAStaph and purified by cation exchange chromatography, concentrated, and protein concentration was determined by Bradford assay. With 20 mM sodium acetate pH 4.5 and 20 mM sodium acetate, 1 M NaCl pH 4.5, as eluent. Peaks containing the desired product were pooled, concentrated with Vivaspin 500 centrifugal concentrators (Sigma) and protein concentration was determined by Bradford Assay (BioRad). For EPO cyclization, 300 μL of Ni-NTA eluate (0.101 mg/mL total protein) was incubated with 100 μM SrtA and sortase buffer in 400 μL total volume at 25 °C for 16 h. For two-step transacylation reactions, 150 μM substrate was incubated with 50 μM SrtAprep and 2 mM probe in 100 mM Tris, 150 mM NaCl pH 8.0 for 4 h at 37 °C. SrtAprep activity was halted by incubation with 500 μM of the protease inhibitor E-64 on ice for 1 h. Crude reaction mixtures were then supplemented with 10 mM imidazole and subjected to Ni-NTA chromatography (Qiagen) to remove prematurely cyclized material. Protein was eluted with 50 mM Tris, 150 mM NaCl, 500 mM imidazole, and buffer exchanged into SrtAStaph buffer (50 mM Tris, 150 mM NaCl, and 10 mM CaCl₂) with a PD10 desalting column (GE Healthcare). For cyclization, this material was incubated overnight with 50 μM SrtAStaph and purified by cation exchange as described for other IFNα2a reactions. Concentrated, purified circular IFNα2 bearing the Aminoxyacetic acid (AOAA) group was then diluted with 1 volume of 50 mM sodium acetate pH 4.5, 150 mM NaCl containing 2 mM methoxy-capped PEG-

propionaldehyde, and 100 mM aniline (JT Baker) and incubated at 30 °C for 3 h without agitation. This reaction mixture was again purified by cation exchange chromatography, concentrated, and protein concentration was determined by Bradford assay.

Thermal Denaturation Assays. Thermal shift assays were performed in a Roche 480 lightcycler and fluorescence was measured with Excitation = 533 nm, Emission = 610 nm. For GCSF-3, 1 μg of each variant was mixed with 1 μL of 100x Sypro orange in 25 mM total volume of 50 mM acetate pH 4.0, 150 mM NaCl n = 4 for all samples with buffer as a blank control and lysozyme as a positive control. For IFNα2, 1 μg of each variant was mixed with
1 μL of 100× Sypro orange (Invitrogen) in 25 μL total volume of 50 mM MES ph 5.0, 150 mM NaCl, n = 4 for all samples with buffer as a blank control and lysosome as a positive control. Samples were heated from ambient temperature to 95°C at 0.01°C/s with 6 acquisitions/°C. The included Roche software was used to calculate the negative first derivative of the temperature change as a function of time and the minima were used as the 

Cell-Based Bioactivity Assays. Daudi cell proliferation inhibition assays to measure the activity of IFNα conjugates were performed as described (8) and compared to commercial IFNα2b (PBL Interferon Source) with low passage Daudi cells (ATCC), cultured in RPMI medium 1640/10% Heat inactivated fetal calf serum (FCS)/50 units/mL penicillin, 50 μg/mL streptomycin sulfate. Cell proliferation was measured by MIT assay according to manufacturer’s directions (ATCC). For the denaturation assay, samples diluted to 1 μg/mL in RPMI medium 1640/10% IFS were boiled for 4 min, allowing to cool at room temperature for 16 h, and assayed for Daudi cell proliferation inhibition. NFS-60 cell proliferation assays to measure G-CSF conjugate activity were performed as follows. NFS-60 cells (a kind gift from James Ihle, St. Jude Children’s Research Hospital) were cultured in RPMI medium 1640/10% IFCS/50 units/mL penicillin, 50 μg/mL streptomycin sulfate. Cells were washed extensively in complete RPMI medium 1640 medium lacking IL-3 and resuspended at 1 × 10⁵ cells/mL in complete RPMI medium 1640 lacking IL-3. Titrated GCSF conjugates (50 μL) in complete RPMI medium 1640 were aliquoted into a flat bottom 96 well plate and 50 μL of cells (0.5 × 10⁴ cells/well) were added to each well. Cells were cultured for 3 d and an MIT assay (ATCC) was performed according to manufacturer’s directions. Each plate contained a titration of commercial GCSF3 (Peprotech) and readings were blanked against wells containing only NFS-60 cells. The activity of each conjugate was measured a minimum of n = 3 times. BaF3 cells stably expressing the EPO receptor (BaF3 EPO-R cells, a kind gift from Harvey Lodish, Whitehead Institute) were used to measure EPO activity. BaF3 EPO-R cells were cultured as described for NFS-60 cells and assays were performed essentially as described for G-CSF, except EPO circularization reactions incubated with or without sortase for 16 h at 37°C were used. The total protein concentration of the EPO input material (measured by the Bradford method) was used and was not adjusted for impurities. Commercial preparations of EPO (eBioscience) were used as standards and readings were blanked against BaF3 EPO-R cells cultured with no cytokines. Activities were measured a minimum of n = 3 times.

Circulatory Half-Life Assays. For circulatory half-life assays, mice were injected in the tail vein with each protein (10 μg per mouse for IFNα2 conjugates, 5 μg per mouse for G-CSF conjugates) and subjected to retroorbital eye bleed at the indicated time points. Blood was harvested, centrifuged at 1,957g in a tabletop centrifuge, and serum was collected and snap-frozen. Elisa assays to measure the quantity of cytokine in serum samples were performed according to the manufacturer’s directions (IFNα from PBL Interferon Source, G-CSF from Invitrogen). Each conjugate was injected into n = 3 mice. Data was fit to a two phase exponential decay in GraphPad Prism.

Granulocyte Proliferation Assay. Peripheral blood was collected retroorbitally into EDTA collection tubes. Red blood cells were lysed in hypotonic lysis buffer and the remaining peripheral blood mononuclear cells were stained with anti-myeloid differentiation antigen-1 (Gr-1) antibody labeled with phycoerythrin (PE) (BD Pharmingen), anti-cluster of differentiation 11b protein antibody labeled with FITC (anti-CD11b-FITC) (BD Pharmingen), and 7-Aminoactinomycin D (7-AAD) (ViaProbe, BD Pharmingen). Cells were analyzed using a FACS Calibur flow cytometer (BD).

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