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An organometallic swap strategy for bottlebrush polymer–protein conjugate synthesis†

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Polymer–protein bioconjugation offers a powerful strategy to alter the physical properties of proteins, and various synthetic polymer compositions and architectures have been investigated for this purpose. Nevertheless, conjugation of molecular bottlebrush polymers (BPs) to proteins remains an unsolved challenge due to the large size of BPs and a general lack of methods to transform the chain ends of BPs into functional groups suitable for bioconjugation. Here, we present a strategy to address this challenge in the context of BPs prepared by “graft-through” ring-opening metathesis polymerization (ROMP), one of the most powerful methods for BP synthesis. Quenching ROMP of PEGylated norbornene macromonomers with an activated enyne terminator facilitates the transformation of the BP Ru alkylidene chain ends into Pd oxidative addition complexes (OACs) for facile bioconjugation. This strategy is shown to be effective for the synthesis of two BP–protein conjugates (albumin and ERG), setting the stage for a new class of BP–protein conjugates for future therapeutic and imaging applications.

Protein–polymer conjugates have garnered significant interest due to their applications in materials science and medicine.¹ While a wide range of polymers have been utilized for protein conjugation,¹ polyethylene glycol (PEG) is the most extensively studied and translationally successful, with over 25 “PEGylated” proteins approved by the United States Food and Drug Administration (FDA) to date.² PEGylation can improve the biophysical properties of proteins in several ways.³ For example, the increased size of PEGylated proteins can reduce their renal clearance rate and, as a consequence, increase their circulation half-life.^{2c–g,3} Additionally, PEGylation can protect proteins from

rapid degradation, improve their solubility, and augment their bioavailability and therapeutic efficacy.

Most PEGylated proteins rely on linear PEG macromolecules (Fig. 1a), where features such as molecular weight, number of conjugated PEG chains per protein, and PEG conformation are key variables that impact the biological performance of the resulting conjugates.^{2c,fg,3} “Branched” PEGs have also been explored for protein conjugation, where features such as number of branches and branch length can be used to further vary the PEG conformation and physical properties of the resulting conjugates (Fig. 1a).⁴ For example, Chilkoti and others have utilized polyacrylates with oligoethylene glycol sidechains (~8–9 ethylene glycol repeat units) for protein conjugation (Fig. 1a). These constructs display many of the desirable properties of linear PEGylated proteins while showing reduced immunogenicity in preclinical studies.⁵

These results, along with observations of reduced anti-PEG antibody binding to densely-grafted PEGylated surfaces,

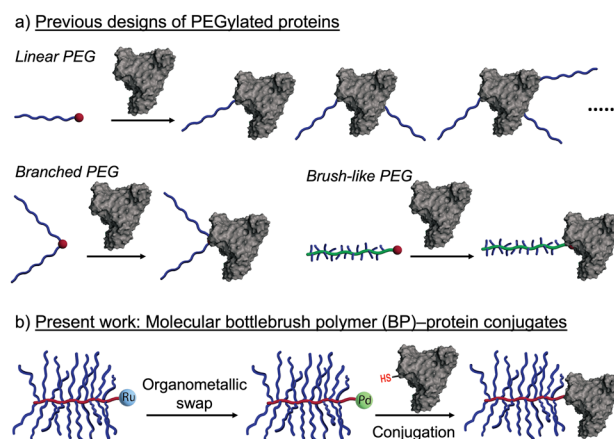


Fig. 1 (a) Previous designs of PEGylated proteins with linear, branched, or brush-like architectures. The red dots represent reactive moieties on the polymers used for conjugation. (b) This work introduces molecular bottlebrush polymer (BP)–protein conjugates prepared through a BP chain-end organometallic swap strategy.

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Boc-protected amine ends (see ESI† for details). PEGylated BPs terminated by **1** (“BP-NHBoc”) were synthesized by ROMP as follows: 3 kDa PEG-based MM (PEG-MM, 20 equiv.) was exposed to Grubbs 3rd-generation bis-pyridyl complex (G3, 1 equiv.) at room temperature (RT) for 30 min in THF solvent to give Ru-terminated BPs “BP-Ru”. The reactions were quenched by the addition of **1** (5 equiv.) and stirring for another 2 h at RT. Size exclusion chromatography (SEC) analysis of the crude reaction revealed a highly efficient polymerization, with nearly quantitative conversion of PEG-MM to a unimodal peak corresponding to putative BP-NHBoc (M_n , SEC = 64 kDa, $D = 1.04$) (Fig. 2b). BP-NHBoc was purified by precipitation in cold diethyl ether to remove excess enyne terminator. The ^1H NMR spectrum for BP-NHBoc showed a unique resonance for the Boc end group (Fig. 2c and Fig. S1a, ESI†); the ratio of the integral of the backbone olefinic resonances to the Boc resonance was 40:9, which is consistent with the theoretical backbone degree of polymerization of 20. Together, these results suggest that **1** is an effective terminator for ROMP of PEGylated BPs.

Next, we sought to further modify the end of BP-NHBoc for bioconjugation using Pd(II) OACs. Exposure to trifluoroacetic acid gave complete conversion to the resulting amine-terminated BP BP-NH₂ (Fig. S1b, ESI†). Then, mixing with NHS ester **2** (Fig. 2a)^{8b} in phosphate buffer (pH = 8.5) for 12 h gave BP-OAC “BP-Pd”. Inductively coupled plasma-mass spectrometry (ICP-MS) was consistent with nearly quantitative introduction of Pd onto the chain ends (calculated 1000 ppb versus observed 1086 ppb) (Fig. S2, ESI†), with each BP-Pd having one Pd atom. ^1H NMR spectroscopy further showed the presence of resonances associated with the OAC (Fig. S3, ESI†), while the size of the BP was conserved as indicated by SEC (Fig. 2b).

With BP-Pd in hand, we explored bioconjugation using BSA (583 amino acids; 66.5 kDa) as a model protein as it contains a single free cysteine available for site-specific conjugation.¹⁰ BSA and BP-Pd were combined either in pure water or in phosphate-buffered saline (PBS) (pH = 7.4). Analysis of the crude reaction by SDS-PAGE gel electrophoresis (Fig. 3a and Fig. S4, ESI†) showed a new smear band with a significantly higher molecular weight (~180 kDa) compared to BSA alone, suggesting the successful formation of conjugate “BP-BSA”. The band at ~120 kDa for the crude conjugate (Fig. 3a and Fig. S4, ESI†) is assigned to the dimer of BSA. While separation of BP-BSA from free BSA and BP-Pd was difficult using preparatory SEC due to the similar hydrodynamic sizes of each component (Fig. S5, ESI†), anion exchange fast protein liquid chromatography (FPLC) using pH 8.5 buffer (in which BSA is negatively charged; pI = 4.7) enabled facile purification of the conjugates (Fig. 3b) as confirmed by SDS PAGE gel electrophoresis (Fig. 3a). The circular dichroism (CD) spectrum of purified BP-BSA (Fig. 3c) was nearly identical to that of the crude conjugation reaction mixture and BSA alone, suggesting that BSA maintains its folded structure following conjugation and purification.

FRET experiments using cyanine 3 (Cy3, $\lambda_{\text{ex}} = 555$ nm, $\lambda_{\text{em}} = 569$ nm) and cyanine 5 (Cy5, $\lambda_{\text{ex}} = 651$ nm, $\lambda_{\text{em}} = 670$ nm) dyes was designed to provide further evidence for the successful

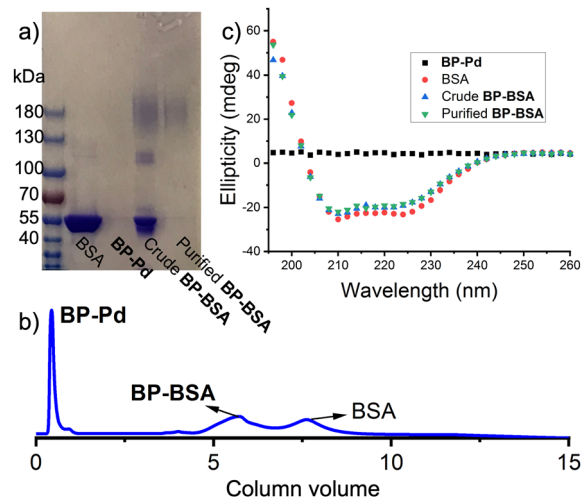


Fig. 3 BP-BSA synthesis, purification, and characterization. (a) SDS PAGE Gel showing BSA, BP-Pd, crude BP-BSA, and purified BP-BSA. (b) FPLC trace for crude BP-BSA. (c) CD spectra for BP-Pd, BSA, crude BP-BSA, and purified BP-BSA.

conjugation of BPs to BSA. First, a Cy3-labeled BP “BP^{Cy3}-Pd” was synthesized following the same general procedure used for the synthesis of BP-Pd but using a mixture of PEG-MM and 5% of a Cy3-labeled PEG MM (Fig. S6 and S7, ESI†). Meanwhile, Cy5-labeled BSA “BSA^{Cy5}” was prepared through lysine conjugation using a commercially available Cy-5 NHS ester. Mixing BP^{Cy3}-Pd and BSA^{Cy5} gave conjugate BP^{Cy3}-BSA^{Cy5} via cysteine arylation. A control conjugate BP^{Cy3}-BSA was also prepared using unlabeled BSA. Both conjugates were purified by FPLC as described for BP-BSA (Fig. S8, ESI†). SDS-PAGE gel electrophoresis was used to characterize the proposed conjugates. As expected, BP^{Cy3}-BSA^{Cy5} showed strong signals in both the Cy3 and Cy5 channels, while BP^{Cy3}-BSA and BSA^{Cy5} only showed bands in the Cy3 and Cy5 channels, respectively (Fig. 4a). UV-vis spectroscopy supported these findings; the conjugate BP^{Cy3}-BSA^{Cy5} displayed absorption peaks that overlap with BP^{Cy3}-Pd and BSA^{Cy5} (Fig. 4b). Fluorescence emission spectra ($\lambda_{\text{ex}} = 550$ nm; Cy3 absorption) were collected for BP^{Cy3}, BSA^{Cy5}, a physical mixture of BP^{Cy3} and BSA^{Cy5}, and FPLC-purified BP^{Cy3}-BSA^{Cy5}. In support of the proposed conjugate structure, FRET-induced Cy5 emission ($\lambda_{\text{em}} = 670$ nm) was only observed for the conjugate BP^{Cy3}-BSA^{Cy5} (Fig. 4c).

Next, we evaluated the stability of BP-BSA, which features aryl thioether linkages, compared to analogous conjugates prepared using the cysteine-maleimide conjugation reaction (BP-BSA-Mal). Maleimide-terminated BP “BP-Mal” was prepared from BP-NH₂ and a commercially available NHS-ester maleimide under similar conditions as were used for the synthesis of BP-Pd from BP-NH₂ and **2** (Fig. S9, ESI†), demonstrating generality of our BP end-functionalization strategy. Conjugation of BP-Mal to BSA was conducted following commonly reported conditions (in PBS, 24 h). Notably, the conjugation conversion was much lower than for the Pd-mediated arylation reaction, as determined by FPLC (Fig. 3b and Fig. S9c, ESI†). Nevertheless, conjugate BP-BSA-Mal could be



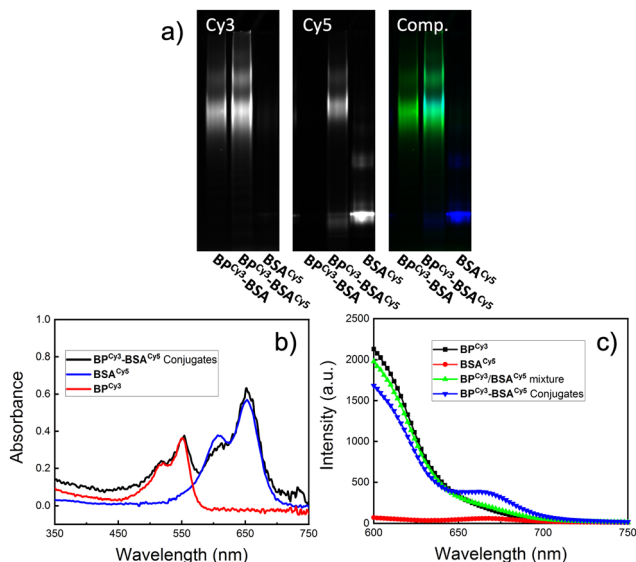


Fig. 4 Dye-functionalized BP-BSA conjugates for FRET experiments. (a) Fluorescence gel images under Cy3/Cy5 channels. (b) UV-vis absorbance of BSA^{Cy5}, BP^{Cy3}-Pd, and BP^{Cy3}-BSA^{Cy5} conjugates. (c) Fluorescence emission spectra for BP^{Cy3}-Pd, BSA^{Cy5}, a physical mixture of BP^{Cy3}-Pd and BSA^{Cy5}, and BP^{Cy3}-BSA^{Cy5} ($\lambda_{\text{ex}} = 550$ nm).

isolated following FPLC purification (Fig. S10, ESI[†]). Exposing BP-BSA and BP-BSA-Mal to glutathione (~1000 equiv.; 10 mM), which is present in mM concentrations in the cytosol and is known to induce thiolate exchange with thiosuccinimides,¹¹ induced no changes for BP-BSA but led to the emergence of a new SDS-PAGE gel band consistent with free BSA for BP-BSA-Mal. Together, these findings support the successful conjugation of BP and BSA using either Pd(II)-induced cysteine arylation or maleimide conjugation, with the former displaying improved stability toward glutathione.

Finally, to demonstrate the generality of this approach, we formed conjugates between BP-Pd and a chemically synthesized protein, ERG,¹² (94 amino acids; ~11 kDa; Fig. S11a, ESI[†]) containing a single cysteine residue. Conjugation following the same general procedure used for BSA followed by FPLC purification gave "BP-ERG" in high conversion as indicated by FPLC (Fig. S11b, ESI[†]) and SDS-PAGE gel electrophoresis (Fig. S11c, ESI[†]).

In conclusion, we report a strategy to conjugate BPs directly to proteins. Our approach leverages ROMP for BP synthesis and achieves efficient conjugation to cysteine residues of proteins *via* an "organometallic swap" of Ru to Pd made possible by an enyne ROMP terminator. This approach allows for the merger of two independent methods that are each powerful for the applications in which they were developed (*e.g.*, ROMP for BP synthesis and Pd-mediated cysteine arylation for bioconjugation) but are traditionally orthogonal. The result is a new class of BP-protein conjugates with numerous potential applications that could leverage the utility of BPs for drug delivery and imaging¹³ with the therapeutic and targeting potential of proteins.

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Conflicts of interest

There are no conflicts to declare.

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