A High-Throughput Platform for Efficient Exploration of Functional Polypeptides Chemical Space via Automation and Machine Learning

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Abstract

Rapid and in-depth exploration of the chemical space of high molecular weight synthetic polypeptides via the ring-opening polymerization (ROP) of N-carboxyanhydride (NCA) is a viable approach towards protein mimics and functional biomaterials. Here, we develop an efficient chemistry for the high throughput diversification of polypeptides based on a click-like reaction between selenolate and various electrophiles in aqueous solutions. With the assistance of automation and machine learning, iterative exploration of the random heteropolypeptides (RHPs) library efficiently and effectively identifies hit materials from a model system of which we have little prior knowledge. This automated and high-throughput platform provides a useful interface between wet and dry experiment, which would accelerate the discovery of new polypeptide materials for unmet challenges such as *de novo* design of artificial enzyme, biomacromolecule delivery, and understanding of intrinsically disordered proteins.

1 Introduction

Proteins are natural biopolymers with vast chemical space and sophisticated functions such as binding, catalysis, transportation and signaling. For decades, an overarching goal of polymer science is to create protein-like functional polymeric materials for not only fundamental understanding of proteins but also solving real-world challenges [1–5]. To this end, synthetic polypeptides prepared by the ring-opening polymerization (ROP) of *N*-carboxyanhydrides (NCA) have emerged as promising protein mimics with the potential to combine the advantages of both peptides and synthetic polymers [6–11]. Specifically, polypeptides possess the same backbone and secondary conformations as protein and can be efficiently produced at up to kilogram scales in a high number-averaged molecular weight (M_n) [12]. Nevertheless, similar to other polymers, polypeptides are subjected to the curse of dimensionality, *i.e.* the combination of just a few residues can lead to a chemical space that is too

*The experimental part of this work was mainly finished when he was a postdoctoral fellow in Peking University.

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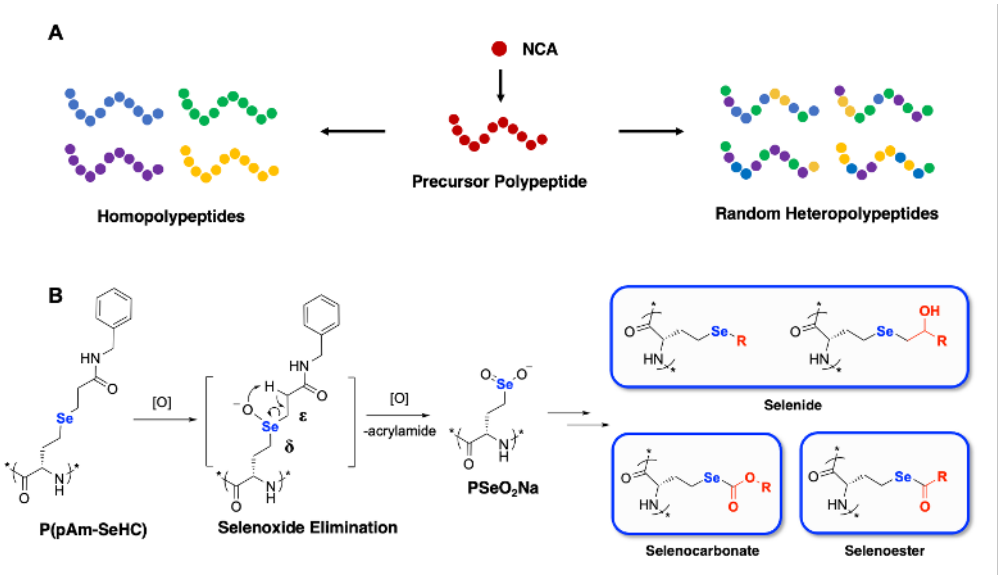

Figure 1: (A) Schematic illustration of the post polymerization modification strategy for making homopolypeptides (left) and random heteropolypeptides (RHP, right). (B) The selenopolypeptide $PSeO_2Na$, derived from the selenoxide elimination of P(pAm-SeHC), could be derivatized to various structures.

large to be fully explored [13, 14]. To reach functional protein-mimicking polypeptides from the enormous chemical space, one needs to:

1. Facilely prepare polypeptides from the design space with high fidelity,

2. Establish an efficient strategy for effective exploration of the space at affordable labor and time cost.

While application of automated and data-driven technologies to accelerated discovery was proven to be effective for many materials [14–20], attempts to incorporate the NCA and polypeptide chemistry to this workflow have been challenging and sparse. This is mainly owing to the high moisture sensitivity of NCA, which makes the purification, storage and polymerization of the monomer really tricky. In a pioneer work, Deming *et al.* synthesized around 500 RHPs within 2 weeks through parallel polymerization [21]. Though the recent advance of methodology might increase the water tolerance during polymerization [22–24], most of the strategies were still performed in a low throughput fashion because of the instability of the monomer and experimental setup. Meanwhile, nowadays there is still limited data available for machine learning (ML)-assisted polymer design [25]. While most studies exploited data from literature and virtual experiments (e.g., electronic structure calculations or simulations), an ideal platform should be capable of performing new experiments to support model training.

To address these challenges, we developed a high-throughput synthesis (HTS) platform in aqueous solutions for polypeptides based on a click-like reaction between selenolate and electrophiles (Figure 1). This quantitative chemistry gave accurate control of the structure and molecular composition of polypeptides. The process was amenable to off-the-shelf automated liquid handling platform and allowed efficient generation and purification of over 1200 polymers within one day, which greatly increase the synthesis capability of the materials. With the assistance of ML model-guided optimization, a closed-loop discovery workflow was established. We were able to perform iterative exploration of the RHP chemical space for enzyme mimics and identified candidates with improved activity in a more efficient and effective way.

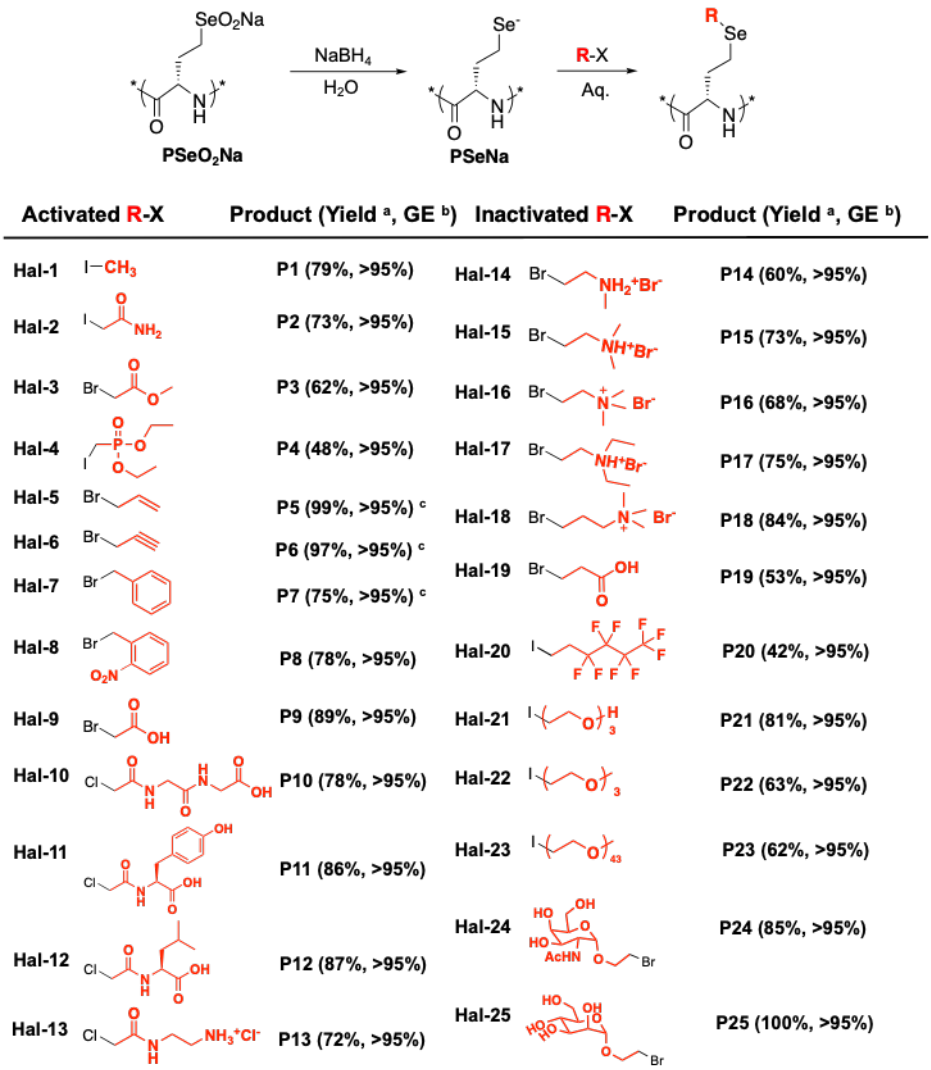

Figure 2: Post polymerization of $PSeO_2Na$ with activated and inactivated halides.[a] yield = purification yield, [b] GE: grafting efficiency based on the ^1H NMR spectra of the product, [c] Prepared from PEG-*b*-$PSeO_2Na$, a poly(ethylene glycol) block copolymer of $PSeO_2Na$.

2 Results

We designed and synthesized a selenopolypeptide, P(pAm-SeHC), whose pendant group is a latent selenolate, a highly nucleophilic species in organic chemistry. Oxidation of P(pAm-SeHC) leads to selenoxide elimination, generating $PSeO_2Na$ (Figure 1B). $PSeO_2Na$ could be reduced with $NaBH_4$ in water, affording the selenolate-bearing polypeptide (PSeNa) for further functionalization with organohalides (Figure 2). The modification of PSeNa showed remarkable tolerance to various functionalities. We were able to prepare many polypeptides with potential applications in biomedical engineering including those that are hard to be introduced directly through the ROP of NCA (Figure 2). When tried feeding with more than one organohalides, we found the molecular composition correlated well with the feeding volume ratio of the organohalides (Figure S1). A map from the feeding volume ratio to the molecular composition was thus directly created, which saves tremendous amount of times from additional characterization.

Based on these findings, the HTS of RHPs was established with the assistance of a commercialized automated workstation for dispensing stock solutions of organohalides to plates. This semi-automated workflow greatly boosted the synthesis capability and enabled the parallel preparation of 400 RHPs

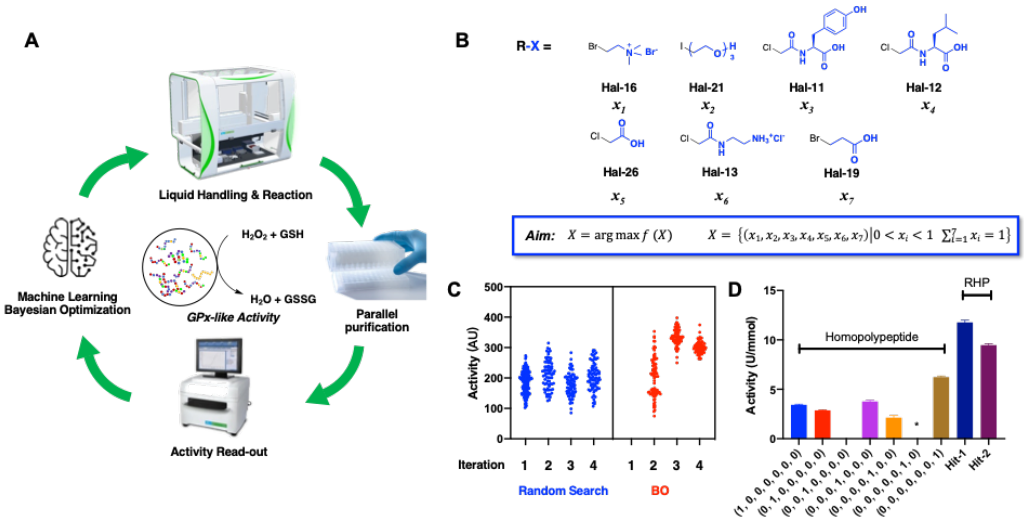

Figure 3: Closed-loop optimization of GPx activity of the RHPs via HTS and machine learning. (A) Cartoon illustration of the closed-loop workflow containing four modules, namely HTS, parallel purification, activity read-out, and Bayesian optimization. (B) Structure of the seven selected organohalides for RHP library generation and aim of optimization. The molecular composition of RHPs are described as seven-dimensional vectors $\boldsymbol{x} = (x_1, \ldots, x_7)$, where x_n (n = 1 to 7) is the relative volume ratio of the organohalides and the program will perform BO on this seven-dimensional consecutive space,. (C) GPx-like activity of RHPs in each iteration via random searching (blue) or Bayesian optimization (red). (D) Comparison of the GPx-like activity of the two RHP hits with the seven homopolypeptides each modified with one individual organohalide used in HTS (n = 3). **Hit-1**: (0.12, 0.12, 0, 0, 0, 0, 0.76) and **Hit-2**: (0, 0.24, 0.22, 0, 0, 0, 0.54). All polymers are synthesized in flask and then purified for GPx activity. Error bars represent the standard deviation. *Activity of the homopolypeptide (0, 0, 0, 0, 0, 1, 0) cannot be measured properly owing to precipitation during testing.

(4 plates) in one day. The throughput could be easily improved to 1200 RHPs (12 plates) per day if only activated organohalides were used for modification. We applied a Bayesian optimization (BO) framework based on BoTorch and Ax [26] and established a closed-loop material discovery workflow (Figure 3A).

For demonstration, we chose glutathione peroxidase-like (GPx-like) activity [27] of the materials as a optimization target (Figure 3A). Seven organohalides with different properties were selected for modification (Figure 3B). Within 4 days, four iterations comprising a total of 660 experiments were performed with 166 experiments per iteration. We did not find any similar system that studies the influence of the side chain structure and composition on the GPx-like activity of the selenopolypeptide the literature. So 166 RHPs were randomly chosen initially from the designed space to train a Gaussian process (GP) regression model. Candidates for successive iterations were chosen by selecting compositions that optimized an expected improvement (EI) acquisition function, subject to the constraint that total mole fractions equal 1. To avoid trapping in local minimums, random search and BO were performed simultaneously in each round. Both were used to select 83 RHPs compositions to synthesize, evaluate, and retrain the surrogate GP before proposing the candidates for the next iteration. The results showed that while random search consistently found candidates with activities near a range of 150-200, BO efficiently found RHPs with substantially higher GPx-like activity, particularly in the third and fourth iteration (Figure 3C). T-distributed stochastic neighbor embeddings (t-SNE) showed that BO quickly identified an area in the design space that achieves higher activity (Figure S2). Two hits from BO were synthesized in flask and their GPx-like activity normalized to the amount of selenium was evaluated. **Hit-1** exhibited 2 times higher GPx-like activity than the most active homopolypeptide in the design space (Figure 3D), which meant that activity of RHPs is not merely the normalized average of the activity of each component.

3 Discussion

While the above results indicate the establishment of a closed-loop discovery workflow for polypeptides, there are still remaining challenges. The primary challenge is the precipitation during modification. In the preliminary trials, precipitation was observed when (1) the content of relatively hydrophobic modifiers was high (e.g. higher than 0.5 in some cases), (2) the contents of negatively and positively charged modifiers were roughly equal to each other, which neutralized the net charge and led to insoluble polyplex, (3) the conversion of the side chain was incomplete and the residual selenolate were gradually oxidized into diselenide and formed a crosslinked network. To avoid such undesired precipitation, one could try adding organic solvent and adjusting the pH during the modification. Attaching a polyethylene glycol (PEG) block to the precursor polymer were also proven to be useful. Meanwhile, under such synthesis throughput, the property characterization could be a rate-limiting step. For the characterization assays that are feasible to set up and quick to perform, such as reading fluorescent signal directly with microplate reader, it is possible to perform the synthesis and characterization of 1200 polypeptides within one day. But for many other assays (such as the GPx assay in this manuscript), the maximum throughput per day is limited because of human intervention. We believe further application of automation on characterization could boost the throughput, which will further accelerate the process.

The application of this platform is not limited to the discovery of catalytic materials. Since organohalides, the most abundant building blocks in organic chemistry, were used as the modifiers, the strategy opens many possibility for applications. For example, by integrating different pendant groups (positively charged, hydrophobic and zwitterionic *etc.*) and redox property of selenium, the platform could be used to the development of novel antimicrobial materials. As the modification is mostly carried out in aqueous solution, products from HTS could be easily adapted to cellular assay with only one additional parallel purification step. Thus the platform would also enable accelerated discovery of biomaterials for therapeutic purposes such as bio-molecules delivery. We understand the presence of selenium might not be necessary for some applications. In that case, the strategy could still offer a viable way for rapid prototyping of polypeptides for the exploration design space. Compared with other click-type reactions, this modification reaction only introduce a selenium atom as a miniature linker, which pose minimum influence on the overall polymer structure and makes generalization to other types of polypeptide more likely to succeed. After gathering enough knowledge of the system through HTS, a non-selenium version could be synthesized by *e.g.* replacing selenium to carbon.

4 Conclusion

In summary, we report a robust, quantitative, and divergent strategy for the rapid expansion of polypeptide library based on a universal precursor selenopolypeptide. This post polymerization modification strategy avoided the laborious efforts of making a variety of NCA that are synthetically challenging. The potential of this modification chemistry was highlighted by the establishment of a closed-loop optimization workflow for the discovery of functional RHP. Enabled by the efficiency of the reaction, a map from the feeding volume ratio to the molecular composition was directly created. Because all polypeptides were derivatized from the same precursor, this strategy could be particularly useful to generate standardized dataset. Moreover, the HTS was performed in aqueous solutions and open air, which allowed convenient transferring of the resulting polymers to subsequent biological assays. As a proof-of-concept, we demonstrated a concise workflow enabling the rapid identification of RHPs with promising GPx-like activity. While detailed structure-activity relationship is still under investigation, these results underscored the power of this system in accelerating material discovery by exploring polypeptide chemical space of which people have little knowledge. We envision that the potential of this platform is far beyond artificial enzymes and can accelerate the discovery of antimicrobial agents, understanding of protein phase separation, and development of intracellular delivery systems for therapeutic biomacromolecules, *etc.*

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