Total synthesis of micrococcin P1 and thiocillin I enabled by Mo\textsuperscript{(vi)} catalyst†

Siddhartha Akasapu,‡ Aaron B. Hinds,‡ Wyatt C. Powell† and Maciej A. Walczak†*

Thiopeptides are a class of potent antibiotics with promising therapeutic potential. We developed a novel Mo\textsuperscript{(vi)}-oxide/picolinic acid catalyst for the cyclodehydration of cysteine peptides to form thiazoline heterocycles. With this powerful tool in hand, we completed the total syntheses of two representative thiopeptide antibiotics: micrococcin P1 and thiocillin I. These two concise syntheses (15 steps, longest linear sequence) feature a C–H activation strategy to install the trisubstituted pyridine core and thiazole groups. The synthetic material displays promising antimicrobial properties measured against a series of Gram-positive bacteria.

Our retrosynthetic analysis of the synthetic targets led to the dissection of the macrocycle into two “top” and “bottom” fragments, which could be united through a peptide coupling and then macrocyclised at the thiazole carboxylic acid adjacent to valine to furnish the final product(s) (Fig. 1). For construction of the two fragments, we envisioned a convergent approach involving the strategic introduction of selected thiazole rings through a catalytic cysteine cyclodehydration. Catalytic methods for cysteine cyclodehydrations are scarce despite the myriad obstacles encountered when employing common stoichiometric reagents due to their high Lewis acidity, likely incompatibility with acid-sensitive groups, possible epimerization, and generation of undesired by-products. We hypothesized that a MoO\textsubscript{2}(L\textsubscript{2}) complex with the appropriate ligands might minimize epimerization of the endo- and exocyclic methylene groups since the cyclization event occurs under neutral conditions. Furthermore, bidentate ligands may extend the lifetime of the catalyst and prevent precipitation of heterogeneous molybdenum particles.

To validate the feasibility of this proposal, we evaluated a series of Mo\textsuperscript{(vi)} oxide complexes (Table 1). Initially, we studied
We rationalized the reactivity trend from Table 1 by a mechanism depicted in Scheme 1A: complex 11 undergoes a ligand exchange with amide 12, replacing one of the pyridine coordination sites. Picolinic acid-based ligands that contain electron-donating groups (e.g., 8d, 9a, 9b) retard the initial displacement step because the electron-rich heterocycle forms a tighter complex with the electrophilic Mo(VI), whereas electron-withdrawing groups at C4 and C6 of the pyridine ring (e.g., 9c) facilitate the displacement. Once the amide is bound to Mo (13), a proton transfer occurs from the amide NH to one of the oxo ligands. This step is likely promoted by a neighbouring nitrogen atom on the pyridine ring and may proceed intramolecularly. Ring closure from 14 followed by elimination of H₂O and azoline product 16 regenerates catalyst 11. The highest rate of cyclodehydration of 6 with 8b can be rationalized by its electron-donating ability combined with steric hindrance of the methyl group that likely distorts the geometry of the MoO₂(L₂) complex, thus accelerating access of the amide substrate. This mechanistic proposal is consistent with DFT calculations (Scheme 1B). The most stable configuration of the MoO₂(pic)₂ complex is the one with pyridine nitrogen atoms in a cis configuration (e.g., 11). The Mo–N bond in the unsubstituted picolinic acid complex is 2.38 Å. This linkage is elongated in complexes substituted at C4 with an electron-withdrawing group (9c) and in sterically-congested complexes with the 6-Me group making the initial ligand exchange more facile. On the contrary, attachment of an electron-donating group at the para position increases the bond strength between Mo and N, demonstrated by a shortened Mo–N distance in a complex with 9a.

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cyclodehydration conditions were applied to two dipeptides followed by oxidation to thiazoles in excellent yields for both substrates. The remaining portion of the bottom fragment was prepared via a modified Hantzsch method using thioamidate and bromopyruvate in 94% yield. Coupling of with serine followed by a stereoselective (dr > 99 : 1) installation of the trisubstituted olefin with MsCl and a base (DABCO, Et3NH) resulted in thiazole. With this key precursor in hand, the amine and carboxylic groups in and were liberated and the subsequent amide couplings resulted in gram-scale syntheses of bottom fragments in seven steps for both micrococcin P1 and thiocillin I in 47% and 51% overall yield, respectively.

The synthesis of top fragment 37, common to D series thiopeptides, started from a Pd-catalyzed C–H activation of thiazole 26 (Scheme 3). We found that the yield of this reaction was critically dependent on the size of the ester group and the methyl group was incompatible with the cross-coupling conditions. The reaction of ethyl thiazole ester 26b with Pd(OAc)2 (5 mol%) and CyJohnPhos (15 mol%) gave, after conversion from 28a, methyl ester 28b which was then coupled with amine 30 following the two-step, selective chlorination of the pyridine core (97%). At this stage, the sulfur protective group was removed, and MoO4(acac)2-catalyzed cyclodehydration and oxidation afforded 32 in 86% yield. We found that the pyridine scaffold in 31 was sufficient to stabilize the Mo(VI) catalyst and prevented decomposition of the Mo complex in the cyclodehydration reaction thus alleviating the need of further stabilization by additional ligands. Next, the Stille coupling with ethyl vinyl ether followed by bromination with NBS afforded bromoketone. Inspired by the prior work of Williams, we converted 34 into thiazole 36 in 86%. Because the exocyclic methylene group in the Hantzsch intermediate can undergo epimerization, we optimized the cyclization step by buffering the conditions with a bulky base (2,6-lutidine) whereas larger bases (e.g., 2,6-di-i-butyridine) were ineffective in promoting this transformation. To confirm the optical purity of the newly formed thiazole 36, the carbamate was removed, and the resultant amine was converted into a Mosher amide giving a 95 : 5 dr (determined by 19F NMR). Finally, site-selective hydrolysis of the methyl ester in proceeded without concomitant removal of the i-Pr group to yield top fragment in 73%.

In preparation for the union of the two fragments, the Boc protective group was removed from bottom segments to yield free amines which were then coupled with top unit to afford oligopeptides. Next, the i-Pr ester in 39 was removed under more forcing conditions (NaOH/H2O), and the resultant acid was merged with dipeptide. The installation of the olefin was accomplished by elimination of the hydroxsyl group in threonine with MsCl in exclusive Z selectivity. The final steps of the synthesis involved global deprotection with HCl to cleave all alcohol, amine, and carboxylic acid protective groups in one step, followed by macrocyclization of the resulting amino acid intermediate with PyAOP furnished micrococcin P1 in 22% yield. The similarity of micrococcin P1 and thiocillin I, which differ only by a mutation of L-valine into 3-hydroxy-L-valine, led us to adopt identical conditions for both syntheses, with the exception of the deprotection for thiocillin I. We found that acidic conditions alone were insufficient and resulted in only partial cleavage of the silicon group at the hydroxyvaline position (ca. 30%); thus, following the final macrocyclization, the resultant precursor was subjected to TBAF to reveal thiocillin (2) in 15%. Micrococcin P1 was completed in 14 steps and thiocillin I was completed in 15 steps from known commercial materials (longest linear sequence).

Having access to two representative members of the thiopeptide family, we evaluated the in vitro antimicrobial activity against a panel of recent Gram-positive bacterial strains (Table 2). Micrococcin P1 and thiocillin I exhibited similar potencies, showing 2- to 4-fold difference in their minimum inhibitory concentration (MIC) values in nearly all of the test bacterial isolates. An exception to this trend was observed for . Micrococcin P1 was completed in 14 steps and thiocillin I was completed in 15 steps from known commercial materials (longest linear sequence).

In summary, we described a general synthetic route toward thiopeptide antibiotics belonging to the D series. Given the
structural commonalities shared by all family members of this class, the presented method is easily adaptable to suit the preparation of thiopeptides belonging to other series as well as derivatives. The novel molybdenum catalyst eliminates the need for stoichiometric reagents and generates water as the only by-product. Moreover, the modular approach lends itself to future SAR studies to attain compounds with desirable properties for pre-clinical and clinical development.

Conflits of interest

There are no conflicts to declare.

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