Unnatural natural triterpenes produced by altering isoleucine into alanine at position 261 in hopene synthase and the importance of having the appropriate bulk size at this position for directing the stereochemical destiny during the polycyclization cascade[†]

Tsutomu Hoshino,* Takamasa Abe and Masanori Kouda

Department of Applied Biological Chemistry, Faculty of Agriculture and Graduate School of Science and Technology, Niigata University, Ikarashi, Niigata 950-2181, Japan. E-mail: hoshitsu@agr.niigata-u.ac.jp

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Incubation of squalene with the site-directed mutant of Ile261Ala of squalene-hopene cyclase from *Alicyclobacillus acidocaldarius* afforded multiple triterpenes consisting of tri-, tetra- and penta-cyclic skeletons, together with a final product of hopene, among which the previously unknown 6/6/6/6-fused tetracyclic skeletal compounds, denoted prohopene A and B, are included.

Squalene-hopene cyclase (SHC) catalyses the cyclization reaction of squalene 1 into pentacyclic triterpenes, hopene 2 and hopanol 3, under a fine regio- and stereo-chemical specificity. The reaction has been believed to proceed through all pre-chair conformation,¹ but recent studies on the site-directed mutagenesis have indicated that the reaction proceeds via two expansion steps from the 5-membered C- and D-ring intermediates, which had been previously formed under Markovnikov closure, into the corresponding 6-membered rings (anti-Markovnikov adduct), as shown in Scheme 1.2a,b The ring-expansion processes have been further supported by trapping experiments of the 6/6/5-fused tricyclic intermediate $\hat{6}$ and the 6/6/6/5-fused tetracyclic intermediate 8 (Markovnikov adducts) using the substrate analogues having a highly nucleophilic hydroxyl group.^{2a,b} The stereochemistry of 13H in **6** and 17H in **8** have been established to be of β -configuration; no enzymic products having the α -configurations have been obtained in the trapping experiments. Recently, we and Poralla's group have reported the isolation of the enzymatic products derived from the carbocation intermediates of mono- 4^{3} bi- $5^{4a,c}$ tri- $6^{2b,4c}$ and



† Electronic supplementary information (ESI) available: EIMS and NMR assignments. See http://www.rsc.org/suppdata/cc/b0/b000711k/

tetra-cyclic $\mathbf{8}$; 2a,b,4b,c these discrete cationic intermediates were produced by a single amino acid replacement of D377N (D377C), F365A, Y420A, F601A, W169F, W169 H or W489F in A. acidocaldarius SHC (Scheme 1). The abortive cyclization products formed by each point mutation have revealed not only the catalytic function of given amino acids but also the cyclization mechanism for 1; the cyclization is triggered by the DXDDTA motif;³ D377 stabilises monocyclic cation 4 probably via the carboxylate anion; and both F365^{4a} and $\hat{F}601^{2b}$ stabilise the transient carbocations at each cyclization stage $5 \rightarrow$ **8** possibly *via* a cation $-\pi$ interaction. The aromatic residues of W169, W489 and Y420 are likely to play a significant role for folding the substrate $1.^{2a,4c}$ In a series of the site-directed mutagenesis experiments, we have focused on Ile261 as a next experiment, which is highly conserved among all the known SHCs and oxidosqualene cyclases. The mutated SHCs of I261A produced the unknown 6/6/6/6-fused tetracyclic 14 and 15 ('unnatural' natural products) together with the known 11, 12, 13 and 16.5 The stereochemistry at 13- and 17-positions of premature products 11 and 12 was of α -configuration and in contrast to those of true intermediates 6 and 8. We report here, that the appropriate bulk size and shape at position 261 has a critical role in directing the steric control for constructing the hopane skeleton.

With the cell-free homogenates (150 ml), prepared from a 3 L culture of *E. coli* clone encoding I261A SHC, 100 mg of **1** was incubated for 15 h at optimum catalytic conditions (pH 6 and 55 °C). The GC analysis (30 m DB1, capillary column) showed six new enzymic products other than **2** in a hexane-extract of the reaction mixture.

Column chromatography over SiO₂ eluting with hexane afforded five fractions in the following order: **16**, **2** + **13**, **12** + **14** + **15**, **11** and the recovered **1**. The complete separation of each product was achieved by reverse-phase HPLC (C18) with THF–H₂O (6:4). The yields of each product, estimated by GC, were as follows: 4.0, 19.0, 4.1, 4.1, 3.7, 3.2, 48.6 and 3.1 mg for **11**, **12**, **13**, **14**, **15**, **16**, **2** and **3**, respectively, and 0.6 mg for the recovered **1**. No other products were observed in a detectable amount.

Structures of all the isolated compounds were determined as shown in Fig. 1 by EIMS and NMR spectra (H–H COSY 45, HOHAHA, NOESY, DEPT, HMQC and HMBC).[†] The EIMS, ¹H and ¹³C NMR spectra of **11** were identical to those of the authentic (17*E*)-(13 α H)-malabarica-14(27),17,21-triene,^{2b} the stereochemistry of H13 being further confirmed to be of α configuration by a strong NOE between H9 and H13. The epimer of **11**, (13 β H)-malabaricatriene **11**^{'2b} with a longer retention time (rt) on the GC than **11**, was never detected in the reaction mixture. The fragmentation pattern of **12** in the EIMS spectrum was superimposable to that of 17-*epi*-dammara-20(21),24-diene **12'**,^{2a} but the rt of **12** on the GC is shorter than that of **12'**, and the NOE between 30-Me and H17 was found, thus proving the α -orientation of H17 in **12**. The double bond of **13** was $\Delta^{13,17}$ by HMBC correlation both from 30-Me to C13



Fig. 1 Structures of the enzymatic products by the mutated I261A SHC.

and from 21-Me for C17. The proton chemical shift of 21-Me was 0.919 ppm (J 6.7 Hz) in CDCl₃, which allowed the assignment of 20*R*-stereochemistry.⁶ The EIMS spectrum of 14 was essentially the same as that of 15. The 6/6/6/6-fused tetracyclic skeletons of 14 and 15 were revealed by NMR analyses. An HMBC correlation between 28-Me and C13 was observed for 15, but not for 14. A strong NOE was observed between H16 and H19 for 15, while no NOE was seen for 14. Product 16 differed from 2 only in the double bond position, which was determined by the HMBC cross peaks of 28-Me/C17, 29-Me/C21 and 30-Me/C21.

Tricyclic 11 could be produced *via* 6' and two tetracyclics 12 and 13, *via* 8' (Scheme 2). Proton elimination from 21-Me of 8' could give 12, but a hydride shift to C18 of 8' followed by deprotonation of the 13H could afford 13. Formation of tri- and tetra-cyclic skeletons 11–13 may have occurred owing to the local change, especially near the site(s) responsible for the C/Dring formation; the mutated SHC replaced by a smaller bulk size of Ala could not perfectly fit with 1.7 Compounds 11–13 were accumulated, while the corresponding epimers 11' and 12' from 6 and 8 were not detected. This suggests that 6' and 8' cannot undergo further cyclizations, whereas the intermediates 6 and 8, which had been produced by this mutated SHC, could undergo





subsequent cyclizations to yield 2. Therefore, it is likely that the $(13\beta H)$ - and $(17\beta H)$ -configurations in 6/6/5- and 6/6/6/5-ring systems are required for the completion of two ring-expansion processes to give 9. This hypothesis agrees well with the previous results^{2a,b} that only **6** and **8** were trapped when the squalene analogues having a hydroxy group were incubated with the native SHC, but that 6' and 8' were not. The secondary cation 9 has been assumed as an intermediate in hopene biosynthesis, but no experimental evidence has been given. Formation of 14 and 15 gave definitive evidence for the involvement of intermediate 9. The 1,2-shift of 28-Me to the C17 cation could give 14 (path a in Scheme 2), whereas rearrangement of the isoprenoid side chain to the cation could afford 15 (path b). Triterpenes 14 and 15 have never been reported before. We propose to denote the prohopane skeleton for 9, prohopene A for 14 and prohopene B for 15. It is noteworthy that 8' is the biosynthetic intermediate of some plant triterpenes.¹ A looser binding near the C/D-ring could also perturb the correct positioning of the Δ^{21} double bond in 9, thus leading to the accumulation of 14 and 15; the appropriate arrangement of the double bond could allow a further cyclization to give 10 through the nucleophilic attack of the double bond toward cation 9. Product 16 could be formed perhaps due to the erroneous positioning of the deprotonation site for introducing the $\Delta^{22,29}$ double bond of 2, which may have also occurred concomitantly with the local change near the C/Drings

With respect to the mutated I261V SHC, no abortive cyclization product was found and the kinetic data were almost the same as that of the wild-type SHC,⁷ but the mutant I261A gave a looser affinity and a slower velocity for hopene biosynthesis.⁷ Site-directed mutagenesis not only helps to understand the fundamental issue of the reaction mechanism (molecular recognition and catalytic function), but also generates the previously unknown 'unnatural' natural products,^{8a} as represented by **14** and **15**. The rational genetic engineering of the active and/or recognition sites is a promising tool for the creation of novel natural products.^{4a,8b}

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