Elucidation of stability determinants of cold-adapted monomeric isocitrate dehydrogenase from a psychrophilic bacterium, Colwellia maris, by construction of chimeric enzymes

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To elucidate determinants of differences in thermostability between mesophilic and psychrophilic monomeric isocitrate dehydrogenases (IDHs) from Azotobacter vinelandii (AvIDH) and Colwellia maris (CmIDH), respectively, chimeric enzymes derived from the two IDHs were constructed based on the recently resolved three-dimensional structure of AvIDH, and several characteristics of the two wild-type and six chimeric IDHs were examined. These characteristics were then compared with those of dimeric IDH from Escherichia coli (EcIDH). All recombinant enzymes with a (His)₆-tag attached to the N-terminal were overexpressed in the E. coli cells and purified by Ni²⁺-affinity chromatography. The catalytic activity (kcat) and catalytic efficiency (kcat/Km) of the wild-type AvIDH and CmIDH were higher than those of EcIDH, implying that an improved catalytic rate more than compensates for the loss of a catalytic site in the former two IDHs due to monomerization. Analyses of the thermostability and kinetic parameters of the chimeric enzymes indicated that region 2, corresponding to domain II, and particularly region 3 located in the C-terminal part of domain I, are involved in the thermolability of CmIDH, and that the corresponding two regions of AvIDH are important for exhibiting higher catalytic activity and affinity for isocitrate than CmIDH. The relationships between the stability, catalytic activity and structural characteristics of AvIDH and CmIDH are discussed.

INTRODUCTION

NAD(P)⁺-dependent isocitrate dehydrogenase [IDH, EC 1.1.1.41(42)] occupies a key position in the TCA cycle and catalyses a reaction consisting of dehydrogenation and concomitant decarboxylation, as follows:

\[
\text{isocitrate} + \text{NAD(P)}^+ \rightarrow \text{2-oxoglutarate} + \text{CO}_2 + \text{NAD(P)}\text{H}^+
\]

The catalytic mechanism and structure of IDH have been studied most extensively in Escherichia coli (EcIDH). From these studies, it has been clarified that EcIDH binds to a coenzyme by using a unique motif, other than the Rossmann fold shared by many NAD(P)⁺-dependent dehydrogenases (Chen & Jeong, 2000). NADP⁺-IDHs of many bacteria, including E. coli, are known to be homodimers of subunits of about 40–45 kDa, although a monomeric IDH with a molecular mass of about 80–100 kDa is also found in eubacteria. Bacteria generally possess only one type of IDH. The monomeric and dimeric IDHs differ in amino acid sequence and immunological cross-reactivity (Ishii et al., 1993; Eikmanns et al., 1995; Sahara et al., 2002). The dimeric EcIDH and a monomeric IDH from Azotobacter vinelandii show only a 7–8% identity in amino acid sequence alignment, based on their structures. This implies that the monomeric and dimeric IDHs have evolved convergently.

A psychrophilic bacterium, Colwellia maris (Takada et al., 1979; Yumoto et al., 1998), has both monomeric and dimeric IDHs (Ochiai et al., 1979). Its monomeric IDH (CmIDH) exhibits maximal activity at 20°C, and even at 30°C is rapidly inactivated, indicating that it is a typical cold-adapted enzyme. Such psychrophilic enzymes are one of the mechanisms for biological adaptation to permanently cold environments and have two common
characteristics: high catalytic activity at low temperatures and low thermostability compared to mesophilic and thermophilic counterparts (Gerday et al., 1997). These characteristics are considered to be closely related to each other, because the enhanced conformational flexibility of the enzyme proteins responsible for the thermostability may be necessary to accommodate the substrates, the diffusion rates of which are inevitably diminished at low temperatures, and to bring about rapid conformational changes for the catalysis without energy loss (Fields & Somero, 1998). Recent structural comparisons of homologous enzyme proteins from psychrophilic, mesophilic and thermophilic organisms indicate that there may be numerous structural features of psychrophilic enzymes responsible for increased thermostability (Fields & Somero, 1998; Russell et al., 1998; Alvarez et al., 1998; Kim et al., 1999; Bentahir et al., 2000; de Backer et al., 2002).

The monomeric IDH of a mesophilic nitrogen-fixing bacterium, *Azotobacter vinelandii*, (AvIDH) showed 66% identity and 78% similarity in amino acid sequence to CnIDH (Ishii et al., 1993; Sahara et al., 2002), indicating that their tertiary structures are similar to each other. However, the former was found to be a typical mesophilic enzyme (optimal temperature for activity, 40–45°C), and the two IDHs differed in thermostability and optimal temperature for activity. On the other hand, the three-dimensional structure and active site of AvIDH recently resolved by crystallographic analysis (Yasutake et al., 2002) allow us to analyse the relationship between the temperature-dependent characteristics and structure of enzymes. Therefore, based on the three-dimensional structure of AvIDH, we constructed chimeric enzymes, in which various combinations of three regions of AvIDH and CnIDH were fused, and examined their temperature-dependent characteristics for catalytic function and structural stability.

The dimeric EcIDH has two catalytic sites, which are located at the interfaces of the two identical subunits and are formed by amino acid residues derived from both subunits (Hurley et al., 1989, 1991). On the other hand, the crystal structure of the monomeric AvIDH (Yasutake et al., 2002) reveals that this enzyme contains domain I, consisting of N- and C-terminal segments (regions 1 and 3, respectively), and domain II, corresponding to the intermediate segment (region 2), and that the single polypeptide chain acquires the ability to catalyse a reaction identical to the dimeric IDH by fusing domain B’–C’ of the second subunit to the first subunit with the same spatial relationship (Fig. 1). This suggests that monomeric IDH may have evolved through the duplication of domain B–C in an ancestral dimeric IDH, rather than convergently. Although monomeric CmIDH and AvIDH and dimeric EcIDH catalyse the same reaction, and exhibit the same specificities for the coenzyme (NADP+) and metal ion (Mn2+ or Mg2+), the former two IDHs can be considered to have lost one catalytic site by the monomerization. Accordingly, in this paper, we also compared the catalytic properties of monomeric and dimeric bacterial IDHs.

### METHODS

**Construction of genes encoding chimeras between CmIDH and AvIDH.** The *icd* genes encoding AvIDH, CnIDH and EcIDH were amplified by PCR to introduce restriction sites for BamHI and SacI at the 5’- and 3’-terminals of the ORFs, respectively. Therefore, the following primers were synthesized: for AvIDH, AF0 5’-ggcc-gggaattc-TCCACACCGAGATTATC-3’ (29-mer) and AR0 5’-ggcc-gggaattc-CTATGGAGGTGCCAG-3’ (28-mer); for CnIDH, CF0 5’-ggcc-gggaattc-ACGACCTGATAAATACAAAATCT-3’ (32-mer) and CR0 5’-ggcc-gggaattc-CTAAAGTACGGATGAAATG-3’ (33-mer); for EcIDH, EF5 5’-ggccgaattc-GAAGTAAGAGTGTG-3’ (27-mer) and ER5 5’-ggccgaattc-TTACATGTTCGTGATGATC-3’ (29-mer) [lower-case type indicates additional bases for introducing digestion sites for SacI and BamHI (underlined)]. PCR was carried out in a DNA thermal cycler 2400 (Perkin-Elmer) in a 50 µl reaction mixture containing about 10 pmol of each primer, 1 U KOD-plus DNA polymerase (Toyobo) and 100 ng pAVESc (Sahara et al., 2002), pIS202 (Ishii et al., 1993) or pTK512 (Thorsness & Koshland, 1987) carrying the *icd* genes of *A. vinelandii*, *C. maris* and *E. coli*, respectively, as template DNA in a buffer system prepared by the manufacturer. Cycling conditions were as follows: denaturation at 94°C for 15 s, annealing at 50°C for 30 s, and extension at 68°C for time periods calculated based on an extension rate of 1 kbp min⁻¹. Each amplified PCR fragment was ligated to the BamHI–SacI site of pTrcHisB (Invitrogen), a plasmid vector for conferring the N-terminal (His)₆-tag on the expressed proteins, to obtain the plasmids pHisAvWT, pHisCmWT and pHisEcWT, respectively.

The *icd* gene of AvIDH possesses BssHI and NspV sites between regions 1 and 2 and between regions 2 and 3, respectively (Fig. 1c), but a BssHI site is absent in the corresponding region of the *C. maris icd* gene. Therefore, to exchange each domain of AvIDH and CmIDH, a BssHI site was introduced into the *icd* of *C. maris* by PCR, as described above. For this reaction, the following two primers were used: *C.m*. *BssHI*-s 5’-GGTAACCTCTCTGCTGCACGCCAGCG-3’ (27-mer) and *C.m*. *BssHI*-as 5’-CGCTGGCGGGGGAGCATGAGTTACC-3’ (27-mer) [lower-case type indicates bases substituted to introduce the BssHI site (underlined)]. Two PCR products were obtained in separate reactions with the primer sets CF0 plus *C.m*. *BssHI*-as and then *C.m*. *BssHI*-s plus CR0. The products were used as template DNAs for a third PCR reaction with the primers CF0 and CR0. The resultant PCR product was digested with *Bam*HI and SacI, and then ligated to the *Bam*HI–SacI site of pTrcHisB to obtain the plasmid pHisCm-BssHI. The introduction of the BssHI site in CmIDH resulted in no change of amino acid residues, because the codon of Arg116, CGT, was replaced by another codon for Arg, CGC. After the *A. vinelandii* and *C. maris icd* genes had been amplified by PCR with pHisAvWT and pHisCm-BssHI as template DNA and the primer sets AF0 plus AR0 and CF0 plus CR0, respectively, the resulting products were digested with BssHI and NspV to obtain six DNA fragments corresponding to regions 1 to 3 of AvIDH and CmIDH (fragments 1Av–3Av and 1Cm–3Cm respectively). Fragments 1Av, 2Av and 3Av and fragments 1Cm, 2Cm and 3Cm were ligated to the *Bam*HI–SacI site of pTrcHisB to obtain the plasmids pHisACA and pHisACG, respectively. Similarly, for the exchange of region 1 of the two enzymes, four DNA fragments produced by the digestion of the amplified AvIDH and CmIDH ORFs with BssHI were ligated with combinations of fragments 1Cm and 2–3Av and fragments 1Av and 2–3Cm to obtain pHiCACAA and pHisACG, respectively. To construct chimeric IDHs with replacements of region 3, the NspV site in the vector pTrcHisB located downstream of the inserted *icd* gene was utilized. The NspV fragments of pHisCmWT and pHisAvWT were

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**Note:** The text continues with further details on the methods and results, which are not included in this snippet. The full document would provide a detailed account of the experimental procedures and findings related to the construction and analysis of chimeric IDHs from different bacterial sources.
Fig. 1. Structure of dimeric and monomeric IDHs. (a) Ribbon model of dimeric EcIDH. Two identical (first and second) subunits are coloured in blue and light blue, respectively. Isocitrate and Mg$^{2+}$ bound to catalytic sites are shown by violet sticks and green spheres, respectively. (b) Ribbon model of monomeric AvIDH (red) superimposed onto (a). Isocitrate, Mg$^{2+}$ and NADP$^{+}$ are depicted as in (a). (c) and (d) Respective schematic representations of the catalytic sites of dimeric EcIDH and monomeric AvIDH. The colour of each region is the same as in (a) and (b). Closed and open circles indicate amino acid residues bound to isocitrate plus Mn$^{2+}$ (or Mg$^{2+}$) and NADP$^{+}$, respectively. Crosses represent the catalytic sites. N and C show each terminal of the protein. In EcIDH, the second subunit and its amino acid residues are prime-signed. In (d), numbers in parentheses show the positions of the corresponding amino acid residues in CmIDH. (e) Schematic representation of each region in monomeric IDH.
exchanged and ligated to yield the plasmids pHisCCA and pHisAAC. The coding regions of these chimeric genes were confirmed by subsequent DNA sequencing in both directions.

**Overexpression and purification of His-tagged IDHs.** Cells of an *E. coli* mutant defective in IDH, DEK2004 (Thorness & Koshland, 1987; LaPorte et al., 1985), harbouring the expression plasmid for the His-tagged wild-type AvIDH, CmIDH and EcIDH (AvWT, CmWT and EcWT, respectively) and chimeric IDHs (AAC, ACA, CAA, CCA, CAC and ACC) were grown at 37 °C to a turbidity of 0.6–0.8 at 600 nm in Super broth medium (12 g tryptone, 24 g yeast extract, 5 g NaCl, 3.81 g KH2PO4 and 12.5 g K2HPO4.12H2O, pH 7.0) containing 50 mg ampicillin l−1 and 15 mg tetracycline l−1. The cultures were then rapidly cooled on ice and further incubated for 18–24 h at 15 °C after the addition of 1 mM IPTG to induce the expression of the IDH protein. The inductions of gene expression by IPTG were carried out at low temperatures, such as 15 °C, because of the marked thermostability of CmIDH (Ochiai et al., 1979). Cells were harvested and resuspended in 20 ml Buffer A (50 mM sodium phosphate, pH 8.0, containing 2 mM MgCl2, 0.5 M NaCl, 10 mM 2-mercaptoethanol and 10 mM imidazole) per litre of the culture. Hen-egg lysozyme was added to the cell suspension at a concentration of 2 mg ml−1 and the mixture was gently shaken overnight at 4 °C. The cells were then disrupted by ultrasonic oscillation. After the centrifugation of the cell lysate at 39 120 g for 30 min at 4 °C to remove cell debris, the supernatant was centrifuged at 105 000 g for 6 h at 4 °C. The resultant supernatant was loaded onto a Hi-NTA column (25 ml, Qiagen) equilibrated with Buffer A. After a thorough washing with the same buffer, the column was further washed with 50 ml Buffer B (Buffer A containing 10%, v/v, glycerol and 20 mM imidazole instead of 10 mM imidazole) and next with 50 ml Buffer C (Buffer B containing 30 mM instead of 20 mM imidazole). The enzymes were then eluted with 50 ml Buffer D (Buffer B containing 250 mM instead of 20 mM imidazole). The eluant was concentrated by acetone chilled at −20 °C and then added to the extracts. After cooling for 1 h at −80 °C, the mixture was centrifuged at 39 120 g for 15 min at 4 °C. The precipitates were then dried and dissolved in a small volume of 0.1% (w/v) SDS. The solutions were coated onto a PVDF membrane (Hybond-P, Amersham Pharmacia Biotech), N-terminal amino acid sequences of the peptide fragments were confirmed by automated Edman degradation on a Hewlett Packard protein sequencer G1005A to clarify the digestive site with trypsin. To determine the C-terminal structure of the proteolytic intermediate from CmWT, the peptides precipitated by aceton were digested at room temperature with carboxypeptidase Y (Oriental Yeast) in 50 μl of 100 mM potassium phosphate (pH 5.6) containing 0.1% (w/v) SDS and 0.1 mM DL-norleucine (as a standard amino acid) at an enzyme:substrate ratio of 1:100. After digestion for various times between 0 and 20 min, 5 μl of the reaction mixture was withdrawn and mixed with an equal volume of 20% (v/v) acetic acid. The liberated amino acids were determined by a JEOL AminoTac JLC-500/V automatic amino acid analyser. The molecular mass of the proteolytic intermediates from CmWT in 0.1% (w/v) SDS solution was determined using a MALDI-TOF mass spectrometer (Voyager DE Pro, PE biosystems).

### RESULTS

**Overexpression and purification of wild-type and chimeric IDHs**

As shown in Fig. 2a, SDS-PAGE analysis revealed that the purities of the recombinant enzymes with His-tags at the N-terminal were at least 90–95%, and the apparent molecular masses of the monomeric IDHs (AvWT and CmWT and their chimeric IDHs) and dimeric EcWT were 80 kDa and 43 kDa, respectively, similar to those of the respective native enzymes (Sahara et al., 2002; Thorness & Koshland, 1987; Ishii et al., 1987). All the purified recombinant IDHs were able to cross-react with antibody against His-tag (Fig. 2c), but no cross-reactivity with antibody against monomeric IDH was observed in EcWT (Fig. 2b), as reported previously (Fukunaga et al., 1992).

**Optimal temperature for activity and thermostability**

The effect of temperature on the activities of wild-type and chimeric IDHs was examined (Fig. 3a). The optimal temperatures for activity (T_{opt}) of AvWT and CmWT with

**Digestion with trypsin.** The purified recombinant IDHs were dialysed overnight at 4 °C against 0.1 M NaHCO3, pH 8.1. The enzyme samples (1 mg ml−1) were incubated for various times at 25 °C with trypsin (0.01 mg ml−1). The proteolysis was stopped by the addition of an equal volume of 2 × SDS-PAGE sample buffer. The mixtures were immediately boiled and analysed by SDS-PAGE.

**Amino acid sequencing and matrix-assisted laser desorption/ ionization time-of-flight (MALDI-TOF) mass spectrometry.**

After SDS-PAGE of CmWT, ACA, CAC, AAC, CCA and ACC digested for 30 min with trypsin under the conditions described above, the gels including 58–62 kDa peptide fragments were cut off and broken in 20 mM Tris/HCl (pH 8.0) containing 1% (w/v) SDS. The peptide fragments were extracted from the gels by vigorous mixing overnight. A four-fold volume of acetone chilled at −20 °C was then added to the extracts. After cooling for 1 h at −80 °C, the mixture was centrifuged at 39 120 g for 15 min at 4 °C. The precipitates were then dried and dissolved in a small volume of 0.1% (w/v) SDS. The solutions were coated onto a PVDF membrane (Hybond-P, Amersham Pharmacia Biotech). N-terminal amino acid sequences of the peptide fragments were confirmed by automated Edman degradation on a Hewlett Packard protein sequencer G1005A to clarify the digestive site with trypsin. To determine the C-terminal structure of the proteolytic intermediate from CmWT, the peptides precipitated by aceton were digested at room temperature with carboxypeptidase Y (Oriental Yeast) in 50 μl of 100 mM potassium phosphate (pH 5.6) containing 0.1% (w/v) SDS and 0.1 mM DL-norleucine (as a standard amino acid) at an enzyme:substrate ratio of 1:100. After digestion for various times between 0 and 20 min, 5 μl of the reaction mixture was withdrawn and mixed with an equal volume of 20% (v/v) acetic acid. The liberated amino acids were determined by a JEOL AminoTac JLC-500/V automatic amino acid analyser. The molecular mass of the proteolytic intermediates from CmWT in 0.1% (w/v) SDS solution was determined using a MALDI-TOF mass spectrometer (Voyager DE Pro, PE biosystems).
His-tags (47.5°C and 25°C, respectively) were analogous to those of the respective native enzymes (40–45°C and 20°C, respectively) (Sahara, 2000; Ochiai et al., 1979). All chimeric IDHs exhibited $T_{opt}$ values within the range of those of AvWT and CmWT. The $T_{opt}$ of CAC, AAC and ACC (27.5°C) was only slightly higher than that of CmWT, while the corresponding values of ACA, CCA and CAA (32.5°C, 32.5–37.5°C and 42.5°C, respectively) were higher than those of the former three chimeric IDHs. These results suggest that region 3, located at the C-terminal of CmIDH and AvIDH, is involved in determining $T_{opt}$. The dimeric EcWT exhibited a similar $T_{opt}$ to AvWT.

**Fig. 2.** SDS-PAGE (a) and immunoblot analysis (b, c) of purified wild-type and chimeric IDHs. AvIDH indicates the native enzyme protein purified from the A. vinelandii cells. M, marker proteins. (a) Five micrograms of each protein was applied. Protein on the gel was stained with Coomassie brilliant blue. (b) and (c) After SDS-PAGE of 2.5 μg protein per lane, antibodies against monomeric IDH of V. parahaemolyticus (b) and N-terminal His-tag (c) were used for immunoblotting. Both of the antibodies (20 mg ml⁻¹) were diluted 1:2500.

**Fig. 3.** Effect of temperature on specific activities (a) and thermostability (b, c) of wild-type and chimeric IDHs. Red, AvWT; blue, CmWT; light green, CAC; orange, ACA; pink, AAC; sky blue, CCA; light blue, ACC; yellow, CAA; grey, EcWT. (b) Inactivation of enzymes by incubation at various temperatures. (c) Thermal unfolding of the enzyme proteins monitored by CD.
AvWT and CmWT exhibited the same thermostability of activity as the respective native enzymes (Ochiai et al., 1979; Sahara, 2000) (Fig. 3b). Furthermore, the thermostability of EcWT activity was similar to that of AvWT. Half-lives (t½) for the heat-inactivation of the chimeric enzymes were intermediate between those of the two wild-types, AvWT and CmWT. The thermostability of chimeric IDHs was fundamentally correlated with the optimal temperatures, that is, chimeric IDHs showing lower optimal temperatures were more thermolabile. However, the t½ values of ACA and CAC were 38 °C and 40-5 °C, respectively, and CAC was more thermostable than ACA, in spite of its lower Tm. Similarly, the Tm of CCA was higher than that of AAC, but the t½ values of CCA and AAC were 37-5 °C and 40-5 °C, respectively.

In addition, the thermostability of the structure of the IDH proteins was monitored by CD (Fig. 3c). The wild-type and chimeric IDHs were classified into two groups based on the thermal denaturation profiles. The first group comprised AvWT, CmWT, ACA, CCA, ACC and CAA with a monophasic denaturation process. The second was composed of CAC and AAC, which are denatured in two steps with the presence of a stable intermediate. ACC possessed almost the same Tm (temperature at which a half-change in the ellipticity occurred) as CmWT (31-5 °C and 30-5 °C, respectively), whereas the Tm value of CAA was closest to that of AvWT of all the chimeric IDHs (45 °C and 51 °C, respectively), indicating that the exchange of region 1 had little effect on the thermostability of AvWT and CmWT. This possibility was supported by the finding that ACA had almost the same denaturation curves and Tm values as CCA (39-5 °C and 41 °C, respectively). Conversely, since ACA and CCA showed Tm values intermediate between those of AvWT and CmWT, region 2 of AvIDH and region 3 of CmIDH may be determinants of thermostability. On the other hand, Tm values for the first step of denaturation of CAC and AAC (31 °C and 33 °C, respectively) were similar to the Tm of CmWT. This result suggests that the region(s) derived from CmIDH in these chimeric enzymes are denatured in preference to the one(s) from AvIDH. After the incubation above 40 °C, at which the second denaturation step started, the activities of CAC and AAC could not be recovered (Fig. 3b), indicating an irreversible inactivation. In contrast, only a slight inactivation of CAC was observed after incubation at temperatures between 28 °C and 40 °C, at which the first denaturation step proceeded (Fig. 3b, c). These results indicate that domain I of CAC is unfolded reversibly between 30 °C and 40 °C. Thus, the exceptional thermostability of CAC and AAC activities at the moderate temperatures described above (Fig. 3b) may be attributable to the renaturation of the enzymes on cooling after the incubation.

Fig. 4. Digestion of wild-type and chimeric IDHs with trypsin. (a) Time-course of tryptic digestion. The IDH samples were treated for the indicated times with trypsin under the standard conditions described in Methods. Ten micromolars of the enzyme was withdrawn and immediately electrophoresed. After electrophoresis, protein on the gel was stained with Coomassie brilliant blue. Left and right panels indicate the bands of undigested molecules and major digestive intermediates [corresponding to white triangles in (b)], respectively. (b) SDS-PAGE after partial digestion with trypsin. Lane 1, AvWT; lane 2, CmWT; lane 3, ACA; lane 4, CAC; lane 5, ACC; lane 6, CCA; lane 7, CAA. All IDH samples (10 μg) were digested for 30 min under standard conditions. White triangles show major digestive intermediates. M, molecular marker proteins. (c) Effect of ligands on the digestion of CmWT with trypsin. CmWT (1 mg ml⁻¹) was incubated for 30 or 60 min at 25 °C with trypsin (0-01 mg ml⁻¹) in the absence (lanes a) or presence of 10 mM isocitrate and 6-7 mM Mn²⁺ (lanes b), 1-2 mM NADP⁺ (lanes c) or 10 mM isocitrate and 1-2 mM NADP⁺ (lanes d). The digestion was terminated by the addition of 2 × SDS-PAGE sample buffer and subsequent boiling.
Resistance to trypsin

The sensitivity of wild-type and chimeric IDHs to trypsic digestion was examined (Fig. 4a). At 25 °C, AvWT and EcWT were little digested after incubation for 120 min with trypsin, while CmWT was rapidly digested with a t1/2 of about 5 min. Six chimeric IDHs were classified into the following three groups based on sensitivity to trypsin: CAC and ACC, exhibiting a sensitivity to trypsin similar to CmWT;CAA, resistant to trypsin in a similar manner to AvWT; and ACA, AAC and CCA, with an intermediate level of resistance. The sensitivity of wild-type and chimeric IDHs to trypsic digestion was significantly correlated to the thermostability of their activity and protein structure (Fig. 3b, c). SDS-PAGE of CmWT, ACA, CAC, AAC, CCA and ACC digested with trypsin (Fig. 4b, lanes 2–7) revealed that the undigested enzyme proteins (83 kDa) and their digestive intermediates (58–62 kDa, white triangles in Fig. 4b) were contained as two major bands, and that the latter accumulated with the decrease of the former. The proteolytic intermediates of chimeric IDHs appeared later than those of CmWT, indicating that the chimeric proteins are more resistant to digestion than CmWT (Fig. 4a, right-hand panel). The apparent molecular masses of the digestive intermediates estimated by SDS-PAGE indicated that none of them are regions 1–3 themselves. N-terminal amino acids of the digestive intermediates from Lys157 to Ala164 in AvIDH have an N-terminal sequence (KHPHKMGA) corresponding to the sequence from Asn159 to Ala166 in CmIDH. On the other hand, the N-terminal sequence of intermediates from CmWT, CCA and ACC was found to be NNPHSMGA, which is the homologous sequence from Asn159 to Ala166 in CmIDH. Because the six IDH enzymes were digested at homologous positions with trypsin, we conclude that the slight differences in the molecular masses of their intermediates were due to different cleavage sites at the C-terminus. Digestion with carboxypeptidase Y, the C-terminal structure of the intermediate from CmWT was identified as EEK, corresponding to the sequence from Lys157 to Ala164 in AvIDH. Furthermore, a major value of 58646.23 Da obtained by MALDI-TOF mass spectrometry was nearly consistent with the theoretical mass of the fragment from Asn159 to Lys698 of CmIDH (58663.87 Da). These results indicate that the proteolytic intermediates were produced by the digestion of region 1 and the C-terminal part of region 3 in domain I (Fig. 5b). Although the effects of ligands such as substrate and coenzyme on the trypsic digestion of CmWT were also examined, Mg2+, isocitrate and NADP+, even when more than one of them was added, were not able to protect CmWT from digestion (Fig. 4c).

Comparison between wild-type AvWT, CmWT and EcWT and chimeric IDH activity

Both of the monomeric IDHs, AvWT and CmWT, exhibited much higher specific activity at low temperatures than the dimeric EcWT (Fig. 3a). A larger difference was observed when the molar catalytic activity (kcat) of the former two IDHs was compared with that of EcWT (Table 1). The affinity for NADP+ of the three IDHs was similar, but the Km value for isocitrate of AvWT was eightfold smaller than that of CmWT and almost the same as that of EcWT. In contrast to EcWT, AvWT maintained higher specific and molar catalytic activities even at low temperatures than the cold-adapted CmWT, indicating that AvIDH can perform its catalytic function over a wide range of temperatures, in spite of its mesophilic characteristics. Based on the relationship between the stability and activity of the enzyme, the chimeric IDHs could be classified into two groups. ACA and CCA were more stable, but had lower activity at low temperatures than CmWT. On the other hand, CAC and ACC had almost the same optimal temperature for activity as CmWT, but the activities of the two chimeric IDHs were enhanced at low temperatures. Furthermore, the Km values for isocitrate of ACA, CCA and CAA were comparable to that of AvWT, indicating that region 3 of AvWT is required to increase affinity for this substrate.

DISCUSSION

The cold-adapted monomeric IDH-II from C. maris (CmIDH) has been shown to be much more thermolabile than its mesophilic counterpart in A. vinelandii (AvIDH) (Ochiai et al., 1979; Sahara, 2000), in spite of the similarity in their amino acid sequences (Sahara et al., 2002) and protein structures, as estimated from far-UV CD spectra (data not shown). The three-dimensional structure of AvIDH (Yasutake et al., 2002, 2003) consists of three regions (Fig. 1e). Therefore, to specify the structural characteristics responsible for the psychrophilic nature of CmIDH, chimeric IDHs exchanging each region of the two enzymes were constructed and characterized. CAA and ACC showed characteristics similar to AvWT and CmWT, respectively (Fig. 3 and Table 1), indicating that region 1 of the two wild-type IDHs contributes little to their stability and temperature dependence. This region exhibited the highest level of homology in amino acid sequence (74% identity) among the three regions of AvIDH and CmIDH (Sahara et al., 2002). On the other hand, region 2 of AvIDH is necessary for the thermostability and high catalytic activity, but not the affinity for isocitrate (Fig. 3 and Table 1). Domain II (region 2) of monomeric IDH consists of two repetitive structural motifs, corresponding to domains B–C from the same two subunits of the dimeric IDH (Fig. 1a–d). A bundle of four helices, formed by two helices from the two motifs, is very hydrophobic in the AvIDH and CmIDH proteins, but several hydrophobic amino acid residues of AvIDH (Met356, Ile357, Val388, Ile390 and Ile392) are replaced by other hydrophobic ones with smaller side-chain volumes in CmIDH (Ala356, Leu357, Ala388, Val388 and Val388, respectively). Dimeric isopropylmalate dehydrogenase (IPMDH) has a similar structural framework to the dimeric IDH (Imada et al., 1991). The increased hydrophobicity of the helix bundle in mesophilic IPMDH caused by mutations leads to a strengthened thermostability comparable to that of the thermophilic
Fig. 5. Major digestive intermediate of CmWT. (a) Ribbon model of monomeric AvIDH and its respective regions. Region 1 (Thr^3 to Arg^146, red), region 2 (Ala^147 to Leu^577, blue), region 3 (Phe^578 to Leu^740, yellow). N and C indicate each terminus. (b) Structure of a major digestive intermediate of CmWT. Region M (Asn^159 to Lys^698, light blue) corresponds to the digestive intermediate. (c) Ca trace of domain I of CmWT. The helix bundle consisting of α1 from region 1 and α21–24 from region 3 is shown as red cylinders. The orange region is region C in (b). (d) and (e) Partial amino acid sequence alignments of AvIDH and CmIDH. Bold type indicates the amino acid residues conserved between the two enzymes. Stars represent the amino acid residues involved in the catalytic site (see Fig. 1d). Coloured bars under the sequence correspond to the coloured regions in (b). Secondary structures, α-helix (rectangles) and β-sheet (arrows), are shown on the sequence. Red-outlined rectangles are α-helices forming the bundle in domain I represented in (c). Dotted letters are amino acid residues determined by N-terminal sequencing of the digestive intermediates (see text).
Table 1. Kinetic parameters for wild-type and chimeric IDHs at 15 °C

Values shown are the mean of three independent experiments ± SEM.

<table>
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<th>Enzyme</th>
<th>Specific activity (µmol min⁻¹ mg⁻¹)</th>
<th>k_cat (s⁻¹)</th>
<th>Kₘ (µM)</th>
<th>kcat/Kₘ × 10² (s⁻¹ M⁻¹)</th>
<th>Kcat/Kₘ (M⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AvWT</td>
<td>75.5 ± 3.3</td>
<td>105.5 ± 5.5</td>
<td>7.9 ± 0.5</td>
<td>73.0 ± 6.0</td>
<td>92.7</td>
</tr>
<tr>
<td>CmWT</td>
<td>50.5 ± 1.5</td>
<td>70.8 ± 2.1</td>
<td>62.2 ± 3.2</td>
<td>57.5 ± 0.8</td>
<td>9.2</td>
</tr>
<tr>
<td>ACA</td>
<td>33 ± 2.2</td>
<td>47.4 ± 3.1</td>
<td>11.3 ± 0.4</td>
<td>45.9 ± 2.2</td>
<td>4.0</td>
</tr>
<tr>
<td>CAC</td>
<td>89.8 ± 2.9</td>
<td>129.9 ± 4.1</td>
<td>93.4 ± 1.3</td>
<td>97.1 ± 4.7</td>
<td>10.4</td>
</tr>
<tr>
<td>AAC</td>
<td>75.0 ± 9.0</td>
<td>117.4 ± 12.6</td>
<td>154.3 ± 10.3</td>
<td>138.9 ± 17.1</td>
<td>9.0</td>
</tr>
<tr>
<td>CCA</td>
<td>37.0 ± 0.6</td>
<td>51.9 ± 0.8</td>
<td>8.5 ± 0.8</td>
<td>44.2 ± 5.8</td>
<td>51.9</td>
</tr>
<tr>
<td>ACC</td>
<td>26.6 ± 0.8</td>
<td>37.2 ± 1.1</td>
<td>28.3 ± 2.2</td>
<td>35.5 ± 4.2</td>
<td>12.5</td>
</tr>
<tr>
<td>CAA</td>
<td>63.5 ± 0.0</td>
<td>89.3 ± 0.0</td>
<td>12.0 ± 2.5</td>
<td>89.1 ± 7.9</td>
<td>74.6</td>
</tr>
<tr>
<td>EwWT</td>
<td>13.4 ± 0.3</td>
<td>22.0 ± 0.5</td>
<td>3.3 ± 0.1</td>
<td>15.4 ± 1.1</td>
<td>4.7</td>
</tr>
</tbody>
</table>

*The reaction mixture contained 0.12 mM NADP⁺ and 2 mM isocitrate, as described in Methods.
†The Kₘ values for isocitrate and NADP⁺ were determined by varying the concentrations of isocitrate and NADP⁺ under standard assay conditions. The data were analysed by Lineweaver–Burk plotting. The following molecular masses of His-tagged recombinant IDHs were used for calculation: AvWT (83 898 Da, 774 aa), CmWT (84 134 Da, 774 aa), ACA (83 949 Da, 773 aa), CAC (84 083 Da, 774 aa), AAC (83 835 Da, 772 aa), CCA (84 197 Da, 775 aa), ACC (83 886 Da, 772 aa), CAA (84 146 Da, 775 aa) and EwWT (98 531 Da, 448 aa).
‡k_cat values per catalytic site.

counterpart (Kirino et al., 1994; Wallon et al., 1997a). As reported in a psychrophilic IPMDH (Wallon et al., 1997b), larger cavities between helices in the bundle of CmIDH, which are derived from substitution by amino acid residues with smaller side chains, might be responsible for the low stability. The reduced stability of psychrophilic enzymes is considered to give them activation energies lower than those of their mesophilic and thermophilic homologues (Fields, 2001). In fact, the activation energy of CmWT calculated by Arrhenius plotting of the data in Fig. 3a was smaller than that of AvWT (8.9 and 17.1 kJ mol⁻¹, respectively).

Region 3 of CmIDH is related to some unique properties of the chimeric enzymes. First, the results of the thermal denaturation of the wild-type and chimeric IDHs and the thermostability of their activities (Fig. 3b, c) indicated that region 3 of CmIDH is responsible for its thermostability and may initially unfold when this enzyme is heat-denatured. Second, the introduction of CmIDH region 3 into the chimeric IDHs led to a reduction of the affinity for isocitrate (CAC, AAC and ACC in Table 1). This can be explained by the general insight for cold-adapted enzymes that their thermalability is attributable to an enhanced structural flexibility compared to their mesophilic and thermophilic counterparts, and that such a flexible structure accompanies a broader distribution of conformational states and results in poor binding to the ligand and high Kₘ values (Gerday et al., 1997). It has been reported that the high flexibility of cold-adapted lactate dehydrogenases from Antarctic fishes is localized in a limited region involved in catalytic conformational changes, rather than the entire molecule (Fields & Somero, 1998).

Limited proteolysis is useful to clarify the structural configuration of proteins and to identify exposed and flexible regions in the native structure (Aghajanian et al., 2003). The resistance of wild-type and chimeric IDHs to digestion with trypsin is in good agreement with their thermostability (Figs 3 and 4). N-terminal amino acid sequencing and MALDI-TOF mass spectrometric analysis of the intermediates of CmWT and of five chimeric IDHs, not including CAA, revealed that trypsin cleavage occurred between Arg158 and Asn159 and between Lys598 and Ile699 in the CmIDH sequence, with the resultant generation of the light-blue-coloured fragment (region M) in Fig. 5(b, d, e). Since CAA was resistant to trypsin in a similar manner to AvWT (Fig. 4a, b), trypsin should digest the C-terminal fragment containing 44 amino acid residues of CmIDH (orange-coloured region C in Fig. 5b, c, e) prior to the N-terminal fragment of 149 amino acid residues (violet-coloured region N). Region C consists of three short z-helices, is located at the surface of the molecule, far from the activesite cleft, and contains no amino acid residue involved in the active site (Fig. 5e), suggesting that the coexistence of ligands such as isocitrate, NADP⁺ and Mg²⁺ cannot protect the IDH proteins from tryptic digestion. The data in Fig. 4c support this possibility. Therefore, region 3, in particular region C, of CmIDH, responsible for the thermostability, is concluded to be more sensitive to tryptic digestion than the other regions. Domain I of monomeric IDH contains many z-helices, and four helices in region 3, z21–z24, form a helix bundle together with z1 in region 1 (red cylinders in Fig. 5c). In contrast to these tight interactions, region C, located on the surface, should be flexible, since Pro709, Pro718 and Pro739 in this region of AvIDH possess much
higher $B$ factors than the mean for the whole molecule (data not shown). Therefore, region C of CmlIDH might be more flexible than that of AvlIDH. On the other hand, CmlIDH has a smaller number and content of Pro residues than AvlIDH (the former, 31 and 4.2%; the latter, 37 and 5.0%). This has been proposed to be a general characteristic of cold-adapted enzymes (Gerday et al., 1997; Wallon et al., 1997b). Notably, a Pro residue in a loop region diminishes the flexibility of the main chains of the protein as well as the entropy of unfolding, since the pyrrolidine ring severely restricts possible conformations of the preceding residue (Matthews et al., 1987). In short loops in region C, the Pro$^{218}$ and Pro$^{739}$ of AvlIDH are substituted for Ala$^{719}$ and Ala$^{740}$, respectively, in CmlIDH (Fig. 5e). Furthermore, the replacement of His$^{217}$ of AvlIDH with Phe in CmlIDH may weaken the stability of region C in the latter enzyme, because the His residue forms a hydrogen bond with Tyr$^{105}$ of region N in AvlIDH, but the His residue is lost in CmlIDH, in spite of the conservation of the Tyr residue (Tyr$^{107}$ in CmlIDH).

NADP$^+$-IDH is a member of the $\beta$-decarboxylating dehydrogenase family, which catalyses metal ion- and NAD(P)$^+$-dependent dehydrogenation and subsequent metal ion-dependent decarboxylation of 2R,3S-2-hydroxy acids. NAD$^+$-IDH, NAD$^+$-IPMDH, NAD$^+$-homoo-isocitrate dehydrogenase (HDH) and NAD$^+$-tartrate dehydrogenase (TDH) are contained in this family (Chen & Jeong, 2000). Among them, all IPMDHs, HDHs and TDHs, and most IDHs, are dimers. From phylogenetic analyses and comparisons of the crystal structures of NADP$^+$-EcIDH, pig mitochondrial and human cytosolic dimeric NADP$^+$-IDHs and dimeric NAD$^+$-IPMDH of Thermus thermophilus, it has been proposed that the ancestor had to be a dimeric enzyme with a broad specificity for substrates and coenzymes (Hurley et al., 1989, 1991; Imada et al., 1991; Dean & Golding, 1997; Steen et al., 2001; Stoddard et al., 1993; Ceccarelli et al., 2002; Xu et al., 2004; Hurley & Dean, 1994). On the other hand, the structure of monomeric AvlIDH (Fig. 1) suggests that the monomeric IDHs did not evolve convergently but originated from the common ancestor for this enzyme family by a unique domain duplication ( Yasutake et al., 2002). The specific activities of monomeric AvlIDH and CmlIDH at 15°C were higher than that of dimeric EcIDH (5.6- and 3.8-fold, respectively; Table 1). Furthermore, at all temperatures tested, AvlIDH showed higher activities than EcIDH (Fig. 3a). Similar results have been reported for other monomeric IDHs from mesophilic bacteria (Chen & Yang, 2000; Kanao et al., 2002). At 15°C, the $K_m$ values for isocitrate and NADP$^+$ of AvlIDH were almost the same as those of EcIDH, but the catalytic efficiency ($k_{cat}/K_m$) of the former was 20-fold higher than that of the latter (Table 1). Similarly, at 37°C, the $K_m$ for isocitrate and NADP$^+$ and $k_{cat}/K_m$ of the two IDHs has been reported to be 36 and 23 $\mu$M and 3.1 $\times$ 10$^{-4}$ M$^{-1}$ s$^{-1}$ for AvlIDH and 17 and 11 $\mu$M and 7.3 $\times$ 10$^{-4}$ M$^{-1}$ s$^{-1}$ for EcIDH, respectively (Barrera & Jurshuk, 1970; Chen & Yang, 2000). This implies that the monomeric IDHs cope with the loss of a catalytic site due to the monomerization through improving the catalytic rates. The amino acid residues involved in the binding to isocitrate and Mn$^{2+}$ (or Mg$^{2+}$) are conserved between AvlIDH and EcIDH (Fig. 1c, d). EcIDH is bound to NADP$^+$ by hydrogen bonds between the 2’-phosphate of NADP$^+$ and some of the amino acid residues and by electrostatic attractions to the charged isocitrate–Mg$^{2+}$ complex as the true substrate (Hurley et al., 1991; Stoddard et al., 1993). Moreover, AvlIDH can form an additional hydrogen bond between the nicotinamide ring of the bound NADP$^+$ and the side chain of Ser$^{87}$ (Fig. 1d) (Yasutake et al., 2003), implying that the resultant stabilized Michaelis ES complex leads to a rapid conversion to reaction products. The similar $K_m$ values for NADP$^+$ of AvlIDH and EcIDH (Table 1) suggest that the catalysis of AvlIDH is due to the random binding mechanism between ligand(s), as reported for EcIDH (Stoddard et al., 1993).

It is noteworthy that AvlIDH exhibited higher specific activity at low temperatures than mesophilic EcIDH and even than cold-adapted CmlIDH (Fig. 3a). Nevertheless, this enzyme does not possess the unique characteristics in amino acid sequence and structure which have been reported in cold-adapted and/or -active enzymes, such as lower numbers of several hydrophobic and/or charged amino acid residues than their mesophilic and thermophilic counterparts (Gerday et al., 1997; Russell et al., 1998; Bentahir et al., 2000), extension of the surface loop and optimization of the surface potentials (Kim et al., 1999; de Bacter et al., 2002), which are responsible for the weakened intermolecular interactions, and increased structural flexibility. In fact, AvlIDH shows typical mesophilic thermostability and the same resistance to trypsin as EcIDH (Figs 3 and 4). Similar results were reported for a mutant, 3-2G7, of the cold-adapted subtilisin S41 from Antarctic Bacillus TA41 which retains psychrophilic characteristics and acquires markedly increased thermostability (Miyazaki et al., 2000). The existence of such enzymes, including AvlIDH, indicates that the thermolability of the enzyme proteins is not always essential for high catalytic activity under cold conditions. Thus, further detailed studies of AvlIDH, of which the three-dimensional structure has been resolved, should provide valuable information for solving this problem. On the other hand, in vivo transcription of the CmlIDH gene is induced by low temperature, and the growth of the E. coli icd-defective mutant at low temperatures is improved by the transformation of a plasmid carrying the gene encoding CmlIDH (Suzuki et al., 1995; Sahara et al., 1999). Furthermore, isocitrate lyase of C. maris, which catalyses the cleavage of isocitrate to glyoxylate and succinate, is markedly thermolabile, and the expression of the gene encoding the enzyme is also cold-inducible (Watanabe et al., 2001, 2002). Such a cold-inducible expression of genes for cold-adapted metabolic enzymes seems to be one strategy for adaptation to cold environments. In C. maris, the lower catalytic activity of CmlIDH at low temperatures than that of AvlIDH might be
partially compensated by this cold-inducible transcriptional mechanism. These lines of study are in progress in our laboratory.

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REFERENCES


