Letter to the Editor: ¹H, ¹³C and ¹⁵N resonance assignments of human 5,10-methenyltetrahydrofolate synthetase

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Biological context

Folate-mediated one-carbon metabolism plays a crucial role in several major cellular processes. The thermodynamically stable 5-formyltetrahydrofolate (5-FTHF, leucovorin), which is not utilized as a one-carbon donor is transferred back to the folate pool by the 5,10-methenyltetrahydrofolate synthetase (MTHFS), the only enzyme that catalyzes its conversion to other reduced folates. The role of human MTHFS, a 202 amino acid protein of 23 kDa is potentially important in the treatment of certain cancers. 5-FTHF has been administered in chemotherapy to rescue normal cells from high dose levels of the antifolate methotrexate (Jolivet et al., 1983). 5-FTHF was also used to potentiate the antitumor activity of fluorouracil, a potent inhibitor of thymidylate synthase, the enzyme involved in deoxyuridylate methylation (Machover et al., 1982).

Endogenously, 5,10 methenyl-THF can be converted to 5-FTHF by a 'side' reaction catalyzed by serine hydroxymethyltransferase (SHMT). SHMT is involved in the generation of glycine and one-carbon units. The polyglutamated form of 5-FTHF is an inhibitor of SHMT and may regulate SHMT activity (Stover and Schirch, 1990). Through modulation of intracellular levels of 5-FTHF polyglutamates, which are potent inhibitors of many folate-dependent enzymes, MTHFS may regulate folic acid-dependent reactions of amino acid, purine and pyrimidine synthesis. This enzyme is a potential target for pharmaceutical applications in the manipulation of cell growth and development, which are significant in cancer prevention and treatment. We have undertaken structural studies of human MTHFS in solution using NMR spectroscopy in order to gain insight into the reaction mechanism, cofactor binding and role of Mg²⁺. Here we report the first assignment of ¹H, ¹³C and ¹⁵N chemical shifts for hMTHFS as a basis for the determination of its three-dimensional structure and characterization of dynamic processes within these protein-ligand complexes.

A truncated 197-residue construct of MTHFS, which retains full enzymatic activity, was used in this NMR study. Sequence alignment with homologous proteins showed that the mammalian protein contains a hydrophobic pentapeptide on the N-terminus. Solubility conditions were optimized for the deletion mutant, MTHFS₆₋₂₀₂, in which these five amino acids were removed.

Methods and experiments

Human MTHFS_{6–202} was cloned into the *Ndel/Bam*HI restriction sites of the pET 11c vector (Stratagene) and expressed in *E. coli* BL21 (DE3) cells carrying plasmid pLysS. Uniformly ¹⁵N- as well as ¹⁵N-, ¹³C-labeled protein was grown in ¹⁵N-NH₄Cl and ¹³C-glucose enriched M9 minimal media supplemented with thiamine and trace metals. The expressed protein was purified by affinity chromatography and eluted by substrate competition. Column preparation included coupling of substrate carboxyl groups to primary amines on Poros NH support. Samples for NMR measurements contained 1 mM to 1.5 mM MTHFS in 20 mM pipes buffer pH 6.5, 100 mM KCl, 15 mM 2-mercaptoethanol and 1.5 mM leucov-

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Figure 1. 1 H- 15 N HSQC spectrum of the 23 kDa human MTHFS collected at 30 °C, pH 6.5. For clarity, only a portion of residue-specific assignments of backbone amide groups is indicated. Side-chain amide cross peaks are connected by lines and other side-chain correlations are annotated (sc).

orin with the addition of ${}^{2}\text{H}_{2}\text{O}$ to 10% v/v. NMR experiments were carried out at 30 °C either on the Bruker DRX500, Bruker DRX800 or Varian UNITY plus 800 MHz spectrometers. NMR data were processed with GIFA (Pons et al., 1996) and NMRPipe software (Delagio et al., 1995) and analyzed using a combination of XEASY (Bartels et al., 1995) and NMRView (Johnson and Blevins, 1994). Backbone and side-chainresonances were assigned using 3D-HNCACB, CBCA(CO)NH, HN(CA)CO, HNCO, HNCA, HNHA, HCCH-COSY, NOESY-HSQC (mixing time 90 ms), and HCCH-TOCSY (mixing time 18 ms) experiments. DSS was used as a chemicalshift reference standard at 0 ppm to calibrate proton chemical shifts (in ppm). ¹⁵N and ¹³C shifts were referenced indirectly assuming the gyromagnetic ratios of $\gamma^{15}N/\gamma^{1}H = 0.101329118$ and $\gamma^{13}C/\gamma^{1}H =$ 0.251449530 (Wishart et al., 1995).

Extent of assignments and data deposition

Analysis from triple resonance experiments provided the resonance assignments for MTHFS. Degenerate resonances were confirmed by sequential NOE data. 99% completeness was obtained for amide ¹H and ¹⁵N backbone resonance assignments missing only for residues S2 and Y147. In total, 98% of ¹H^{α}, 95% of ¹H^{β}, 98% of ¹³C^{α} and ¹³C^{β}, and, 96% of ¹³CO resonances were assigned. Figure 1 shows the ¹H-¹⁵N HSQC spectrum of uniformly ¹⁵N labeled MTHFS (197 residues). Mostly complete assignment of side-chain ¹H resonances was obtained with over 85% assignment of nonlabile ¹H resonances. Main chain and side-chain ¹H, ¹³C and ¹⁵N resonances of hMTHFS have been deposited in the BioMagResBank (http://www.bmrb.wisc.edu) under accession number 5983.

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