

Genetic Aspects of Hyperhomocysteinemia in Chronic Kidney Disease

Gere Sunder-Plassmann, Wolfgang C. Winkelmayer, and Manuela Födinger

Patients with chronic kidney disease who are on dialysis or with a kidney transplant have higher total plasma homocysteine concentrations than individuals who are free from kidney disease. Several single-nucleotide polymorphisms of genes encoding enzymes that are involved in homocysteine metabolism have been studied in these patients. These polymorphisms are located in genes encoding of 5,10-methylenetetrahydrofolate reductase (MTHFR), methionine synthase reductase, methionine synthase, cystathionine β -synthase, glutamate carboxy peptidase II, reduced folate carrier 1, and transcobalamin II. Among the single-nucleotide polymorphisms studied, only MTHFR 677C>T was associated consistently with total plasma homocysteine levels, but there currently is no evidence of any association between MTHFR 677C>T genotype and long-term outcomes. Semin Nephrol 26:8-13 © 2006 Elsevier Inc. All rights reserved.

KEYWORDS chronic kidney disease, homocysteine, genetics, MTHFR, hyperhomocysteinemia

A mong the determinants and correlates of total plasma homocysteine (tHcy) levels, the genetics of enzymes involved in the metabolism of homocysteine has yielded a large and fast-growing body of scientific literature. As a result, several single-nucleotide polymorphisms (SNPs) were identified and their associations with tHcy concentrations were tested. Rare autosomal-recessive disorders such as severe deficiencies of cystathionine β synthase (CBS)¹ or 5,10-methylenetetrahydrofolate reductase (MTHFR)² often are associated with severe hyperhomocysteinemia (plasma tHcy concentrations > 100 μ mol/L) and urinary excretion of excess homocysteine (homocystinuria). Patients suffering from severe CBS or MTHFR deficiency frequently experience vascular complications early in life, providing the basis for the homocysteine theory of atherosclerosis.³

By contrast, several SNPs of proteins involved in vitamin flux or of Hcy-converting enzymes are prevalent⁴ and can be associated with mild hyperhomocysteinemia (tHcy plasma concentrations, 10-15 μ mol/L, the higher normal range) or moderately increased tHcy levels (tHcy plasma concentrations, 15-30 μ mol/L). The most interesting SNPs including MTHFR 677C>T,⁵ MTHFR 1298A>C,⁶ MTHFR 1793G>A,⁷ MTRR 66A>G,⁸ MTRR 997C>G,⁹ MTR 2756A>G,¹⁰CBS 844ins68,¹¹ GCP2 1561C>T,¹² RFC1 80G>A,¹³ and TCN2 776C>G¹⁴ are summarized in Table 1.

Genetic Polymorphisms of MTHFR and tHcy Plasma Concentrations in Chronic Kidney Disease Patients

MTHFR (EC 1.5.1.20) is a key enzyme of the folate cycle.¹⁵ It catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, thus generating the active form of folate that is required for remethylation of homocysteine to methionine.

In the *MTHFR* gene (OMIM 607093), several SNPs have been identified, such as at nucleotide position 677 (*MTHFR* 677C>T),⁵ position 1298 (*MTHFR* 1298A>C),^{6,16,17} position 1317 (*MTHFR* 1317T>C),⁶ and position 1793 (*MTHFR* 1793G>A).⁷ *MTHFR* 677C>T is located at the folate-binding site, changing an alanine into a valine residue (A222V). The most important milestones of this SNP are listed in Table 2. *MTHFR* 1298A>C is located in the presumptive regulatory domain, changing glutamic acid into an alanine residue (E429A), whereas *MTHFR* 1317T>C is a silent mutation. *MTHFR* 1793G>A results in an amino acid substitution

Division of Nephrology and Dialysis, Department of Medicine III, and the Institute of Medical and Chemical Laboratory Diagnostics, Medical University Vienna, Vienna, Austria; and the Division of Pharmacoepidemiology and Pharmacoeconomics and Renal Division, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, MA.

Address reprint requests to Gere Sunder-Plassmann, MD, Klinische Abteilung für Nephrologie und Dialyse Universitätsklinik für Innere Medizin III, Medizinische Universität Wien, Währinger Gürtel 18-20, A-1090 Wien, Austria. E-mail: gere.sunder-plassmann@meduniwien.ac.at

| Table I SNPs with Potential Relevance to Hey Metable |
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|---|

| | Gene Locus | Sequence Variation | Study |
|--|------------|--------------------|-----------------------------|
| 5,10-methylenetetrahydrofolate reductase | MTHFR | 677C>T | Frosst et al ⁵ |
| | | 1298A>C | Weisberg et al ⁶ |
| | | 1793 G>A | Rady et al ⁷ |
| Methionine synthase reductase | MTRR | 66A>G | Wilson et al ⁸ |
| - | | 997C>G | Wilson et al ⁹ |
| Methionine synthase | MTR | 2756A>G | Leclerc et al ¹⁰ |
| Cystathionine β -synthase | CBS | 844ins68 | Tsai et al ¹¹ |
| Glutamate carboxy peptidase II | GCP2 | 1561C>T | Devlin et al ¹² |
| Reduced folate carrier 1 | RFC1 | 80G>A | Chango et al ¹³ |
| Transcobalamin II | TCN2 | 776C>G | Namour et al ¹⁴ |

(R594Q). MTHFR 677C>T, MTHFR 1298A>C, and compound heterozygosity for 1289A>C and 677C>T are associated with a reduced enzyme activity of 45%, 68%, and 42%, respectively.¹⁸ The functional consequences of the 1793G>A mutation currently are unknown.

Bagley and Selhub¹⁹ showed that red blood cell folate is represented exclusively by 5-methyltetrahydrofolate in *MTHFR* 677CC individuals, whereas individuals with the 677TT genotype accumulated formylated folates, which pointed to a disruption of the folate cycle. Functional analysis of recombinant expressed human MTHFR showed that 677TT led to an enhanced propensity to dissociate into monomers and to losing its flavin adenine dinucleotide cofactor on dilution, resulting in a loss of activity.²⁰ In this context it was shown that riboflavin deficiency aggravated hyperhomocysteinemia in *MTHFR* 677TT individuals²¹ and in end-stage renal disease patients.²² The 677TT genotype also was associated with alterations of genomic DNA methylation, which is essential for the regulation of gene expression and genomic integrity. Hypomethylation of DNA was correlated positively with formylated folates, hyperhomocysteinemia, and correlated inversely with methylated folate derivatives.²³

The effect of MTHFR 677C>T on plasma tHcy plasma concentrations has been investigated in several studies of chronic kidney disease patients.²⁴ Hemodialysis,²⁵ peritoneal dialysis patients,²⁶ and kidney graft recipients²⁷ who were homozygous for the *MTHFR* 677T allele had higher tHcy plasma concentrations as compared with patients with wild-type alleles (Table 3). In the majority of studies, this effect even was sustained when patients received folic acid (\geq 10 mg/d).²⁸ By contrast, neither the *MTHFR* 1298A>C polymorphism alone nor compound heterozygosity for *MTHFR* 677T and *MTHFR* 1298C had a major effect on tHcy plasma

| Table 2 | Milestones | of MTHFR | 677C>T |
|---------|------------|----------|--------|
| | | - | |

| Year | Finding | Reference |
|-----------|--|--|
| 1991 | Thermolabile MTHFR Associated with Coronary Artery Disease and tHcy | Kang et al ⁵¹ |
| 1994 | cDNA cloning of MTHFR gene | Goyette et al ⁵² |
| 1995 | Description of 677C>T: association of TT genotype with reduced enzyme activity and elevated plasma tHcy | Frosst et al ⁵ |
| 1996 | Interaction of 677TT with poor folate status is responsible for increase of tHcy | Jacques et al ⁵³ |
| 1997 | Association of 677TT with better tHcy response to folic acid therapy | Malinow et al ⁵⁴ |
| 1997/1998 | Association of 677TT with low cellular 5-CH ₃ -tetrahydrofolate | Molloy et al ⁵⁵ ; Bagley and Selhub ¹⁹ |
| 1999 | Association of 677TT with enhanced vitamin B ₂ dissociation rate | Guenther et al ⁵⁶ |
| 2002 | Association of 677TT with impaired DNA methylation | Friso et al ²³ |
| 2002 | Meta-analysis of the association of 677TT with coronary artery disease risk | Klerk et al ³⁸ |
| 2003 | Meta-analysis of 677C>T / 1298A>C haplotypes | Ogino and Wilson ⁵⁷ |

| Table 3 Iviean they Plasma Concentrations (μ moi/L) According to IVII HFR 6/7C>1 Genotypes in Individuals From | m Austri |
|---|----------|
|---|----------|

| | МТІ | | | |
|------------------------------|------|------|------|------------------------------|
| Patient Population | СС | СТ | тт | Study |
| Hemodialysis | 25.4 | 28.7 | 36.4 | Födinger et al ²⁵ |
| Peritoneal dialysis | 22.2 | 23.1 | 61.7 | Vychytil et al ²⁶ |
| Kidney transplant recipients | 14.9 | 14.6 | 18.6 | Födinger et al ²⁷ |
| Healthy controls | 9.7 | 9.9 | 12.2 | Födinger et al ²⁵ |

| | Types of Cases | Ν | tHcy | Plasma Folate | Study |
|---------------|-----------------|------|------|---------------|---------------------------------|
| MTHFR 677C>T | HD | 69 | Yes | Yes | Födinger et al ²⁵ |
| MTHFR 677C>T | PD | 178 | Yes | Yes | Vychytil et al ²⁶ |
| MTHFR 677C>T | KTR | 636 | Yes | Yes | Födinger et al ²⁷ |
| MTHFR 677C>T | HD, PD | 415 | Yes | Νο | Födinger et al ²⁹ |
| MTHFR 1298A>C | KTR | 733 | No | Yes* | Födinger et al ³⁰ |
| MTHFR 1298A>C | HD, PD | 415 | No | Νο | Födinger et al ²⁹ |
| MTHFR 1793G>A | KTR | 730 | No | Yes | Winkelmayer et al ³² |
| MTR 2756A>G | KTR, HD, PD, CO | 1716 | No | No | Feix et al ⁴⁵ |
| MTRR 66A>G | KTR | 733 | No | No | Feix et al ⁴⁶ |

 Table 4
 Associations Between Common Genetic Polymorphisms of MTHFR, MTR, and MTRR on tHcy Concentrations in Chronic Kidney Disease Patients

Abbreviations: HD, hemodialysis patients; PD, peritoneal dialysis patients; KTR, kidney transplant recipients; CO, controls. *Compound heterozygosity for *MTHFR* 677C>T/1298 A>C.

concentration of hemodialysis and peritoneal dialysis patients,²⁹ or kidney graft recipients.³⁰ The *MTHFR* 1298A>C mutation was associated weakly with low folate concentrations as shown in *MTHFR* 677T/1298C compound heterozygous kidney graft recipients (Table 4).³⁰

In other studies,^{31,32} heterozygosity or homozygosity for *MTHFR* 1793G>A was not associated independently with plasma levels of tHcy or vitamin B_{12} in kidney graft recipients, but showed an association with higher folate concentrations. In these studies, Winkelmayer et al^{31,32} also found evidence for strong positive interactions between the *MTHFR* 1793G>A and 1298A>C mutations on vitamin B_{12} concentrations.

Pharmacogenetics of Homocysteine-Decreasing Therapies in Chronic Kidney Disease Patients

The response to homocysteine-decreasing therapy of renal failure patients appears to be influenced by genetic polymorphisms in *MTHFR*. Hemodialysis patients with the *MTHFR* 677TT genotype receiving high-dose folic acid orally attained normal total homocysteine levels more frequently than patients with the *CC* or *CT* genotype.³³ A better response to therapy also was observed in hemodialysis patients with the *MTHFR* 677TT/1298AA and the *MTHFR* 677CT/1298AC genotype who were treated intravenously with 15 mg of folic acid and an equimolar amount of folinic acid,³⁴ and among *MTHFR* 677TT genotype patients receiving 15 mg of folic

acid orally.³⁵ The more pronounced response to folate therapy of *MTHFR* 677TT patients possibly is caused by the correction of the intracellular deficiency of 5-methyltetrahydrofolate in TT genotype patients.¹⁹

MTHFR 677C>T and Outcomes of Chronic Kidney Disease Patients

In one cross-sectional study of dialysis patients, the MTHFR 677C>T mutation was associated with greater rates of cardiovascular disease.³⁶ When following-up these patients for 2 years, no association between this mutation and cardiovascular disease outcomes was detected.37 However, the observation of an independent role of MTHFR 677C>T in cardiovascular disease risk received support by a recent metaanalysis of 11,162 cases with coronary artery disease and 12,758 control individuals without renal failure. In that study, it was shown clearly that patients with the MTHFR 677TT genotype had a significantly higher risk for coronary heart disease, particularly in the presence of low folate levels.38 The idea of an independent association of MTHFR 677C>T with vascular disease risk was supported further by the observation of an association between the MTHFR 677T allele with increased intima-media thickness of the common carotid arteries³⁹ and an increased risk for vascular access thrombosis.40

Based on these observations, the *MTHFR* 677C>T mutation in individuals with and without renal failure may be an independent cardiovascular disease risk factor, which sup-

 Table 5
 Associations Between Common Genetic Polymorphisms of GCP2 and RFC1 on tHcy, Plasma Folate, and Red Blood Cell

 Folate Levels in Chronic Kidney Disease Patients

| | Types of Cases | Ν | tHcy | Folate | Red Blood Cell Folate | Study |
|--------------|----------------|-----|------|--------|-----------------------|---------------------------------|
| GCP2 1561C>T | HD, PD | 120 | No | No | Yes | Födinger et al ⁴⁷ |
| GCP2 1561C>T | KTR | 730 | No | Yes | ND | Winkelmayer et al ⁴⁸ |
| RFC1 80G>A | HD, PD | 120 | No | No | Νο | Födinger et al47 |
| RFC1 80G>A | KTR | 730 | No | No | ND | Winkelmayer et al ⁴⁸ |

Abbreviations: HD, hemodialysis patients; PD, peritoneal dialysis patients; KTR, kidney transplant recipients; ND, not done.

Table 6 Associations Between a Common Genetic Polymorphism in *TCN2* on tHcy, Vitamin B₁₂ and Holotranscobalamin II Levels in Chronic Kidney Disease Patients

| | Types of Cases | Ν | tHcy | Vitamin B ₁₂ | Holotranscobalamin II | Study |
|-------------|----------------|-----|------|-------------------------|-----------------------|---------------------------------|
| TCN2 776C>G | HD, PD | 120 | No | No | No | Födinger et al ⁴⁹ |
| TCN2 776C>G | KTR | 732 | No | No | ND | Winkelmayer et al ⁵⁰ |

Abbreviations: HD, hemodialysis patients; PD, peritoneal dialysis patients, KTR, kidney transplant recipients; ND, not done.

| Table 7 Associations Between GCP2 C>T on Plasma or Red Blood Cell Folate Concern | trations. |
|--|-----------|
|--|-----------|

| | Mean Red Blood Cell or Plasma Folate (nmol/L) | | | | | | | |
|----------------------------|---|-------------------|-----------------|-----------------|-------------------------------------|--|--|--|
| Types of Cases | Ν | CC | СТ | тт | Study | | | |
| Framingham offspring study | 1,913 | 12.7* (n = 1,713) | 13.5* (n = 190) | 13.5* (n = 190) | Vargas-Martinez et al ⁵⁸ | | | |
| HD, PD | 120 | 1,337† (n = 111) | 2,055† (n = 9) | 2,055† (n = 9) | Födinger et al ⁴⁷ | | | |
| KTR | 730 | 14.7* (n = 654) | 15.6* (n = 74) | 24.7* (n = 2) | Winkelmayer et al ⁴⁸ | | | |
| СО | 180 | 685† (n = 161) | 863† (n = 19) | — | Melse-Boonstra et al ⁵⁹ | | | |

Abbreviations: HD, hemodialysis patients; PD, peritoneal dialysis patients; KTR, kidney transplant recipients; CO, controls. *Plasma folate.

tRed blood cell folate.

ports the concept that impaired folate metabolism is related causally to increased coronary heart disease and vascular disease risk.

It has been speculated that hyperhomocysteinemia in kidney transplant patients might contribute to an increased risk for graft loss.⁴¹ In this context, *MTHFR* 677C>T and *MTHFR* 1298A>C mutations were studied for a putative relation with kidney transplant survival. The studies available thus far have shown that (1) neither *MTHFR* 677C>T⁴² nor *MTHFR* 1298A>C^{42,43} were important determinants of renal transplant survival, (2) the *MTHFR* genotype of the donor kidney did not influence tHcy plasma levels,²⁷ and (3) the *MTHFR* 677TT genotype might be associated with occurrence of acute rejection episodes within 90 days after kidney transplantation. In this small study the TT genotype had no effect on 1-year graft survival rate.⁴⁴

Other Common Genetic Polymorphisms and Hyperhomocysteinemia in Chronic Kidney Disease Patients

Several other SNPs in candidate genes encoding enzymes that are involved in the metabolism of folate and homocysteine (Tables 4-6) have been investigated in renal failure patients.²⁴ These include *MTR* 2756A>G of the gene encoding methionine synthase,⁴⁵ *MTRR* 66G>A and 997C>G of the gene coding for methionine synthase reductase,⁴⁶ *RFC1* 80G>A of the gene coding for the reduced folate carrier 1,^{47,48} *GCP2* 1561C>T encoding glutamate carboxypetidase II,^{47,48} and *TCN2* 776C>G coding for transcobalamin II.^{49,50} Among these SNPs only *GCP2* 1561C>T showed a significant influence on folate status, whereas none of these SNPs showed a major association with tHcy plasma concentrations (Table 7).

Summary

In summary, tHcy plasma concentrations in patients with chronic kidney disease are increased compared with patients without kidney disease, and several genetic factors were tested for association with tHcy levels in these patients. Polymorphisms have also been identified in genes potentially modifying the metabolism of folate or vitamin B_{12} , and thus affecting tHcy plasma concentrations. The most consistent effect on tHcy plasma concentrations, however, only was observed for 677C>T of *MTHFR*, whereas all other polymorphisms investigated to date showed no major effect on tHcy concentrations.

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