Increased Frequency of the MTHFR A1298C Mutation in an Irish Population

Cathal McCarthy  
*Technological University Dublin*

Fergus Ryan  
*Technological University Dublin*, fergus.x.ryan@tudublin.ie

Joseph Vaughan  
*Technological University Dublin*

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structural issues and can be resolved. The p53 resequencing microarray is currently undergoing a redesign (Roche Molecular Diagnostics, personal communication). Given the cost-effectiveness of chip technology, it is reasonable to expect a next-generation Chip in which most of these limitations have been addressed. Such improvements could lead to a more useful and productive tool in cancer research and diagnostics.

References

Antonette C.P. Allen* Francis A. Chiafari
BRT Laboratories, Inc. 400 West Franklin St. Baltimore, MD 21201

*Author for correspondence. Fax 410-383-0938; e-mail allen@brtlabs.com.

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To the Editor:
We would like to thank Drs. Allen and Chiafari for their comments. They reiterate many of the points we made in our report (1). We are glad that they also had similar findings. However, they suggest that we differ in the detection of polymorphisms. In the Discussion section of our report (1), we speculated that our cut-off score might be too high because we observed that a polymorphism in exon 6 had a score of 6. In their study, the GeneChip detected one of six exon 4 (codon 72) polymorphisms, whereas we were unable to detect any in 12 cases from which we obtained a PCR product. We would argue that this was not a significant difference because both sample sizes are small. In fact, it actually supports our conclusion that a combination of both microarray and sequencing is required to identify p53 alterations, as they would have missed five polymorphisms. We also look forward to being able to use the next-generation p53 microarray, as we stated in our report (1), because this methodology definitely has a role to play in sequencing of the p53 gene.

Reference

Rita Kandel1* Thomas Rohan2
1 University of Toronto Toronto, Canada
2 Albert Einstein College of Medicine Bronx, NY

* Address correspondence to this author at: Pathology and Laboratory Medicine, Mt. Sinai Hospital, 600 University Ave, Toronto, ON M5G1X5 Canada. Fax 416-586-8628; e-mail rkandel@mtsinai.on.ca.

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To the Editor:
The enzyme methylenetetrahydrofolate reductase (MTHFR) catalyzes the reduction of methylene tetrahydrofolate to 5-methyltetrahydrofolate, the cosubstrate required for the remethylation of homocysteine to methionine. Mutations in the MTHFR enzyme are reported as causes of hyperhomocysteinemia (1). Hyperhomocysteinemia is generally, although not universally, seen as an independent and graded risk factor for venous thrombosis and neural tube defects (2). Several polymorphisms have been reported in the MTHFR gene, but two particular mutations generate the most interest, the recently described A1298C (3) and the most-characterized C677T (4). The A1298C polymorphism in the MTHFR gene encodes for a glutamate to alanine substitution and leads to a decrease in enzyme activity. Combined heterozygosity for the C677T/A1298C polymorphisms in some studies (5) is associated with higher homocysteine concentrations and decreased plasma folate.

Amplification Refractory Mutation System (ARMS) PCR determination of the MTHFR C677T mutation has been described by Hessner et al. (6). To determine the frequency of the A1298C mutation in the Irish population, we developed a reliable and rapid ARMS PCR method. We compared the results with those obtained with the standard method for detection, PCR followed by restriction fragment length polymorphism (RFLP) analysis (3).

Our cohort consisted of 120 blood donors, none of whom had experienced any past or current thrombotic events or had a family history of thrombosis. Informed consent was obtained from all study participants. Total genomic DNA was isolated from blood leukocytes, and MTHFR A1298C was analyzed by PCR-RFLP (3).

ARMS PCR was also used to determine the frequency of this mutation. A typical ARMS PCR set-up for the wild-type reaction consisted of 200 ng of genomic DNA, 2.5 mM MgCl2, 0.4 mM each deoxynucleotide triphosphate (Invitrogen, BioSciences), 2.5 µL of 10× buffer [200 mM Tris-HCl (pH 8.4), 500 mM KCl; Invitrogen], 1.5 U of Platinum Taq polymerase (Invitrogen), and 50 mL/L dimethyl sulfoxide (Sigma-Aldrich). ARMS PCR primers used in the wild-type reaction were as follows: A1298C forward consensus primer (5'-CTTTTGCGGAGCAGTGACACTAC-3'); A1298C wild-type reverse primer (5'-CAAAGACTCCAGAAGAGTC-3'); cystic fibrosis 22 (CF22) forward primer (5'-AAACGCTGAGCCTACAAAGA-3'); and CF22 reverse primer (5'-TGTCACCATGACAGGCAT-3'; Sigma-Aldrich). The mutant reaction
had the same components as above, with the replacement of A1298C wild-type reverse primer with A1298C mutant reverse primer, which had the following sequence:

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5\'\text{-GTTAAGAACCACACTCTACAAGACACTGTG-3}\']

which had the following sequence: wild-type reverse primer with the replacement of A1298C.

ARMS PCR conditions were 95 °C for 5 min; 40 cycles of 95 °C for 30 s, 57 °C for 30 s, and 72 °C for 30 s; and 72 °C for 5 min. The wild-type reaction produces a 127-bp fragment (Fig. 1). The CF22 primers were used as internal control primers and produce a 578-bp fragment in each reaction. The Chaim Sheba Medical Center, Institute of Thrombosis and Hemostasis, (Department of Hematology, Institute of Thorombosis and Hemostasis, The Chaim Sheba Medical Center, Tel-Hashomer, Israel) for the 1298C positive controls.

We thank Dr. A Davern, Dublin Blood Transfusion Centre, for the blood samples. We would like to also thank Drs. Valeria Capra (Laboratorio del Servizio di Neurochirurgia, Instituto Scientifico G. Gaslini, Genova, Italy) and Nurit Rosenberg (Department of Hematology, Institute of Thorombosis and Hemostasis, The Chaim Sheba Medical Center, Tel-Hashomer, Israel) for the 1298C positive controls.

**References**

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**Interference in Measurement of Potassium Caused by Bacterial Contamination of an Analyzer**

To the Editor: We encountered a problem with potassium measurement after periods of standby on a Beckman Synchron LX20 Pro. Initial potassium measurements were rejected because of excessive reference drift, and potassium results for quality-control (QC) samples were as much as 2.5 mmol/L above the previous mean. Replicate analyses of control material immediately after standby revealed a decreasing trend in potassium concentration, whereas simultaneously