University of Colorado Denver

Mail Stop 8313
12800 East 19th Avenue, Room 4404K
Aurora, CO 80045

Department of Pediatrics
DNA Diagnostic Laboratory

Office: 303-724-3801
Fax: 303-724-3802
www.uchsc.edu/dnalab

DNA ANALYSIS REPORT

DATE: 12/08/2010 DATE RECEIVED: 11/16/2010

REPORT TO: David Johnson, MD; Colorado Retina Associates

PATIENT Paul Martz	DATE OF BIRTH 1/7/1963	SPECIMEN TYPE Blood
DIAGNOSTIC REQUEST ADRP panel	CASE # / ACCESSION # ADRP-090 / #10-3134	HOSPITAL# / SPECIMEN # 59229

INDICATION FOR STUDY: Autosomal Dominant Retinitis Pigmentosa

RESULT: likely positive

INTERPRETATION: Paul Martz possesses a novel variation in the *RP1* gene, namely p.D2066N:c.6196G>A. The variation was predicted to be probably damaging by PolyPhen-2 with a score of 0.995 (the highest score for a damaging variation is 1.0). An additional novel variation was also identified in the *PRPF31* gene, namely p.N413N:c.1239C>T. The variation is likely benign. Finally, a reported variation with an allele frequency of 0.129 was also identified in the *RDH12* gene, namely p.R161Q:c.482G>A. The variation was predicted to be probably damaging with a score of 0.941. The variation was identified in three other RP patients with different mutations. Therefore, this variation may be a modifier of the condition. All of the variations identified in the patient are listed in Table 1 (see page 2). The clinical significance of these identified variations was predicted based on our current knowledge. Whether or not some of these identified variations can modify disease presentation is not clear at this time.

(sequence variations are reported according to nomenclature by *den Dunnen and Antonarakis (Hum Genet 109(1):121-124, 2001)*

TECHNIQUES: Direct testing for mutations in the 21 known adRP genes including *ASCC3L1*, *BEST1*, *CA4*, *CRX*, *FSCN2*, *GUCA1B*, *IMPDH1*, *KLHL7*, *NRL*, *NR2E3*, *PRPF3*, *PRPF8*, *PRPF31*, *RDH12*, *RDS*, *RHO*, *ROM1*, *RP1*, *RP9*, *RP31* and *SEMA4A* is performed by PCR amplification and DNA sequencing in two directions of all coding exons and the exon/intron borders. Codon 1 corresponds to the start ATG and nucleotide 1 to the A.

LIMITATIONS: Only the coding regions of the gene and immediately flanking intron sequences were examined. Changes in the promoter region, farther into the introns, or in other non-coding regions of the gene would not be detected. The sensitivity of DNA sequencing is 99% for the detection of nucleotide base changes, small deletions and insertions in the regions analyzed. Multiple exon deletions, multiple exon insertions, complete deletion of one allele may not be identified using these methods.

If you have any questions concerning the information in this report, please feel free to contact Dr. Pei-Wen Chiang (pei-wen.chiang@ucdenver.edu; 303-724-3805).