Polymorphisms in the Delta-Aminolevulinic Acid Dehydratase (δ-ALAD) and Vitamin D Receptor (VDR) Genes in Lead-Exposed Children

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**Supplementary Material**

The δ-ALAD and VDR Genes primers along with nucleotide sequence, fragment sizes and their allelic variants upon RFLP

**ALAD**

Primers: CAGAGCATGGACAGGGAGCAA / TAGGCAGCGGTGGAGGCATCTCT

[product length = 917]

AGACAGACATTAGCTCAGTAGAGGAAAGGGTTTCCCCGGGGCCAGAGCTGTTCCACAGTGGAAGGGGCAGCCCCATAAAGTAAAGAGCTACCCATCACCCGAGACGTCGTGGCAGAGGCTGTTGCAGAAGGGAGCTGAACTGCAGATGGGAGTTCAAAAAGAGGGCCTCGAAGGAGCCTTCCACAGCCGAATTC↓CGGAGCTCTGCTACTCAGGGCCTCAGTCTTCCCTCCTATTTAGTGGATGCATCCCTGCCCCTTCTGTCCTGGGGGCTTGAGCCCTCCTGGTGCCATATGCAGCTTGGTTTCTAACAGAGGCACACAGTGTGGTGGGGTC↓CGGAGGACCGTTGCCTGGGACCTGCCTTCCTTCAACCCCTCTACCCACACCCACACAGGTATGGTGTGAAG↓CGGCTGGAAGAGATGCTGAGGCCCTTGGTGGAAGAGGGCCTACGCTGTGTCTTGATCTTTGGCGTCCCCAGCAGAGTTCCCAAGGTGAAGAATCAAAGGAAGGGCTAAGAAGGGAGGTTGCGCTCACGCCCGTAATCCCAGCACTTTGGGAGGCCAAAGTGGGTGGATCACTTGAGCCCAGGATTTTGAGACCAGCCTGGACAACATGGCAAAACCCATCTCTACAAAAAATACAAAAGTTAGCTGGGTGTGGGGGTATGTGCCTGTAGTCCCAGCTACTCGGGAGGTGGAGAGGTGGGAGGATTGCTTGAGCCCAGAAAGTCGAGGCTGCAGTGAGCCAAAATCGCGCCAGTGCACTCTAGCCTGGGTGACAGAGCAAGACCCTGTCTCCAATACAAACAGAAAAAGGAAGGGAGGTTGGGCAAAGGTGGACTGAGGGTCCACACTGACTGCACCCTCACTCCCACATTGTGCTGGCCCTGGGGCCACAGGTGAATGGACGTGGTCTTTGCC

MspI: (rs1800435): G to C polymorphism exists (AAG to AAC)

Msp-I-cutsite_1

|  |  |  |  |
| --- | --- | --- | --- |
| Wild type | ALAD 1-1 (GG) | 3 fragments | 584 +158 + 139 bp |
| Heterozygous | ALAD 1-2 (GC) | 4 fragments | 584 + 513 + 158 + 139 bp |
| Homozygous mutant | ALAD 2-2 (CC) | 3 fragments | 513 + 158 + 139 bp |

**VDR – FokI**

Primers: AGCTGGCCCTGGCACTGACTCTGGCT / ATGGAAACACCTTGCTTCTTCTCCCTC [product length = 267]

AGCTGGCCCTGGCACTGACTCTGGCTCTGACCGTGGCCTGCTTGCTGTTCTTACAGGGATGGAGGCAATG↓GCGGCCAGCACTTCCCTGCCTGACCCTGGAGACTTTGACCGGAACGTGCCCCGGATCTGTGGGGTGTGTGGAGACCGAGCCACTGGCTTTCACTTCAATGCTATGACCTGTGAAGGCTGCAAAGGCTTCTTCAGGTGAGCCCTCCTCCCAGGCTCTCCCCAGTGGAAAGGGAGGGAGAAGAAGCAAGGTGTTTCCAT

FokI: (rs2228570): T to C polymorphism exists (ATG to ACG)

Fok-I-cutsite_1

|  |  |  |  |
| --- | --- | --- | --- |
| Wild type | TT | 2 fragments | 197 + 70 bp |
| Heterozygous | TC | 3 fragments | 267 + 197 + 70 bp |
| Homozygous mutant | CC | 1 fragment | 267 bp |

**VDR - BsmI**

Primers: GACCTGTGGCAACCAAGACT / AACCAGCGGAAGAGGTCAAG

[product length = 831]

GACCTGTGGCAACCAAGACTACAAGTACCGCGTCAGTGACGTGACCAAAGGTATGCCTAGACTCCACCTCCTGGGGAGTCTTTTTCAGCTCCCAGATTCTGGCTCCACCCGTCCTGGGGTTTGGCTCCAATCAGATACATGGGAGGGAGTTAGGCACCAACAGGGAGAGAAGGGCGAGGGTCAGACCCATGGGGTTGGAGGTGGGTGGGCGGCTCCTCAGCTCTGCCCGCAGTACCTGGCCATTGTCTCTCACAGCCGGACACAGCCTGGAGCTGATTGAGCCCCTCATCAAGTTCCAGGTGGGACTGAAGAAGCTGAACTTGCATGAGGAGGAGCATGTCCTGCTCATGGCCATCTGCATCGTCTCCCCAGGTATGGGGCCAGGCAGGGAGGAGCTCAGGGACCTGGGGAGCGGGGAGTATGAAGGACAAAGACCTGCTGAGGGCCAGCTGGGCAACCTGAAGGGAGACGTAGCAAAAGGAGACACAGATAAGGAAATACCTACTTTGCTGGTTTGCAGAGCCCCTGTGGTGTGTGGACGCTGAGGTGCCCCTCACTGCCCTTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTCGTAGGGGGGATTCTGAGGAACTAGATAAGCAGGGTTCCTGGGGCCACAGACAGGCCTGCG↓CATTCCCAATACTCAGGCTCTGCTCTTGCGTGAACTGGGCTCAACATTCCTGTTATTTGAGGTTTCTTGCGGGCAGGGTACAAAACTTTGGAGCCTGAGAGATGGTTCTGCCTATATAGTTTACCTGATTGATTTTGGAGGCAATGTGCAGTGACCCTTGACCTCTTCCGCTGGTT

BsmI: (rs1544410) [G>A polymorphism]

|  |  |  |  |
| --- | --- | --- | --- |
| Wild type | GG | 2 fragments | 655 + 176 bp |
| Heterozygous | GA | 3 fragments | 831 + 655 + 176 bp |
| Homozygous mutant | AA | 1 fragment | 831 bp |

Bsm-I-cutsite_1

**VDR - ApaI**

Primers: CAGAGCATGGACAGGGAGCAA / TAGGCAGCGGTGGAGGCATCTCT

[product length = 832]

CAGAGCATGGACAGGGAGCAAGGCCAGGCAGGGACAGGGCCAGGTGCGCCCATGGAAGGACCTAGGTCTGGATCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGTCATAGAGGGGTGGCCTAGGGGGTGCTGCCGTTGAGTGTCTGTGTGGGTGGGGGGTGGTGGGATTGAGCAGTGAGGGGCC↓CAGCTGAGAGCTCCTGTGCCTTCTTCTCTATCCCCGTGCCCACAGATCGTCCTGGGGTGCAGGACGCCGCGCTGATTGAGGCCATCCAGGACCGCCTGTCCAACACACTGCAGACGTACATCCGCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTATGCCAAGATGATCCAGAAGCTAGCCGACCTGCGCAGCCTCAATGAGGAGCACTCCAAGCAGTACCGCTGCCTCTCCTTCCAGCCTGAGTGCAGCATGAAGCTAACGCCCCTTGTGCTCGAAGTGTTTGGCAATGAGATCTCCTGACTAGGACAGCCTGTGGCGGTGCCTGGGTGGGGCTGCTCCTCCAGGGCCACGTGCCAGGCCCGGGGCTGGCGGCTACTCAGCAGCCCTCCTCACCCCGTCTGGGGTTCAGCCCCTCCTCTGCCACCTCCCCTATCCACCCAGCCCATTCTCTCTCCTGTCCAACCTAACCCCTTTCCTGCGGGCTTTTCCCCGGTCCCTTGAGACCTCAGCCATGAGGAGTTGCTGTTTGTTTGACAAAGAAACCCAAGTGGGGGCAGAGGGCAGAGGCTGGAGGCAGGGCCTTGCCCAGAGATGCCTCCACCGCTGCCTA

**ApaI**: (rs7975232) [G>T polymorphism]

Apa-I-cutsite_1

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| --- | --- | --- | --- |
| Wild type | GG | 2 fragments | 615 + 217 bp |
| Heterozygous | GT | 3 fragments | 832 + 615 + 217 bp |
| Homozygous mutant | TT | 1 fragment | 832 bp |

**VDR - TaqI**

Primers: CAGAGCATGGACAGGGAGCAA / TAGGCAGCGGTGGAGGCATCTCT

[product length = 832]

CAGAGCATGGACAGGGAGCAAGGCCAGGCAGGGACAGGGCCAGGTGCGCCCATGGAAGGACCTAGGTCTGGATCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGTCATAGAGGGGTGGCCTAGGGGGTGCTGCCGTTGAGTGTCTGTGTGGGTGGGGGGTGGTGGGATTGAGCAGTGAGGGGCCCAGCTGAGAGCTCCTGTGCCTTCTTCTCTATCCCCGTGCCCACAGATCGTCCTGGGGTGCAGGACGCCGCGCTGATTGAGGCCATCCAGGACCGCCTGTCCAACACACTGCAGACGTACATCCGCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTATGCCAAGATGATCCAGAAGCTAGCCGACCTGCGCAGCCTCAATGAGGAGCACTCCAAGCAGTACCGCTGCCTCTCCTTCCAGCCTGAGTGCAGCATGAAGCTAACGCCCCTTGTGCT↓CGAAGTGTTTGGCAATGAGATCTCCTGACTAGGACAGCCTGTGGCGGTGCCTGGGTGGGGCTGCTCCTCCAGGGCCACGTGCCAGGCCCGGGGCTGGCGGCTACTCAGCAGCCCTCCTCACCCCGTCTGGGGTTCAGCCCCTCCTCTGCCACCTCCCCTATCCACCCAGCCCATTCTCTCTCCTGTCCAACCTAACCCCTTTCCTGCGGGCTTTTCCCCGGTCCCTTGAGACCTCAGCCATGAGGAGTTGCTGTTTGTTTGACAAAGAAACCCAAGTGGGGGCAGAGGGCAGAGGCTGGAGGCAGGGCCTTGCCCAGAGATGCCTCCACCGCTGCCTA

**TaqI**: (rs731236): T to C polymorphism exists (ATT to ATC)

Taq-I-cutsite_1

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| --- | --- | --- | --- |
| Wild type | TT | 2 fragments | 494 + 338 bp |
| Heterozygous | TC | 4 fragments | 494 + 338 + 293 + 201 bp |
| Homozygous mutant | CC | 3 fragment | 338 + 293 + 201 bp |