



# THE PRIMARY CARE COMPANION FOR CNS DISORDERS

## Supplementary Material

**Article Title:** Genetic and Clinical Factors Affecting Plasma Clozapine Concentration

**Author(s):** Eric Olsson, MD; Gunnar Edman, PhD; Leif Bertilsson, PhD; Dzana Sudic Hukic; Catharina Lavebratt, PhD; Sven V. Eriksson, MD, PhD; and Urban Ösby, MD, PhD

**DOI Number:** 10.4088/PCC.14m01704

### List of Supplementary Material for the article

1. [Table 1](#) Primer Sequences for Amplification of Polymerase Chain Reaction Fragments That Contained the Polymorphism, Polymerase Chain Reaction Fragment Size, and Restriction Endonucleases Used in Polymerase Chain Reaction-Restriction Fragment Length Polymorphism\*
2. [Table 2](#) Assay Identification and Sequences of Interest For Genotype Determination\*
3. [Table 3](#) Polymerase Chain Reaction Primers, Sequencing Primers, and Dispensing Order Used For MDR1 -2677G>T Genotype Determination\*
4. [Table 4](#) Genotype Frequencies With Corresponding Concentration-To-Dose Ratios of Clozapine\*

### Disclaimer

This Supplementary Material has been provided by the author(s) as an enhancement to the published article. It has been approved by peer review; however, it has undergone neither editing nor formatting by in-house editorial staff. The material is presented in the manner supplied by the author.

**Supplementary Table 1.** Primer Sequences for Amplification of Polymerase Chain Reaction Fragments That Contained the Polymorphism, Polymerase Chain Reaction Fragment Size, and Restriction Endonucleases Used in Polymerase Chain Reaction-Restriction Fragment Length Polymorphism\*

<b>Gene and Single Nucleotide Polymorphism</b>	<b>Primer (5'-3')</b>	<b>Fragment Length (bp)</b>	<b>Restriction Enzyme</b>	<b>Reference</b>
UGT1A4 -142T>G rs2011425	fo-GTTGGGCCCAT AACGAAAGGCAGTT re-GCTCCACACACAACACCTATGAAG	576	FastDigest StuI (Eco1471)	[18]

\*DNA fragments spanning the single nucleotide polymorphism were amplified in individual reactions by polymerase chain reaction (10 ng DNA/reaction) containing the forward and reverse primers. The temperature program was 95°C for 5 min, followed by 50 cycles of 95°C for 30 s, 55.5°C for 1 min, and 72°C for 1 min. The amplified 576-bp fragment was digested (FastDigest StuI, Eco1471, Fischer Scientific, Stockholm, Sweden) for 10 min at 37°C and analyzed on 1% agarose gels. The wild type allele, and not the mutant allele, was cut into 324- and 252-bp fragments.

**Supplementary Table 2.** Assay Identification and Sequences of Interest For Genotype Determination\*

<b>Gene and Single Nucleotide Polymorphism</b>	<b>Assay Identification</b>	<b>Sequence of Interest</b>
CYP1A2 -729C>T rs12720461	C__30634146_10	GGCTAGGTGTAGGGGTCCTGAGTTC[C/T]GGGCTTTGCTACCCAGCTCTTGACT
CYP1A2 -163C>A rs762551	C__8881221_40	TGCTCAAAGGGTGAGCTCTGTGGGC[C/A]CAGGACGCATGGTAGATGGAGCTTA
CYP1A2 -2467delT rs35694136	C__60142977_10	TGCAGTGAGCCATGATTGTGGCACA[T/-]GAACCCCAACCTGGGTGACAGAGCA
MDR1 -3435C>T rs4005995	C__7586657_20	TGTTGGCCTCCTTTGCTGCCCTCAC[A/G]ATCTCTTCCTGTGACACCACCCGGC

\*Primers and probes were obtained commercially (Life Technologies, Stockholm, Sweden). DNA fragments spanning the single nucleotide polymorphisms were amplified in individual reactions by polymerase chain reaction (10 ng DNA/reaction) containing forward primer, reverse primer, and probes for the single nucleotide polymorphisms. Polymerase chain reaction was performed in 96- or 384-well formats with 2 negative controls distributed per assay. The temperature program was 95°C for 10 min followed by 50 cycles of 92°C for 15 s and 60°C for 90 s.

**Supplementary Table 3.** Polymerase Chain Reaction Primers, Sequencing Primers, and Dispensing Order Used For MDR1 -2677G>T

Genotype Determination\*

<b>Gene and Single Nucleotide Polymorphism</b>	<b>Primer (5'-3')</b>	<b>Dispensing Order</b>
MDR1 -142T>G	foB-CTGGACAAGCACTGAAAGATAAGA	GCAGCTAGCT
rs2032582	re-TGGCTTTGCTACTTTCTGTAAGTT seq-TTAGTTTGACTCACCTTCC	

\*Forward, reverse, and sequencing primers were obtained commercially (Fischer Scientific, Stockholm, Sweden). DNA fragments spanning the single nucleotide polymorphism were amplified in individual reactions by polymerase chain reaction (10 ng DNA/reaction) containing the forward and reverse primers for the single nucleotide polymorphism. The temperature program was 95°C for 10 min followed by 50 cycles of 92°C for 15 s and 58.5°C for 90 s. The amplified DNA fragments spanning the single nucleotide polymorphism were analyzed with a sequencer (PSQ96, QIAGEN Nordic, Solna, Sweden).

**Supplementary Table 4.** Genotype Frequencies With Corresponding Concentration-To-Dose Ratios of Clozapine\*

<b>Gene and Single Nucleotide Polymorphism</b>	<b>Genotype</b>	<b>No. of Patients (%)</b>	<b>Concentration-To-Dose Ratios</b>
<i>CYP1A2</i>			
rs35694136	TT	86 (91)	5 ± 4
CYP1A2*1D -2467delT	T/del	7 (7)	5 ± 3
	del/del	2 (2)	2.7 ± 0.5
rs12720461	CC	95 (100)	5 ± 4
CYP1A2*K -729C>T	CT	0 (0)	
	TT	0 (0)	
rs762551	CC	9 (9)	4 ± 2
CYP1A2*F -163C>A	CA	35 (37)	6 ± 4
	AA	51 (54)	4 ± 2
<i>MDR1</i>			
rs1045642	TT	32 (34)	5 ± 3
-3435C>T	CT	49 (52)	5 ± 4
	CC	14 (15)	5 ± 4
rs2032582	TT	13 (14)	5 ± 3
-2677G>T	GT	51 (54)	6 ± 4
	GG	26 (27)	4 ± 2
	TA	2 (2)	4 ± 2
	GA	3 (3)	8 ± 8
	AA	0 (0)	
<i>UGT1A4</i>			
rs2011425	TT	84 (88)	5 ± 4
L48V -142T>G	TG	10 (11)	5 ± 3
	GG	1 (1)	4.1

\*Data reported as mean ± SD.