

**Table E3: Analysis of gene-environment interactions (PD cases only versus controls) after adjustment\*.**

Genetic polymorphisms	Candidate genotype	Exposure <sup>†</sup> Low vs High	Multiplicative interaction Odds Ratio (95% CI)	p value
<i>CYP2D6</i>	*4*4	Solvents	1.95 (0.43-8.88)	0.39
<i>CYP1B1</i>	*3*3	Solvents	1.29 (0.53-3.15)	0.57
<i>GSTM1</i>	Null	Solvents	2.34 (1.08-4.62)	0.03
<i>GSTT1</i>	Null	Solvents	0.81 (0.32-2.00)	0.63
<i>GSTM3</i>	AB/BB	Solvents	0.95 (0.43-2.07)	0.88
<i>GSTP1</i> haplotype	AB, AC, AD, BB, BC, CC	Solvents	1.32 (0.65-2.66)	0.44
<i>NQO1</i>	*1*2/*2*2	Solvents	0.68 (0.32-1.44)	0.31
<i>SOD2 A<sub>16</sub>V</i>	AV	Solvents	1.44 (0.56-3.73)	0.44**
	VV	Solvents	1.94 (0.70-5.34)	
<i>NAT2</i>	FS/SS	Solvents	1.14 (0.56-2.29)	0.72
<i>CYP2D6</i>	*4*4	Pesticides	1.33 (0.31-5.80)	0.70
<i>PON1 L55M</i>	LL/LM	Pesticides	0.55 (0.24-1.30)	0.18
<i>PON1 Q192R</i>	QR/RR	Pesticides	1.49 (0.64-3.45)	0.36
<i>GSTM1</i>	Null	Pesticides	0.71 (0.31-1.65)	0.43
<i>GSTT1</i>	Null	Pesticides	1.81 (0.58-5.63)	0.31
<i>GSTM3</i>	AB/BB	Pesticides	1.08 (0.43-2.71)	0.87
<i>GSTP1</i> haplotype	AC/AD/BC/CC	Pesticides	3.01 (0.75-12.02)	0.12
<i>NQO1</i>	*1*2/*2*2	Pesticides	1.09 (0.47-2.54)	0.84
<i>CYP1B1</i>	*3*3	Pesticides	0.69 (0.21-2.32)	0.55
<i>NAT2</i>	FS/SS	Pesticides	0.67 (0.29-1.56)	0.35
<i>GSTM1</i>	Null	Iron	1.13 (0.54-2.33)	0.75
<i>CYP1B1</i>	*3*3	Iron	1.64 (0.63-4.27)	0.31
<i>SOD2 A<sub>16</sub>V</i>	AV	Iron	0.69 (0.28-1.70)	0.71**
	VV	Iron	0.72 (0.27-1.94)	
<i>NAT2</i>	FS/SS	Iron	0.77 (0.37-1.63)	0.51
<i>SOD2 A<sub>16</sub>V</i>	AV	Copper	0.89 (0.31-2.58)	0.46**
	VV	Copper	1.65 (0.51-5.34)	
<i>CYP2D6</i>	*4*4	Manganese	1.63 (0.35-7.62)	0.54
<i>NQO1</i>	*1*2/*2*2	Manganese	1.06 (0.49-2.33)	0.88
<i>CYP1B1</i>	*3*3	Manganese	1.93 (0.71-5.21)	0.20
<i>SOD2</i>	AV	Manganese	0.73 (0.27-1.93)	0.67**
	VV	Manganese	1.07 (0.38-3.01)	

\* logistic regression adjusting for age, sex, country, ever used tobacco containing product, ever knocked unconscious and first degree family history of Parkinson's disease. MAO-A and MAO-B are not adjusted for sex but are presented for males and females separately.

\*\* For three category factors p-value for trend derived from logistic regression coding genetic factors as 0, 1 and 2 variable

† cut-offs for low /high exposure:

solvents/iron/manganese: 20% of an OEL (AAI)  
pesticides/copper: 2% of an OEL (AAI)

**Table E3: Analysis of gene-gene interactions (PD cases only versus controls) after adjustment\*.**

Gene-gene interactions		Multiplicative interaction Odds Ratio (95% CI)	p value
<i>CYP2D6</i>	<i>GSTM1</i>	0.86 (0.36-2.09)	0.86
<i>PON55</i>	<i>GSTM1</i>	1.18 (0.82-1.68)	0.38
<i>PON192</i>	<i>GSTM1</i>	0.88 (0.62-1.26)	0.50
<i>GSTT1</i>	<i>GSTM1</i>	1.35 (0.84-2.16)	0.22
<i>GSTM3</i>	<i>GSTM1</i>	0.73 (0.49-1.10)	0.13
<i>GSTP1</i> haplotype AB/AC/AD vs. AA BB/BC/CC vs. AA	<i>GSTM1</i> Null vs. Pos Null vs. Pos	0.73 (0.50-1.07) 1.02 (0.55-1.87)	0.23**
<i>NQO1</i>	<i>GSTM1</i>	0.95 (0.66-1.37)	0.78
<i>NAT2</i>	<i>GSTM1</i>	1.02 (0.72-1.46)	0.90
<i>CYP2D6</i>	<i>GSTT1</i>	1.62 (0.47-5.58)	0.44
<i>GSTP1</i> haplotype AB/AC/AD vs. AA BB/BC/CC vs. AA	<i>GSTT1</i> Null vs. Pos Null vs. Pos	0.99 (0.59-1.63) 1.72 (0.77-3.83)	0.38**
<i>MAO-B</i> (males only)	<i>NQO1</i>	0.95 (0.58-1.57)	0.85
<i>MAO-B</i> (females only) AG vs. AA GG vs. AA	<i>NQO1</i>	0.97 (0.52-1.84) 0.85 (0.39-1.84)	0.91**
<i>MAO-B</i> (males only)	<i>DRD2A</i> <sup>2</sup>	1.57 (0.55-4.51)	0.40
<i>MAO-B</i> (females only) AG vs. AA GG vs. AA	<i>DRD2A</i> <sup>2</sup>	0.62 (0.18-1.97) 0.67 (0.16-2.81)	0.71**
<i>MAO-B</i> (males only)	<i>DRD2B</i> <sup>1</sup>	0.59 (0.33-1.09)	0.09
<i>MAO-B</i> (females only) AG vs. AA GG vs. AA	<i>DRD2B</i> <sup>1</sup>	0.97 (0.46-2.02) 0.64 (0.25-1.61)	0.58**

\* logistic regression adjusting for age, sex, country, ever used tobacco containing product, ever knocked unconscious and first degree family history of Parkinson's disease. MAO-A and MAO-B are not adjusted for sex but are presented for males and females separately.

\*\* For three category factors p-value for trend derived from logistic regression coding genetic factors as 0, 1 and 2 variable

<sup>1</sup> Excludes Malta

<sup>2</sup> Excludes Sweden and Malta.