CHAPTER IV

RESULTS

Allele frequencies of three common SNPs of *MDR1* (C1236T, G2677T/A and C3435T) accordance with Hardy-Weinberg equilibrium were determined among 204 healthy women and the result is shown in Table 2. The allele frequencies of C and T at position 1236 (C1236T) were 35.05% and 64.95%, respectively. At locus 2677 (G2677T/A), the frequencies of G, T and A alleles were 52.94%, 41.42% and 5.64%, respectively. At locus 3435 (C3435T), frequencies of C and T alleles were 50.74% and 49.26%, respectively. Our results showed that the allele frequencies of three common SNPs of *MDR1* for Thai women were in Hardy-Weinberg equilibrium ($p > 0.05$).

Table 2 Hardy-Weinberg equilibrium of three common *MDR1* SNPs in Thai women

***MDR1* allele**	**1236**		**2677**			**3435**	
	C	**T**	**G**	**T**	**A**	**C**	**T**
Allele frequency, n (%)	143 (35.05)	265 (64.95)	216 (52.94)	169 (41.42)	23 (5.64)	207 (50.74)	201 (49.26)
P-value	0.5264		0.0549			0.4857	

The association between *MDR1* (C1236T) polymorphism and cervical cancer risk is presented in Table 3. The genotype frequencies of CC, CT and TT were 11.76%, 47.06% and 41.18% in the cervical cancer patient group, respectively and 11.27%, 47.55% and 41.18% in the healthy control group, respectively. The association between *MDR1* (C1236T) polymorphism and cervical cancer risk was not observed ($p > 0.05$).

Table 3 Association between *MDR1* (C1236T) polymorphism and the risk for cervical cancer

***MDR1* (C1236T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
CC	23 (11.27)	24 (11.76)	1	1
CT	97 (47.55)	96 (47.06)	0.95 [0.48-1.89, 0.8708]	0.84 [0.33-2.16, 0.722]
TT	84 (41.18)	84 (41.18)	0.96 [0.48-1.93, 0.8974]	0.85 [0.33-2.19, 0.735]
CT+TT	181 (88.73)	180 (88.24)	0.95 [0.50-1.83, 0.8768]	0.85 [0.35-2.07, 0.714]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

Table 4 Association between *MDR1* (G2677T/A) polymorphism and the risk for cervical cancer

***MDR1* (G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
GG	59 (28.92)	55 (26.96)	1	1
GA	6 (2.94)	10 (4.90)	1.79 [0.54-6.38, 0.2856]	1.69 [0.39-7.33, 0.484]
GT	92 (45.10)	84 (41.18)	0.98 [0.59 -1.61, 0.9312]	0.86 [0.42-1.73, 0.667]
TA	13 (6.37)	7 (3.43)	0.58 [0.18-1.70, 0.2732]	0.27 [0.07-1.08, 0.064]
TT	32 (15.69)	47 (23.04)	1.58 [0.85-2.94, 0.1238]	1.59 [0.68-3.70, 0.284]
AA	2 (0.98)	1 (0.49)	0.54 [0.01-10.62, 0.5323]	0.70 [0.01-47.98, 0.870]
GA+TA+AA	21 (10.29)	18 (8.82)	0.92 [0.41-2.03, 0.8214]	0.75 [0.28-2.01, 0.571]
GT+TA+TT	137 (67.16)	138 (67.65)	1.08 [0.68-1.71, 0.7281]	0.95 [0.50-1.79, 0.870]
GA+GT	98 (48.04)	94 (46.08)	1.03 [0.63-1.68, 0.9040]	0.94 [0.47-1.87, 0.858]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

The association between variation of *MDR1* (G2677T/A) and cervical cancer risk is exhibited in Table 4. The genotype frequencies of GG, GA, GT, TA, TT and AA were 28.92%, 2.94%, 45.10%, 6.37%, 15.69%, 0.98%, respectively in healthy controls and 26.96%, 4.90%, 41.18%, 3.43%, 23.04%, 0.49%, respectively in cervical cancer patients. Women carrying TA genotype presented a trend to decrease the risk for cervical cancer with adjusted OR = 0.27 (95%CI = 0.07-1.08, *p* = 0.064).

Table 5 Association between *MDR1* (C3435T) polymorphism and the risk for cervical cancer

***MDR1* (C3435T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR^{a} [95%CI, *p*]**
CC	55 (26.96)	47 (23.04)	1	1
CT	97 (47.55)	84 (41.18)	1.01 [0.61-1.70, 0.9573]	0.92 [0.46-1.88, 0.828]
TT	52 (25.49)	73 (35.78)	1.64 [0.94-2.88, 0.0643]	1.50 [0.70-3.21, 0.300]
CT+TT	149 (73.04)	157 (76.96)	1.23 [0.77-1.98, 0.3604]	1.13 [0.59-2.17, 0.723]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

The association between polymorphism of *MDR1* (C3435T) and the risk for cervical cancer is showed in Table 5. The genotype frequencies of CC, CT and TT were 26.96%, 47.55% and 25.49% in the healthy controls, respectively and 23.04%, 41.18% and 35.78% in the cervical cancer patients, respectively. The TT genotype (C3435T) showed a trend to elevate risk for cervical cancer with OR= 1.64 (95%CI = 0.94-2.88, *p* = 0.0643).

Table 6 Correlation between *MDR1* polymorphism (C1236T and G2677T/A) and the risk for cervical cancer

MDR1 **(C1236T) genotype**	***MDR1*** **(G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
CC	GG	17 (73.90)	18 (75.00)	1	1
	GA	2 (8.70)	5 (20.83)	2.36 [0.32-27.42, 0.2935]	2.71 [0.31-23.68, 0.368]
	GT	2 (8.70)	0 (0.00)	-[b]	-[b]
	TA	0 (0.00)	0 (0.00)	-[b]	-[b]
	TT	0 (0.00)	0 (0.00)	-[b]	-[b]
	AA	2 (8.70)	1 (4.17)	0.47 [0.01-10.05, 0.5000]	0.54 [0.01-21.47, 0.740]
	GA+TA+AA	4 (17.40)	6 (25.00)	1.42 [0.28-8.02, 0.4544]	1.81 [0.28-11.87, 0.536]
	GT+TA+TT	2 (8.70)	0 (0.00)	-[b]	-[b]
	GA+GT	4 (17.40)	5 (20.83)	1.18 [0.21-6.99, 0.5618]	1.02 [0.17-6.12, 0.978]
CT	GG	29 (29.90)	28 (29.17)	1	1
	GA	4 (4.12)	5 (5.21)	1.30 [0.25-7.21, 0.5000]	0.77 [0.09-6.33, 0.808]
	GT	49 (50.52)	55 (57.29)	1.16 [0.58-2.34, 0.6479]	0.97 [0.34-2.77, 0.952]
	TA	13 (13.40)	7 (7.29)	0.56 [0.16-1.79, 0.2751]	0.18 [0.03-0.92, 0.039*]
	TT	2 (2.06)	1 (1.04)	0.52 [0.01-10.59, 0.5254]	0.04 [0.00-0.96, 0.047*]
	AA	0 (0.00)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	17 (17.52)	12 (12.50)	0.73 [0.27-1.98, 0.4961]	0.34 [0.08-1.42, 0.138]
	GT+TA+TT	64 (65.98)	63 (65.62)	1.02 [0.52-2.00, 0.9516]	0.75 [0.29-1.95, 0.550]
	GA+GT	53 (54.64)	60 (62.50)	1.17 [0.59-2.33, 0.6244]	0.96 [0.33-2.77, 0.936]

OR: odds ratio, CI: confidence interval, * $p<0.05$

[a] adjusted multiple logistic regression for partners’ smoking, contraceptive use and HPV infection

[b] drop because confidence levels not possible with zero count cells

Table 6 Correlation between *MDR1* polymorphism (C1236T and G2677T/A) and the risk for cervical cancer (Cont.)

***MDR1* (C1236T) genotype**	***MDR1* (G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
TT	GG	13 (15.48)	9 (10.71)	1	1
	GA	0 (0.00)	0 (0.00)	-[b]	-[b]
	GT	41 (48.81)	29 (34.53)	1.02 [0.35-3.10, 0.9656]	1.10 [0.27-4.50, 0.898]
	TA	0 (0.00)	0 (0.00)	-[b]	-[b]
	TT	30 (35.71)	46 (54.76)	2.21 [0.76-6.62, 0.1025]	3.35 [0.81-13.80, 0.094]
	AA	0 (0.00)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	0 (0.00)	0 (0.00)	-[b]	-[b]
	GT+TA+TT	71 (84.52)	75 (89.29)	1.53 [0.56-4.30, 0.3603]	1.96 [0.53-7.22, 0.314]
	GA+GT	41 (48.81)	29 (34.53)	1.02 [0.35-3.10, 0.9656]	1.05 [0.27-4.14, 0.942]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

[b] drop because confidence levels not possible with zero count cells

The correlation between *MDR1* (C1236T and G2677T/A) and the risk for cervical cancer is exhibited in Table 6. The carriers of CT genotype (C1236T) together with TA genotype or TT genotype (G2677T/A) were significantly decreased risk for cervical cancer adjusted by partners' smoking, contraceptive use and HPV infection with adjusted OR = 0.18 (95%CI = 0.03-0.92, p = 0.039) and 0.04 (95%CI = 0.00-0.96, p = 0.047), respectively.

Table 7 Correlation between *MDR1* polymorphism (C3435T and G2677T/A) and the risk for cervical cancer

MDR1 **(C3435T) genotype**	***MDR1*** **(G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
CC	GG	37 (67.27)	30 (63.83)	1	1
	GA	5 (9.09)	4 (8.51)	0.99 [0.18-5.04, 0.6348]	1.29 [0.22-7.48, 0.780]
	GT	7 (12.72)	6 (12.77)	1.06 [0.26-4.12, 0.9272]	0.90 [0.15-5.34, 0.911]
	TA	1 (1.82)	0 (0.00)	-[b]	-[b]
	TT	3 (5.46)	7 (14.89)	2.88 [0.59-18.47, 0.1250]	1.58 [0.23-11.08, 0.645]
	AA	2 (3.64)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	8 (14.55)	4 (8.51)	0.62 [0.12-2.59, 0.4610]	1.01 [0.21-4.89, 0.989]
	GT+TA+TT	11 (20.00)	13 (27.66)	1.46 [0.52-4.15, 0.4291]	1.13 [0.29-4.32, 0.863]
	GA+GT	12 (21.81)	10 (21.28)	1.03 [0.35-3.01, 0.9557]	1.05 [0.29-3.86, 0.939]
CT	GG	7 (7.22)	7 (8.33)	1	1
	GA	1 (1.03)	1 (1.19)	1.00 [0.01-89.58, 0.7677]	2.47 [0.02-262.47, 0.705]
	GT	80 (82.47)	62 (73.82)	0.78 [0.22-2.74, 0.6487]	1.53 [0.28-8.20, 0.622]
	TA	7 (7.22)	5 (5.95)	0.71 [0.11-4.33, 0.6709]	0.73 [0.07-7.39, 0.788]
	TT	2 (2.06)	8 (9.52)	4.00 [0.48-49.16, 0.1426]	3.61 [0.27-48.31, 0.332]
	AA	0 (0.00)	1 (1.19)	-[b]	-[b]
	GA+TA+AA	8 (8.25)	7 (8.33)	0.88 [0.16-4.73, 0.8575]	0.61 [0.08-4.77, 0.640]
	GT+TA+TT	89 (92.02)	75 (89.29)	0.84 [0.24-2.96, 0.7584]	1.51 [0.29-7.94, 0.628]
	GA+GT	81 (83.50)	63 (75.01)	0.78 [0.22-2.75, 0.6531]	1.56 [0.29-8.36, 0.603]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

[b] drop because confidence levels not possible with zero count cells

Table 7 Correlation between *MDR1* polymorphism (C3435T and G2677T/A) and the risk for cervical cancer (Cont.)

MDR1 **(C3435T) genotype**	***MDR1*** **(G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
TT	GG	15 (28.84)	18 (24.66)	1	1
	GA	0 (0.00)	5 (6.84)	-[b]	-[b]
	GT	5 (9.62)	16 (21.92)	2.67 [0.70-11.37, 0.1083]	0.60 [0.11-3.32, 0.560]
	TA	5 (9.62)	2 (2.74)	0.33 [0.03-2.47, 0.2037]	0.13 [0.01-1.29, 0.081]
	TT	27 (51.92)	32 (43.84)	0.99 [0.38-2.53, 0.9773]	0.91 [0.27-3.03, 0.873]
	AA	0 (0.00)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	5 (9.62)	7 (9.58)	1.17 [0.25-5.68, 0.8211]	0.21 [0.01-3.75, 0.290]
	GT+TA+TT	37 (61.54)	50 (68.50)	1.13 [0.46-2.72, 0.7727]	0.73 [0.23-2.27, 0.587]
	GA+GT	5 (9.62)	21 (28.76)	3.50 [0.94-14.52, 0.0346*]	1.40 [0.15-12.68, 0.766]

OR: odds ratio, CI: confidence interval, * $p<0.05$,

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

[b] drop because confidence levels not possible with zero count cells

The correlation between genotype of *MDR1* (C3435T and G2677T/A) and the risk for cervical cancer is given in Table 7. Women carrying TT genotype (C3435T) in combination with GA and GT genotypes (G2677T/A) were significantly increased cervical cancer risk with OR = 3.50 (95%CI = 0.94-14.52, p = 0.0346).

Table 8 Correlation between *MDR1* polymorphism (C1236T and C3435T) and the risk for cervical cancer

***MDR1* (C1236T) genotype**	***MDR1* (C3435T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
CC	CC	13 (56.52)	9 (37.50)	1	1
	CT	5 (21.74)	3 (12.50)	0.87 [0.11-5.94, 0.6041]	0.55 [0.06-4.86, 0.589]
	TT	5 (21.74)	12 (50.00)	3.47 [0.76-16.85, 0.0652]	2.37 [0.43-13.01, 0.320]
	CT+TT	10 (43.48)	15 (62.50)	2.17 [0.58-8.17, 0.1914]	1.49 [0.33-6.77, 0.608]
CT	CC	24 (25.81)	28 (28.00)	1	1
	CT	53 (56.99)	48 (48.00)	1.06 [0.51-2.19, 0.8722]	1.00 [0.35-2.82, 0.994]
	TT	16 (17.20)	24 (24.00)	1.75 [0.70-4.40, 0.1875]	1.32 [0.37-4.74, 0.670]
	CT+TT	69 (74.19)	72 (72.00)	1.22 [0.61-2.42, 0.5450]	1.08 [0.40-2.91, 0.883]
TT	CC	14 (16.67)	14 (16.67)	1	1
	CT	39 (46.43)	33 (39.29)	0.85 [0.32-2.22, 0.7078]	0.93 [0.27-3.22, 0.915]
	TT	31 (36.90)	37 (44.04)	1.19 [0.45-3.16, 0.6938]	1.49 [0.43-5.19, 0.530]
	CT+TT	70 (83.33)	70 (83.33)	1.00 [0.41-2.45, 1.00]	1.17 [0.37-3.68, 0.784]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking, contraceptive use and HPV infection

Table 8 exhibits the association between *MDR1* polymorphism (C1236T and C3435T) and the risk for cervical cancer. The carriers of CC genotype (C1236T) combined with TT genotype (C3435T) presented increasing trend of cervical cancer risk with OR = 3.47 (95%CI = 0.76-16.85, p = 0.0652).

Table 9 Relationship between *MDR1* (C1236T) polymorphism and the risk for cervical cancer in combination with status of partners' smoking

Partners' smoking	***MDR1* (C1236T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	CC	13 (13.68)	7 (12.50)	1	1
	CT	48 (50.53)	25 (44.64)	0.97 [0.31-3.25, 0.9499]	0.74 [0.18-2.99, 0.667]
	TT	34 (35.79)	24 (42.86)	1.31 [0.41-4.48, 0.6152]	0.98 [0.23-4.12, 0.981]
	CT+TT	82 (86.32)	49 (87.50)	1.11 [0.38-3.52, 0.8357]	0.84 [0.22-3.16, 0.793]
Yes	CC	10 (9.17)	17 (11.49)	1	1
	CT	49 (44.95)	71 (47.97)	0.85 [0.32-2.17, 0.7162]	0.95 [0.27-3.39, 0.942]
	TT	50 (45.88)	60 (40.54)	0.71 [0.26-1.81, 0.4296]	0.82 [0.23-2.91, 0.755]
	CT+TT	99 (90.83)	131 (81.51)	0.78 [0.30-1.89,0.5502]	0.88 [0.26-2.96, 0.842]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for contraceptive use and HPV infection

Table 9 presents the relationship between *MDR1* (C1236T) and the risk for cervical cancer in combination with status of partners' smoking. The results showed that *MDR1* (C1236T) polymorphism was not correlated with cervical cancer risk both non-smoking partner and smoking partner group ($p > 0.05$).

Table 10 reveals the relationship between variation of *MDR1* (G2677T/A) and the risk for cervical cancer in combination with status of partners' smoking. Among women with non-smoking partners, the significantly elevated risk for cervical cancer was observed in women carrying GA with OR = 11.64 (95%CI = 0.96-590.26, p = 0.0281). Moreover, women with TT genotype were significantly elevated cervical cancer risk with OR = 4.36 (95%CI = 1.44-13.42, p = 0.0031) and adjusted OR = 5.18 (95%CI = 1.31-20.45, p = 0.019), adjusted by contraceptive use and HPV infection.

Table 10 Relationship between *MDR1* (G2677T/A) polymorphism and the risk for cervical cancer in combination with status of partners' smoking

Partners' smoking	***MDR1* (G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	GG	32 (33.69)	11 (19.65)	1	1
	GA	1 (1.05)	4 (7.14)	11.64 [0.96-590.26, 0.0281*]	6.58 [0.33-131.53, 0.217]
	GT	40 (42.11)	22 (39.29)	1.60 [0.63-4.21, 0.2824]	1.54 [0.49-4.84, 0.457]
	TA	8 (8.42)	1 (1.78)	0.36 [0.01-3.33, 0.3252]	0.23 [0.02-2.78, 0.249]
	TT	12 (12.63)	18 (32.14)	4.36 [1.44-13.42, 0.0031*]	5.18 [1.31-20.45, 0.019*]
	AA	2 (2.10)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	11 (11.57)	5 (8.92)	1.32 [0.29-5.37, 0.4486]	0.98 [0.21-4.61, 0.975]
	GT+TA+TT	60 (63.16)	41 (73.21)	1.99 [0.85-4.87, 0.0861]	1.88 [0.67-5.26, 0.229]
	GA+GT	41 (43.16)	26 (46.43)	1.84 [0.74-4.77, 0.1520]	1.81 [0.60-5.47, 0.294]
Yes	GG	27 (24.76)	44 (29.73)	1	1
	GA	5 (4.59)	6 (4.05)	0.74 [0.17-3.38, 0.4384]	0.96 [0.15-6.07, 0.964]
	GT	52 (47.71)	62 (41.89)	0.73 [0.38-1.40, 0.3104]	0.61 [0.25-1.50, 0.281]
	TA	5 (4.59)	6 (4.05)	0.74 [0.17-3.38, 0.4384]	0.29 [0.04-1.84, 0.189]
	TT	20 (18.35)	29 (19.59)	0.89 [0.40-2.01, 0.7584]	0.76 [0.25-2.27, 0.619]
	AA	0 (0.00)	1 (0.69)	-[b]	-[b]
	GA+TA+AA	10 (9.18)	13 (8.79)	0.80 [0.28-2.34, 0.6420]	0.64 [0.18-2.26, 0.485]
	GT+TA+TT	77 (70.65)	97 (65.53)	0.77 [0.42-1.41, 0.3712]	0.62 [0.27-1.43, 0.263]
	GA+GT	57 (52.30)	68 (45.94)	0.73 [0.39-1.38, 0.3032]	0.64 [0.26-1.57, 0.334]

OR: odds ratio, CI: confidence interval, * $p<0.05$,

[a] adjusted multiple logistic regression for contraceptive use and HPV infection

[b] drop because confidence levels not possible with zero count cells

Table 11 Relationship between *MDR1* (C3435T) polymorphism and the risk for cervical cancer in combination with status of partners' smoking

Partners' smoking	***MDR1* (C3435T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	CC	26 (27.37)	12 (21.42)	1	1
	CT	42 (44.21)	22 (39.29)	1.13 [0.45-2.96, 0.7721]	1.32 [0.42-4.17, 0.641]
	TT	27 (28.42)	22 (39.29)	1.77 [0.67-4.74, 0.2067]	1.37 [0.41-4.58, 0.607]
	CT+TT	69 (72.63)	44 (78.58)	1.38 [0.60-3.33, 0.4165]	1.34 [0.46-3.87, 0.588]
Yes	CC	29 (26.60)	35 (23.65)	1	1
	CT	55 (50.46)	62 (41.89)	0.93 [0.48-1.80, 0.8269]	0.74 [0.30-1.85, 0.519]
	TT	25 (22.94)	51 34.46	1.69 [0.80-3.56, 0.1327]	1.68 [0.62-4.56, 0.307]
	CT+TT	80 (73.40)	113 (76.35)	1.17 [0.63-2.15, 0.5880]	1.02 [0.44-2.36, 0.963]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for contraceptive use and HPV infection

Table 11 presents the relationship between *MDR1* genotype (C3435T) and the risk for cervical cancer in combination with status of partners' smoking. The correlation between *MDR1* (C3435T) combined with partners' smoking and cervical cancer risk was not found ($p > 0.05$).

Table 12 Relationship between *MDR1* (C1236T) polymorphism and the risk for cervical cancer in combination with use of hormonal contraceptive

Contraceptive use	***MDR1* (C1236T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	CC	10 (9.52)	10 (11.24)	1	1
	CT	56 (53.34)	42 (47.19)	0.75 [0.25-2.22, 0.5576]	0.81 [0.21-3.15, 0.765]
	TT	39 (37.14)	37 (41.57)	0.95 [0.31-2.87, 0.9166]	0.96 [0.24-3.89, 0.958]
	CT+TT	95 (90.48)	79 (88.76)	0.83 [0.29-2.35, 0.6960]	0.87 [0.24-3.22, 0.839]
Yes	CC	13 (13.13)	14 (12.17)	1	1
	CT	41 (41.41)	54 (46.96)	1.22 [0.47-3.14, 0.6450]	0.88 [0.24-3.29, 0.852]
	TT	45 (45.46)	47 (40.87)	0.97 [0.37-2.50, 0.9443]	0.77 [0.21-2.83, 0.689]
	CT+TT	86 (86.87)	101 (87.83)	1.09 [0.45-2.65, 0.8334]	0.82 [0.24-2.84, 0.753]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking and HPV infection

Table 12 reveals the relationship between *MDR1* (C1236T) gene and the risk for cervical cancer in combination with contraceptive use. Combination of *MDR1* (C1236T) polymorphism and hormonal contraceptive use was not significantly altered the risk for cervical cancer ($p > 0.05$).

Table 13 exhibits the correlation between polymorphism of *MDR1* (G2677T/A) and the risk for cervical cancer in combination with contraceptive use. The significantly correlation between *MDR1* polymorphism (G2677T/A) combined with use of hormonal contraceptive and the risk for cervical cancer was not observed ($p > 0.05$).

Table 13 Relationship between *MDR1* (G2677T/A) polymorphism and the risk for cervical cancer in combination with use of hormonal contraceptive

Contraceptive use	***MDR1* (G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	GG	37 (35.24)	26 (29.22)	1	1
	GA	4 (3.81)	5 (5.62)	1.78 [0.34-9.80, 0.3238]	2.01 [0.33-12.16, 0.446]
	GT	38 (36.19)	37 (41.57)	1.39 [0.67-2.88, 0.3435]	1.34 [0.51-3.54, 0.552]
	TA	9 (8.57)	3 (3.37)	0.47 [0.08-2.17, 0.2338]	0.20 [0.03-1.32, 0.094]
	TT	16 (15.24)	18 (20.22)	1.60 [0.64-4.04, 0.2706]	1.12 [0.33-3.82, 0.852]
	AA	1 (0.95)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	14 (13.33)	8 (8.99)	0.81 [0.26-2.45, 0.6859]	0.70 [0.18-2.75, 0.610]
	GT+TA+TT	63 (60.00)	58 (65.16)	1.31 [0.68-2.55, 0.3892]	1.09 [0.46-2.59, 0.844]
	GA+GT	42 (40.00)	42 (47.19)	1.42 [0.70-2.90, 0.2935]	1.40 [0.56-3.53, 0.472]
Yes	GG	22 (22.22)	29 (25.21)	1	1
	GA	2 (2.02)	5 (4.35)	1.90 [0.27-21.46, 0.3807]	1.27 [0.09-17.20, 0.859]
	GT	54 (54.55)	47 (40.87)	0.66 [0.32-1.37, 0.2292]	0.55 [0.19-1.58, 0.269]
	TA	4 (4.04)	4 (3.48)	0.76 [0.13-4.58, 0.5030]	0.38 [0.05-3.08, 0.367]
	TT	16 (16.16)	29 (25.22)	1.38 [0.56-3.41, 0.4484]	1.98 [0.59-6.65, 0.268]
	AA	1 (1.01)	1 (0.87)	0.76 [0.01-62.22, 0.6843]	0.89 [0.00-166.18, 0.964]
	GA+TA+AA	7 (7.07)	10 (8.70)	1.08 [0.31-3.93, 0.8874]	0.84 [0.20-3.53, 0.814]
	GT+TA+TT	74 (74.75)	80 (69.57)	0.82 [0.41-1.63, 0.5421]	0.81 [0.32-22.07, 0.662]
	GA+GT	56 (56.57)	52 (45.22)	0.70 [0.34-1.45, 0.3049]	0.57 [0.20-1.65, 0.303]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking and HPV infection

[b] drop because confidence levels not possible with zero count cells

Table 14 Relationship between *MDR1* (C3435T) polymorphism and the risk for cervical cancer in combination with use of hormonal contraceptive

Contraceptive use	***MDR1* (C3435T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR^a [95%CI, *p*]**
No	CC	32 (30.48)	24 (26.97)	1	1
	CT	46 (43.81)	37 (41.57)	1.07 [0.51-2.25, 0.8410]	0.77 [0.29-2.01, 0.588]
	TT	27 (25.71)	28 (31.46)	1.38 [0.61-3.13, 0.3953]	0.74 [0.25-2.16, 0.584]
	CT+TT	73 (69.52)	65 (73.03)	1.19 [0.61-2.34, 0.5909]	0.76 [0.31-1.84, 0.538]
Yes	CC	23 (23.23)	23 (20.00)	1	1
	CT	51 (51.52)	47 (40.87)	0.92 [0.43-1.97, 0.8193]	1.26 [0.44-3.63, 0.664]
	TT	25 (25.25)	45 (39.13)	1.80 [0.79-4.11, 0.1265]	3.30 [1.05-10.43, 0.042*]
	CT+TT	76 (76.77)	92 (80.00)	1.21 [0.60-2.45, 0.5660]	1.87 [0.70-5.01, 0.215]

OR: odds ratio, CI: confidence interval, * $p<0.05$,

^{a}adjusted multiple logistic regression for partners' smoking and HPV infection

Table 14 presents the association between genotypes of *MDR1* (C3435T) and the risk for cervical cancer in combination with use of hormonal contraceptive. Among women who taking hormonal contraceptives, the TT genotype was significantly elevated risk for cervical cancer about 3.30-fold (95%CI = 1.05-10.43, *p* = 0.042), adjusted by partners' smoking and HPV infection.

Table 15 The interaction between *MDR1* (C1236T) polymorphism and HPV infection in cervical cancer risk

HPV infection	***MDR1* (C1236T) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	CC	19 (10.74)	5 (16.12)	1	1
	CT	85 (48.02)	13 (41.94)	0.58 [0.17-2.35, 0.3488]	0.54 [0.17-1.73, 0.299]
	TT	73 (41.24)	13 (41.94)	0.68 [0.19-2.74, 0.5032]	0.60 [0.18-1.92, 0.385]
	CT+TT	158 (89.26)	26 (83.88)	0.63 [0.20-2.34, 0.3858]	0.57 [0.19-1.68, 0.306]
Yes	CC	4 (14.82)	19 (10.98)	1	1
	CT	12 (44.44)	83 (47.98)	1.46 [0.31-5.52, 0.5497]	1.48 [0.41-5.27, 0.548]
	TT	11 (40.74)	71 (41.04)	1.36 [0.28-5.27, 0.6301]	1.38 [0.38-5.02, 0.622]
	CT+TT	23 (85.18)	154 (89.02)	1.41 [0.32-4.78, 0.5616]	1.43 [0.43-4.75, 0.557]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking and contraceptive use

The interaction between variation of *MDR1* gene (C1236T) and HPV infection in cervical cancer risk is revealed in Table 15. The result indicated that interaction between *MDR1* (C1236T) genotype and HPV infection was not significantly altered cervical cancer risk (p > 0.05).

Table 16 presents the interaction between *MDR1* (G2677T/A) polymorphism and HPV infection in the risk for cervical cancer. Among HPV-infected women, carriers of TT genotype (G2677T/A) revealed a trend to increase risk for cervical cancer with OR= 3.10 (95%CI = 0.72-18.58, p = 0.0904) and adjusted OR =3.89 (95%CI = 0.95-15.90, p = 0.059).

Table 16 The interaction between *MDR1* (G2677T/A) polymorphism and HPV infection in cervical cancer risk

HPV infection	***MDR1*** **(G2677T/A) genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	GG	49 (27.68)	12 (38.71)	1	1
	GA	6 (3.39)	1 (3.23)	0.68 [0.01-6.53, 0.5981]	0.55 [0.06-5.14, 0.603]
	GT	82 (46.33)	10 (32.25)	0.50 [0.18-1.37, 0.1287]	0.46 [0.18-1.17, 0.103]
	TA	9 (5.08)	1 (3.23)	0.45 [0.01-3.92, 0.4128]	0.49 [0.06-4.34, 0.523]
	TT	29 (16.39)	7 (22.58)	0.99 [0.29-3.09, 0.9782]	0.91 [0.32-2.63, 0.863]
	AA	2 (1.13)	0 (0.00)	-[b]	-[b]
	GA+TA+AA	17 (9.60)	2 (6.46)	0.48 [0.05-2.53, 0.2952]	0.48 [0.09-2.48, 0.380]
	GT+TA+ TT	120 (67.80)	18 (58.06)	0.61 [0.26-1.51, 0.2282]	0.57 [0.25-1.29, 0.178]
	GT+GA	88 (49.72)	11 (35.48)	0.51 [0.19-1.37, 0.1338]	0.48 [0.19-1.20, 0.117]
Yes	GG	10 (37.04)	43 (24.86)	1	1
	GA	0 (0.00)	9 (5.20)	-[b]	-[b]
	GT	10 (37.04)	74 (42.77)	1.72 [0.59-5.00, 0.2609]	1.88 [0.70-5.08, 0.212]
	TA	4 (14.81)	6 (3.47)	0.35 [0.07-2.04, 0.1449]	0.33 [0.07-1.51, 0.155]
	TT	3 (11.11)	40 (23.12)	3.10 [0.72-18.58, 0.0904]	3.89 [0.95-15.90, 0.059]
	AA	0 (0.00)	1 (0.58)	-[b]	-[b]
	GA+TA+AA	4 (14.81)	16 (9.25)	0.93 [0.23-4.65, 0.5759]	1.08 [0.28-4.26, 0.907]
	GT+TA+ TT	17 (62.96)	120 (69.36)	1.64 [0.62-4.14, 0.2528]	1.82 [0.75-4.44, 0.186]
	GT+GA	10 (37.04)	83 (47.97)	1.93 [0.66-5.59, 0.1703]	2.28 [0.83-6.23, 0.109]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking and contraceptive use

[b] drop because confidence levels not possible with zero count cells

Table 17 The interaction between *MDR1* (C3435T) polymorphism and HPV infection in cervical cancer risk

HPV infection	***MDR1 (C3435T)*** **genotype**	**Control n (%)**	**Case n (%)**	**Crude OR [95%CI, *p*]**	**Adjusted OR[a] [95%CI, *p*]**
No	CC	48 (27.12)	8 (25.81)	1	1
	CT	86 (48.59)	11 (35.48)	0.77 [0.26-2.36, 0.5946]	0.76 [0.28-2.04, 0.584]
	TT	43 (24.29)	12 (38.71)	1.67 [0.56-5.18, 0.3019]	1.69 [0.62-4.59, 0.302]
	CT+TT	129 (72.88)	23 (74.19)	1.07 [0.43-2.96, 0.8792]	1.07 [0.44-2.57, 0.889]
Yes	CC	7 (25.93)	39 (22.54)	1	1
	CT	11 (40.74)	73 (42.20)	1.19 [0.36-3.68, 0.7376]	1.14 [0.40-3.27, 0.805]
	TT	9 (33.33)	61 (35.26)	1.22 [0.35-4.01, 0.7184]	1.30 [0.43-3.90, 0.640]
	CT+TT	20 (74.07)	134 (77.46)	1.20 [0.40-3.24, 0.6977]	1.21 [0.46-3.16, 0.695]

OR: odds ratio, CI: confidence interval

[a] adjusted multiple logistic regression for partners' smoking and contraceptive use

No significantly correlation between *MDR1* (C3435T) genotype in combination with HPV infection and the risk for cervical cancer was observed, as shown in Table 17 ($p > 0.05$).