Association of Single Nucleotide Polymorphisms from Angiogenesis-Related Genes, *ANGPT2*, *TLR2* and *TLR9,* with Spontaneous Preterm Labor

Table S1. APTT and PLT parameters during the development of pregnancy.

Parameters	Pregnancy period (weeks)		*p*-value [a]
	22-35	**37-41**	
Controls			
APTT [b]	27.77 ± 2.14	27.89 ± 2.17	0.290
PLT [c]	240 (164-324)	213 (151-398)	0.018
PDW [d]	12.57 ± 2.05	13.73 ± 1.96	≤ 0.001
MPV [e]	10.66 ± 0.89	11.11 ± 0.90	≤ 0.001
PCT [f]	0.26 ± 0.05	0.26 ± 0.05	1.000
PTL [g] cases			
APTT	27.83 ± 2.45	27.78 ± 2.24	0.393
PLT	220 (125-387)	215 (144-326)	0.006
PDW	12.55 (9.3-20.3)	14.1 (9.7-19.3)	≤ 0.001
MPV	10.81 ± 0.79	11.36 ± 0.98	≤ 0.001
PCT	0.23 (0.14-0.39)	0.24 (0.16-0.34)	0.974
All pregnant women			
APTT	27.81 ± 2.34	27.82 ± 2.20	0.483
PLT	232.41 ± 42.60	221.43 ± 45.62	≤ 0.001
PDW	12.55 (8.8-20.3)	13.9 (9.0-23.7)	≤ 0.001
MPV	10.76 ± 0.83	11.27 ± 0.96	≤ 0.001
PCT	0.24 (0.14-0.39)	0.24 (0.16-0.40)	0.969

[a] *p*-value, $p \leq 0.050$ is considered significant; [b] APTT, activated partial thromboplastin time; [c] PLT, platelet; [d] PDW, PLT distribution width; [e] MPV, mean PLT volume; [f] PCT, plateletcrit; [g] PTL, spontaneous preterm labor.

Table S2. Correlations among PLT parameters in the pregnant women.

PLT [a] parameters	R [b]	*t*-value	*p*-value [c]
Between 22 and 35 weeks of pregnancy			
PLT & PDW [d]	-0.3373	4.912	≤ 0.001
PLT & MPV [e]	-0.3739	5.439	≤ 0.001
PLT & PCT [f]	0.8693	24.117	≤ 0.001
PDW & MPV	0.9419	37.820	≤ 0.001
PDW & PCT	0.0362	0.497	0.620
MPV & PCT	-0.0071	0.096	0.923
Between 37 and 41 weeks of pregnancy			
PLT & PDW	-0.3555	5.680	≤ 0.001
PLT & MPV	-0.3821	6.161	≤ 0.001
PLT & PCT	0.9118	33.165	≤ 0.001
PDW & MPV	0.9673	56.802	≤ 0.001
PDW & PCT	-0.0175	0.261	0.794
MPV & PCT	-0.0278	0.415	0.679

[a] PLT, platelet; [b] R, Spearman rank correlation coefficient; [c] *p*-value, $p \leq 0.050$ is considered significant; [d] PDW, PLT distribution width; [e] MPV, mean PLT volume; [f] PCT, plateletcrit.

Table S3. Distribution of genotypes in *ANGPT2*, *CSF2*, *FLT1*, *TLR2*, *TLR6* and *TLR9* genes between the women with PTL and the controls.

Polymorphism	Genetic model	Genotype	Genotype prevalence, n [a] (%)		OR [b] (95 % CI [c])	*p*-value [d]	AIC [e]
			Controls	Cases			
ANGPT2 rs3020221	Codominant	GG	65 (40.6%)	64 (40.0%)	1.00	0.640	448.7
		GA	73 (45.6%)	79 (49.4%)	1.10 (0.69-1.76)		
		AA	22 (13.8%)	17 (10.6%)	0.78 (0.38-1.61)		
	Dominant	GG	65 (40.6%)	64 (40.0%)	1.00	0.910	447.6
		GA-AA	95 (59.4%)	96 (60.0%)	1.03 (0.66-1.60)		
	Recessive	GG-GA	138 (86.2%)	143 (89.4%)	1.00	0.390	446.9
		AA	22 (13.8%)	17 (10.6%)	0.75 (0.38-1.46)		
	Over-dominant	GG-AA	87 (54.4%)	81 (50.6%)	1.00	0.500	447.2
		GA	73 (45.6%)	79 (49.4%)	1.16 (0.75-1.80)		
CSF2 rs25882	Codominant	TT	109 (68.1%)	109 (68.1%)	1.00	0.730	449.0
		TC	41 (25.6%)	44 (27.5%)	1.07 (0.65-1.77)		
		CC	10 (6.2%)	7 (4.4%)	0.70 (0.26-1.91)		
	Dominant	TT	109 (68.1%)	109 (68.1%)	1.00	1.000	447.6
		TC-CC	51 (31.9%)	51 (31.9%)	1.00 (0.62-1.60)		
	Recessive	TT-TC	150 (93.8%)	153 (95.6%)	1.00	0.450	447.1
		CC	10 (6.2%)	7 (4.4%)	0.69 (0.25-1.85)		
	Over-dominant	TT-CC	119 (74.4%)	116 (72.5%)	1.00	0.700	447.5
		TC	41 (25.6%)	44 (27.5%)	1.10 (0.67-1.81)		
FLT1 rs722503	Codominant	TT	96 (60.0%)	94 (58.8%)	1.00	0.380	447.7
		CT	53 (33.1%)	60 (37.5%)	1.16 (0.73-1.84)		
		CC	11 (6.9%)	6 (3.8%)	0.56 (0.20-1.57)		
	Dominant	TT	96 (60.0%)	94 (58.8%)	1.00	0.820	447.6

		CT-CC	64 (40.0%)	66 (41.2%)	1.05 (0.67-1.65)		
	Recessive	TT-CT	149 (93.1%)	154 (96.2%)	1.00	0.210	446.0
		CC	11 (6.9%)	6 (3.8%)	0.53 (0.19-1.46)		
	Over-dominant	TT-CC	107 (66.9%)	100 (62.5%)	1.00	0.410	446.9
		CT	53 (33.1%)	60 (37.5%)	1.21 (0.77-1.92)		
TLR2 rs3804099	Codominant	TT	48 (30.0%)	56 (35.0%)	1.00	0.190	446.2
		TC	88 (55.0%)	72 (45.0%)	0.70 (0.43-1.15)		
		CC	24 (15.0%)	32 (20.0%)	1.14 (0.59-2.20)		
	Dominant	TT	48 (30.0%)	56 (35.0%)	1.00	0.340	446.7
		TC-CC	112 (70.0%)	104 (65.0%)	0.80 (0.50-1.27)		
	Recessive	TT-TC	136 (85.0%)	128 (80.0%)	1.00	0.240	446.2
		CC	24 (15.0%)	32 (20.0%)	1.42 (0.79-2.53)		
	Over-dominant	TT-CC	72 (45.0%)	88 (55.0%)	1.00	0.073	444.4
		TC	88 (55.0%)	72 (45.0%)	0.67 (0.43-1.04)		
TLR6 rs5743810	Codominant	CC	62 (38.8%)	59 (36.9%)	1.00	0.350	447.5
		CT	80 (50.0%)	74 (46.2%)	0.97 (0.60-1.57)		
		TT	18 (11.2%)	27 (16.9%)	1.58 (0.79-3.16)		
	Dominant	CC	62 (38.8%)	59 (36.9%)	1.00	0.730	447.5
		CT-TT	98 (61.2%)	101 (63.1%)	1.08 (0.69-1.70)		
	Recessive	CC-CT	142 (88.8%)	133 (83.1%)	1.00	0.150	445.5
		TT	18 (11.2%)	27 (16.9%)	1.60 (0.84-3.04)		
	Over-dominant	CC-TT	80 (50.0%)	86 (53.8%)	1.00	0.500	447.2
		CT	80 (50.0%)	74 (46.2%)	0.86 (0.55-1.33)		
TLR9 rs187084	Codominant	TT	37 (23.1%)	50 (31.2%)	1.00	0.230	446.6
		TC	89 (55.6%)	76 (47.5%)	0.63 (0.37-1.07)		
		CC	34 (21.2%)	34 (21.2%)	0.74 (0.39-1.40)		
	Dominant	TT	37 (23.1%)	50 (31.2%)	1.00	0.100	444.9
		TC-CC	123 (76.9%)	110 (68.8%)	0.66 (0.40-1.09)		

Recessive	TT-TC	126 (78.8%)	126 (78.8%)	1.00	NA [f]	447.6
	CC	34 (21.2%)	34 (21.2%)	1.00 (0.59-1.71)		
Over-dominant	TT-CC	71 (44.4%)	84 (52.5%)	1.00	0.150	445.5
	TC	89 (55.6%)	76 (47.5%)	0.72 (0.46-1.12)		

[a] n, number; [b] OR, odds ratio; [c] 95% CI, confidence interval; [d] *p*-value, $p \leq 0.050$ is considered significant; [e] AIC, Akaike information criterion; [f] NA, not analyzed.

Table S4. The frequency of alleles from angiogenesis-related genes in the women with spontaneous preterm labor and the controls.

| Polymorphism | Allele | No. [a] of alleles (%) | | Chi-Square | p-value [b] |
		Controls	Cases		
ANGPT2 rs3020221	A G	117 (36.6%) 203 (63.4%)	113 (35.3%) 207 (64.7%)	0.109	0.742
CSF2 rs25882	C T	61 (19.1%) 259 (80.9%)	58 (18.1%) 262 (81.9%)	0.093	0.761
FLT1 rs722503	C T	75 (23.4%) 245 (76.6%)	72 (22.5%) 248 (77.5%)	0.079	0.778
TLR2 rs3804099	C T	136 (42.5%) 184 (57.5%)	136 (42.5%) 184 (57.5%)	0.000	1.000
TLR6 rs5743810	C T	204 (63.8%) 116 (36.2%)	192 (60.0%) 128 (40.0%)	0.954	0.329
TLR9 rs187084	C T	157 (49.1%) 163 (50.9%)	144 (45.0%) 176 (55.0%)	1.060	0.303

[a] No., number; [b] p-value, $P \leq 0.050$ is considered significant.