

Fms-Like Tyrosine Kinase-1 (Flt-1) And The Vascular Endothelial Growth Factor (VEGF) As Biomarkers For Associated Preeclampsia

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ABSTRACT- Vascular endothelial growth factor (VEGF), the major factor for angiogenesis, is necessary for modulating angiogenesis processes in the placenta, fms-like tyrosine kinase 1 (Flt-1) is an anti-angiogenic protein that inhibits formation of new blood vessels resulting in potential pregnancy complications. The current study aims to study the placental gene expression of VEGF and (Flt1), genes involved in placental angiogenesis to correlate the degree of angiogenesis imbalance with the degree of preeclampsia. Fifty pre-eclamptic women specimens were collected as follow: 25 women with mild PE, 25 patients with severe PE. While 24 normotensive pregnant women matched for age as a control group. Placental mRNA expression of VEGF and Flt1 were measured by real time PCR (RTPCR). The mean VEGF expression was statistically higher in cases of severe PE than mild PE, both were higher than control group ($p < 0.0005$). On the other hand, the mean Flt1 expression was statistically significantly higher in control group as compared to either of the two PE groups ($p < 0.0005$) and there is no statistically significantly difference between sPE and mPE groups. The increase of VEGF and decrease of Flt1 genes expression in placenta tissue predict the risk of preeclampsia.

Keywords: VEGF, Flt-1, Angiogenesis, PE.

1 INTRODUCTION

Abnormal vascular growth and impaired endothelial function in placentas are associated with abnormal pregnancy conditions such as pre-eclampsia. Pre-eclampsia, a life threatening complication of pregnancy, is characterized by the onset of high blood pressure and proteinuria. Pre-eclampsia occurs in about 7-10 % of all pregnancies (1). The pathogenesis of pre-eclampsia is thought to act at three levels, defective placentation, placental ischemia, and endothelial cell dysfunction. Of these, endothelial dysfunction is considered to be a key factor associated with pre-eclampsia (2). The vascular endothelial growth factor (VEGF) family of angiogenic

growth factors are important molecules regulating early placental vascular changes. The key molecules VEGF-A and placental growth factor (PlGF) and the receptors VEGF receptor 1 (fms-like-tyrosine-kinase receptor 1, FLT-1) and VEGF receptor 2 (kinase insert domain receptor, KDR) are expressed in the human placenta throughout gestation, and the VEGF family is known to regulate placental angiogenesis and maternal spiral artery remodeling (3,4).

A number of studies have examined the mRNA levels of different angiogenesis regulating factors in placenta from PE patients although results are inconsistent. Some studies report increased VEGF expression (5-6), while others report reduced expression (7,8) in pre-eclamptic women. Other studies found no difference in VEGF expression

(9,10). Similarly expression of FLT-1 (11,12) and KDR (9,12,13) have also been examined. Very few studies have simultaneously examined the expression of VEGF and both its receptors in the human placenta in PE (14,15). The majority of these studies evaluate the role of VEGF and its receptors in normal vs PE pregnancy as well as their genetic variations, in predicting these pregnancy complications. The current study aims to study the placental gene expression of VEGF and (Flt1), genes involved in placental angiogenesis to correlate the degree of angiogenesis imbalance with the degree of preeclampsia.

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2 Patients AND METHODS

1-Patients:

Fifty patients diagnosed with Preeclampsia were collected from the Obstetrics and Gynecology department, Mansoura University, Egypt (Their mean age (years) \pm SD were 28.15 ± 5.25) during the period from July 2015 and May 2017. Preeclamptic women were divided into 25 women diagnosed as mild preeclampsia (MPE) and 25 women were diagnosed as severe preeclampsia (SPE). The control group comprised 24 normotensive pregnant women. The blood samples were taken from all participants during prenatal visits at second trimester between 20 to 24 gestational weeks. Maternal ages, weights, and height, gravidity, systolic and diastolic blood pressure, were recorded. Exclusion criteria included twin pregnancy, Women with a history of diabetes; thyroid, liver, or chronic renal disease; or preexisting chronic hypertension (defined as blood pressure $>140/90$ or need for antihypertensive medications before pregnancy or before 20 wk gestation) also if they had a pregnancy termination, a major anomaly all these cases were excluded or if the pregnancy outcome was unknown (i.e. if they did not deliver at our hospital). Control group were taken from women who entered Mansoura University Hospital, Egypt, Obstetric department, Maternal Study cohort within 2wk of each case and who remained normotensive and non-proteinuric throughout pregnancy. Ethical approval: A written informed consent was taken before sample withdrawal. The study was performed in accordance with the ethical standards laid down in Mansoura Faculty of Medicine.

2-METHODS :

Urine Collection: For pregnant women, a midstream clean-catch technique is usually adequate. Ten ml of urine for protein detection by dipstick in at least two random urine specimens obtained at least 4 h apart was required. proteinuria means protein ≥ 5 gr in a 24 hr (medi-test combi).

RNA extraction from placental tissue:

Fresh samples of 74 human placentas were obtained within 30 min after placental delivery in gynaecological and obstetric department, Mansoura University, Egypt. After a rinse of the samples with normal saline, the amniotic membranes and the maternal decidua were removed, then the samples were snap frozen in liquid nitrogen and stored at -70°C until RNA isolation by using miRNeasy mini kit (Qiagen, cat no. 217004, Germany). RNA was quantified by spectrometry (16).

TaqMan real-time PCR (provided by Thermo Scientific, U.S.A, cat No. #K1641) was used to quantify the expression of VEGF gene in placenta.

Reverse Transcription of Extracted RNA to Produce cDNA (17).

One μg (1000 ng) of RNA was reverse-transcribed using Maxima[®] First Strand cDNA Synthesis Kit provided by

Thermo Scientific, USA, cat. no. #K1641. The volume of RNA taken was calculated for each sample separately according to RNA concentration measured by nanodrop. The reaction was done by adding the following to calculated volume of RNA: 4 μl 5X reaction mix (containing the remaining reaction components: reaction buffer, dNTPs, oligo (dT), and random hexamer primers) and 2 μl Maxima enzyme mix (containing Maxima reverse transcriptase and Thermo Scientific Ribolock RNase inhibitor) and the reaction was completed to 20 μl by nuclease-free water. Thus, each 1 μl of the reaction contains 50 ng of RNA. The tubes were incubated for 10 minutes at 25°C followed by 15 minutes at 50°C . The reaction was terminated by heating at 85°C for 5 minutes. PCR was done using the 2x PCR master-mix solution (i-Taq) provided by iNtRON Biotechnology to check for Tm and product length (18). It was done in a total reaction volume of 20 μl using 10 μl PCR reaction mixture (1X), 1.6 μl template DNA (80 ng), 0.8 μl of 10 μM forward primer (400 nM), 0.8 μl of 10 μM reverse primer (400 nM), and 6.8 μl distilled water. Gene-specific primers were purchased from Invitrogen by Thermo Fisher Scientific. Primer sets for the PCR amplification genes were selected after testing the sequence of the three genes from NCBI database (19). Then, these sequences were submitted in Primer3 tool and checked for product length, melting temperature, GC ratio, self-complementarity, and 3' complementarity. The following assays targeting specific mRNAs were included in the study: VEGF: forward5, -GGGGCAGAATCATCACGAA-3, reverse 5-CCAGGTCTCGATTGGATGG-3. and Flt1: Forward CTGCAAGATTCAGGCACCTATG, Reverse GTTTCGAGGAGGTATGGTGCT.

Quantitative PCR Analysis (20).

Real-time PCR was done for quantification of VEGF gene using SensiFAST SYBR[®] Lo-ROX (purchased from Biorline, London, UK, catalog number: BIO-94005). For each reaction, the following was used: 10 μl of SensiFAST SYBR Lo-ROX (1X), 0.8 μl of 10 μM forward primer (400 nM), 0.8 μl of 10 μM reverse primer (400 nM), and 1.6 μl of template (80 ng), and each reaction was completed to reach a total volume of 20 μl by nuclease free water (6.8 μl). Initial denaturation was done by heating for 1 min at 95°C followed by 40 cycles of denaturation at 95°C for 5 seconds and annealing /extension at 60°C for 30 seconds in 7500 Fast & 7500 Real-Time PCR System (Applied Biosystem, Thermo Fisher Scientific, Life Technologies Corporation, USA). Melting curve analysis was done after amplification to confirm the specificity of the product and to exclude the presence of primer-dimers. The relative gene expression analysis was done by Delta cycle threshold (DDCT) method, and the average DCT of the healthy volunteers for each target gene was used as the calibrator sample (21,22). The amount of target, normalized to an endogenous reference and relative to a calibrator, was calculated. The fold change

is obtained by 2-DDCT. This method assigns a value of 0.7 to the calibrator sample, and all other quantities are expressed as an n-fold difference relative to the calibrator.

3 STATISTICAL ANALYSES

Data analysis was done by Statistical package for social science software (SPSS) version 25. Data are presented as mean ± SD and compared by One-Way ANOVA and they are presented as median (IQR) and compared by Kruskal-Wallis (K-W) test. Significance was considered at p value less than 0.05.

4 RESULTS

This study involved 74 subjects divided into 3 groups: The first is control group: 24 pregnant ladies with no current or previous pre-eclampsia. Their mean age (years) ± SD = 27.8 ± 4.7 years. The second is mild pre-eclampsia group: 25 pregnant ladies fulfilling the criteria of mild pre-eclampsia. Their mean age ± SD were 27.5 ± 4.3 years. The third is severe pre-eclampsia group: 25 pregnant ladies fulfilling the criteria of severe pre-eclampsia. Their mean age (years) ± SD = 28.8 ± 6.2 years. There was no statistically significant difference between the three study groups as regards age, women weight, gravida and para Table (1).

Table (1): Comparison of the clinical variables between the three study groups:

Variable	Group			Statistic	P value
	Control (n=24)	Mild PE (n=25)	Severe PE (n=25)		
Age (years)	27.8 ± 4.7	27.5 ± 4.3	28.8 ± 6.2	F = 0.459	*0.634
Weight (kg)	82.8 ± 14.8	77.6 ± 13.1	80.3 ± 14.1	F = 0.828	*0.441
Gravida:					
1					
2	2 (8.3%)	0 (0%)	1 (4%)		
3	2 (8.3%)	8 (32%)	7 (28%)		
4	10 (41.7%)	11 (44%)	11 (44%)	χ ² = 8.506	**0.404
5	8 (33.3%)	6 (24%)	5 (20%)		
	2 (8.3%)	0 (0%)	1 (4%)		

*Data are presented as mean ± SD and compared by One-Way ANOVA. **Data are presented as frequency (percentage) and compared by Chi-Square test (Monte Carlo significance). ***Data are presented as median (IQR) and compared by Kruskal-Wallis (K-W) test. Pairwise comparisons are presented as capital letters (similar letters = no significant difference, while different letters = significant difference).

Table 2 showed that a statistically significant difference existed for the other variables; SBP, DBP, MAP, and fetal weight. Fetal weight was significantly higher in control group than either of the PE groups (P<0.0005). As regards SBP, DBP and MAP, they all were statistically significantly higher in severe PE > Mild PE > Control.

Table (2): Comparison of the clinical variables between the three study groups:

Variable	Group			Statistic	P value
	Control (n=24)	Mild PE (n=25)	Severe PE (n=25)		
Para:					
0	4 (16.7%)	3 (12%)	6 (24%)		
1	5 (20.8%)	7 (28%)	6 (24%)		
2	9 (37.5%)	11 (44%)	9 (36%)	χ ² = 3.830	**0.939
3	5 (20.8%)	4 (16%)	4 (16%)		
4	1 (4.2%)	0 (0%)	0 (0%)		
Fetal weight (g)	3125 (3012.5-3237.5) A	2500 (2135-2875) B	2450 (1800-2725) B	K-W = 31.87	***<0.0005
SBP (mmHg)	115 (110-120) A	140 (135-140) B	170 (165-172.5) C	K-W = 61.02	***<0.0005
DBP (mmHg)	75 (75-80) A	85 (80-90) B	110 (107.5-115) C	K-W = 61.66	***<0.0005
MAP (mmHg)	90 (86.6-91.7) A	103 (99.1-105.8) B	130 (126.6-134) C	K-W = 64.24	***<0.0005

*Data are presented as mean ± SD and compared by One-Way ANOVA. **Data are presented as frequency (percentage) and compared by Chi-Square test (Monte Carlo significance). ***Data are presented as median (IQR) and compared by Kruskal-Wallis (K-W) test. Pairwise comparisons are presented as capital letters (similar letters = no significant difference, while different letters = significant difference).

Table 3 showed that a statistically significant difference between the three study groups as regards 2 studied laboratory variables (VEGF and FLT-1). FLT-1 level was statistically significantly higher in control group as compared to either of the two PE groups (p<0.0005) and there is no statistically significant difference between sPE and mPE but, VEGF was statistically significantly higher in severe PE > Mild PE > Control (P<0.0005).

Table (3): Comparison of the VEGF and FLT-1 between the three study groups.

Variable	Group			Statistic	P value
	Control (n=24)	Mild PE (n=25)	Severe PE (n=25)		
VEGF	1.3 (1.2-1.37) A	2 (1.9-2.45) B	2.8 (2.55-3.35) C	K-W = 58.07	**<0.0005
FLT-1	1.2 (1.1-1.3) A	0.72 (0.64-0.82) B	0.53 (0.42-0.72) B	K-W = 51.35	**<0.0005

*Data are presented as median (IQR) and compared by Kruskal-Wallis (K-W) test. Pairwise comparisons are presented as capital letters (similar letters = no significant difference, while different letters = significant difference).

Table 4 showed that no statistically significant difference in the proportions of subjects with previous history of PE (P=0.208) and in the starting of PE (P=0.305). There was statistically significant difference in the level of protein in urine with trace and + in mild cases, but ++ and +++ in severe cases (P<0.0005).

Table (4): Comparison of proteinuria and previous PE between mild and severe PE.

Variable	Group		Statistic	P value
	Mild PE (n=25)	Severe PE (n=25)		
Protein in urine:				
Nil	1 (4%) a	0 (0%) a	$\chi^2=50.000$	**<0.0005
Trace	13 (52%) a	0 (0%) b		
+	11 (44%) a	0 (0%) b		
++	0 (0%) a	12 (48%) b		
+++	0 (0%) a	13 (52%) b		
Previous PE, Yes	5 (20%)	9 (36%)	$\chi^2=1.587$	*0.208
Onset of PE (weeks)	30 (27-34)	30 (28-35)	Z=-1.025	***0.305

Data are presented as frequency (percentage) and compared by Chi-Square test (Monte Carlo significance**). Comparison between column proportions was done by Bonferroni adjustments.***

This table showed that there was no statistically significant difference in the proportions of subjects with previous history of PE and in the timing of PE. There was statistically significant difference in the proportions of protein in urine with trace and + in mild cases and ++ and +++ in severe cases.

5 DISCUSSION

Vascular endothelial growth factor (VEGF) is a potent regulator of placental vascular function (24). The gene encoding VEGF is highly polymorphic and its functional polymorphisms may be useful as indicators of susceptibility to PE (25). Keshavarzi et al. found that The relative mRNA expression of VEGF gene in placental tissue was significantly higher in PE women compared to controls (35). Also, Chung et al. showed that total VEGF mRNA expression was increased 2.8-fold ($p < 0.05$) in PE versus normal placenta (25). The present study, is agree with both of Keshavarzi et al. and Chung et al., it has analyzed and compared mRNA expression of VEGF in placenta of normotensive and preeclampsia cases. We found that, VEGF expression was statistically significantly higher in severe PE > Mild PE > Control ($p < 0.0005$). Also, the present finding supports the results of a number of studies which have reported increasing of VEGF expression in preeclampsia (26,27).

In contrast, some studies have showed an decreased VEGF expression in placental tissues of preeclampsia, Cooper et al found that levels of VEGF mRNA were significantly lower in the pre-eclamptic women compared with the control women (28). Andraweera et al. (15) compared mRNA placental expression of VEGFA in placental tissue obtained at delivery from PE (n = 18), gestational hypertension (n = 15) and uncomplicated pregnancy (n = 30). Compared to placental mRNA from ncomplicated pregnancies, VEGFA were reduced in PE ($p = 0.006$) and gestational hypertension ($p < 0.001$) placentae (15). Kim et al also reported decreased expressions of VEGF in both level

of mRNA and protein in placenta of preeclamptic patients compared with the normotensive controls(8) . A few studies have also reported unaltered expression of VEGFA in placental tissues in PE women (29, 30). Sgambati et al reported that in the cases of preeclampsia, the levels of VEGF mRNA were the same as the control group (31). Ranheim et al. reported that there were no statistically significant differences in expression of VEGF in mRNA levels for either the decidua basalis or placental tissues in a study conducted in 25 PE and 19 uneventful pregnancies (32).

Flt1 gene produces two mRNAs in placenta and vascular endothelial cells, a long form for the full-length receptor Flt1 and a short form for sFlt1 which carries only the ligand binding region (33) . Toft *et al* studied on the transcriptomes of placental tissues from PE and small for gestational age (SGA) pregnancies by whole-genome microarray and quantitative Real time PCR. it showed that increased expression of Flt1 was detected by QRT-PCR in the PE +SGA group but microarray analysis did not reveal any significant differences between groups (9). But, Marni showed that no clear evidence of an association between sFlt-1 levels in first trimester and adverse pregnancy outcomes (36). The present study has analyzed and compared mRNA expression of Flt1 in placenta of normotensive and preeclampsia cases and our findings revealed that, Flt1 gene Expression in placenta tissue was statistically significantly higher in control group as compared to either of the two PE groups ($p < 0.0005$) and there is no statistically significantly difference between two groups of pre-eclamps.

Results inconsistency of these studies may be due to the differences in phenotypic classification of PE chosen sample size, phenotypic classification of PE chosen, the timing of placental tissue sampling, the method of VEGF quantification and out comedepiction and the references taken for comparison (37,38). There are many genetic and environmental factors that may further alter gene expression of preeclampsia. Also, the pathophysiology of VEGF expression in PE is far from complete decipherment with numerous postulates available for explaining different obtained results (30, 38), However, findings were affected by ethodological, biological and testing variations between studies; highlighting the need for consistent testing of new biomarkers and reporting of outcome measures.

6 Conclusion:

The increase of VEGF and decrease of Flt1 gene Expression in placenta tissue predict the risk of preeclampsia.

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