Molecular pathogenesis of preeclampsia: microRNA hypothesis

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Abstract. The discovery of micro RNA (miRNA) in 1993 by Ambros and colleagues has a huge influence in pathogenesis theory, diagnosis and treatment approach of some diseases. Some studies have conducted to seek the association alterations of miRNA expression to incidences and severity of preeclampsia (PE). We have reviewed some studies that conducted to seek the association of miRNA and PE and we discussed the role of various miRNAs in PE pathogenesis. In summary, we have shown that many researchers have given evident that the different placental and plasma miRNA expression is associated with PE. Some studies also identified the novel candidate of miRNAs (and their pathways) that may be of etiologic relevance in the pathogenesis of PE. Base on review, specific miRNA have a role to down regulate of anti apoptosis genes, regulate angiogenics growth factors such as angiogenin, vascular endothelial growth factor (VEGF) B (VEGF-β), cysteine-rich 61 (CYR61), Placental growth factor (PlGF) and VEGF-A that have a role in angiogenesis. miRNA also have a role in survival, migration, and capillary tube formation of HUVEC by targeted of c-kit. Some miRNAs target genes that participate in immunologic dysfunction, cell adhesion, cell cycle, and signaling. miRNA also have a roles in endothelial cell response to hypoxia, cell differentiation, and survival. A miRNA influence calcium signaling through negative regulations of the calmodulin-coding mRNAs, Mef2a and Gata4, mainly in smooth muscle cells that contribute to PE pathogenesis. These investigations provide novel targets for further investigation of the pathogenesis of PE and these differential miRNAs may be potential markers for the diagnosis and provide a potential therapeutic target for PE. Further investigations on posttranscriptional regulation in PE to evaluate biologic effects of identified miRNAs (including confirmations of miRNA and target gene interactions) are needed.

Key words: Preeclampsia, microRNA, miRNA, preeclampsia pathogenesis.

Introduction

Preeclampsia (PE) is a disease of pregnancy characterized by hypertension (defined as systolic blood pressure ≥140 mm Hg or diastolic blood pressure ≥90 mm Hg) and proteinuria (300 mg or greater in a 24-h urine specimen and/or protein to creatinine ratio of > 0.30), developing after 20 weeks of gestation (Sibai et al., 2005). It has been estimated that PE affects 3%–5% of pregnancies worldwide, recently, it has been reported that PE complicates 3-8% of pregnancies (Duley, 2009; WHO, 2005). There is much evidence shown that PE originates in the placenta and thus the placenta is believed as the central basis to the pathogenesis of PE (Young et al., 2010). But the molecular basis for placental dysregulation of these pathogenic factors remains unknown.

Many hypotheses have emerged that attempt together a causal framework for the disease, causing PE to be named the 'disease of theories' (Cerdeira & Karumanchi, 2010). Here, we hypothesize that microRNA has a main role in PE patoghenesis: microRNA hypothesis. MicroRNAs (miRNAs) are small, non coding RNAs ~22 nucleotides (nt) in length that regulate gene expression with important functions in the regulation of a variety of biological processes involved in development, cell differentiation, regulation of cell cycle, metabolism and apoptosis (Bushati & Cohen, 2007; Garzon et al., 2009). Albeit only 1% of the genomic transcripts in mammalian cells encode miRNA, miRNAs are predicted to control the activity of more than 60% of all protein-coding genes (Friedman et al., 2009; Sun et al., 2010). It has been estimated that miRNAs regulate ~30% of human genes (Bartel, 2004). MicroRNAs regulate mRNA, which encodes proteins that modulate cellular functions, therefore, miRNAs play important roles in physiological homeostasis in health and pathophysiological derangement in disease (Sun et al., 2010). MicroRNAs are known to have function in pathological process and prognosis of diseases such as diabetes (Poy et al., 2004), neurodegenerative disorder (Jin et al., 2004), gastrointestinal diseases (Pellish et al., 2008) and cancer and its resistant for chemotherapy (Garofalo & Croce, 2011). Certain miRNAs are tissue-specific and the temporal expression of the tissue-specific miRNAs correlates closely with the specific physiological or pathological status of the corresponding organs (Sun et al., 2010).

Functional studies indicate that miRNAs participate in the regulation of almost every cellular process investigated so far and that changes in their expression are associated with many human pathologies (Krol et al., 2010). Some scientifically proven theories have been proposed to seek the association of alterations of miRNA expression to incidences and severity of preeclampsia (PE). Research conducted by Pineles et al. (2007) shows that PE is associated with alterations in placental miRNA expression. This research reported that miR-210 and -182 are expressed differentially in the human placentas of patients with PE compared with control subjects. In this review we explore the result of such investigations that discuss the association of miRNA and PE along with the role of various mRNAs in PE pathogenesis.

Biogenesis and Mechanism Action of miRNA

MicroRNAs are processed from RNA polymerase II (RNAPII)-specific transcripts of independent genes or from introns of protein-coding genes (Carthew & Sontheimer, 2009). These initial miRNA precursors, known as pri-miRNAs, are processed into ~70 nt hairpin structures known as pre-miRNAs - in the nucleus - by a nuclear enzyme complex known as the microprocessor that contains an endoribonuclease - Drosha - and a double-stranded RNA binding protein - DiGeorge syndrome critical region 8 (DGCR8)**.** This process called as Drosha–DGCR8 step (Fabian et al., 2010a; Krol et al., 2010). Drosha is an RNase III enzyme which contains two RNase domains which cleave the 5` and 3` ends, releasing the pre-miRNA (Fabian et al., 2010b).

The pre-miRNA is exported from the nucleus to the cytoplasm by Exportin-5 (XPO5) (Yi et al., 2003). In the cytoplasm, the pre-miRNA is further cleaved by another RNase III enzyme – Dicer, which removes the loop to yield the ~22 nucleotide miRNA duplext (Sun et at., 2010). After being unwound by a helicase, one strand of miRNA is destined to be the mature miRNA called as guide strand and the complementary strand - called as passenger strand or miRNA* - is rapidly degraded (Sun et al., 2010). The thermodynamic stability of the miRNA duplex termini and the identity of the nucleotides in the 3′ overhang determine which strands act as guide strand (Ryan et al., 2010). Then the guide strand is incorporated into a miRNA-induced silencing complex (miRISC) (Bartel, 2004), see Figure 1.

Guided by the sequence complementarity between the small RNA and the target mRNA, miRNA-RISC-mediated gene inhibition is commonly divided into three processes: (a) site-specific cleavage, (b) enhanced mRNA degradation and (c) translational inhibition (Gu & Kay, 2010). The miRISC-mRNA interaction can lead to several modes of direct and indirect on translational repression (Sun et al., 2010). Direct on translational repression involved: (a). Initiation block: The miRISC inhibits translation initiation by interfering with eIF4F-cap recognition and 40S small ribosomal subunit recruitment or by antagonizing 60S subunit joining and preventing 80S ribosomal complex formation. (b) Postinitiation block: premature ribosomal drop-off, the 40S/60S ribosomes are dissociated from mRNA, stalled or slowed elongation, the 40S/60S ribosomes are prohibited from joining during the elongation process or facilitating proteolysis of nascent polypeptides (Fabian et al., 2010b; Nilsen, 2007; Sun et al., 2010).

The indirect on translational repression occurs via mRNA deadenylation and degradation (Nilsen, 2007; Sun et al., 2010). Deadenylation of mRNAs is mediated by glycine-tryptophan protein of 182 kDa (GW182) proteins - the components of miRISC, poly(A)-binding protein (PABP), and Argonaute (AGO) protein (Fabian et al., 2010b; Gu & Kay, 2010; Krol et al., 2010). Argonaute (AGO) proteins are core components of the miRISC which are directly associated with miRNAs (Krol et al., 2010). Then this molecule will interacts with the CCR4/CAF1 deadenylase complex to facilitate deadenylation of the poly(A) tail (Fabian et al., 2010b; Krol et al., 2010). Following deadenylation, the 5`-terminal cap is removed by the decapping enzyme - decapping DCP1-DCP2 complex (Fabian et al., 2010b). Endonucleolytic cleavage and mRNA degradation that miRNA-mediated by AGO2 (Ender & Meister, 2010; Krol et al., 2010).

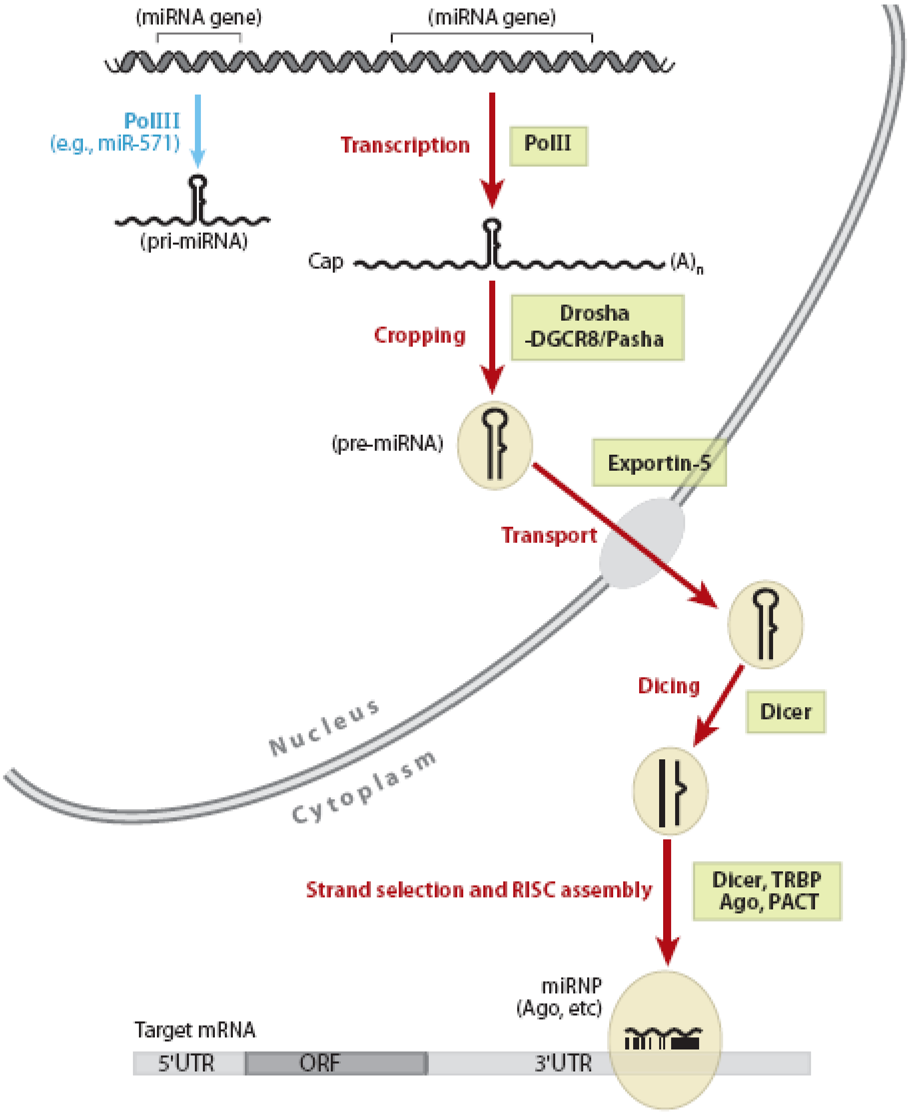

Figure 1. Pathways of microRNA (miRNA) biogenesis and action (Lee & Dutta, 2009). Abbreviations: miRNP, ribonucleoprotein complex containing miRNA; ORF, open reading frame; P-body, PACT, interferon-inducible double-stranded RNA-dependent activator; RISC, RNA-induced silencing complex; TRBP, human immunodeficiency virus–transactivating RNA-binding protein; UTR, untranslated region of mRNA.

Molecular Mechanisms of Preeclampsia

Angiogenic factor such as placental growth factor (PlGF) and vascular endothelial growth factor (VEGF) and their receptors Flt1 [also known as vascular endothelial growth factor receptor 1 (VEGFR-1)], VEGFR-2, Tie-1, and Tie-2, are essential for normal placental vascular development (Young et al., 2010). Alterations in the regulation and signaling of angiogenic pathways in early gestation contribute to the inadequate cytotrophoblast invasion seen in preeclampsia (Young et al., 2010). Additionally, perturbation of the renin–aldosterone–angiotensin II axis, excessive oxidative stress, inflammation, immune maladaptation, and genetic susceptibility may all contribute to the pathogenesis of preeclampsia (Young et al., 2010).

Several placentally derived "toxins" were suggested, including cytokines, anti-angiogenic factors, syncytiotrophoblast microparticles (STBM), and formed blood products activated in the intervillus space (Roberts & Hubel, 2009). The role of these anti-angiogenic factors such as soluble fms-like tyrosine kinase 1 (sFlt1) and soluble endoglin (sEng) in early placental vascular development and in trophoblast invasion is just the beginning to be explored in placental dysregulation. Hypoxia is likely to be an important regulator (Young et al., 2010). Oxidative stress was an attractive component as part of the linkage (Mellembakken et al., 2002). Reactive oxygen species could be generated by the reduced perfusion of the placenta with consequent activation of monocytes and neutrophils passing through the intervillus space. Oxidative stress would also stimulate release of cytokines, antiangiogenic factors, microparticles and other potential linkers (Roberts & Hubel, 2009).

Some factors such as genetic factors, oxidative stress, catechol-O-methyltransferase (COMT) deficiency, hemoxygenase deficiency and immunological/inflammatory factors cause placental dysfunction which leads angiogenic imbalance, increase sFlt1 and sEng, decrease of PlGF and VEGF (Maynard et al., 2008; Mutter & Karumanchi, 2008; Young et al., 2010). sFlt1 and sEng levels have been shown to be elevated in the serum of preeclamptic women, as compared to normal preganant women, weeks before the appearance of overt clinical manifestations of the disease (Levine et al., 2004, 2006). Compared to normo-tensive controls, in patients with severe preeclampsia, free PlGF and VEGF levels are significantly declined and sFlt1 levels are significantly elevated (Levine et al., 2004, 2006).

It`s clear that the increase of sFlt1 expression associated with decreased PlGF and VEGF signaling, cause inadequate placental vascular development (Levine et al., 2004; Maynard et al., 2003; Venkatesha et al., 2006). This alterations causes widespread endothelial dysfunction that results in hypertension, proteinuria, and other systemic manifestations of preeclampsia (Maynard et al., 2003; Mutter & Karumanchi, 2008).

The Role of miRNA in Preeclampsia Pathogenesis

The first research that linked miRNA and PE was conducted by Pineles et al. (2007) The study was performed to determine whether PE and small-for-gestational age (SGA) are associated with alterations in placental miRNA expression. Thus they evaluated placental miRNAs expression from patients with PE, SGA, PE + SGA along with a control group. They found that seven miRNAs (miR-210, miR-155, miR-181b, miR-182*, miR-200b, miR-154*, and miR-183) were significantly higher expressed between PE+SGA and the control group. The expression of miR-182 and miR-210 was significantly higher in PE than in the control group. Based on Gene Ontology (GO) analysis, miR-182 have a role to down-regulate anti-apoptosis genes. They speculated that high expression of miR-182 in PE may contribute to the increased apoptosis in the placentas of patients with preeclampsia. The targets of both miR-182 and miR-210 are enriched in immune processes, which support the association between abnormal immune responses and PE as descripted previously by Kim et al. (2005) Beside that, angiogenin and VEGF-β are potential targets of miR-182 and miR-182*, respectively (Pineles et al.,2007). These molecules have a role in angiogenesis. A study by et al.(2005) elucidates miRNA essentiality, that in mice with deficient miRNA, defective angiogenesis is caused that leads to embryonic lethality.

A study with small sample in China found expression of miR-130a, miR-181a, miR-222, miR-16, miR-26b, miR-29b and miR-195 in placenta of severe PE women (Fei et al., 2009). The other reseacrh by Hu et al. (2009) reported that miR-16, miR-29b, miR-195, miR-26b, miR-181a, miR-335 and miR-222 were significantly increased in placenta from women with severe PE. This research revealed that some angiogenic growth factors were potential targets of the altered miRNA, such as cysteine-rich 61 (CYR61), PlGF, VEGF-A which were targets of miR-222, miR-335 and miR-195, respectively. It describes the role of this angiogenics factors for the development of PE. It is well known that the expressions of VEGF-A and VEGF receptor-1 are down-regulated in cytotrophoblasts of PE placenta (Mutter & Karumanchi, 2008; Zhou et al., 2002). Several articles reviewed by Lam et al. (2005) provides sufficient evidenence that PlGF is also dysregulated in serum or placental tissue of women with PE.

The research by Mo et al. (2002) found that CYR61 is essential for placental development and vascular integrity. Gellhaus et al. (2006) found that CYR61 is significantly decreased in PE placenta. CYR61 is a secreted matrix protein expressed by nearly all types of vascular cells and trophoblasts and implicated in diverse cellular processes such as proliferation, migration, differentiation, and adhesion. It was found that the expression of CYR61 in human placenta was significantly lower than that of the normal control.[46] Recently, study reported that overexpression of miR-155 contributes to PE development by targeting and down-regulating angiogenic regulating factor CYR61 (Zhang et al., 2010). It was also reported that CYR61 has been demonstrated to be one of the important early angiogenic factors during pregnancy, this role is probably because CYR61 can induce the expression of VEGF (Zhang et al., 2010).

Poliseno et al*.* (2006) found that overexpression of miR-221/222 inhibits tube formation, migration, and wound healing in response to stem cell factor in human umbilical endothelial cells (HUVEC). This effect, arises because c-kit is a target of miR-221/222. c-kit is a tyrosine kinase receptor for stem cell factor and has been shown to promote survival, migration, and capillary tube formation HUVEC (Matsui et al., 2004).

The other study by Zhu et al*.* (2009) was conducted in China population. They investigated that 34 miRNAs were expressed differentially in PE placentas, compared to normal placentas. Of these, 11 microRNAs were over-expressed, and 23 miRNAs were under-expressed in PE placentas. miR-518b showed significant overexpression in severe PE vs control; miR-18a, -363, and -542-3p were significantly underexpressed in severe PE vs control. miR-152 showed significant overexpression in mild PE vs control specimens and in severe PE vs control specimens. miR-411 and miR-377 were under-expressed in mild PE vs control specimens and in severe PE vs control. Zhu et al*.* (2009) also found that miR-210 was significantly underexpressed in mild PE vs the other 2 groups; while significant overexpression was found in severe PE vs all other groups. In their comments, they mention that the increase in miR-210 expression in sPE induced by focal regions of ischemia/hypoxia in placentas is cause of poor placentation in PE pregnancies, as previous study showed that the expression of miR-210 was increased on exposure to hypoxia (Fasanaro et al., 2008). They speculated that the decrease of miR-210 in mPE as a compensatory mechanism in the pregnancies with mPE, but there isn`t a sufficient explanation.

Recently, Enquobahrie et al*.* (2011) found that eight miRNAs were differentially expressed (miR-210 up-regulated and 7 - miR-328, miR-584, miR-139-5p, miR-500, miR-1247, miR-34C-5p and miR-1-down-regulated) among PE cases compared with controls. These miRNAs target genes that participate in organ/system development (cardiovascular and reproductive system), immunologic dysfunction, cell adhesion, cell cycle, and signaling. In their comment consistent with the other scientist, they stated that miR-210 plays roles in endothelial cell response to hypoxia, formation of capillary-like structures, vascular endothelial growth factor– driven cell migration, cell differentiation, and survival, events that are integral to preeclampsia pathogenesis. Enquobahrie et al*.* (2011) utilizing the results of previous study conducted by Ikeda et al*.* (2009) speculated that miR-1 influence risk of PE through its effect on calcium signaling. They demonstrated that miR-1 influence calcium signaling through negative regulations of the calmodulin-coding mRNAs, Mef2a and Gata4, mainly in smooth muscle cells. It`s believed that PE has associated with abnormal calcium metabolism and related consequences (Thway et al., 2004).

The association between PE and altered miRNA expression suggests the possibility of a functional role for miRNA in this disease. These different miRNAs may play an important role in pathogenesis of PE and may become diagnostic markers and therapeutic target for PE.

Conclusion

In summary, we have shown that there are many scientific evidences that have proven the fact that the differential placental and plasma miRNA expression is associated with PE. Some researches also identify novel candidate miRNAs (and pathways they regulate) that may be of etiologic relevance in the pathogenesis of PE. It provides novel targets for further investigation of the pathogenesis of PE and these differential miRNAs may be potential markers for the diagnosis and provide a potential therapeutic target for PE. Further investigations on posttranscriptional regulation in PE to evaluate biologic effects of identified miRNAs (including confirmations of miRNA and target gene interactions) are needed.

References

Bartel D.P. 2004. MicroRNAs: genomics, biogenesis, mechanism, and function. Cell, 116:281–97.

Bushati N, Cohen SM. MicroRNA functions. Annu Rev Cell Dev Biol 2007;23:175-205.

Carthew R.W. and Sontheimer E.J. 2009. Origins and mechanisms of miRNAs and siRNAs. Cell, 136:642–55.

Cerdeira A.S. and Karumanchi S.A. 2010. Biomarkers in Preeclampsia. In Biomarkers in Kidney Disease. Biomarkers in Kidney Disease, Elsevier Inc. 385-426.

Duley L. 2009. The global impact of pre-eclampsia and eclampsia. Semin Perinatol, 33:130e7.

Ender C. and Meister G. 2010. Argonaute proteins at a glance. Cell Sci, 123:1819-23.

Enquobahrie D.A., Abetew D.F., Sorensen T.K., Willoughby D., Chidambaram K. and Williams M.A. 2011. Placental microRNA expression in pregnancies complicated by preeclampsia. Am J Obstet Gynecol, 204(2):178.e12-21

Fabian M.R., Sonenberg N. and Filipowicz W. 2010a. Regulation of mRNA translation and stability by microRNAs. Annu. Rev. Biochem, 79:351–379.

Fabian M.R., Sundermeier T.R. and Sonenberg N. 2010b. Understanding How miRNAs Post-Transcriptionally Regulate Gene Expression. In Rhoads RE (Ed). miRNA Regulation of the Translational Machinery Progress in Molecular and Subcellular Biology 50. Springer-Verlag Berlin Heidelberg: 1-20.

Fasanaro P., D'Alessandra Y., Di Stefano V., Melchionna R., Romani S., Pompilio G., Capogrossi M.C. and Martelli F. 2008. MicroRNA-210 modulates endothelial cell response to hypoxia and inhibits the receptor tyrosine-kinase ligand Ephrin-A3. J Biol Chem, 283:15878-83.

Fei L.P., Li H.Y., Sha H., Liu L., Li Z.J. and Yi H.Y. 2009. The expression of microRNA in placenca from severe preeclampsia patients. Chinese Journal of Practical Gynecology and Obstetrics, 25(12):911-4.

Friedman R.C., Farh K.K., Burge C.B. and Bartel D.P. 2009. Most mammalian mRNAs are conserved targets of microRNAs. Genome Res, 9:92–105.

Garofalo M. and Croce C.M. 2011. microRNAs: Master Regulators as Potential Therapeutics in Cancer. Annu Rev Pharmacol Toxicol, 51:25–43.

Garzon R. Calin G.A. and Croce C.M. 2009. MicroRNAs in Cancer. Annu Rev Med, 60:167–79.

Gellhaus A., Schmidt M., Dunk C., Lye S.J., Kimmig R. and Winterhager E. 2006. Decreased expression of the angiogenic regulators CYR61 (CCN1) and NOV (CCN3) in human placenta is associated with pre-eclampsia. Mol Hum Reprod, 12:389-99.

Gu S. and Kay M.A. 2010. How do miRNAs mediate translational repression? Silence, 1:11-15

Hu Y., Li P., Hao S., Liu L., Zhao J. and Hou Y. 2009. Differential expression of microRNAs in the placentae of Chinese patients with severe pre-eclampsia. Clin Chem Lab Med, 47(8):923–9

Ikeda S., He A., Kong S.W., Lu J., Bejar R., Bodyak N., Lee K.H., Ma Q., Kang P.M., Golub T.R. and Pu W.T. 2009. MicroRNA-1 negatively regulates expression of the hypertrophy-associated calmodulin and Mef2a genes. Mol Cell Biol, 29:2193-204.

Jin P., Alisch R.S. and Warren S.T. 2004. RNA and microRNAs in fragile X mental retardation. Nat Cell Biol, 6:1048–53.

Kim Y.M., Romero R., Oh S.Y., Kim C.J., Kilburn B.A., Armant .R, Nien J.K., Gomez R., Mazor M., Saito S., Abrahams V.M. and Mor G. 2005. Toll-like receptor 4: a potential link between "danger signals," the innate immune system, and preeclampsia? Am J Obstet Gynecol, 193:921-7.

Krol J., Loedige I. and Filipowicz W. 2010. The widespread regulation of microRNA biogenesis, function and decay. Nat Rev Gene. AOP. doi:10.1038/nrg2843.

Lam C., Lim K.H. and Karumanchi SA. 2005. Circulating angiogenic factors in the pathogenesis and prediction of preeclampsia. Hypertension, 46:1077–85.

Lee Y.S. and Dutta A. 2009. MicroRNAs in Cancer. Annu. Rev. Pathol. Mech. Dis. 4:199–227

Levine R.J., Lam C., Qian C., Yu K.F., Maynard S.E., Sachs B.P., Sibai B.M., Epstein F.H., Romero R., Thadhani R. and Karumanchi S.A. 2006. 2006. Soluble endoglin and other circulating antiangiogenic factors in preeclampsia. N Engl J Med, 355:992e1005.

Levine R.J., Maynard S.E., Qian C., Lim K.H., England L.J., Yu K.F., Schisterman E.F., Thadhani R., Sachs B.P., Epstein F.H., Sibai B.M., Sukhatme V.P. and Karumanchi S.A. 2004. Circulating angiogenic factors and the risk of preeclampsia. N Engl J Med 350:672e83.

Matsui J., Wakabayashi T., Asada M., Yoshimatsu K. and Okada M. 2004. Stem cell factor/c-kit signaling promotes the survival, migration, and capillary tube formation of human umbilical vein endothelial cells. J Biol Chem, 279:18600–7.

Maynard S.E., Epstein F.H., Karumanchi S.A. 2008. Preeclampsia and angiogenic imbalance. Annu Rev Med, 59:61–78.

Maynard S.E., Min J.Y., Merchan J., Lim .K.H, Li J., Mondal S., Libermann T.A., Morgan J.P., Sellke F.W., Stillman I.E., Epstein F.H., Sukhatme V.P. and Karumanchi S.A. 2003. Excess placental soluble fms-like tyrosine kinase 1 (sFlt1) may contribute to endothelial dysfunction, hypertension, and proteinuria in preeclampsia. J Clin Investig, 111:649–58.

Mellembakken J.R., Aukrust P., Olafsen M.K., Ueland T., Hestdal K. and Videm V. 2002. Activation of leukocytes during the uteroplacental passage in preeclampsia. Hypertension 39:155–60.

Mo F.E., Muntean A.G., Chen C.C., Stolz D.B., Watkins S.C. and Lau L.F. 2002. CYR61 (CCN1) is essential for placental development and vascular integrity. Mol Cell Biol, 22:8709–20.

Mutter W.P. and Karumanchi S.A. 2008. Molecular mechanisms of preeclampsia. Microvascular Research, 75:1–8.

Nilsen T.W. 2007. Mechanisms of microRNA-mediated gene regulation in animal cells. Trends in Genetics, 23:243-249.

Pellish R.S., Nasir A., Ramratnam B. and Moss S.F. 2008. Review article: RNA interference - potential therapeutic applications for the gastroenterologist. Aliment Pharmacol Ther, 27:715–723

Pineles B.L., Romero R., Montenegro D., Tarca A.L., Han Y.M., Kim Y.M., Draghici S., Espinoza J., Kusanovic J.P., Mittal P., Hassan S.S. and Kim C.J. 2007. Distinct subsets of microRNAs are expressed differentially in the human placentas of patients with preeclampsia. Am J Obstet Gynecol, 196:261.e1-6.

Poliseno L., Tuccoli A., Mariani L., Evangelista M., Citti L., Woods K., Mercatanti A., Hammond S. and Rainaldi G. 2006. MicroRNAs modulate the angiogenic properties of HUVECs. Blood, 108:3068 –71.

Poy M.N., Eliasson L., Krutzfeldt J., Kuwajima S., Ma X., Macdonald P.E., Pfeffer S., Tuschl T., Rajewsky N., Rorsman P. and Stoffel M. 2004. A pancreatic islet-specific microRNA regulates insulin secretion. Nature, 432:226–30

Roberts J.M. and Hubel C.A. 2009. The Two Stage Model of Preeclampsia: Variations on the Theme. Placenta, 30 (23):S32–S37.

Ryan B.M., Robles A.I. and Harris C.C. 2010. Genetic variation in microRNA networks: the implications for cancer research. Nature Reviews Cancer, 10: 389-402.

Sibai B., Dekker G. and Kupferminc M. 2005. Pre-eclampsia. Lancet, 365:785–99.

Sun W., Li Y.S.J., Huang H.D., Shyy J.Y.J. and Chien S. 2010. microRNA: A Master Regulator of Cellular Processes for Bioengineering Systems. Annu Rev Biomed Eng, 12:1–27.

Thway T.M., Shlykov S.G., Day M.C., Sanborn B.M., Gilstrap L.C., Xia Y. and Kellems R.E. 2004. Antibodies from preeclamptic patients stimulate increased intracellular Ca^{2+} mobilization through angiotensin receptor activation. Circulation, 110:1612-9.

Venkatesha S., Toporsian M., Lam C., Hanai J., Mammoto T., Kim Y.M., Bdolah Y., Lim K.H., Yuan H.T., Libermann T.A., Stillman I.E., Roberts D., D'Amore P.A., Epstein F.H., Sellke F.W., Romero R., Sukhatme V.P., Letarte M. and Karumanchi S.A. 2006. Soluble endoglin contributes to the pathogenesis of preeclampsia. Nat Med, 12:642–49

WHO. 2005. World health report: Make every mother and child count. Geneva: World Health Organization.

Yang W.J., Yang D.D., Na S., Sandusky G.E., Zhang Q. and Zhao G. 2005. Dicer is required for embryonic angiogenesis during mouse development. J Biol Chem, 280:9330-5.

Yi R., Qin Y., Macara I.G. and Cullen B.R. 2003. Exportin-5 mediates the nuclear export of pre-microRNAs and short hairpin RNAs. Genes Dev, 17:3011–16.

Young B.C., Levine R.J. and Karumanchi S.A. 2010. Pathogenesis of Preeclampsia. Annu Rev Pathol Mech Dis, 5:173–92.

Zhang Y., Diao Z., Su L., Sun H., Li R., Cui H. and Hu Y. 2010. MicroRNA-155 contributes to preeclampsia by down-regulating CYR61. Am J Obstet Gynecol, 202:466.e1-7.

Zhou Y., McMaster M., Woo K., Janatpour M., Perry J., Karpanen T., Alitalo K., Damsky C. and Fisher S.J. 2002. Vascular endothelial growth factor ligands and receptors that regulate human cytotrophoblast survival are dysregulated in severe preeclampsia and hemolysis, elevated liver enzymes, and low platelets syndrome. Am J Pathol, 160:1405–23.

Zhu X.M., Han T., Sargent I.L., Yin G.W. and Yao Y.Q. 2009. Differential expression profile of microRNAs in human placentas from preeclamptic pregnancies vs normal pregnancies. Am J Obstet Gynecol, 200:661.e1-661.e7.