

# Genetics of Pre-eclampsia

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Pre-eclampsia is a major cause of maternal and perinatal mortality and morbidity worldwide, but remains unclear about the underlying disease mechanisms. Pre-eclampsia is currently believed to be a two-stage disease. The first stage involves shallow cytotrophoblast invasion of maternal spiral arteriole, resulting in placental insufficiency. The hypoxic placenta release soluble factors, cytokines, and trophoblastic debris into maternal circulation, which induce systemic endothelial damage and dysfunction. This cause the second stage of the disease: maternal syndrome. Epidemiological research has consistently demonstrated a familial predisposition to pre-eclampsia. Intensive research efforts have been made to discover susceptibility genes that will inform our understanding of the pathophysiology of pre-eclampsia and that may provide direction for therapeutic or preventative strategies. In this review, we summarize the current understanding of the role of genetic factors in the pathophysiology of pre-eclampsia and explain the molecular approach to search for genetic clues in pre-eclampsia.

**Key Words:** Pre-eclampsia, Genetics, Susceptibility gene

## Introduction

Pre-eclampsia is a pregnancy-specific syndrome that carries a high risk of maternal and perinatal mortality and morbidity. Pre-eclampsia affects 5 to 10% of all pregnancies and is characterized by the onset of hypertension and proteinuria after 20 weeks of gestation. It can progress to HELLP (hemolysis, elevated liver enzymes, and low platelet counts) syndrome and seizures (eclampsia). Despite decades of intense research on the problem, the mechanisms of the disease onset remains unclear.

Despite extensive clinical trials, no therapeutic approaches are currently available to either treat or prevent pre-eclampsia. Anti-hypertensive drugs, corticosteroids for lung maturation, and/or magnesium sulfate to prevent eclampsia are administered to handle (or prevent the worsening of) symptoms as a temporization strategy to allow safe delivery of a more mature fetus. However, when temporizing management, the maternal risks must be carefully weighed against the possible fetal benefits, as the risk of fatal deterioration of the health of the mother and/or fetus is high. Several prophylactic therapies (anti-oxidant vitamins, calcium or folic acid supplementation, aspirin) have so far not proved efficacious at preventing pre-eclampsia in healthy, nulliparous subjects, although these therapies have shown some benefits in groups<sup>1-4</sup>. As a consequence, the sole, albeit radical, way to resolve pre-eclampsia is to remove the placenta; in the case of prematurity, this results in delivery of a preterm baby.

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Therefore, pre-eclampsia, with or without intrauterine growth retardation (IUGR), remains a major cause of maternal and neonatal mortality and morbidity worldwide.

A number of epidemiological studies have confirmed that preeclampsia has a maternal genetic component. Daughters of pre-eclamptic women have a higher chance of themselves developing pre-eclampsia<sup>5)</sup>. Phenotyping patients with pre-eclampsia are vital for any genetic study. Furthermore, previous studies have provided compelling evidence that nulliparity, a family history of pre-eclampsia (sister/mother who suffered pre-eclampsia), a personal history of a previous pregnancy with pre-eclampsia, an increase in the trophoblastic mass (multiple pregnancy, molar pregnancy), paternity changes between pregnancies, age over 40 years, obesity, and some maternal chronic conditions such as diabetes, chronic hypertension, renal disease, autoimmune disease, and antiphospholipid syndrome are risk factors for pre-eclampsia<sup>6, 7)</sup>.

It has been recognized for many years that pre-eclampsia has a familial component, and the identification of susceptibility genes is one of a number of strategies designed to elucidate the underlying pathogenetic mechanisms of this condition. The objective of this review is to summarize our understanding of what role genetic factors play in the pathophysiology of pre-eclampsia and to describe the molecular approach to search for genetic clues in pre-eclampsia.

## Diagnosis

Pre-eclampsia is usually diagnosed by the presence of hypertension associated with proteinuria. Hypertension is defined as a blood pressure of at least 140 mm Hg (systolic) or at least 90 mm Hg (diastolic) on at least two occasions and at least 4-6 hrs apart after the 20 weeks of gestation in women known to be normotensive beforehand<sup>8-10)</sup>. Blood-pressure recordings to establish the diagnosis should be no more than 7 days apart<sup>8, 9, 11)</sup>. Hypertension is regarded as severe if there

are sustained rises in blood pressure to at least 160 mm Hg (systolic), at least 110 mm Hg (diastolic), or both<sup>8, 9, 11, 12)</sup>. Proteinuria is defined as excretion of 300 mg or more of protein every 24 hrs. If 24 hrs urine samples are not available, proteinuria is defined as a protein concentration of 300 mg/L or more ( $\geq 1+$  on dipstick) in at least two random urine samples taken at least 4-6 hrs apart<sup>8, 9)</sup>. The urine dipstick measurements used to establish proteinuria should be performed no more than 7 days apart<sup>8, 9, 11)</sup>.

Dependent on the amount of systemic involvement, several other symptoms, such as edema, disturbance of hemostasis, renal or liver failure, and HELLP syndrome also complicate the clinical picture. Pre-eclampsia can be early onset (pre-eclampsia starting before 34 weeks of gestation) or late onset (pre-eclampsia starting after 34 weeks of gestation), can show mild or severe symptoms (systolic blood pressure  $\geq 160$  mmHg or diastolic blood pressure  $\geq 110$  mmHg, proteinuria  $>5$  g/24 hrs, oliguria, neurological symptoms, other clinical symptoms such as deranged liver function, thrombocytopenia  $<100,000$  mm<sup>3</sup>, HELLP syndrome), and can evolve into eclampsia in the most severe cases (Table 1)<sup>13)</sup>. In addition, it can manifest as a maternal disorder only, with normal fetal growth, or intrauterine growth restric-

**Table 1.** Indicators of Severity of Pre-eclampsia<sup>13)</sup>

Abnormality	Nonsevere	Severe
Diastolic blood pressure	$<110$ mmHg	$\geq 110$ mmHg
Systolic blood pressure	$<160$ mmHg	$\geq 160$ mmHg
Proteinuria	$\leq 2+$	$\geq 3+$
Headache	Absent	Present
Visual disturbances	Absent	Present
Upper abdominal pain	Absent	Present
Oliguria	Absent	Present
Convulsion (eclampsia)	Absent	Present
Serum creatinine	Normal	Elevated
Thrombocytopenia	Absent	Present
Serum transaminase elevation	Minimal	Marked
Fetal-growth restriction	Absent	Obvious
Pulmonary edema	Absent	Present

tion of the fetus (IUGR) or sudden fetal distress may occur.

The traditional criteria used to confirm a diagnosis of pre-eclampsia (new onset of both hypertension and proteinuria after 20 weeks' gestation) are applicable to most healthy, nulliparous women. However, the criteria mentioned so far are not reliable in women who have either hypertension or proteinuria before 20 weeks' gestation, especially those receiving antihypertensive drugs<sup>10, 14, 15</sup>. Because of the physiological changes leading to raised maternal blood pressure and increased protein excretion with advanced gestation in such women, more stringent criteria should be used to diagnose pre-eclampsia in those with microvascular disease<sup>10, 14, 15</sup>. Consequently, markers to predict and methods to prevent pre-eclampsia in these women are probably different from those in healthy nulliparous women.

## Pathophysiology

The precise origin of pre-eclampsia remains elusive, but it is believed to be multifactorial. A certainty is the central role played by the placenta<sup>16, 17</sup>. A long standing hypothesis has been that pre-eclampsia develops as a

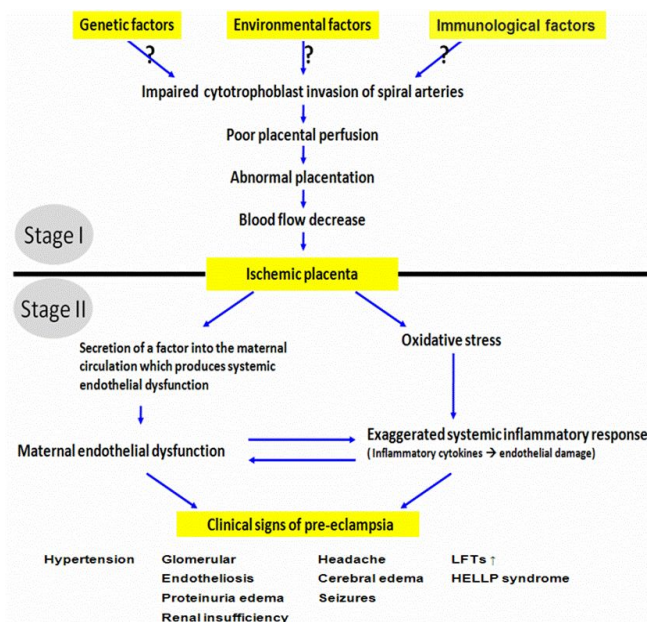


Fig. 1. Pathophysiological mechanisms in pre-eclampsia<sup>18</sup>.

consequence of some kind of immune maladaptation between the mother and the fetus during the very first weeks of pregnancy, leading to the following two-stage progression (Fig. 1)<sup>18</sup>. In the first asymptomatic stage, local aberrant feto-maternal immune interactions within the uterine wall lead to impaired tissue and arterial invasion by trophoblast cells (Fig. 2)<sup>19</sup>. This results in failed transformation of the uterine spiral arteries and subsequently poor placental perfusion. Chronic hypoxia or alternate periods of hypoxia/re-oxygenation within the intervillous space are expected to trigger tissue oxidative stress and increase placental apoptosis and

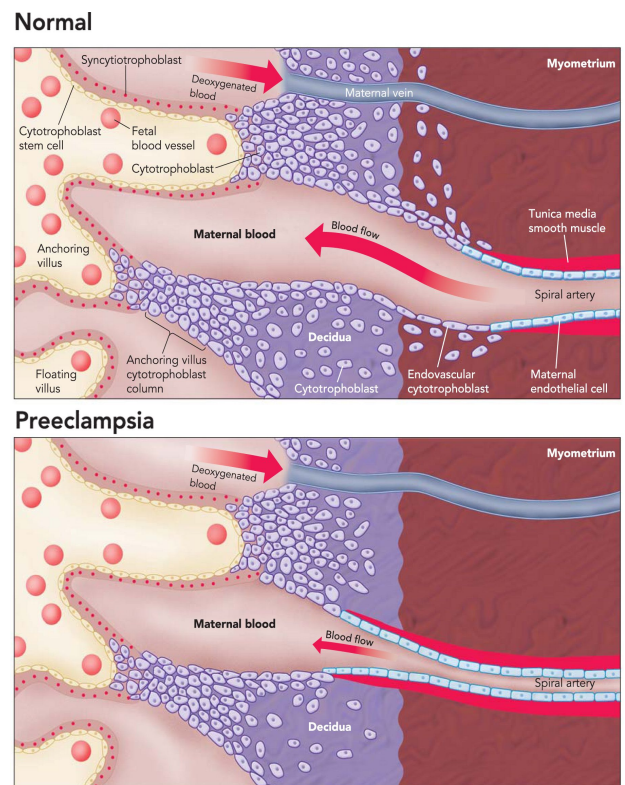


Fig. 2. Abnormal placentation in pre-eclampsia<sup>19</sup>. In normal placental development, invasive cytotrophoblasts of fetal origin invade the maternal spiral arteries, transforming them from small-caliber resistance vessels to high-caliber capacitance vessels capable of providing placental perfusion adequate to sustain the growing fetus. During the process of vascular invasion, the cytotrophoblasts differentiate from an epithelial phenotype to an endothelial phenotype, a process referred to as "pseudovasculogenesis" or "vascular mimicry" (top). In preeclampsia, cytotrophoblasts fail to adopt an invasive endothelial phenotype. Instead, invasion of the spiral arteries is shallow, and they remain small caliber, resistance vessels (bottom).

necrosis<sup>20, 21</sup>). In the second stage, the clinical disorder arises, when the maternal vascular and immune systems can no longer handle the high levels of shedding of placentally produced debris and the aberrant expression of pro-inflammatory, anti-angiogenic and angiogenic factors, leading to systemic endothelial cell dysfunction and an exaggerated inflammatory response<sup>22-24</sup>). Recently, this hypothesis has been challenged<sup>25</sup>). It was proposed instead that an intrinsic failure of trophoblast differentiation at different time points of ontogeny may lead to either a mild disorder with late-onset appearance, or IUGR, with or without maternal symptoms. However, the origin of pre-eclampsia might not be restricted to an alteration in trophoblast differentiation, but may also in some cases depend on underlying maternal constitutional factors such as genetic factors, obesity, dysfunctional maternal clearance, or a dysfunctional maternal inflammatory system<sup>26</sup>).

### Candidate genes

Various candidate gene studies have been performed to identify associations between pre-eclampsia and genetic polymorphisms in specific genes between cases and controls. Candidate genes are genes with documented biological actions in pathways known to be active in pre-eclampsia that are polymorphic. Single nucleotide polymorphisms (SNPs) are the markers most commonly used to determine genetic associations. Recent initiatives such as the HapMap project (<http://www.hapmap.org/>) and the establishment of the dbSNP database (<http://www.ncbi.nlm.nih.gov/projects/SNP/>) have resulted in the identification of multiple SNPs in all human genes.

In association studies, the frequency of alleles and genotypes (homozygous and heterozygous) in the disease group and a healthy population are compared. The most advanced type of association study is a case-control study, where subjects are matched for age and ethnicity. Association studies involving unrelated sub-

jects allow the detection of common variants or common alleles of small effect. In these types of studies, it is also possible to determine those genes that have a weak influence on disease risk. Currently, more than 60 candidate genes related to pre-eclampsia development have been identified, and several groups of candidate genes have been distinguished based on the pathophysiology of pre-eclampsia. The genes that have been most frequently investigated are those involved in blood pressure regulation (angiotensinogen, angiotensin-converting enzyme, and angiotensin receptors), inherited thrombophilias (coagulation factor V Leiden variant, prothrombin, and methylene tetrahydrofolate reductase), vasodilatation regulating genes (endothelial nitric oxide synthase, eNOS), and the gene encoding the cytokine tumor necrosis factor alpha (TNF  $\alpha$ ) (Table 2)<sup>27-69</sup>). However, our studies based on examinations in Korean population have suggested that the contribution of genetic polymorphism of  *$\beta$ -adrenoceptor*, *EDNI*, *ICAM-1*, *INHA*, *STOX1*, and *TNF* genes to the occurrence of pre-eclampsia is few. It seems that pre-eclampsia is a disease with polygenic inheritance patterns, influenced by environmental factors, gene-gene and gene-environmental interactions<sup>70-75</sup>).

It must be conceded that over a decade of molecular genetic research has failed to identify a single universally accepted susceptibility gene for pre-eclampsia. There has been a lack of reproducibility of results, as has been the experience with many complex disorders. Possible explanations have been discussed widely<sup>76</sup>), and studies of pre-eclampsia share some of these generic problems. Progress in this field will require attention to both study design and the choice of candidate genes.

### Meta-analyses

It has been argued that the stringent criteria used in association studies may be impractical and that more insight might be gained by combining the results of

**Table 2.** Candidate Gene Studies in Pre-eclampsia

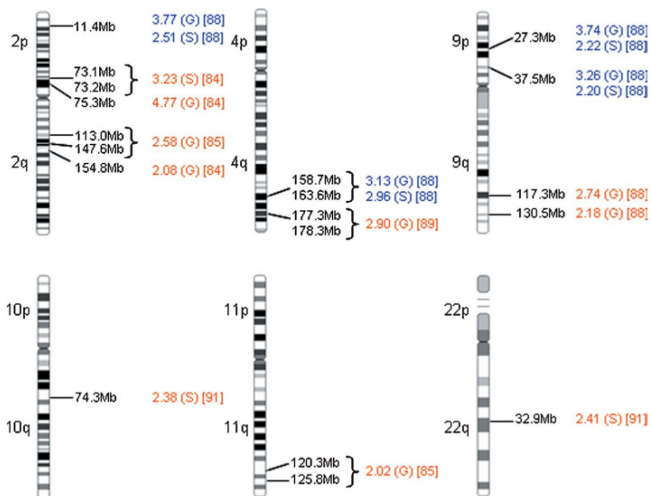
Gene name	Gene symbol	References	Gene name	Gene symbol	References
Thrombophilia			Interleukin 1 $\beta$	<i>IL1B</i>	48
Factor V Leiden	<i>F5</i>	27-29	Interleukin 1 receptor antagonist	<i>ILIRN</i>	49
Prothrombin 20210	<i>F2</i>	29,30	Interlukin 10	<i>IL10</i>	50
Methylene tetrahydrofolate reductase	<i>MTHFR</i>	27-29,31,32	T-lymphocyte-associated protein 4	<i>CTLA4</i>	51
Cystathione $\beta$ -synthase	<i>CBS</i>	28	TNF-receptor supergamilt member 6	<i>FAS</i>	52
Plasminogen activator inhibitor 1	<i>SERPINE1</i>	29,32	Oxidative stress		
$\beta$ -Fibrinoten	<i>FGB</i>	33	Microsomal epoxide hydrolase	<i>EPHX1</i>	53
Platelet glycoprotein IIIa	<i>ITGB3</i>	30	Glutathione S-transferase pi	<i>GSTP1</i>	41,54
Thrombomodulin	<i>THBD</i>	34	Glutathione S-transferase mu 1	<i>GSTM1</i>	54,55
Factor VII	<i>F7</i>	33	Glutathione S-transferase theta I	<i>GSTT1</i>	54,55
Platelet collafen receptor $\alpha$ 2 $\beta$ 1	<i>ITGA2</i>	29	Myeloperoxidase	<i>MPO</i>	55
Factor XIII A-subunit	<i>F13A1</i>	35	Manganese superoxidase dismutase	<i>SOD2</i>	55
Haemodnamics			Cytochrome IAI	<i>CYP1A1</i>	54,55
Angiotensinoten	<i>AGT</i>	32,36	Haptoglobin	<i>HP</i>	56
Renin	<i>REN</i>	37	p22 <sup>phox</sup>	<i>CYBA</i>	57
Angiotenin-converting enzyme	<i>ACE</i>	32,36	Lipid metabolism		
AT1 receptor	<i>AGTR1</i>	32,36	Lipoprotein lipase	<i>LPL</i>	58
AT2 receptor	<i>AGTR2</i>	38	Apolipoprotein E	<i>APOE</i>	59
Epithelial sodium channel	<i>SCNN1B</i>	39	Peroxisome-proliferator-activated receptor $\gamma$	<i>PPARG</i>	60
Endothelial function			Cholesteryl ester transfer protein	<i>CETP</i>	61
Enos	<i>NOS3</i>	40	$\beta$ 3-Adrenergicreceptor	<i>ADRB3</i>	62
Endothelin 1	<i>EDN1</i>	41	Endocrine		
Dimethylarginne dimethylaminohydrolase 1	<i>DDAH1</i>	42	Oestrogen receptor	<i>ESR1</i>	63
Dimethylarginne dimethylaminohydrolase 2	<i>DDAH2</i>	42	Oestrogen receptor	<i>ESR2</i>	64
G-protein $\beta$ 3	<i>GNB3</i>	43	Androgen receptor	<i>AR</i>	65
Cytokines			Inhibin $\alpha$	<i>INHHA</i>	66
TNF $\alpha$	<i>TNF</i>	32,44	Angiogenesis		
TGF $\beta$ 1	<i>TGF</i>	45	VEGF	<i>VEGF</i>	67
IGF II	<i>IGF2</i>	46	Matrix metallopeptidase 1	<i>MMP1</i>	68
Interleukin 1 $\alpha$	<i>IL1A</i>	47	Catechol-methyltransferase	<i>COMT</i>	69

several smaller studies in a Meta-analyses. One recent Meta-analyses failed to find any evidence for an increased risk of pre-eclampsia associated with the *MTHFR* 677C>T variant [pooled odds ratio, 1.01 (95% CI, 0.79-1.29)]<sup>77</sup>; an earlier Meta-analyses suggested that 677C>T may be associated with severe pre-eclampsia only [diastolic blood pressure  $\geq$ 110 mm Hg; odds ratio, 1.41 (95% CI, 1.03-1.73)]<sup>78</sup>. Meta-analyses of prothrombin 20210G>A did not support a role for this polymorphism in pre-eclampsia [odds ratio, 1.37 (95% CI, 0.72-2.57)]<sup>77</sup>. Factor V Leiden was associated with an approx. 2-fold increase in risk of pre-eclampsia

in three separate meta-analyses, although many of the same studies were incorporated in these particular meta-analyses<sup>77, 79, 80</sup>. Some important general points have emerged from these meta-analyses. There was considerable variation in the recruitment protocols for case-control studies and in the phenotypic profile of affected women. Furthermore, there was statistical evidence of heterogeneity between the results of studies; in particular, large studies and studies published within the last few years tended to yield negative results, whereas the majority of positive results came from earlier and smaller studies.

## Genome-wide linkage analysis

Genome-wide linkage analysis is the study of genetic variations across the entire human genome. Genome-wide screening has the potential to detect genetic loci that contribute to susceptibility to pre-eclampsia and identify susceptibility loci for development of this disease. Linkage analysis has proved its worth in identifying the molecular basis of many Mendelian disorders, but has been less successful in guiding the search for susceptibility genes for complex disorders. This may be due to underlying genetic heterogeneity (susceptibility loci may differ between affected pedigrees) or to the relatively low genetic risk of disease conferred by individual genes in a complex mode of inheritance. Ascertainment of multicaser families presents difficulties in studies of pre-eclampsia, as there is no known male phenotype, and susceptibility in females is apparent only during pregnancy. Nevertheless, research groups from Iceland, Australia, Finland, and Netherlands have undertaken genome-wide linkage screens which have yielded encouraging results (Fig. 3)<sup>81</sup>. The studies in



**Fig. 3.** Chromosomal loci linked to pre-eclampsia<sup>81</sup>. Chromosomal position is given according to NCBI (National Center for Biotechnology Information) Build 35.1. LOD scores (red) or non-parametric linkage scores (blue) are shown; the highest scores provide the strongest evidence of linkage. The results of linkage analysis using both strict diagnostic criteria (S, pre-eclampsia/eclampsia only) and general diagnostic criteria (G, includes pregnancy-induced hypertension) are shown.

Australia indicated the *PREG1* gene as a contributor of pre-eclampsia development<sup>82</sup>. In a genome-wide linkage analysis of Icelandic families representing 343 affected women, a significant locus was found on chromosome 2 (2p13)<sup>83</sup>, while in another genome-wide linkage study of pre-eclampsia, evidence was found for a candidate region on 4q<sup>84</sup>. In a large Norwegian population (case-control study, 1139 cases, 2269 controls), 71 SNPs within candidate genes in the region 2q22-23 were genotyped. The gene encoding activin receptor 2 (*ACVR2A*) lies within this region. Activin is a possible autocrine/paracrine regulator of the human placenta<sup>85</sup>. The type II activin receptor has a molecular weight of 85 kD, and there are two receptor isoforms (*ACVR2A* and *ACVR2B*) that have tissue- and temporal-specific differences. The available evidence suggests that *ACVR2A* may play a role in the etiology of pre-eclampsia<sup>86, 87</sup>.

Epigenetic markers and gene-gene interactions have also been investigated in genome-wide association studies to elucidate the pathophysiological processes involved in pre-eclampsia. It has been proposed that *SERPIN* (serine protease inhibitor) proteins could contribute to the development of pre-eclampsia. *SERPIN* genes encode more than 36 proteins with various functions ranging from protease inhibitors, storage proteins, carrier proteins, to hormone precursors without an inhibitory function. *SERPIN* family proteins are involved in the coagulation and fibrinolysis cascade, inflammatory processes, complement activation, and phagocytosis. Alterations in promoter methylation (hypomethylation or total methylation) of the genes encoding *SERPIN* proteins could play a role in transcriptional regulation (alterations in CpG methylation can influence the binding of transcription factors) and activity of *SERPIN* genes.

Much attention has been paid to the gene coding for *SERPINA3* (alpha-1-antichymotrypsin), which is thought to be involved in pre-eclampsia<sup>88</sup>. Recently, *STOX1* (storkhead box 1) missense mutations have been suggested to predispose to pre-eclampsia in Dutch families<sup>89</sup>. *STOX1* is a transcriptional factor that is encoded by

a gene on chromosome 10 (10q22). This factor is placentally expressed and controls polyploidization of extravillous trophoblasts. Four *STOX1* transcripts are expressed in the early placenta (including extravillous trophoblasts), and alterations in *STOX1* activity have been implicated in pre-eclampsia susceptibility. Several recent studies, however, have contested the generality of the involvement of this gene<sup>90</sup>. Further investigation into the function of *STOX1* is therefore required to determine if this gene is indeed involved in the pathophysiological cascades that lead to the onset of pre-eclampsia.

It should be noted that there is little overlap between the loci identified in different populations in these analyses, possibly because of genetic differences between populations, highlighting the importance of carrying out genetic studies in different parts of the world.

## Conclusion

Genetic screening could potentially be the initial step in pre-eclampsia prevention/treatment and could increase our understanding of the pathophysiological mechanisms underlying pre-eclampsia. Where should genetic studies of pre-eclampsia be directed? Recent genome-wide linkage analysis of families affected by pre-eclampsia has yielded encouraging results. In contrast, the credibility of candidate gene studies has been undermined by conflicting and inconclusive results. It is clear that large studies that have adequate statistical power to detect small genetic effects are needed to reliably identify or exclude susceptibility genes. This invites a multicentre collaborative approach between clinicians and geneticists to develop common recruitment protocols for the establishment of large DNA resource databases that can be used by statisticians to conduct meaningful meta-analyses. The results of pathophysiological and genetic studies have provided some insights into the nature of pre-eclampsia, but an understanding of the fundamental causes of pre-eclampsia remains tantalizingly elusive.

## 국문초록

자간전증은 전세계적으로 모성 및 주산기 사망과 이환의 주된 원인이나 아직까지 병인기전은 명확하게 규명되지 않은 실정이다. 자간전증은 일반적으로 두 단계 질환으로 알려져 있으며, 그 임상상의 첫 단계는 모체의 나선동맥의 얇은 세포영양아층 침투에 의한 태반 부전이 발생한다. 태반 부전에 의한 허혈성 태반이 모체의 순환 혈류 내로 용해성 인자와 싸이토카인, 영양막 조직파편을 유리하면, 전신적인 내피세포 손상 및 기능 부전을 야기하고, 이로 인하여 자간전증 이차 단계인 모체 증후군이 나타난다. 역학적 연구에서 자간전증에 대한 유전적 소인이 일관되게 증명되었다. 집중적 연구 노력에 의한 감수성 유전자 발견은 자간전증의 병태생리를 이해하는데 있어서 유용한 정보를 줄 것이며 자간전증의 치료 및 예방 방법에 대한 방향을 제시할 것이다. 본 주제에서는 자간전증의 병태생리에 있어서 유전적 요인의 역할에 대한 최신 이해를 요약하고 자간전증의 유전적 실마리를 찾기 위한 분자적 접근에 대해 설명하고자 한다.

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