



Genome-wide association study identifies *WWC2* as a possible locus associated with persistent pulmonary hypertension of the newborn in the Thai population

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Background: There is known to be significant genetic involvement in persistent pulmonary hypertension of the newborn (PPHN), but to date there is not a clear understanding of this situation, and clarifying that involvement would be of considerable assistance in devising effective treatments for the disease. This case-control study was undertaken to search for genetic variants associated with PPHN in the Thai population using a genome-wide association study (GWAS).

Methods: A 659,184 single nucleotide polymorphisms from 387 participants (54 PPHN cases and 333 healthy participants) were genotyped across the human genome using an Illumina Asian Screening Array-24 v1.0 BeadChip Array. After quality control, we obtained 443,063 autosomal SNPs for the GWAS analysis. The FaST-LMM and R packages were used for all statistical analyses.

Results: For the case-control analysis, the genomic inflation factor (λ) was 1.016, rs149768622 T>C in the first intron of *WWC2* gene showed the strongest association with a P value of 3.76E-08 and odds ratio (OR) of 13.24 (95% CI: 3.91–44.78). The variants at the *LOC102723906/LOC105377599*, *CADM4*, *GPM6A*, *CIT*, *RIMBP2*, *LOC105374510*, *LOC105375193*, *PTPRN2*, *CDK14*, and *LCORL* loci showed suggestive evidence of associations with PPHN ($P < 1E-05$).

Conclusions: This GWAS found that rs149768622 T>C in the *WWC2* gene was possibly associated with PPHN. However, replication and functional studies are needed to validate this association and further explore the role(s) of the *WWC2* gene in PPHN.

Keywords: *WWC2*; persistent pulmonary hypertension of the newborn (PPHN); genetic variant; single nucleotide polymorphism (SNP); genome-wide association study (GWAS)

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Introduction

Persistent pulmonary hypertension of the newborn (PPHN) is a serious respiratory disease characterized by an elevation in pulmonary vascular resistance in the neonatal pulmonary circulation (1). PPHN results from a failure of pulmonary vasculature relaxation, which in turn results in shunting of non-oxygenated blood from the pulmonary to the systemic circulation at birth. Recent studies have reported incidences of PPHN ranging between 1.2 and 4.6 per 1,000 live-births (2,3). There are various etiologies of PPHN, most commonly meconium aspiration syndrome, transient tachypnea of the newborn, and respiratory distress syndrome. PPHN also manifests in patients with congenital anomalies (e.g., congenital diaphragmatic hernia or lung hypoplasia) (2,4,5). Other causes of PPHN that are unrelated to respiratory conditions include sepsis, birth asphyxia, and maternal drug/smoke exposure (6,7). A small

fraction of patients without any of the above-mentioned risk factors are diagnosed with idiopathic PPHN.

PPHN is a complex disease that is attributable to genetic variants of multiple genes and environmental influences. Proper lung development depends on timely action from various genes, and mutations in any of these genes can result in maldevelopment of abnormal growth in the lungs, which can lead to pulmonary hypertension (8). Genetic mutations also can adversely result in either maladaptation or abnormal growth of the lung, which ultimately leading to pulmonary hypertension (8). To date, little is conclusively known concerning genetic involvement with PPHN. Numerous studies have examined the genes that encode certain proteins related to proper lung development, such as vasodilators, vasoconstrictors, surfactants, vascular growth factors, and serotonin receptors, from which studies only a few genetic loci have been identified in patients with PPHN, including the *CRHR1*, *CPS1*, *EDN1*, *NOTCH3*, *EPAS1*, *TTL3*, *ITGAM*, *TBX4*, and *SMAD9* genes (9-16). Few of these studies used a genome-wide approaches (13,14). Genetic studies in individuals with pulmonary arterial hypertension (PAH) are also helpful in understanding the contributions to PPHN, although the disease mechanisms of this condition are slightly different from PAH (17,18). An extensive literature review by Morrell *et al.* summarized the presence of causal mutations of genes, identifying *BMPR2*, *EIL2AK4*, *TBX4*, *ATP13A3*, *GDF2*, *SOX17*, *AQP1*, *ACVRL1*, *SMAD9*, *ENG*, *KCNK3*, *CAV1*, *SMAD4*, *SMAD1*, *KLF2*, *BMPR1B*, and *KCNA51* in adult or childhood onset PAH (19).

A genome-wide association study (GWAS) is a study in which genotypes of multiple genetic loci of the human genome of patients and healthy controls are analyzed to search for specific genetic variations that are associated with a particular disease in order to gain a better understand of how these genes contribute to the disease. In this study, we performed a GWAS to search for genetic variants associated with PPHN. We also summarized the genetic findings related to PPHN from previous studies. We present the following article in accordance with the STREGA reporting checklist (available at <https://tp.amegroups.com/article/view/10.21037/tp-22-280/rc>).

Highlight box

Key findings

- A genome-wide association study (GWAS) showed that a single nucleotide polymorphism (SNP) rs149768622 T>C in the *WWC2* gene was associated with persistent pulmonary hypertension of the newborn (PPHN) (P=3.76E-08, odds ratio 13.24, and 95% CI: 3.91–44.78). *WWC2* protein plays a role in the formation of critical alveoli.

What is known and what is new?

- PPHN is attributable to genetic polymorphisms of multiple genes and environment. SNPs in genes, such as *CRHR1*, *CPS1*, *EDN1*, *NOTCH3*, *EPAS1*, and *SMAD9* were reportedly associated with PPHN.
- This study is the first to utilize GWAS in searching for genetic polymorphisms associated with PPHN.
- *WWC* gene is a possible candidate gene modulating the risk for PPHN.

What is the implication?

- Further studies regarding functional effects of *WWC2* gene in PPHN should be carried out.
- Genetic testing of identified genetic variants in at risk families provides information whether the next children should be closed monitoring during perinatal period.

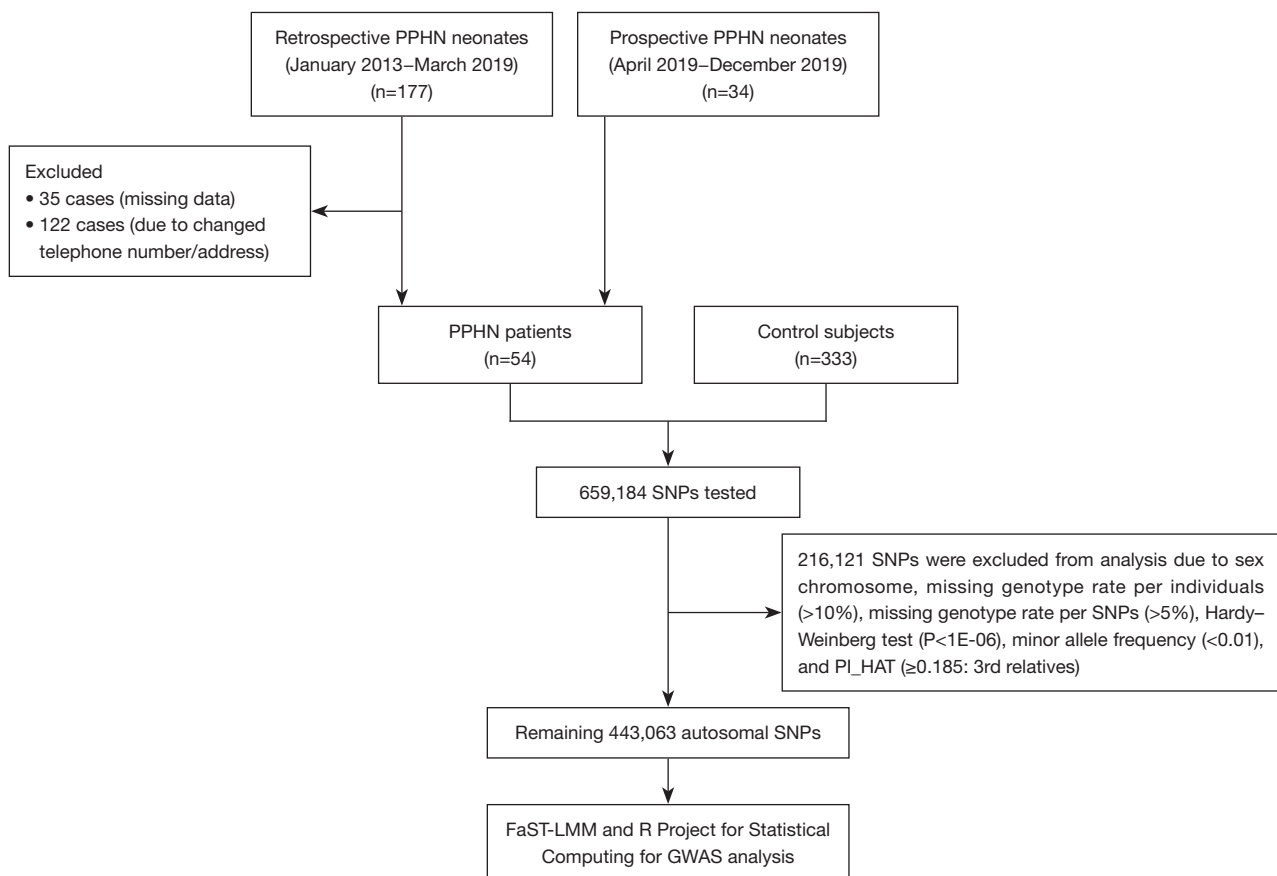


Figure 1 A flow chart illustrating subject selection and study workflow. PPHN, persistent pulmonary hypertension of the newborn; SNPs, single nucleotide polymorphisms; FaST-LMM, Factored Spectrally Transformed Linear Mixed Models; R, R Program for statistical analysis; GWAS, genome-wide association study.

Methods

Study population

The GWAS data were obtained from a previous study in which we investigated associations between selected genes involved in the pathogenesis of PPHN (16). A total of 54 infants, who were diagnosed with PPHN between January 2013 and December 2019, were recruited into this case-control study. The inclusion criteria were infants who were diagnosed with PPHN and were born to mothers with gestational age of ≥ 35 weeks and birth weight of $\geq 2,000$ g. Infants who had congenital malformations or recognizable genetic diseases, e.g., congenital cyanotic heart disease, congenital diaphragmatic hernia, or chromosomal disorders, were excluded from the study. The diagnostic criteria for PPHN were refractory hypoxia and one of the

three following conditions: (I) documented pulmonary hypertension as defined by echocardiographic evidence of elevated pulmonary pressure (right to left or bidirectional shunt); (II) a pre- to post ductal partial pressure of oxygen gradients equal to or greater than 20 mmHg; and/or (III) a pulse oximetry oxygen saturation gradient equal to or greater than 10% (20). For a control group, we recruited 100 healthy newborns. In addition, we included 233 healthy adults who had participated in the Thai SNP Database Project of Ramathibodi Hospital, 333 control participants were finally included in this study. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The study was approved by the Research Ethics Committee of Hat Yai Hospital (No. 24/2562) and informed consent was taken from the patients' parents. A flow diagram of the analysis is shown in *Figure 1*.

Table 1 Baseline characteristics of the 54 enrolled PPHN patients

Characteristic	Values
Gestational age (weeks)	39.5±2.1
Birth weight (g)	3,105±471
Age	
PPHN subjects from prospective recruitment (days) (n=25)	2 (1.0–4.0)
PPHN subjects from retrospective data (years) (n=20)	2.3 (1.0–3.5)
Gender	
Male	32 (59.3)
Female	22 (40.7)
Perinatal history	
Apgar score at 1 minute	8 (7–9)
Apgar score at 5 minutes	9 (8–9)
Causes of PPHN	
Meconium aspiration syndrome	25 (46.3)
Transient tachypnea of the newborn	13 (24.1)
Congenital pneumonia	7 (13.0)
Respiratory distress syndrome	5 (9.3)
Neonatal sepsis	2 (3.7)
Idiopathic PPHN	1 (1.9)
Birth asphyxia	1 (1.9)
Treatment modalities of PPHN	
High-frequency oscillatory ventilation	38 (70.4)
Intravenous iloprost	15 (27.8)
Intragastric sildenafil	39 (72.2)
Inhaled nitric oxide	46 (85.2)
Intravenous milrinone	25 (46.3)
Hydrocortisone	23 (42.6)
Sedation	54 (100.0)
Analgesia	54 (100.0)
Inotropic agents	54 (100.0)
Outcomes	
Length of supplemental oxygenation (days)	24 (16–30)
Length of hospital stay (days)	22 (16–34)
In-hospital mortality	2 (3.7)

Data are presented as mean ± standard deviation, median (interquartile range), or n (%). PPHN, persistent pulmonary hypertension of the newborn.

Genotyping and quality control in the GWAS

We performed single nucleotide polymorphism (SNP) genotyping by using an Illumina Asian Screening Array-24 v1.0 BeadChip, following the Illumina Infinium HTS Assay protocol (Illumina, San Diego, CA, USA). The array platform contained 659,184 SNPs probes across the genome. We applied standard SNP quality control filters to exclude SNPs with a low call rate of <98%, a missing genotype rate per individual of >10%, a missing genotype rate per SNPs of >5%, gender inconsistency based on the heterozygosity rate of the X chromosome (maleTh =0.8, femaleTh =0.2), Hardy-Weinberg equilibrium test ($P < 1E-06$), minor allele frequency (MAF) of each SNP of <0.01, and genome-wide estimates of identity-by-descent ($\text{pihat} \geq 0.185$ (3rd generation)). We were left with 443,063 variants after quality control.

Statistical analysis

This study used the FaST-LMM (V2.02.20121124) and R Project for general statistical analysis. A Manhattan plot of $-\log_{10}P$ was generated using the R package. Quantile-quantile plots (Q-Q plots) were used to assess the overall quality of the GWAS. Significant SNPs with a strong association for PPHN were defined as having statistical significance at the genome-wide association P value threshold of <1E-08 and SNPs with suggestive evidence for PPHN with a P value threshold of <1E-05.

Results

Among the 54 infants with PPHN, approximately two-thirds had meconium aspiration syndrome or transient tachypnea of the newborn, with frequencies of 46.3% and 24.1%, respectively. Idiopathic PPHN was diagnosed in one patient (1.8%). The mean gestational age was 39.5±2.1 weeks, the mean birthweight was 3,105±471 g, and the median Apgar scores at 1 minute and 5 minutes were 8 and 9, respectively. A summary of the baseline characteristics is shown in *Table 1*.

SNP association analysis

The GWAS results for the 443,063 markers that were included in the further analysis of this study showed good overall quality of the GWAS. The genomic inflation factor (λ) was 1.016 (*Figure 2A*). In this study, the rs149768622 T>C SNP, which is located in the intronic area of the *WW*

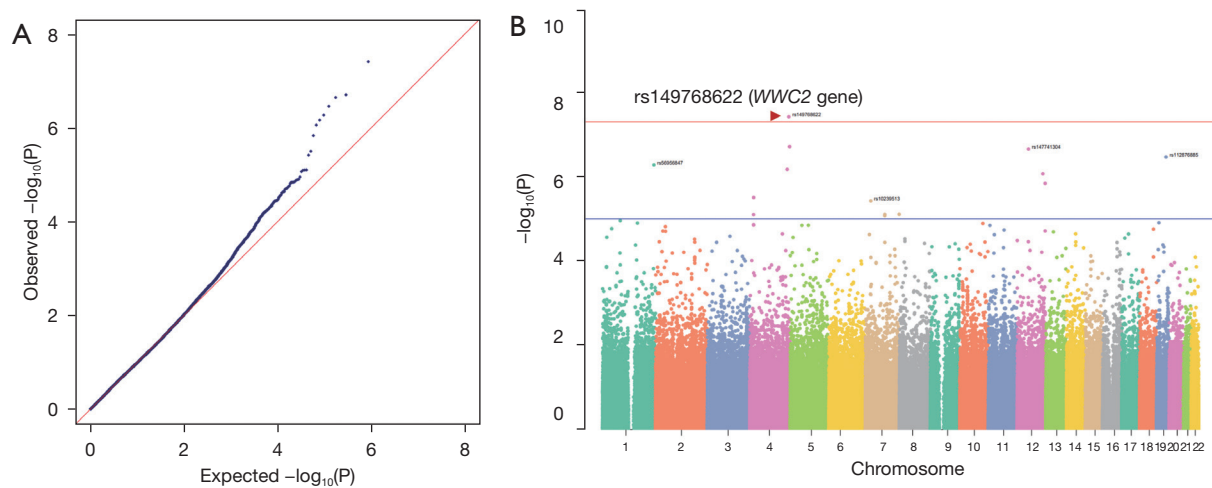


Figure 2 (A) Q-Q plot of the GWAS for PPHN (genomic inflation factor =1.016). (B) The Manhattan plot shows P values for PPHN patients versus healthy controls using logistic regression analysis. The X-axis represents the SNP markers in each chromosome and the Y-axis shows negative logarithm of P values. A total of 443,063 SNPs are included. The highest P value ($P=3.76E-08$) was observed in the rs149768622 gene on the intronic region of the *WWC2* gene (arrowhead). Q-Q plot, quantile-quantile plot; GWAS, genome-wide association study; PPHN, persistent pulmonary hypertension of the newborn; SNP, single nucleotide polymorphism.

and *C2 Domain Containing 2 (WWC2)* gene on chromosome 4 (4q35.1) had the highest P value ($P=3.76E-08$) and odds ratio (OR) 13.24 [95% confidence interval (CI): 3.91–44.78] (Figure 2B). The variants at the rs78232913 (*LOC102723906/LOC105377599*), rs147741304 (intergenic area), rs112876885 (*CADM4*), rs56956847 (intergenic area), rs191330351 (*GPM6A*), rs56074206 (*CIT*), rs7134357 (*RIMBP2*), rs145547469 (*LOC105374510*), rs10239513 (*LOC105375193*), rs11764121 (*PTPRN2*), rs144344757 (*CDK14*), rs187729743 (*LCORL*) and rs79741635 (intergenic area) loci showed suggestive evidence of associations with PPHN (P value $<1E-05$). The significant findings of our GWAS are summarized in Table 2.

For genotype distribution and allele frequency, the allele frequency of the minor allele “C” of rs149768622 in the *WWC2* gene showed a significant difference between the PPHN and control groups (0.074 vs. 0.006, respectively). In addition to *WWC2*, the suggestive candidate polymorphisms of other genes are summarized in Table 2.

Gene network analysis of candidate genes from the GWAS

A gene network of 8 candidate genes in this study (1 strong evidence, the *WWC2* gene, and 7 with suggestive evidence, the *CADM4*, *GPM6A*, *CIT*, *RIMBP2*, *PTPRN2*, *CDK14*, and *LCORL* genes) and previous genes that were reported

to be related to PPHN were analyzed. Genes within the biological network of the *WWC2* gene were also included (Figure S1).

Discussion

A number of genetic studies have been conducted to identify genetic factors contributing to PPHN. Most of these studies have focused on evaluating selective SNPs on genes associated with the biological pathways related to the pathogenic mechanisms that contribute to PPHN, such as pulmonary surfactants, endothelin, phosphodiesterase, enzymes in the corticosteroid pathway, and enzymes in the urea cycle pathway. Genetic associations have been identified on multiple genomic loci across the genome. As PPHN and PAH result from the contributions of multiple genetic variants in conjunction with environmental influences, they are considered a complex disease. For a complex disease, GWAS is a cost-effective method for studying multiple genetic variants across the genomes of large numbers of individuals to identify associations between genotypes and a phenotype. GWAS is typically carried out by genotyping of several hundred thousand SNPs using high throughput technologies (e.g., microarray, next generation sequencing). Unlike traditional gene mapping methods, GWAS can be performed on collections of individuals with unknown

Table 2 List of significant variants found in this study

Chr	SNP	Gene (protein)	Protein function	Ref. allele	Risk allele	MAF		Functional consequence	GWAS	
						PPHN	Control		OR	P
4q35.1	rs149768622	WWC2 (WW and C2 Domain Containing 2)	Modulator in Hippo pathway signaling	T	C	0.074	0.006	Intron variant	13.24 (3.91–44.78)	3.76E-08
4q35.2	rs78232913	LOC102723906; LOC105377599	Uncharacterized gene thought to produce ncRNA	G	A	0.065	0.005	LOC102723906: intron variant; LOC105377599: 2KB upstream variant	15.32 (3.89–60.19)	1.93E-07
12q13.3	rs147741304	None*	None	G	A	0.056	0.003	NA	19.47 (3.88–97.97)	2.19E-07
19q13.31	rs112876885	CADM4 (Cell Adhesion Molecule 4); LOC105372411	Cell-cell adhesion	A	G	0.056	0.003	CADM4: Missense variant; LOC105372411: intron variant	19.53 (3.89–98.08)	3.39E-07
1p21.2	rs56956847	None**	None	A	G	0.129	0.027	NA	5.36 (2.58–11.14)	5.24E-07
4q34.2	rs191330351	GPM6A (Glycoprotein M6A)	Calcium channel activity, neuronal migration, stem cell differentiation	T	C	0.129	0.026	Intron variant	5.69 (2.71–11.94)	6.67E-07
12q24.23	rs56074206	CIT (Citron Rho-Interacting Serine/Threonine Kinase); MIR1178 (MicroRNA 1178)	Cell division, cytokinesis, development of central nervous system	G	A	0.129	0.029	CIT: intron variant; MIR1178: 2KB upstream variant	5.06 (2.45–10.42)	8.52E-07
12q24.33	rs7134357	RIMBP2 (RIMS binding protein 2)	Synaptic transmission	G	A	0.194	0.059	Intron variant	3.87 (2.18–6.88)	1.43E-06
4p15.31	rs145547469	LOC105374510	Uncharacterized gene thought to produce ncRNA	T	C	0.111	0.023	Intron variant	5.38 (2.44–11.83)	3.11E-06
7p15.3	rs10239513	LOC105375193	Uncharacterized gene thought to produce ncRNA	T	C	0.306	0.132	2KB upstream variant	2.93 (1.84–5.67)	3.74E-06
7q36.3	rs11764121	PTPRN2 (Protein Tyrosine Phosphatase Receptor Type N2)	Involved in vesicle-mediated secretory process. May be involved in the regulation of insulin secretion	A	G	0.083	0.015	Intron variant	5.96 (2.37–15.04)	7.76E-06

Table 2 (continued)

Table 2 (continued)

Chr	SNP	Gene (protein)	Protein function	Ref. allele	Risk allele	MAF		Functional consequence	GWAS	
						PPHN	Control		OR	P
7q21.13	rs144344757	CDK14 (Cyclin Dependent Kinase 14)	Regulator of cell cycle progression and cell proliferation, cell-cycle Regulator of Wnt signaling pathway	A	G	0.129	0.032	Intron variant	4.57 (2.25–9.05)	7.79E-06
4p15.31	rs187729743	LCORL (Ligand Dependent Nuclear Receptor Corepressor Like)	May act as transcription activator	C	T	0.065	0.008	Intron variant	9.16 (2.85–29.42)	7.87E-06
7q21.13	rs79741635	None***	None	A	G	0.129	0.032	NA	4.57 (2.49–9.31)	8.40E-06

*, an intergenic region lies between the *KRT82* and *KRT75* genes; **, an intergenic region lies between the *GRM2* and *RGS7* genes; ***, an intergenic region lies between the *CLDN12* and *CKD14* genes. Chr, chromosome; SNP, single nucleotide polymorphism; MAF, minor allele frequency; PPHN, persistent pulmonary hypertension of the newborn; GWAS, genome-wide association study; OR, odds ratio; P, P value of heterogeneity; T, thymine; C, cytosine; ncRNA, noncoding ribonucleic acid; G, guanine; A, adenine; NA, not available.

ancestry. Our study is the first to utilize GWAS to search for genetic variations associated with PPHN. As most of the GWAS identified SNPs that were present in non-coding regions, a functional SNP would be the most likely to affect gene regulation by altering the binding of some transcription factors. In this pilot study, we also identified rs149768622 in the intron 1 of the *WWC2* gene as a strong candidate for association with PPHN at the genome-wide significance level ($P < 1E-08$) and 13 SNPs from 10 genes (*LOC102723906/LOC105377599*, *CADM4*, *GPM6A*, *CIT*, *RIMBP2*, *LOC105374510*, *LOC105375193*, *PTPRN2*, *CDK14*, and *LCORL*) and 2 intergenic areas as having suggestive evidence for associations with PPHN.

The *WWC2* gene encodes a member of the WW-and-C2-domain-containing family of proteins. The *WWC2* gene is expressed in various human tissues, including the lungs, thyroid, uterus, and liver. Its expression is high in lung tissue (21). The *WWC2* protein is an upstream component of the Hippo signaling pathway, which controls organ size in animals through the regulation of cell regulation and apoptosis. In mice, the *WWC2* gene plays role in controlling cell differentiation, cell proliferation, and organ growth. In human beings, experimental data have indicated that the protein plays a role in the formation of critical alveoli, which usually occurs postnatally (22). The formation of critical alveoli consists of 2 steps, alveolar septation and alveologensis. The first step subdivides saccules into alveoli lined by flat type 1 (AT1) cells (i.e., pneumocyte type I) and surfactant-secreting type 2 (AT2) cells (i.e., pneumocyte type II). Pneumocyte type I cells contribute about 95% of the alveolar surface where passive gas exchange between alveoli and capillaries takes place. As a main function of pneumocyte type I cells is for gas exchange, damage or malfunction of these cells could result in the development of neonatal hypoxia and subsequent PPHN. Our study found that rs149768622 T>C, which is located in the first intron of the *WWC2* gene, was present in significantly higher amounts in patients with PPHN than in the healthy controls. YAP (Yes1 Associated Transcriptional Regulator) is a protein involved in the Hippo signaling pathway that has been experimentally determined to be co-expressed with the *WWC2* protein (Figure S1). Bertero *et al.* (23) found that YAP/TAZ-dependent activation of glutaminolysis and anaplerosis is a pathogenic mechanism by which vessel stiffness can stimulate cellular proliferation in pulmonary hypertension. YAP/TAZ forms a complex with TEAD, a transcriptional enhancer factor, which also plays a key role in the Hippo signaling pathway. Duong

et al. (22) suggested that TEAD is enriched in AT1 cells and directs AT1 cell maturation. Their experiment found that the *WWC2* gene had the highest TEAD motif enrichment in AT1 cells. The *WWC2* gene is likely involved in physiologic changes at birth from air-inflated stretching and AT1 cell differentiation via interactions with the Hippo pathway. The *WWC2* gene is likely to play an essential role in alveolar development after birth, it is possible that *WWC2* is a candidate gene for the pathogenesis of PPHN.

Our analysis also found 7 suggestive risk genes, namely the *CADM4*, *GPM6A*, *CIT*, *RIMBP2*, *CDK14*, *PTPRN2*, and *LCORL* genes. The functions of the proteins encoded from these genes are summarized in *Table 2*. Interestingly, one of these genes was the *PTPRN2* gene, which encodes a member of the protein tyrosine phosphatase (PTP) family. The PTPs remove phosphate groups from tyrosine residues, thereby influencing signal transduction and cellular processes such as cell metabolism, motility and survival. Chen *et al.* (24) studied epigenome-wide associations between smoke/allergen exposure and the development of asthma and chronic obstructive pulmonary disease, and found that hypomethylated *PTPRN2* was associated with rapid lung function.

Recently, a number of genes involved in the pathogenesis of PPHN have been identified. The majority of these studies have focused on selected genes. A summary of previous studies regarding the genes involved in PPHN is shown in *Table 3*. The gene most reported to be involved in PPHN is the *CPS1* gene, which encodes the carbamoyl phosphate synthase enzyme in the urea cycle. Pearson *et al.* (9) reported a missense variant, T1405N, (i.e., rs7422339 or rs1047891) in a patient with PPHN and a lower plasma concentration of arginine, which is an intermediate in the urea cycle. In the urea cycle, nitric oxide is synthesized during the conversion of arginine to citrulline. The study suggested that low concentrations of intermediates in the urea cycle and nitric oxide precursors may be associated with PPHN. Kaluarachchi *et al.* (12) also reported 3 SNPs, rs41272673, rs4399666, and rs2287599, in the *CPS1* gene, in US patients with PPHN with low tyrosine levels but high phenylalanine levels. El-Khazragy *et al.* (15) found that the rs4399666 variant in the *CPS1* gene was also significantly associated with PPHN in Egyptian infants. Byers *et al.* (10) studied 32 SNPs in 12 candidate genes involving the pathophysiology of PPHN and found that rs4458044 in the corticotropin-releasing hormone receptor 1 (*CRHR1*) gene was significantly associated with PPHN. They found that the level of 17-hydroxyprogesterone in infants with

PPHN was significantly higher than in the controls. Approximately 14% of the infants in the PPHN group were also found to have congenital adrenal hyperplasia. Mei *et al.* (11) observed significantly higher GT and TT genotypes in the rs2070699 variant in the endothelin 1 (*EDN1*) gene and higher plasma levels of endothelin-1 in patients with PPHN. Liu *et al.* (13) investigated genetic variants associated with 25 reported PPHN/PAH-related genes by panel exome sequencing in 74 PPHN infants. They found that 3 SNPs (rs192759073, rs1047883 and rs2229589) in *CPS1* and one SNP (rs1044008) in *NOTCH3* were significantly associated with PPHN ($P < 0.05$). Wang *et al.* (14) found that the p.E317K and p.P777S variants in the tubulin tyrosine ligase-like family member 3 (*TTL3*) gene and the p.E1071D variant in the integrin subunit alpha M (*ITGAM*) gene were associated with PPHN in high altitude areas (Tibet and Han in China). Recently, we found that the rs17034984 variant in the *EPAS1* gene, which encodes either the endothelial PAS domain-containing protein 1 or the HIF-2 α protein was a possible genetic susceptibility locus associated with PPHN (16). In this GWAS analysis, we found that rs17034984 had nearly reached statistical significance at the genome-wide association P value threshold of $< 1E-08$ ($P = 1.97E-05$), it failed to reach the value, probably due to the dilution effect from the SNPs being tested over the whole genome.

GWAS is a high-throughput genotyping test that evaluates a large set of SNPs across the human genome. In this study, we used a case-control study design to compare the frequency of SNPs between patients with PPHN and a matched control group without PPHN. We found that significant genetic variants were observed more frequently in patients with PPHN than in the controls. These variants may either be causative or more likely associated (in ‘linkage disequilibrium apostrophe’) with the causative mutation. There are various implications these GWAS results could have in terms of their clinical applications for PPHN. One possible clinical application of these genetic associations would be to provide predictive and prognostic information in the presence of other risk factors for PPHN. Since the clinical manifestation of PPHN usually involves a short onset, genotyping of identified genetic variants in a family with a previous PPHN child could be a sign indicating close monitoring of following children during the perinatal period. Biomarkers currently serve as a valuable tool for early diagnosis, disease staging, they can be used as prognostic indicators of the treatment outcomes, monitoring of treatment progress, and determining therapeutic targets.

Table 3 Significant genetic variants reported to be associated with PPHN from previous studies

Reference (years)	No. of PPHN cases	Study methodology	Gene (Chr)	Protein			Variant	
				Name	Protein function	Role in PPHN/ PAH	Name	Functional consequence
Pearson <i>et al.</i> 2001 (9)	31	Study of 3 polymorphisms of the <i>CPS1</i> gene using single-strand conformation polymorphism analysis	<i>CPS1</i> (2q34)	Carbamoyl-phosphate synthetase 1	Enzyme in the first step of the urea cycle	Nitric oxide is endogenously synthesized from a precursor L-arginine by nitric oxide synthase. L-arginine is an amino acid supplied by urea cycle	rs7422339 (rs1047891)	Missense variant
Byers <i>et al.</i> 2012 (10)	88	Family-based candidate gene study (32 SNPs in 12 genes (<i>BMP2, SFTPB, EPAS1, PDE5A, SOD3, NR3C1, CRHBP, VEGFA, NOS, SFTPC, SFTPD, CRHR1</i>) using TaqMan-based quantitative PCR	<i>CRHR1</i> (17q21.31)	Corticotropin Releasing Hormone Receptor 1	A G-protein coupled receptor for corticotropin-releasing factor and urocortin. Required for normal embryonic development of the adrenal gland and for normal hormonal responses to stress	Downstream of rs4458044 is a transcription factor binding site for PPAR- γ . PPAR- γ is a regulator of pulmonary smooth muscle cell proliferation and vascular tone. Decreased expression of PPAR- γ was observed in patients with pulmonary hypertension and neonatal chronic lung disease. Fetal steroid production is also essential for <i>in utero</i> lung development and <i>ex utero</i> pulmonary transition	rs4458044	Intron variant
Mei <i>et al.</i> 2016 (11)	55	Candidate gene sequencing (<i>EDN1, ACE, VEGFA, NOS3</i> genes) using next generation sequencing	<i>EDN1</i> (6p24.1)	Endothelin 1	A potent vasoconstrictor and mitogen for smooth muscles	Endothelin 1 promotes vasoconstriction, which affects pulmonary vasculature (25)	rs2070699	Intron variant
Kaluarachchi <i>et al.</i> 2018 (12)	77	Family-based candidate gene study (48 SNPs in 6 urea cycle genes: <i>CPS1, NAGS, ASS, ASL, ARG1, OTC</i>) using TaqMan-based quantitative PCR	<i>CPS1</i> (2q34)	Same as above	Same as above	Same as above	rs41272673 rs4399666 rs2287599	Intron variant Intron variant Synonymous variant
Liu <i>et al.</i> 2019 (13)	115	Clinical exome sequencing panel (n=115) then SNP analysis for disease-causing variants in 25 PPHN/PAH genes (n=74)	<i>CPS1</i> (2q34)	Same as above	Same as above	Same as above	rs192759073 rs1047883 rs2229589	Synonymous variant Missense variant Synonymous variant
			<i>NOTCH3</i> (19p13.12)	Notch receptor 3	A receptor that belongs to the Notch signaling pathway, which plays roles in the regulation of cell proliferation, differentiation, differentiation and apoptosis cell-fate determination	Expression of NOTCH3 was increased in the pulmonary artery smooth muscle cells of PAH patients. Heterozygous variants might affect cell proliferation and NOTCH3-HES5 signaling resulting in PAH (26)	rs1044008	Synonymous variant
Wang <i>et al.</i> 2020 (14)	100	Whole exome sequencing (n=20) then gene panel sequencing of 237 genes (n=80)	<i>TLL3</i> (3p25.3)	Tubulin tyrosine ligase-like family member 3	Protein with ligase activity that catalyzes ATP-dependent restoration of tyrosine to the C-terminus of α -tubulin. Tubulin is polymerized into microtubules	Abnormality in the detyrosination/tyrosination cycle of tubulin is involved in the development of hypertension. Reduced adhesion of induced pluripotent stem cell-derived endothelial cells obtained from a patient with familial PAH was observed	p.E317K p.P777S	Missense variant Missense variant
			<i>ITGAM</i> (16p11.2)	Integrin subunit alpha M	Integral membrane protein involved in adhesive interactions of monocytes, macrophages, and granulocytes	Unclear	p.E1071D	Missense variant
El-Khazragy <i>et al.</i> 2021 (15)	150	Specific SNP analysis (rs4399666) using TaqMan-based quantitative PCR	<i>CPS1</i> (2q34)	Same as above	Same as above	Same as above	rs4399666	Intron variant
Nakwan <i>et al.</i> 2022 (16)	45	SNP microarray	<i>EPAS1</i> (2p21)	Endothelial PAS Domain Protein1 or HIF-2 α protein	A transcription factor involved in the induction of oxygen regulated genes. It regulates erythropoiesis and physiological responses to hypoxia through the HIFs signaling pathway	HIF-2 α regulates the vascular endothelial growth factor expression, which may be implicated in the development of blood vessels and the tubular system of the lung. HIF-2 α stability is involved in arginase expression and nitric oxide homeostasis. Endothelial HIF-2 α could induce pulmonary hypertension through an increased expression of endothelin-1 and a decrease in vasodilatory apelin receptor signaling	rs17034984	Intron variant

PPHN, persistent pulmonary hypertension of the newborn; Chr, chromosome; PAH, pulmonary arterial hypertension; PPAR- γ , peroxisome proliferator-activated receptor γ ; SNP, single nucleotide polymorphism; PCR, polymerase chain reaction; ATP, adenosine triphosphate; HIF-2 α , hypoxia-inducible factor 2 alpha.

In general, a biomarker is a biological molecule found in the blood or other body fluids or tissues. In addition, a genetic marker that causes a disease or is associated with susceptibility to disease is a potential biomarker because a circulating protein encoding from a gene can be genetically influenced. An example of a potential use of a genetic biomarker in PAH is the use of a SNP of the *COL18A1* gene to predict the outcome of PAH. Lower serum levels of endostatin, which is encoded from *COL18A1*, have been associated with reduced mortality in PAH (27). A loss-of-function missense variant in the *COL18A1* gene, which results in a change in the amino acid composition of endostatin, was linked to lower serum endostatin and was associated with reduced mortality (27). The genotype AG of the rs12483377 SNP had significantly lower serum levels of endostatin compared with the homozygous GG genotype (27). Another example is the use of plasma endothelin-1 as an effective biomarker for monitoring and predicting the outcome of pulmonary hypertension (28,29). In another study, the presence of the rs2070699 T allele of the *EDNI* gene that encodes endothelin-1 was associated with higher plasma endothelin-1 levels, which increase the risk of PPHN in neonates with respiratory distress (11). Other potential biomarkers that confer a risk of developing PPHN are plasma tyrosine and phenylalanine (30). A study on polymorphisms of urea cycle enzymes and intermediate metabolites found that 2 intronic SNPs and a synonymous mutation in the *CPS1* gene were significantly associated with PPHN (12). The same study found that tyrosine levels were significantly lower and phenylalanine levels were significantly higher in patients with PPHN when compared to controls (12). Other biomarkers of pulmonary diseases, including genetic variants, are extensively reviewed elsewhere (31). Biomarkers may be used for risk stratification of PPHN and as a guide for specific treatments when the evidence is sufficient, especially for at risk newborns. For example, the determination of *CPS1* genetic variants and urea cycle intermediate metabolites in newborns with birth asphyxia and meconium-stained amniotic fluid may be a guide for disease vigilance or the use of a selective blockade for endothelin-1 receptor type A to encourage pulmonary vasodilation in newborns with *EDNI* genetic variants.

Unlike rare monogenic diseases in which the variants usually reside within coding regions of genes, variants associated with common complex diseases usually reside within non-coding regions (32). Our study examined

SNPs in the intron of the *WWC2* gene. Intronic SNPs may result in alter RNA splicing. Disrupted RNA splicing results in the loss of exons or the inclusion of introns and an altered protein-coding sequence. Alternative splicing and exon shuffling lead to enhancing the protein diversity. Intron also plays an important role in gene regulation and expression, regulation of mRNA transport, and chromatin assembly (33).

In this study, we were unable to recruit more patients with PPHN in our registry as many former patients were lost to contact and blood samples had not been kept. Therefore, we prospectively studied infants with PPHN together with matching healthy control infants. Since not all neonates with respiratory failure develop PPHN, it seems that PPHN is most likely caused by some type of pulmonary vascular maladaptation precipitated by genetic-environmental interactions. Since environmental factors are a main factor triggering PPHN, genetic studies in patients with idiopathic PPHN might provide powerful insights into the genetics of PPHN. However, recruiting patients with idiopathic PPHN is difficult, as they represent only a small fraction of these patients. In addition, further studies regarding the functional effects of *WWC2* gene variants should be carried out to determine their clinical significance in PPHN. The expression of the *WWC2* gene could be evaluated either in lung and other tissues obtained from deceased patients with PPHN or in animal models of PPHN, such as mice that have elevated pulmonary arterial pressure and some degree of hypoxemia. Functional studies of the *WWC2* gene can be performed by immunohistochemical analysis or western blot using antibodies against the *WWC2* protein. *WWC2* mRNA expression studies can be performed by various methods such as whole-mount *in situ* hybridization or quantitative reverse transcriptase polymerase chain reaction (34,35). In this study, we did not perform a functional study of the *WWC2* gene since we did not have lung tissue samples obtained from deceased patients with PPHN and a mouse model with PPHN could not be created in our setting.

Conclusions

In conclusion, this is the first study to examine possible associations between genetic variations and PPHN using GWAS across the genome. We identified *WWC2* as a possible candidate gene, which may modulate the risk for PPHN. Further studies are required to confirm our findings

and to explore the physiological mechanism behind this association.

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Footnote

Reporting Checklist: The authors have completed the STREGA reporting checklist. Available at <https://tp.amegroups.com/article/view/10.21037/tp-22-280/rc>

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Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at <https://tp.amegroups.com/article/view/10.21037/tp-22-280/coif>). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The study was approved by the Research Ethics Committee of Hat Yai Hospital (No. 24/2562) and informed consent was taken from the patients' parents.

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