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Peroxisome proliferator activated receptor gamma polymorphism Pro12Ala in polycystic ovary syndrome (PCOS) of South Indian Population

Raichel Jacob^{1*}, Chandirasekar Ramachandran¹, Calistus Jude², Uthayakumar Venkatachalam¹, Sasikala Keshav Rao¹

¹Division of Human Genetics, Department of Zoology, Bharathiar University, Coimbatore, India

²Department of Life Sciences, Kristu Jayanti College, Bangalore, India

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ABSTRACT

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Keywords: PPAR gamma Polymorphism Hormones PCOS **Objective:** To investigate the frequency of Pro12Ala polymorphism in PPAR gamma gene among PCOS of South Indian Population. Understanding this polymorphism may help us in better diagnosis prevention and therapeutic approaches towards management of PCOS.

Method: A total of 75 women with the diagnosis of PCOS and 75 healthy controls were included in this study. The Pro12Ala variant in the PPAR gamma gene was analysed by PCR-RFLP.

Results: Genotypic frequencies for PPAR gamma gene Pro12Ala polymorphism showed the frequency of Pro/Pro genotypes was 77% in PCOS and 81% in controls. The odds ratio was 0.71 (95% *CI* 0.31–1.63) and 2.66 (95% *CI* 0.21–32.9) and alleles expressed 0.87 (95% *CI* 0.42–1.79). Regarding hormone levels, there were significant differences between PCOS and non PCOS.

Conclusion: PPAR γ 2 gene Pro12Ala polymorphism was supposed to be susceptible genes in PCOS. The present study demonstrated that there is a statistical difference between the distributions of PPAR gamma Pro12Ala polymorphism in South Indian Population.

1. Introduction

Polycystic ovary syndrome (PCOS) is a common endocrine disorder affecting up to 7% of women of reproductive age [1]. The disorder is characterised mainly by menstrual irregularities acne, hyperandrogenism central obesity, type 2 diabetes [2]. The pathogenesis of PCOS is unknown. Recent reports show that it remains as a complex multigenic disorder characterised by abnormal gonadotropin release and dysregulation of

Tel: +91 9442413152

E-mail: raichelshaju@yahoo.co.in

steroidogenesis [3]. PCOS is a familial condition with autosomal dominant mode of inheritance [4]. It is a combination of genetic abnormalities combined with environmental factors such as nutrition and body weight, which mainly affect the PCOS [5].

Recent studies show that initiation of pathological mechanisms occurs mainly during the foetal life, with high maternal serum levels of androgen/insulin may influence the genetic programme which result in both reproductive and metabolic consequences of PCOS [6]. The peroxisome proliferators activated receptor gamma PPAR gamma gene is located at chromosomal region 3p25 and is mainly expressed in adipose tissue which promotes the differentiation of pre-adipocytes into adipocytes and belong to nuclear hormone receptor family [7]. Peroxisome proliferators-activated receptor-gamma $(PPAR\gamma)$ is a candidate gene involved in glucose homoeostasis, lipid metabolism and adipocyte differentiation also implicated in the pathogenesis of PCOS [8].

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^{*}Corresponding author: Raichel Jacob, Department of Zoology, Bharathiar University, Coimbatore, Tamil Nadu, India.

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PPAR γ is a nuclear receptor which combines with the retinoid X receptors to form heterodimers which controls transcription of genes involved in free fatty acid uptake and lipogenesis, and plays an important role in regulation of insulin sensitivity and adipose tissue metabolism, carcinogenesis and inflammation [9]. A functional polymorphism in exon 2 of PPAR γ 2 gene produces a Pro–Ala substitution at the codon 12 causing the Pro12Ala polymorphism (rs1801282). This CCA-GCA change causes a conformational change in the protein thus affecting the activity [10]. The Pro12Ala polymorphism of PPAR gamma gene has been associated with reduced transcriptional activity of PPAR gamma and presence of Ala isoform has been linked to higher insulin sensitivity and lower body mass index [11].

According to reports of Zargar et al. [12] significant number of PCOS patients show impaired glucose tolerance and are in potential risk of developing type 2 diabetes. The objective of the study was to determine the genetic frequency of Pro12Ala polymorphism in PPAR gamma gene in South Indian PCOS population. The association between the Pro12Ala polymorphism and increased insulin sensitivity in PCOS has been observed in reports of Hahn et al. [13]. PPAR gamma gene associated with the risk of colorectal adenoma was reported in a study [14]. PCOS were diagnosed based on the Rotterdam criteria 2003 [15] which includes polycystic ovarian with >10 small peripheral cysts, hyperandrogenism, anovulation hyperinsulinemia. and Subjects were considered to have oligomenorrhea if they had less than 8 cycles per year and amenorrhea in absence of menses for6 months or more [16]. Clinical hyperandrogenism was diagnosed by hirsutism assessment using F-G scoring if seen with 8 or more [17]. Biochemical hyperandrogenism was diagnosed by elevated levels of serum free testosterone as it is considered the single most predictive evidence of hyperandrogenemia [18].

2. Materials and methods

2.1. Collection of blood samples

Peripheral blood samples of 3 mL was collected from the subjects using a heparinised needle and transported to the laboratory with the help of portable coolers. The subjects were recruited in the study from the women population attending the gynaecology clinic of a tertiary care hospital (n = 75) were served as experimental and were included in the study. Anthropometric details and general clinical characteristics and history of disease were obtained by a standardized health questionnaire. Age matched healthy controls were included in the study. The inclusion criteria of the PCOS were based on the Rotterdam diagnostic criteria. The subjects have not received hormonal therapy for at least 3 months before hormone assays. All the study evaluations and procedures were conducted in accordance with the guidelines of Helsinki Declaration on human experimentation. An ethical committee approval was obtained for the study and written informed consent was obtained from the subjects involved in the study.

The level of serum follicle stimulating hormone FSH luteinizing hormone LH total testosterone T were determined using commercially available human Elisa kits. The intra and inter assay coefficient of variation of all the assays were less than 10%.

2.3. Genotyping

Genomic DNA was isolated from peripheral blood leucocytes by using the standard Phenol-chloroform extraction method [19]. Pro12Ala polymorphism was determined using polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP) method. The PCR reaction mixture contained 50 ng of genomic DNA 0.5 µmol/L of each primer of forward 5'CCA ATT CAA GCC CAG TCC TTT C3' and reverse 5'GCA GAC AGT GTA TCA GTG AAG GAA TCG CTT TCC G and master mix (Promega) USA in a final volume of 25 µL. The reaction mixture was subjected to denaturation at 95 °C for 2 min followed by 35 cycles at 95 °C for 30 s, 52 °C for 30 s, 72 °C for 45 s then by a final extension of 72 °C for 7 min. The PCR products were 237 bp and were digested with BstUI restriction enzyme at 37 °C for 18 h. After the digested products were electrophoresed on a 2.5% agarose gel and visualised by ethidium bromide staining, the C and the G alleles could be distinguished as bands 217 bp and 20 bp respectively.

2.4. Statistical analysis

The standard χ^2 tests were used to compare genotype frequencies among PCOS and control groups. The results were in Hardy–Weinberg equilibrium of genotype frequencies. The results of continuous data were reported as mean and ±SD. Differences in serum hormone levels between PCOS and control groups were assessed by students *t* test *P* < 0.05 was considered significant for all tests. Pearson bivariate correlation was studied for hormones among controls and PCOS. Statistical analysis was performed using the SPSS Version 16 (Statistical Package for the Social Sciences, USA).

3. Results

Table 1 depicts the anthropometric data and hormone levels between PCOS and control groups. There was a significant difference in age, FSH, LH, testosterone hormone levels between the two groups. The subjects were grouped into three based on their age as G I, G II and G III and they were significant at P < 0.05 levels. However, the level of testosterone hormone was significantly higher in the PCOS group when compared to the control subjects. Pearson bivariate correlation was studied among hormones. Correlation was observed among the Group I as r = 0.459, P = 0.006 significant at P < 0.001level. A negative correlation was observed among Group II and Group III individuals with $(r = 0.39 \ P = 0.19, r = 0.43 \ P = 0.15)$.

Table 1

The hormonal concentrations of PCOS and controls.

Groups	Ν	Age	FSH (mIU/mL)	LH (mIU/mL)	Testosterone (ng/mL)
Controls	G I 35	23.25 ± 2.70	9.12 ± 1.80	9.65 ± 2.48	0.60 ± 0.26
	G II 28	33.00 ± 2.56	9.07 ± 2.17	9.53 ± 1.96	0.78 ± 0.24
	G III 12	40.50 ± 2.80	8.80 ± 2.63	10.90 ± 2.02	0.76 ± 0.49
PCOS	G I 35	24.40 ± 1.80	9.30 ± 2.88**	$11.30 \pm 2.85^{**}$	$0.85 \pm 0.30^*$
	G II 28	$32.60 \pm 2.60*$	9.51 ± 2.69	12.30 ± 2.37	$0.90 \pm 0.26^*$
	G III 12	$42.50 \pm 3.14^*$	11.5 ± 2.00	11.90 ± 2.78	$0.48 \pm 0.27*$

Data were expressed as (Mean \pm SD), G I-(18–27) years, G II-(28–37) years, G III-(38–47) years. *Statistically significant values between controls and PCOS at P < 0.05 levels. **Statistically significant values between Group I of controls and PCOS at P < 0.001 levels.

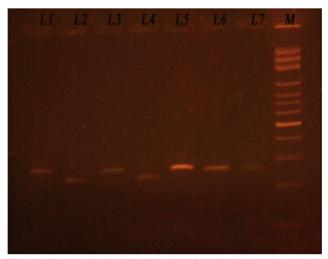


Figure 1. Electrophoresis of PCR product shows Pro12Ala polymorphism in the PPAR gamma gene among the PCOS samples.

Lane-(1, 3, 5, 6 and 7) Ala12Ala homozygote; Lane-(2 and 4) Pro12Pro homozygote; M-100 bp DNA Marker.

Table 2

Genotype frequency distribution of Pro12Ala polymorphism in women with PCOS and controls.

Genotypes	Experimental (n %)	Controls (<i>n</i> %)	<i>P</i> -value	Odds ratio 95% CI				
Allelic frequency								
Pro/Pro	58.0 (77.30)	61.0 (81.30)	1.00	1.0				
Pro/Ala	16.0 (21.00)	12.0 (16.00)	0.64	0.7				
				(0.3–1.63)				
Ala/Ala	1.0 (1.30)	2.0 (2.60)	0.62	2.6				
				(0.21 - 32.9)				
Allelic frequency								
Pro	132.0 (0.88)	134.0 (0.89)	-	_				
Ala	18.0 (0.12)	16.0 (0.10)	0.13	0.87				
				(0.42 - 1.79)				

 $\chi 2$ – Chi-square values or Odds ratio at 95% confidence level.

The allele and genotype frequency distribution (Figure 1) for both PCOS and control groups were consistent with the Hardy– Weinberg equilibrium and are shown in Table 2. Frequencies of the G allele was (0.12) and C allele (0.88) among PCOS and (0.10) and (0.89) in controls. Genotype frequencies was 0.71 *CI* (0.31–1.63) and 2.66 *CI* (0.21–32.9) and alleles expressed 0.87 *CI* (0.42–1.79). Statistically significant values were obtained.

4. Discussion

Polycystic ovary syndrome is a metabolic disorder resulting from the interaction of genetic predisposition and environmental risk factors. The familial tendency of PCOS and the increased levels of hormones play a pathogenic role in the disease. In the current study, we investigated the possible association between Pro12Ala polymorphism at PPAR gamma gene and the occurrence of PCOS.

The metabolic syndrome is evident at an early age in women with PCOS irrespective of race and ethnicity. Due to high impact of PPAR gamma gene as an insulin-sensitising transcription factor involved in adipogenesis and lipogenesis, the occurrence of single nucleotide polymorphisms (SNPs) in the PPAR γ gene was addressed by numerous reports on studying subjects with insulin resistance, type 2 diabetes, arteriosclerosis, and hypertension [20].

Hyperinsulinemia acts as a central factor for critical link between PCOS and metabolic syndrome. Reports [10] showed abdominal adipose was increased in Ala 12 carriers with diabetes and obesity. Metabolic dysfunction in lipid profile and abdominal obesity is regarded as an indicator of CVD cardiovascular disease in the Ala genotype women with PCOS [21]. Studies [22] have shown that Ala allele is associated with high BMI and dyslipidemia in elderly subjects. This may indicate that the functional role of Pro12 Ala substitution differs depending on the degree of obesity. Pro12Ala polymorphism showed an association with PCOS susceptibility in Korean women [23]. Cardona et al. [24] reported Pro12Ala polymorphism is associated with high risk of hyper triglycerides. Kalra et al. [25] found that obese carriers of Pro12Ala polymorphism have a risk for hyperlipidemia and concluded that IR is associated with dyslipidemia in women with PCOS, independent of obesity. Studies of Yang et al. [21] reported Ala allele frequency has a positive association with PCOS. Several studies have described ethnic allelic variation of PPAR gamma with a higher allelic frequency in Caucasians and minor frequency in Asian subjects.

The present study may have some limitations which include relatively small size of the sample, PCOS and non PCOS (controls) were not matched for body weight and this factor may limit the influence of BMI on the hormonal secretion of PCOS group. Mainly from the animal studies data it is seen that the testosterone hormone has both facilitatory and inhibitory effect on LH secretion and suppressive effect on progesterone. Most of the PCOS have higher levels of free testosterone. In general, the testosterone hormone has both negative and positive action on female gonadotropins via modulating the gene expression of LH and FSH.

In conclusion, the study showed close association between the testosterone levels and Pro12Ala polymorphism in PCOS women. They posed partially metabolic dysfunction in PCOS. Relationship between Pro12Ala polymorphism and metabolic dysfunction in PCOS may provide evidence for the individualised treatment and early diagnosis of disorder.

Apart from conventional candidate gene approach, genomic wide scans might be promising. Further cDNA technology would shed light on functional aspect of candidate genes for understanding the genetic aetiology of PCOS. Ala allele of PPAR gamma may be advantageous against the development of PCOS when gene-environment interactions are considered. These results imply that the Pro allele may be a susceptibility factor for PCOS. In conclusion, a significant association was found between the single polymorphism located in the coding region of the PPAR gamma and PCOS.

Conflict of interest statement

The authors declare that we have no conflict of interest.

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