

**MOLECULAR ANALYSIS of CYP21 GENE in
PATIENTS PRESENTING with AMBIGUOUS
GENITALIA**

MZ FUZIAH¹, KM YULIA², A. RUS ANIDA³, MR SIDEK², SF
RAMLI², MN ISA⁴

¹ *Department of Paediatrics*, ² *Human Genome Centre, School of Medicine, USM, 16150 Kubang Kerian*, ³ *Department of Paediatrics, Hospital Kota Bharu, Kelantan*, ⁴ *International Medical University, Putrajaya, Malaysia.*

ABSTRACT

Congenital adrenal hyperplasia (CAH) is a group of autosomal recessive disorders of adrenal steroidogenesis. The genes of the steroidogenic enzymes and the mutations involved have been described. Deficiency of the 21-hydroxylase (21-OH) enzyme is by far the most common form of CAH which arises as a result of deletions or deleterious mutations in the active gene (CYP21) located on chromosome 6p. Many different mutations of the CYP21 gene cause varying degrees of impairment of 21-OH activity that results in a spectrum of disease expression. There is no sharp limit between the salt-wasting, the simple virilizing and the late onset forms.

The objective of our study was to determine the 21-OH deficiency mutation defects and correlate the genotype with their phenotypic expression of the disease.

We performed mutational analysis using PCR-ASOH (Polymerase Chain Reaction - Allele Specific Oligonucleotide Hybridization) technique on six patients who presented with ambiguous genitalia (AG) and or electrolyte derangement as hyponatraemia and hyperkalaemia, suspected to have CAH. The Val281Leu and Pro30Leu mutations result in enzymes with 20-60% of normal activity and both are associated with the non-classical form of CAH. The Gln318stop mutation is categorized under the salt-wasting type.

Among the six patients, three had Val281Leu mutation, two had Pro30Leu mutation and one had Gln318stop mutation. The three patients with Val281Leu mutation had presented with adrenal crises during infancy and was classified as salt losers and treated with glucocorticoids and mineralocorticoids. These 3 patients could well be the other 40% who are categorized as salt-losers. The two patients with Pro30Leu mutations have normal male external genitalia and presented with hyponatraemia and hyperkalaemia. Only one patient required mineralocorticoid therapy that was given for about 5 months duration. Subsequently he had normal electrolytes level even without mineralocorticoid therapy. The Gln318stop mutation was identified in one patient who presented with ambiguous genitalia and adrenal crises.

Our study showed that the patients with genotype Val281Leu, Pro30Leu and Gln318stop mutations correlated with their phenotype. The mutation analysis of CYP21 gene proved to be a good complementary investigation and supportive to the diagnosis and management of our CAH patients.

Key words: *ambiguous genitalia, congenital adrenal hyperplasia, CYP21 gene.*

INTRODUCTION

Ambiguous genitalia (AG) are one of the clinical presentations of congenital adrenal hyperplasia (CAH). Congenital adrenal hyperplasia is an autosomal recessive disease caused by loss or severe decrease in the activity of 21-hydroxylase (21-OH). This enzyme is one of the five enzymes necessary for cortisol biosynthesis. Deficiency of the 21-OH is the most common form of CAH accounting for 90-95% of all cases of CAH^{1,6}.

Congenital adrenal hyperplasia presents a wide spectrum of clinical manifestations and patients are divided into 3 groups: salt wasting (SW), simple virilizing (SV) and non-classical (NC). Salt wasting patients manifest as neonatal electrolyte disturbances together with virilization of external genitalia at birth in girls and early pseudoprecocious puberty in boys, while SV patients present the same manifestation as SW patients, but without electrolyte disturbances. Non-classical patients present with late onset symptoms of androgen excess, ranging from progressive virilization and pseudoprecocious puberty in childhood to menstrual disturbances, infertility and hirsutism in adult women².

It was reported that more than 90% of cases of CAH are caused by mutation of the CYP21 gene. This 21-OH (CYP21) gene is located in the HLA class III gene region on chromosome 6p21.3 and consist of 10 exons³. Majority of the mutations on the CYP21 gene are Val281Leu and Pro30Leu. These mutations were reported to result in 20-60% of normal enzyme activity and both are associated with the non-classical form of CAH^{4,5}.

AIM OF THE STUDY

To detect the presence of point mutations in Pro30Leu, Ile172Asn & Val281Leu of CYP21 gene

RESULTS

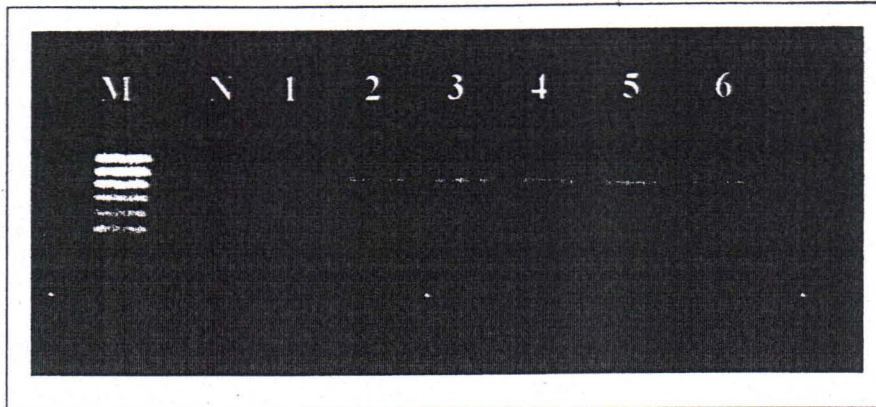


Figure 1: Presence of PCR product (873 bp) for CYP21 gene exon 1-3 using 2.0% agarose gel electrophoresis. Lane M : 100 bp DNA ladder, lane N : negative control, lane 1, 2 : normal samples, lane 3,4,5,6 : samples showing PCR amplification products for CYP21 gene.

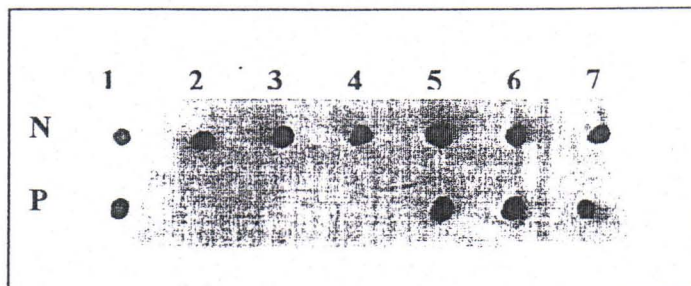


Figure 2: Dot blotting was performed using 1 μ g genomic DNA. The blot was hybridized with 100 pmol/ml of the digoxigenin labeled antiphosphatase (DIG-AP) specific probe from samples of patient 1-7. ASOH of PCR product from CAH patients was performed with the probe corresponding to the site exon. The status N: normal, P: patient.

RESULTS

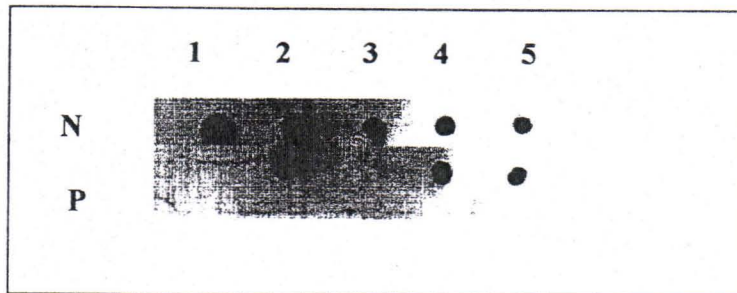


Figure 3: Pro30Leu hybridization DNA samples. Dot blotting was performed using 1 μ g genomic DNA. The blot was hybridized with 100 pmol /ml of the digoxigenin labeled antiphosphatase (DIG-AP) specific probe Pro30Leu. ASOH of PCR product from CAH patients was performed with the probe (Pro30Leu) corresponding to the site exon 1. The status N: normal, P: patient.

RESULTS

Table 1

	Patient I	Patient II	Patient III	Patient IV	Patient V	Patient VI
	4.2	4.3	3.0	3.3	2.8	2.7
	32 days	81 days	2 months	At birth	10 weeks	6 days
	Adrenal crisis Default follow up CPP Mental Retardation	Failure to thrive Normal male external genitalia Both testes descended Sepsis, meningitis & adrenal crisis	Haematuria Salt loss Normal male external genitalia Both testes descended	Normal male external genitalia Both testes descended Hypoglycaemia	Failure to thrive Ambiguous genitalia Phallus 2 cm Single orifice at its base No palpable gonads	Neonatal jaundice Ambiguous genitalia Prominent phallus Single orifice at its base No palpable gonads Registered as male Reassigned as female
	120	110	119	131	92	118

RESULTS

	Patient I	Patient II	Patient III	Patient IV	Patient V	Patient VI
	4.3	4.2	6.5	6.6	7.4	8.2
	28.8	23.0	NA	3.5	NA	NA
	1.6	4.4	NA	NA	NA	NA
	NA	NA	9.9 (0.07-1.7)	NA	>20 (up to 1.1)	33.2 (0.7-2.5)
	48 (139-501)	329 (138-690)	609 (140-500)	650 (138-690)	484 (139-501)	NA

RESULTS

	Patient I	Patient II	Patient III	Patient IV	Patient V	Patient VI
	1.4	NA	4.9	13.3	NA	NA
	46,XY Present	46,XY [*] Present	46,XY Present	46,XY Present	46,XX Not present	46,XX Not present
	-	-	-	-	Uterus & ovaries	Uterus & ovaries
	Val281Leu	Val281Leu	Pro30Leu	Pro30Leu	Val281Leu	Gln318Stop

NA: Not available, CPP: central precocious puberty

DISCUSSION

Majority of the mutations in the CYP21 gene in our patients are Val281Leu and Pro30Leu. These mutations were reported to result in 20-60% of normal enzyme activity and both are associated with the non-classical form of CAH^{4,7}.

In our study, we found that 3/52 patients (5.7%) have Val281Leu while 2/52 patients (3.8%) have Pro30Leu respectively. No mutations were observed in Ile172Asn. Patients with Val281Leu presented with adrenal crisis during infancy and were classified as salt wasting. Two patients with Pro30Leu mutations have normal male external genitalia and presented with hyponatraemia and hyperkalaemia. We did not identify any patient with I172N mutation which is known to result in clearly reduced enzymatic activity. About 1-2% of I172N mutation is usually associated with the SV form^{8,9}.

Our findings showed that patients with Pro30Leu mutations were associated with non-classical form of CAH whereas Val281Leu mutations were associated with salt wasting form of CAH.

CONCLUSION

This study suggested that phenotypes are not always concordant with the genotype in patients with Val281Leu mutations diagnosed with CAH.

ACKNOWLEDGMENT

This project is supported by USM short-term grant
304/PPSP/6131117

REFERENCES

1. M.Natividad Lobato et al. 1999: Mutation Analysis in-patients with congenital adrenal hyperplasia in the Spanish Population: Identification of putative novel steroid 21-hydroxylase deficiency alleles associated with the classic form of the disease. *Human Hered* .**49**: 169-175.
2. Hughes IA, Clark AJL9eds, 2000: Adrenal Disease in Childhood. Clinical and Molecular Aspects. *Endocr Dev Basel, Karger, Vol 2*, 93-111.
3. Phyllis W.Speiser et al. 1992: Disease expression and molecular genotype in congenital adrenal hyperplasia due to 21- hydroxylase deficiency. *J Clin Invest* **90**: 584-595.
4. Anna Nordenstrom et al. 1999: Genotyping Is Valuable Diagnostic Complement to Neonatal Screening for Congenital Adrenal Hyperplasia due to 21- hydroxylase deficiency. *J Clin Endocrinol Metab* **84**: 1505-1509.
5. Owerbach D, Sherman L, Ballard AL, Azziz R. 1992.Mutation in CYP21 is associated with nonclassical steroid 21-hydroxylase deficiency. *Mol Endocrinol* **6** : 1211-5
6. A Wedell. 1998. Molecular genetics of congenital adrenal hyperplasia (21-hydroxylase deficiency): implications for diagnosis, prognosis and treatment. *Acta Paediatr* **87**:159-64.
7. Selma F. Witchel, Rhonda Smith, Carlo Enrico Crivellaro, Thais Della Manna, Vae Dichtchekenian, Nuvarte Setian, Durval Damiani. 2000. CYP21 mutations in Brazil patient with 21-hydroxylase deficiency. *Hum Genet* **106**:414-419.
8. Jarmo Jaaskelainen, Antti Levo, Raimo Voutilainen, Juka Pertanen,1997. Population -Wide Evaluation of Disease Manifestation in relation to Molecular Genotype in Steroid 21-hydroxylase (CYP21) Deficiency: Good Correlation in well Defined Population. *J. Clin. Endocrinol. Metab* **82**: 3293-3297.
9. Catherine Deneux, Veronique Tardy, Anne Dib, Etienne Mornet, Line Billaud, Daniel Charron, Yves Morel, Frederique Kuttenn.2001.Phenotype-Genotype Correlation in 56 Women with Nonclassical Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency. *Journal of Clinical Endocrinology & Metabolism*: **86**;207-213.