

## INVOLVEMENT OF CYP17 GENE POLYMORPHISM WITH BENIGN PROSTATIC HYPERPLASIA IN BABYLON PROVINCE

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**ABSTRACT :** The present study was designed to evaluate the frequency and association of CYP17 gene (-34 T↔C) SNP with benign prostatic hyperplasia (BPH) in Babylon province. To achieve this aim, 146 patients with BPH and 102 apparently healthy control group were subjected to the study. DNA was extracted from whole blood for all samples. Genotyping of CYP17 gene (-34 T↔C) SNP were carried out by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Results indicated that the homozygous genotype (CC) of CYP17 gene (-34 T↔C) SNP was found to be significantly increase the risk of BPH by two folds with respect to those of the wild genotype (TT) of CYP17 gene (-34 T↔C) SNP. The heterozygous genotype (TC) of CYP17 gene (-34 T↔C) SNP was found to be none significantly increase the risk of BPH with respect to those of the wild genotype (CC) of CYP17 gene (-34 T↔C) SNP. The minor allele (C) of CYP17 gene (-34 T↔C) SNP was significantly higher in BPH patients when compared with that of the control group. In conclusion, the CYP17 gene (-34 T↔C) SNP is involved in the pathogenesis of BPH. The homozygous genotype (CC) was found to be significantly increase the risk of BPH by two folds with respect to those of the wild genotype (TT). The minor allele (C) of CYP17 gene (-34 T↔C) SNP was significantly higher in BPH patients when compared with that of the control group.

**Key words :** Benign prostatic hyperplasia, cytochrome 17, polymorphism.

### INTRODUCTION

Benign prostatic hyperplasia (BPH) is the nonmalignant enlargement of the prostate gland. It refers to hyperplasia of stromal and glandular epithelial that arises in the periurethral transition zone of the prostate that surrounds the urethra (Miller *et al*, 2009; Strandberg, 2000). The etiology of BPH is multifactorial and under endocrine control. Laboratory and clinical studies have identified two factors necessary for the BPH development, these factors are dihydrotestosterone and aging. Dihydrotestosterone is very essential for prostate growth. The serum testosterone levels decrease as a result of aging mainly due to decreased stimulation of Leydig cells and increased conversion of testosterone in the peripheral tissues to estrogens which induce androgen receptor. The aging prostate becomes more sensitive to androgens (Gann *et al*, 1996; Wilding, 1992).

Steroidal hormones, essentially androgen and estrogens, play an important role in the physiological growth and development of prostate gland, hence any genetic and environmental factors may play a role in regulating blood levels of circulating steroidal hormones. Thus, genes involved in the metabolic pathways of these hormones, if expressed differentially may alter the risk

of development of BPH (Konwar *et al*, 2008; Habuchi *et al*, 2000). There is an evidence to support the proposition of hormonal etiology of BPH involving androgen action. Androgen is required for differentiation and growth of the prostate in utero and at puberty. Testosterone, the most abundant circulating androgen is synthesized from cholesterol by a series of enzymatic reactions involving several of the cytochrome P450 enzymes such as CYP17 (Neuhausen *et al*, 1990; Picado-Leonard *et al*, 1987).

The cytochrome 17 (CYP17) enzyme functions at key branch points in steroid hormone biosynthesis in the adrenal gland, ovary and gonads. The human CYP17 gene is located in chromosome 10 at position 10q24.3 and contains eight exons. It spans a length of 1527 bp. Transcription initiation site is mapped approximately 180 bp upstream of the initiation codon in exon 1 and ~1.7 kb mRNA is produced (Ranbir *et al*, 2009; Ying *et al*, 2005).

Cytochrome P-450 C17 mediates both steroid 17 - hydroxylase activity, which converts pregnenolone to dehydroepiandrosterone and 17,20-lyase activity, which generates androstenedione from progesterone, precursors of testosterone and estrogen (Ilic *et al*, 1996; Daviglus *et al*, 1996). These androgens may then be converted to

estrone, testosterone and estradiol. Testosterone is converted to dihydrotestosterone in the prostate by the enzyme 5 $\alpha$ -reductase. Dihydrotestosterone binds to androgen receptor and the dihydrotestosterone-androgen receptor complex transstimulates a number of genes with androgen receptor responsive elements. These occasions eventually outcome in cell division in the prostate (Galbraith *et al*, 1997; Brentano *et al*, 1990).

### Aims of the study

To estimate the frequency and association of CYP17 gene (-34 T $\leftrightarrow$ C) SNP with benign prostatic hyperplasia.

## MATERIALS AND METHODS

### Materials

#### Subjects

The study included two groups, the first group comprises patients with benign prostatic hyperplasia while the second group comprises control subjects. All subjects were collected from February 2018 till July 2018. The practical part of this study was done in the laboratory of Biochemistry Department in College of Medicine, Babylon University. The study was performed on 146 patients with BPH and 102 apparently healthy control group. Any subject suffered from problems such as, renal dysfunction, liver dysfunction, diabetes mellitus, malignancies, urinary tract infection, drug dependency such as glucocorticoid, alcohol drinking were excluded from the current study.

#### Blood sampling

Two milliliter of blood collected in EDTA (ethylene diamine tetra acetic acid) containing tube and the samples were kept frozen at -70°C until analysis of CYP17 gene polymorphism.

#### Methods

Genotyping of CYP17 gene -34 T $\leftrightarrow$ C SNP was carried out by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). The DNA extracted from frozen blood by genomic DNA mini kit (Favorgen) (Vogelstein *et al*, 1979). The DNA was amplified by PCR. A 421bp DNA fragment containing the polymorphic site-34 T $\leftrightarrow$ C SNP of CYP17 gene was amplified by using specific primers (forward primer 5'-CCA TTC GCA CTC TGG AGT CAT-3' and reverse primer 5'-GAC AGG AGG CTC TTG GGG TA-3') (Carey *et al*, 1994). The PCR products were digested with MspAII restriction enzyme (Biolabs, New England). The wild genotype (TT) remains uncut (421bp) whereas the homozygous genotype (CC) is digested into 291 and 130bp fragments. The heterozygous genotype (TC) contained three bands sized 421, 291 and 130bp. The

restriction digestion products were analyzed on 2% agarose gel electrophoresis.

### Statistical analysis

The results of phenotypes data were expressed as mean  $\pm$  SD. Student's t-test was used for the evaluation of data. Genotype data expressed as odds ratio (OR), confidence interval (CI) 95%. Statistical analyses were performed with SPSS (version 20). P-value less than 0.05 was considered to be statistically significant.

## RESULTS

The demographic characteristics of patients with BPH and controls groups were shown in Table 1.

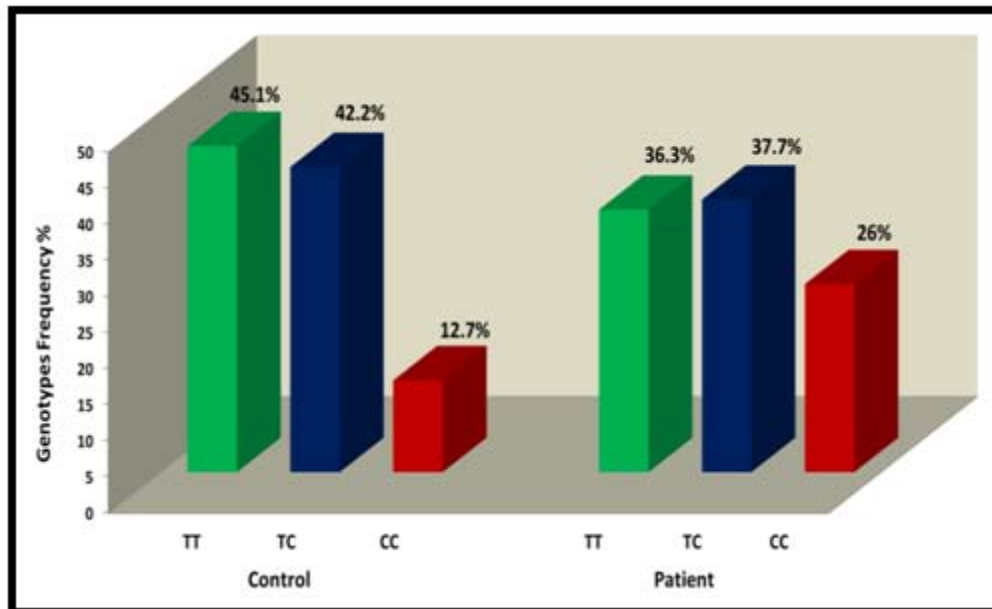
The genotypes distribution and frequency of CYP17 gene (-34 T $\leftrightarrow$ C) SNP as shown in Table 2 and Fig. 1, respectively. The analysis of results indicated that the CYP17 gene (-34 T $\leftrightarrow$ C) SNP genotype frequencies of wild genotype (TT), heterozygous (TC) and homozygous genotype (CC) were 36.3%, 37.7% and 26% in BPH patients and 45.1% 42.2% and 12.7% in controls group, respectively.

The homozygous genotype (CC) of CYP17 gene (-34 T $\leftrightarrow$ C) SNP was found to be significantly increase (OR = 2.537, CI 95% 1.206-5.335, P = 0.013) the risk of BPH by two folds with respect to those of the wild genotype (TT) of CYP17 gene (-34 T $\leftrightarrow$ C) SNP. The heterozygous genotype (TC) of CYP17 gene (-34 T $\leftrightarrow$ C) SNP was found to be none significantly increase (OR = 1.110, CI 95% 0.633-1.946, P=0.715) the risk of BPH with respect to those of the wild genotype (CC) of CYP17 gene (-34 T $\leftrightarrow$ C) SNP.

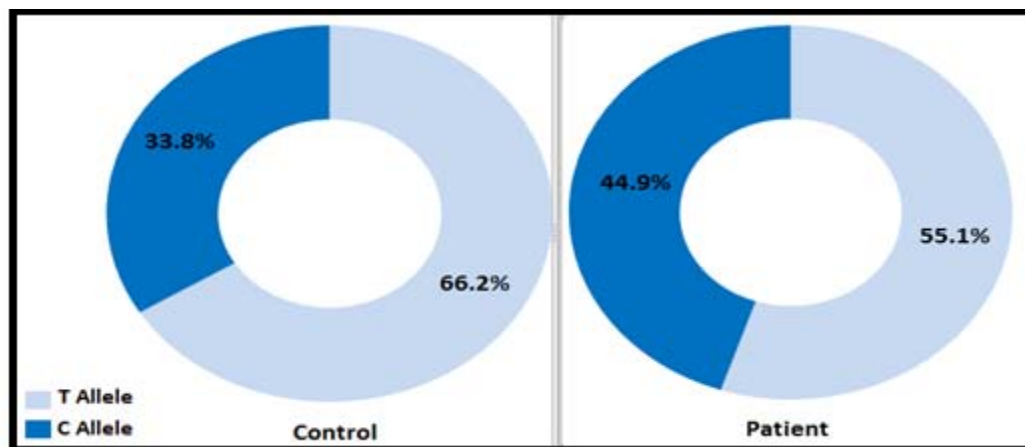
The allele distribution and frequency of CYP17 gene (-34 T $\leftrightarrow$ C) SNP as shown in Table 3 and Fig. 2, respectively. The allele frequencies of T and C of CYP17 gene (-34 T $\leftrightarrow$ C) SNP were found to be 55.1% and 44.9% in benign prostatic hyperplasia patients respectively and 66.2% and 33.8% in the control group, respectively. The minor allele frequencies (C) of CYP17 gene (-34 T $\leftrightarrow$ C) SNP in BPH patients and control groups were found to be 44.9% and 33.8%, respectively. It was significantly higher (P<0.05) in BPH patients when compared with that of the control group.

## DISCUSSION

Several genetic polymorphisms of CYP17 gene have been identified. One of the most common polymorphism of the CYP17 gene is (-34 T $\leftrightarrow$ C) SNP. For CYP17 gene (-34 T $\leftrightarrow$ C) SNP, the 5'-untranslated promoter region of CYP17 gene contains a single base pair thymidine (T) to cytosine (C) polymorphism that may create a new splitting site (CCACC box) at 34 bp upstream from the initiation



**Fig. 1 :** Genotypes frequency of CYP17 gene (-34 T↔C)SNP in patients with Benign Prostatic Hyperplasia and the controls groups. TT: Wild genotype, CC: Heterozygous and CC: Homozygous genotype.



**Fig. 2 :** Alleles Frequency of CYP17 Gene (-34 T↔C)SNP in Patients with Benign Prostatic Hyperplasia and the Controls Groups.

of translation and downstream from the putative transcription start site, therefore providing an additional promoter activity with an increased rate of transcription of CYP17 mRNA, *i.e.* altering the expression level of CYP17 (Sharp *et al*, 2004; Tomonori *et al*, 2000; Ranbir *et al*, 2009).

The CYP17 gene is highly expressed in the human prostate gland and plays an important role in metabolism of steroidal hormones; hence CYP17 polymorphisms which cause changes in enzymatic activity may alter the metabolism of steroidal hormones, possibly altering BPH risk (Ellem *et al*, 2004). A study by Zmuda *et al* (2001) reported that men with the homozygous genotype (CC) of CYP17 gene (-34 T↔C) SNP had a higher bioavailable testosterone level than men with the wild genotype (TT) of CYP17 gene (-34 T↔C) SNP. Heterozygotes genotype (TC) of CYP17 gene (-34 T↔C) SNP had

intermediate testosterone values. This connection is in line with the observation that a subset of BPH has a genetic transmission (Guoqi *et al*, 2013; Sanda *et al*, 1994).

It has been reported that the volume of BPH is positively correlated with serum testosterone and estradiol levels, therefore a distinct sex-steroid hormone caused by the CYP17 genotype will presumably contribute to the development of BPH (Partin *et al*, 1991; Greenwald *et al*, 1974). In this study, the homozygous genotype (CC) of CYP17 gene (-34 T↔C) SNP was found to be significantly increase the risk of BPH by two folds with respect to those of the wild genotype (TT) of CYP17 gene (-34 T↔C) SNP. The presence of (C) allele of CYP17 gene (-34 T↔C) SNP may create an additional promoter activity for CYP17 gene expression than (T) allele of CYP17 gene (-34 T↔C) SNP that lead to

**Table 1 :** Demographic characteristics of patients with benign prostatic hyperplasia and the controls groups.

| Characteristics          | Groups  | Mean ± SD        | Range           | P value |
|--------------------------|---------|------------------|-----------------|---------|
| No.                      | Control |                  | 102             |         |
|                          | Patient |                  | 146             |         |
| Age (y)                  | Control | 54.93 ± 8.68     | 38-65           | > 0.05  |
|                          | Patient | 57.76 ± 6.83     | 40-69           |         |
| Weight (kg)              | Control | 76.07 ± 13.53    | 49-104          | < 0.001 |
|                          | Patient | 86.78 ± 14.4     | 55-120          |         |
| Height (m)               | Control | 1.68 ± 0.09      | 1.49-1.85       | > 0.05  |
|                          | Patient | 1.69 ± 0.08      | 1.51-1.83       |         |
| BMI (kg/m <sup>2</sup> ) | Control | 26.79 ± 4.09     | 19.77-34.72     | < 0.001 |
|                          | Patient | 30.25 ± 3.42     | 19.66-38.07     |         |
| Duration of disease      | Patient | 5.05 ± 2.43 year | 1 month-12 year | -       |

**Table 2 :** Genotypes distribution of CYP17 gene (-34 T↔C)SNP in patients with Benign Prostatic Hyperplasia and the controls groups.

| Genotype | Control | Patient | OR        | 95% CI      | P-value   |
|----------|---------|---------|-----------|-------------|-----------|
| TT       | 46      | 53      | Reference | Reference   | Reference |
| TC       | 43      | 55      | 1.110     | 0.633-1.946 | 0.715     |
| CC       | 13      | 38      | 2.537     | 1.206-5.335 | 0.014     |
| Total    | 102     | 146     |           |             |           |

TT : Wild genotype, CC: Heterozygous and CC: Homozygous genotype.

**Table 3 :** Alleles Distribution of CYP17 Gene (-34 T↔C) SNP in Patients with Benign Prostatic Hyperplasia and the Controls Groups.

| Allele | Control | Patient | OR        | 95% CI      | P-value   |
|--------|---------|---------|-----------|-------------|-----------|
| T      | 135     | 161     | Reference | Reference   | Reference |
| C      | 69      | 131     | 1.592     | 1.099-2.306 | 0.013     |
| Total  | 204     | 292     |           |             |           |

increase the rate of CYP17 gene transcription (mRNA). The increase of CYP17 mRNA cause increase in CYP17 enzyme synthesis (activity), which lead to increasing in androgen production and cell division in the prostate, thereby may increases the risk of BPH.

The current results are in consistence with the results of Lin-Lin *et al* (2017), Ananthan *et al* (2016) and Vivek

*et al* (2014) studies in which the homozygous genotype (CC) of CYP17 gene (-34 T↔C) SNP was found to increase the risk of BPH with respect to those of the wild genotype (TT) of CYP17 gene (-34 T↔C) SNP. Also the minor allele (C) of CYP17 gene (-34 T↔C) SNP was significantly higher in BPH patients when compared with that of the control group. Conversely this results differed from those described by Asmahan *et al* (2014), who did not find an association between CYP17 gene (-34 T↔C) SNP and BPH.

**CONCLUSION**

The CYP17 gene (-34 T↔C) SNP is involved in the pathogenesis of BPH. The homozygous genotype (CC) was found to be significantly increase the risk of BPH by two folds with respect to those of the wild genotype (TT). The minor allele (C) of CYP17 gene (-34 T↔C) SNP was significantly higher in BPH patients when compared with that of the control group.

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