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Research Article

Association of genetic polymorphisms in DNA repair genes in polycystic ovary syndrome

Abstract

Introduction: Polycystic ovary syndrome (PCOS) involves expression of chronic anovulation and hyperandrogenism. Role of environmental and genetic factors in PCOS is strongly supported but the genes that are positively involved in the etiology of the PCOS have not been fully investigated until now.

Material & Methods: A total of 127 patients with PCOS and 140 healthy controls were included in the present study. DNA was isolated from 4mL of blood samples from all the enrolled subjects. The polymorphisms of selected genes (*XRCC*1, *XPD* and *hMSH*2) were carried out by ARMS-PCR and PCR-RFLP.

Results: GA genotype of *XRCC*1 gene were found to be predominant in the PCOS compared to controls (57.5%, 32.9% respectively, p = <0.0001). Significant difference was not observed in the frequency of A allele of *XPD* among the controls and PCOS (0.76 and 0.62 respectively). Heterozygotes of *hMSH*2 gene were found to be predominant in the PCOS group compared to controls with 2.64 folds increased risk for PCOS, which was statistically significant (OR 2.64, 95% CI 1.59–4.39, p=0.0001).

Conclusions: Polymorphisms in *XRCC*1, *XPD* and *hMSH*2 genes were found to be predominant in patients with PCOS. Since different populations have distinct genetic backgrounds, it is necessary to validate or replicate such associations from other ethnic populations.

Introduction

Polycystic ovary syndrome (PCOS) is an endocrine-influenced pathology mostly seen in women of reproductive age [1]. PCOS is characterized by polycystic ovaries, hyperandrogenism and menstrual irregularity [2]. PCOS is an inflammatory disease that usually develops as a consequence of a complex interaction between susceptible genes, the environment and the immune system [2]. Number of candidate genes have been identified which is susceptibility with PCOS [3,4]. Few of these genes have been identified to play an important role in the pathogenesis of the PCOS [3,4]. Many genes have been identified that their changed expression indicating thus that the genetic instability in PCOS disturb the signal transduction ruling steroidogenesis, gonadotrophin action and regulation, steroid hormones action, energy homeostasis, insulin action and secretion, chronic inflammation and others.

Efficient DNA-repair mechanisms help to remove the lesions that cause DNA breaks during replication and prevent propagation of mutations [5]. Previous reports have been demonstrated that polymorphisms in the DNA repair genes modify the clinical outcome [6-8]. However, there is still a paucity of data on the association of genetic polymorphisms in DNA repair genes with the etiopathogenesis of PCOS.

The base excision repair (BER) is one of the important pathways that repairs spontaneous and endogenously produced DNA damage [9]. Though many proteins are involved in BER, the X-ray repair cross-complementing group 1 (*XRCC*1) and apurinic/apyrimidinic (AP) endonuclease (*APE*1) genes play a key role in the repair pathway.

Nucleotide excision repair (NER) is a highly versatile and sophisticated DNA damage repair pathway that counteracts the deleterious effects of a multitude of DNA lesions [10]. NER is a process by which the cells prevent unwanted mutation by removing the vast majority of DNA damage [11]. The *XPD* Lys751Gln (Lysine to Glutamine) substitution is attributed to a (A>C) transversion in exon 23 [12], at 751 codon. Several studies revealed that polymorphisms in this gene may have an effect on prostate cancer [13], age related macular degeneration [14].

Human mutS homolog 2 (*hMSH*2) genes are integral components of the DNA mismatch repair pathway. One of the

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two other mismatch repair proteins, *hMSH6* or *hMSH3* binds with *hMSH2* and can form a heterodimer to perform repair mechanisms [15]. Formation of heterodimer with other proteins can affect by substitution at codon 322 (Gly322Asp) of hMSH2 and which may lead to deficiency in repair mechanisms.

Some studies have shown an association between these polymorphisms and PCOS while some have not [16]. Since many of these studies have emphasized for further studies in different population groups, the present study was undertaken to find out the association of DNA repair genes polymorphism in women susceptibility to develop PCOS.

Materials and Methods

Study population

The study is case control and total of 127 patient with PCOS and 146 controls were recruited in the present study. Written consent was taken from all the enrolled subjects. The study protocol was approved Institutional Review Board. Detailed information on clinical diet, BMI, fasting glucose, LH/FSH ratio was recorded through Performa. PCOS Our sample size of 273 is large enough and exceeds the estimated number of samples (~200 cases + controls) required to obtain a 90 % statistical power.

Molecular analysis

2mL of peripheral blood sample was collected from each participated subjects. DNA was extracted from peripheral blood samples using kit method according to manufactures instruction and genotyping were done for *XRCC1*, *XPD* and *hMSH2* genes. Genotyping of *XRCC1* Arg399Gln (G>A) and *XPD* Lys751Gln (A>C) polymorphism was performed using the Amplification refractory mutation system-polymerase chain reaction (ARMS-PCR). PCR-RFLP (Polymerase chain reaction-Restriction fragment length polymorphism) was performed for *hMSH2* Gly322Asp (G>A) polymorphisms. All amplifications were repeated twice and were analyzed using agarose gel electrophoresis system.

Statistical analysis

The genotypic distribution of *XRCC1*, *XPD* and *hMSH2* gene was performed using χ^2-test. Distribution of genotypes and alleles between PCOS and control groups were tested using Fisher's exact test. Since differences between conditional logistical regression and unconditional logistical regression were small, unconditional logistical regression was used to estimate odds ratio (OR) and 95% confidence interval (CI). The above statistical analysis was performed using Graph pad prism version 5.0 (GraphPad Software, Inc., San Diego, California, USA).

Results

The frequency of 'A' allele of *XRCC1* gene was found to be predominant in PCOS group compared to controls (37% vs 22% respectively) (Table 1).

Heterozygotes (GA) were found to be predominant in the PCOS group compared to controls (57.5%, 32.9% respectively, p = <0.0001) with 3.11 folds increased risk for PCOS, which was statistically significant (OR 3.11, 95% CI 1.86-5.19, p =<0.0001) (Table 2). Based on the dominant model, combination of GA+AA genotypes were also observed to be associated with high risk for PCOS (OR 3.03, 95% CI 1.85– 4.97, p= <0.0001). In recessive model the AA genotype (compared with GG+GA) did not reveal any risk to PCOS (OR 1.47, 95% CI 0.56-3.86, p= 0.43) (Table 2).

Variation in the distribution of allele frequency is reveled in the present study (Table 3). No significant difference was observed in the frequency of A allele among the controls and PCOS (0.76 and 0.62 respectively).

AC genotypic frequency was found to be predominant in PCOS group (53.5%) compared to controls (34.9%) with the difference being statistically significant (p= 0.0002). Based on the dominant model, combination of AC+CC genotype frequency were 64.4% in PCOS and 41.8% in control (OR 2.54, 95%CI 1.56–4.15, p=0.003). Overdominant model revealed AC (Compare with AA+CC genotype) genotype was observed to be associated with PCOS (OR 2.15, 95%CI 1.32–3.49, p=0.0019) (Table 4).

The frequency of 'A' allele was found to be predominant in PCOS group compared to controls (38% vs 25% respectively) (Table 5).

Heterozygotes (GA) were found to be predominant in the PCOS group compared to controls (63.8%, 43.1% respectively, p = 0.0001) with 2.64 folds increased risk for PCOS, which was statistically significant (OR 2.64, 95% CI 1.59–4.39, p=0.0001)

Table 1: *XRCC1* allele frequency distribution in controls and PCOS.

	Controls		Patients	
Allele	Count	Frequency	Count	Frequency
G	228	0.78	161	0.63
A	64	0.22	93	0.37

Table 2: *XRCC1* genotypic frequency distribution in controls and PCOS.

Model	Genotype	Controls	Patients	OR (95% CI)	P-value
Codominant	G/G	90 (61.6%)	44 (34.6%)	1.00	<0.0001
	G/A	48 (32.9%)	73 (57.5%)	3.11 (1.86-5.19)	
	A/A	8 (5.5%)	10 (7.9%)	2.56 (0.94-6.93)	
Dominant	G/G	90 (61.6%)	44 (34.6%)	1.00	<0.0001
	G/A-A/A	56 (38.4%)	83 (65.3%)	3.03 (1.85-4.97)	
Recessive	G/G-G/A	138 (94.5%)	117 (92.1%)	1.00	0.43
	A/A	8 (5.5%)	10 (7.9%)	1.47 (0.56-3.86)	
Overdominant	G/G-A/A	98 (67.1%)	54 (42.5%)	1.00	<0.0001
	G/A	48 (32.9%)	73 (57.5%)	2.76 (1.69-4.52)	

Table 3: *XPD* allele frequency distribution in controls and PCOS.

	Controls		Patients	
Allele	Count	Frequency	Count	Frequency
A	221	0.76	158	0.62
C	71	0.24	96	0.38

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(Table 6). Based on the dominant model, combination of GA+AA genotypes was also observed to be associated with high risk for PCOS (OR 2.69, 95% CI 1.63– 4.43, *p*= 0.001). In recessive model no such variation was observed (compared with GG+GA) (OR 1.90, 95% CI 0.60–5.95, *p*= 0.27) (Table 6). Whereas in the overdominant model, GA (Compared with GG+AA genotype) genotype found to be associated with a 2.32 folds increased risk for PCOS (OR 2.32, 95% CI 1.42-3.78, *p* = 0.004), further confirming the risk of 'A' allele in PCOS.

Discussion

PCOS is a chronic inflammatory disease with unknown aetiology. The pathophysiology of PCOS relates to a dysregulated immune response on a background of genetic susceptibility. The last few decades have seen a discernible shift in the global prevalence of PCOS.

PCOS may represent a polygenic disorder [17-19]. Several genes have been identified which play important role in the pathogenesis of PCOS and the presence of their polymorphisms have been explored [20]. Serum adiponectin plays a vital role in the pathogenesis of insulin resistance of PCOS women [21]. Investigator demonstrated that patients with PCOS have a 7.8-fold higher frequency of CYP1A1 Ile/Val genotype and a 7.4-fold CYP1A1 any Val genotype (Ile/Val or Val/Val) [22].

Table 4: *XPD*genotypic frequency distribution in controls and PCOS

Model	Genotype	Controls	Patients	OR (95% CI)	P-value
Codominant	A/A	85 (58.2%)	45 (35.4%)	1.00	0.0002
	A/C	51 (34.9%)	68 (53.5%)	2.52 (1.51-4.20)	
	C/C	10 (6.8%)	14 (11%)	2.64 (1.09-6.43)	
Dominant	A/A	85 (58.2%)	45 (35.4%)	1.00	0.003
	A/C-C/C	61 (41.8%)	82 (64.6%)	2.54 (1.56-4.15)	
Recessive	A/A-A/C	136 (93.2%)	113 (89%)	1.00	0.22
	C/C	10 (6.8%)	14 (11%)	1.68 (0.72-3.94)	
Overdominant	A/A-C/C	95 (65.1%)	59 (46.5%)	1.00	0.0019
	A/C	51 (34.9%)	68 (53.5%)	2.15 (1.32-3.49)	

Table 5: *hMSH2* allele frequency distribution in controls and PCOS.

	Controls		Patients	
Allele	Count	Frequency	Count	Frequency
G	219	0.75	157	0.62
A	73	0.25	97	0.38

Table 6: *hMSH2* genotypic frequency distribution in controls and PCOS

Model	Genotype	Controls	Patients	OR (95% CI)	P-value
Codominant	G/G	78 (53.4%)	38 (29.9%)	1.00	0.0001
	G/A	63 (43.1%)	81 (63.8%)	2.64 (1.59-4.39)	
	A/A	5 (3.4%)	8 (6.3%)	3.28 (1.01-10.72)	
Dominant	G/G	78 (53.4%)	38 (29.9%)	1.00	0.001
	G/A-A/A	68 (46.6%)	89 (70.1%)	2.69 (1.63-4.43)	
Recessive	G/G-G/A	141 (96.6%)	119 (93.7%)	1.00	0.27
	A/A	5 (3.4%)	8 (6.3%)	1.90 (0.60-5.95)	
Overdominant	G/G-A/A	83 (56.9%)	46 (36.2%)	1.00	0.004
	G/A	63 (43.1%)	81 (63.8%)	2.32 (1.42-3.78)	

Our study demonstrated that heterozygotes (GA) of *XRCC1* gene were found to be predominant in the PCOS group compared to controls (57.5%, 32.9% respectively, *p* = <0.0001) with 3.11 folds increased risk for PCOS, which was statistically significant (OR 3.11, 95% CI 1.86–5.19, *p* =<0.0001). Our results are in contrast to those obtained by Gulbay et al., (2017) [16], reveled that there was no difference between women with PCOS and controls in terms of *XRCC1* Arg194Trp and *XRCC1* Arg399Gln genotypes (OR= 1.15, 95% CI= 0.57-2.32, p= 0.69 for *XRCC1* Arg194Trp and OR= 1.14, 95% CI= 0.87-1.48, p= 0.32 for *XRCC1* Arg399Gln). Gulbay et al., 2017 [16], also reported that the frequency of variant alleles for *XRCC1* Arg194Trp and *XRCC1* Arg399Gln in the study population were 7.02% and 32.90% respectively and similar to controls. Several epidemiological studies have assessed bladder cancer risk and Arg399Gln *XRCC1* polymorphism [7,23,24]. Many of them have suggested a decreased risk for individuals with the variant homozygote genotype (AA) [7,24]. The homozygote variant genotype (AA) was inversely associated with bladder cancer risk [25]. Moullan et al., 2003 [26], demonstrated that the A allele did not appear to be associated with an increased Breast Cancer risk from the analysis of the individual SNPs but whereas A allele have increase in our study. Duell et al. 2001 [27] and Smith et al. 2003 [28], neither group reported an association of the codon 399 A allele with an increased Breast Cancer risk in white American women or Caucasian women.

In 2003, Mort and colleagues, suggested lack of association between *XPD* gene polymorphisms and cancer. AC genotypic frequency was found to be predominant in PCOS group (53.5%) compared to controls (34.9%) with the difference being statistically significant (*p*= 0.0002). Our study also demonstrated that combination of AC+CC genotype frequency were 64.4% in PCOS and 41.8% in control (OR 2.54, 95%CI 1.56–4.15, *p*=0.003). Gln allele was reported to be associated with poor DNA repair capacity in a study conducted on *XPD* Lys751Gln polymorphism [29]. Gulbay et al, (2017) [16], revealed that no statistical differences were observed between PCOS women and the control group in terms Lys751Gln *XPD* polymorphism. Wang et al., (2010) [30], also demonstrated that AC genotype was not associated with breast cancer. In another study, Sanyal et al., (2004) [31], also reported that variant allele in *XPD* did not show any significant difference between the patients with bladder cancer and healthy control. Fontana et al., (2008) [25], demonstrated that the CC and AC genotype of *XPD* were associated with a decreased risk of bladder cancer, but these results were not significant. Stern et al., (2002) [32], also found a small but non-significant decrease in risk for the CC genotype when compared to subjects with the AA or AC genotypes.Most of the published studies did not reveal any association between *XPD* polymorphisms and bladder cancer risk [33-35].

Heterozygotes (GA) of *hMSH2* gene were found to be predominant in the PCOS group compared to controls (63.8%, 43.1% respectively, *p* = 0.0001) with 2.64 folds increased risk for PCOS, which was statistically significant (OR 2.64, 95% CI 1.59–4.39, *p*=0.004) which is in absolute conformity with data of Poplawski et al. (2005) [36], Significant association of

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Gly322Asp polymorphism of the *hMSH2* gene with breast cancer and colorectal cancer [37], was reported. The frequency of A allele was found to be predominant in PCOS group compared to controls.

Since this variation was observed to be statistically significant in the patient group compared to the controls, the possibility of this variation in the pathogenicity of the disease under the influence of other genes and environmental factors cannot be ruled out. The reasons for the disparity in results needs an in depth analysis of the sequel of events that leads to PCOS.

References

1. Battaglia C, Mancini F, Cianciosi A (2008) Vascular risk in young women with polycystic ovary and polycystic ovary syndrome. Obstet Gynecol 111: 385-395. Link: https://goo.gl/gidhGq

2. Urbanek M, Kosova G (2013) Genetics of the polycystic ovary syndrome. Mol Cell Endocrinol 373: 29-38. Link: https://goo.gl/McpMNy

3. Menke MN, Strauss JF (2007) Genetics of polycystic ovarian syndrome. Clin Obstet Gynecol 50: 188-204. Link: https://goo.gl/wXyF8o

4. Celik O, Yesilada E, Hascalık S (2010) Angiotensin converting enzyme gene polymorphism and risk of insulin resistance in PCOS. Reprod Bio Med Online 20: 492-98. Link: https://goo.gl/KhrD5z

5. Wiseman H, Halliwell B (1996) Damage to DNA by reactive oxygen and nitrogen species: role in inflammatory disease and progression to cancer. Biochem J 313: 17–29. Link: https://goo.gl/xc3e8h

6. Ozsavc D (2007) Oxidative DNA damage and repair system. Adv Mol Med 3: 57–61.

7. Kelsey KT, Park S, Nelson HH (2004) A population-based casecontrol study of the XRCC1 Arg399Gln polymorphism and susceptibility to bladder cancer. Cancer Epidemiol Biomarkers Prev 8: 1337-1341. Link: https://goo.gl/Ldkqsg

8. McCarty KM, Smith TJ, Zhou W (2007) Polymorphisms in XPD (Asp312Asn and Lys751Gln) genes, sunburn and arsenic-related skin lesions. Carcinogenesis 28: 1697–1702. Link: https://goo.gl/P5NVtG

9. Zhang X, Miao X, Liang G (2005) Polymorphisms in DNA base excision repair genes ADPRT and XRCC1 and risk of lung cancer. Cancer Res 65: 722-726. Link: https://goo.gl/fwxH6y

10. Dip R, Camenisch U, Naegeli H (2004) Mechanisms of DNA damage recognition and strand discrimination in human nucleotide excision repair. DNA Repair (Amst) 3: 1409-1423. Link: https://goo.gl/9r427F

11. Peterson CL, Côté J (2004) Cellular machineries for chromosomal DNA repair. Genes & Develop 18: 602–616. Link: https://goo.gl/WFX9Wv

12. Shen M, Hung RJ, Brennan P (2003) Polymorphisms of the DNA repair genes XRCC1, XRCC3, XPD, interaction with environmental exposures, and bladder cancer risk in a case control study in northern Italy. Cancer Epidemiol Biomarkers Prev 1: 1234-1240. Link: https://goo.gl/ygShVJ

13. Rybicki AB, Moreira VD, Cicek A (2004) DNA repair gene XRCC1 and XPD polymorphisms and risk of prostate cancer. Cancer Epidemiol Biomarkers Pre 13: 23–29. Link: https://goo.gl/nmrznJ

14. Görgün E, Güven M, Unal M (2010) Polymorphisms of the DNA Repair Genes XPD and XRCC1 and the Risk of Age-Related Macular Degeneration. Invest Ophthalmol Vis Sci 51: 4732-4737. Link: https://goo.gl/hQDGvH

15. Mitchell RJ, Farrington SM, Dunlop (2002) Mismatch Repair Genes hMLH1 and hMSH2 and Colorectal Cancer: A HuGE Review. AJ Epidemiol 56: 885-902. Link: https://goo.gl/QUvKFG

16. Gulbay G, Yesilada E, Celik O (2017) The Investigation of Polymorphisms in DNA Repair Genes (XRCC1, APE1 and XPD) in Women with Polycystic Ovary Syndrome. Asian Pac J Cancer Prev 18: 1219-1223. Link: https://goo.gl/gXqRiA

17. Franks S, Gharani N, Waterworth D (1997) The genetic basis of polycystic ovary syndrome. Hum Rep 12: 2641–2648. Link: https://goo.gl/w7NjEj

18. Legro RS, Driscoll D, Strauss JF (1998) Evidence for a genetic basis for hyperandrogenemia in polycystic ovary syndrome. Proc Natl Acad Sci USA 95: 14956–14960. Link: https://goo.gl/wrXr6U

19. Franks S, McCarthy M (2004) Genetics of ovarian disorders: polycystic ovary syndrome. Rev in End and Met Dis 5: 69–76. Link: https://goo.gl/47wq9B

20. Fratantonio E, Vicari E, Pafumi C (2005) Genetics of polycystic ovarian syndrome. Rep Bio Med Online 10: 713–720.

21. Karkanaki A, Piouka A, Katsilis I, Farmakiotis D (2009) Adiponectin Levels Reflect the Different Phenotypes of Polycystic Ovary Syndrome: Study in Normal Weight, Normoinsulinemic Patients. Fertility and Sterility 92: 2078-2081. Link: https://goo.gl/qvBQpJ

22. Esinler I, Aktas D, Otegen U (2008) CYP1A1 gene polymorphism and polycystic ovary syndrome. Reprod Biomed Online 16: 356-360. Link: https://goo.gl/FdmVud

23. Andrew AS, Nelson HH, Kelsey KT (2006) Concordance of multiple analytical approaches demonstrates a complex relationship between DNA repair gene SNPs, smoking and bladder cancer susceptibility. Carcinogenesis 5: 1030-1037. Link: https://goo.gl/fQj6vJ

24. Matullo G, Guarrera S, Carturan S (2001) DNA repair gene polymorphisms, bulky DNA adducts in white blood cells and bladder cancer in a case-control study. Int J Cancer 92: 562-567. Link: https://goo.gl/BJbbfs

25. Fontana L, Bosviel R , Delort L (2008) DNA repair gene ERCC2, XPC, XRCC1, XRCC3 polymorphisms and associations with bladder cancer risk in a french cohort. Anticancer Res 28: 1853-1856. Link: https://goo.gl/PCd7ba

26. Moullan N, Cox DG,Ange`le S (2003) Polymorphisms in the DNA repair gene XRCC1, breast cancer risk,and response to radiotherapy. Cancer Epidemiol Biomark Prevent 1: 1168–1174. Link: https://goo.gl/KfMPsf

27. Duell EJ, Millikan RC, Pittman GS (2001) Polymorphisms in the DNA repair gene XRCC1 and breast cancer. Cancer Epidemiol Biomark 10: 217–222. Link: https://goo.gl/8Mgvs9

28. Smith TR, Miller MS, Lohman K (2003) Polymorphisms of XRCC1 and XRCC3 genes and susceptibility to breast cancer. Cancer Lett 190: 183–190. Link: https://goo.gl/J6e3eM

29. Shi Q, Wang LE, Bondy ML (2004) Reduced DNA repair of benzo[a]pyrene diol epoxide-induced adducts and common XPD polymorphisms in breast cancer patients. Carcinogenesis 25: 1695-1700. Link: https://goo.gl/pNZSQi

30. Wang HC, Liu CS, Wang HC (2010) Significant Association of XPD Asp312Asn Polymorphism with Breast Cancer in Taiwanese Patients. Chin J Physiol 53: 130-135. Link: https://goo.gl/Vyi38R

31. Sanyal S, Festa F, Sakano S (2004) Polymorphisms in DNA repair and metabolic genes in bladder cancer. Carcinogenesis 25: 729-734. Link: https://goo.gl/2abExs

32. Stern MC, Umbach DM, Lunn RM (2002) DNA repair gene XRCC3 codon 241 polymorphism, its interaction with smoking and XRCC1 polymorphisms, and bladder cancer risk. Cancer Epidemiol Biomarkers Prev 9: 939-943. Link: https://goo.gl/njvfyV

33. Shao J, Gu M, Xu Z (2007) Polymorphisms of the DNA gene XPD and risk of bladder cancer in a Southeastern Chinese population. Cancer Genet Cyto Genet 1: 30-36. Link: https://goo.gl/oMizsC

Citation: Dhaded S, Dabshetty S (2018) Association of genetic polymorphisms in DNA repair genes in polycystic ovary syndrome. J Gynecol Res Obstet 4(3): 044-048. DOI: http://dx.doi.org/10.17352/jgro.000058

34. Schabath MB, Delclos GL, Grossman HB (2005) Polymorphisms in XPD exons 10 and 23 and bladder cancer risk. Cancer Epidemiol Biomarkers Prev 4: 878-884. Link: https://goo.gl/8ErscS

35. Matullo G, Guarrera S, Sacerdote C (2005) Polymorphisms/ haplotypes in DNA repair genes and smoking: a bladder cancer case-control study. Cancer Epidemiol Biomarkers Prev 1: 2569-2578. Link: https://goo.gl/B7m7DP

36. Poplawski T, Zadrozny, M Kolacinska (2005) Polymorphisms of the DNA mismatch repair gene HMSH2 in breast cancer occurence and progression. Breast Cancer Res Treat 94: 199–204. Link: https://goo.gl/QANcLr

37. Chio YH, Cotterchio ME, Neerav GM (2009) Penetrance of colorectal cancer among MLH1/MSH2 carriers participating in the colorectal cancer familial registry in Ontario. Hereditary Cancer. Clin Pra 7: 1-11. Link: https://goo.gl/NU8Mfs

Citation: Dhaded S, Dabshetty S (2018) Association of genetic polymorphisms in DNA repair genes in polycystic ovary syndrome. J Gynecol Res Obstet 4(3): 044-048. DOI: http://dx.doi.org/10.17352/jgro.000058