Program and Abstracts

The 2nd International Conference of the Indonesian Chemical Society 2013

ICICS 2013

Research in Chemistry for Better Quality of Environmental

Universitas Islam Indonesia, Yogyakarta, Indonesia
October, 22 - 23th 2013

Abdul Kahar Muzakkir, Conference Hall
Universitas Islam Indonesia (UII), Yogyakarta.
Preface

The international conference is an annual conference of the Indonesian Chemical Society (Himpunan Kimia Indonesia, HKI). In the year 2013, the mandate of the organizing committee was given to the HKI Yogyakarta branch and also supported by Department of Chemistry of Universitas Negeri Yogyakarta (UNY), Department of Chemistry of Universitas Gadjah Mada (UGM), Department of Chemistry of Universitas Islam Negeri Sunan Kalijaga (UIN Suka), National Nuclear Energy Agency (BATAN Yogyakarta), and Balai Penyelidikan dan Pengembangan Kegununganapian (BPPTK Yogyakarta).

For the year 2013, ICICS 2013 is hosted by Department of Chemistry, Faculty of Mathematics and Natural Sciences, Islamic University of Indonesia, Yogyakarta from October 22 – 23, 2013. This conference was also prepared to celebrate 70th anniversary of Universitas Islam Indonesia.

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The Scientific Programme of ICICS2013 comprises the following:

1. Invited Speaker 11 papers
2. A total 256 paper for parallel session
   a. Organic Chemistry 32 papers
   b. Inorganic Chemistry 43 papers
   c. Physical Chemistry 37 papers
   d. Analytical Chemistry 68 papers
   e. Education Chemistry 23 papers
   f. Biochemistry 43 papers

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<th>Poster</th>
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<tr>
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<td>0</td>
<td>11</td>
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Prevalence of Estrogen Receptor Alpha (ESRα) Gene Polymorphism in Javanese postmenopausal Women with DM type 2

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Abstract

Polymorphisms of estrogen receptor alpha (ESR-α) gene may cause deleterious effect to metabolic action, particularly in the glucose homeostasis due to insulin resistance. Polymorphisms in the ESR-α gene have been associated with the occurrence of breast cancer, menopausal osteoporosis, recurrent abortions, arterial hypertension, T2DM, dyslipidemia, cardiovascular complications such as coronary heart diseases and stroke. It is understood that in postmenopausal women the incidence of T2DM as well as its cardiovascular complications will increase. So far there are two polymorphisms in ER-α that are the most widely studied as risk factor for many diseases, namely the Pvull and XbaI (rs2234693 and rs9340799). Both polymorphisms have been identified as markers of T2DM in postmenopausal women. The distributions of Pvull and XbaI polymorphisms among the postmenopausal women in the world have been studied, and therefore it is interesting to know their distributions in the Javanese postmenopausal population with T2DM. In this cross-sectional study as many as 121 postmenopausal women especially with T2DM, with age ranges from 45 to 70 years, were consecutively entered. Pvull and XbaI polymorphisms were determined by the PCR-restriction fragment length polymorphism (RFLP). The alleles for Pvull and XbaI were denoted as P and X for absence of restriction site and denoted as p and x respectively for presence of restriction site. The results disclosed Pvull genotypes distribution as follows, PP 26.4 %, Pp 46.3 %, and pp 27.3 %, and as for XbaI genotypes were XX 42.1 %, Xx 32.2 % and xx 25.6 %. Four haplotypes were recognized, and their distributions were PX 24.4 %, Px 23.1 %, pX 28.9 % and px 23.6 %. In conclusion, the prevalent gene for ER-α Pvull was heterozygote Pp (46.3 %) and as for XbaI was homozygote XX (41.3 %), and the prevalent for the haplotype was pX (28.9%).

Keywords: Prevalence- ESRα Polymorphism-Javanese Postmenopausal Women.
Certificate

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Organizing Committee
The 2nd International Conference of the Indonesian Chemical Society (ICICS), October 22-23, 2013, Chemistry Department, Islamic University of Indonesia

Prevalence of Estrogen Receptor Alpha (ESRa) Gene Polymorphism in Javenese Postmenopausal Women with DM type 2

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Polymorphisms of estrogen receptor alpha (ESR-a) gene may cause deleterious effect to metabolic action, particularly in the glucose homeostasis due to insulin resistance. Polymorphisms in the ESR-a gene have been associated with the occurrence of breast cancer, menopausal osteoporosis, recurrent abortions, arterial hypertension, type 2 diabetes mellitus (T2DM), dyslipidemia, cardiovascular complications such as coronary heart diseases and stroke. It is understood that in postmenopausal women the incidence of T2DM as well as its cardiovascular complications will increase. So far there are two polymorphisms in ER-a that are the most widely studied as risk factor for many diseases, namely the Pvull and Xbal (rs2234693 and rs9340799). Both polymorphisms have been identified as markers of T2DM in postmenopausal women. The distributions of Pvull and Xbal polymorphisms among the postmenopausal women in the world have been studied, and therefore it is interesting to know their distributions in the Javanese postmenopausal population with T2DM. In this cross-sectional study as many as 121 postmenopausal women especially with T2DM, with age ranges from 45 to 70 years, were consecutively entered. Pvull and Xbal polymorphisms were determined by the PCR-restriction fragment length polymorphism (RFLP). The alleles for Pvull and Xbal were denoted as P and X for absence of restriction site and denoted as p and x respectively for presence of restriction site. The results disclosed Pvull genotypes distribution as follows, PP 26.4 %, Pp 46.3 %, and pp 27.3 %, and as for Xbal genotypes were XX 42.1 %, Xx 32.2 % and xx 25.6 %. Four haplotypes were recognized, and their distributions were PX 24.4 %, Px 23.1 %, pX 28.9 % and px 23.6 %. In conclusion, the prevalent gene for ESR-a Pvull was heterozygote Pp (46, 3 %) and as for Xbal was homozygote XX (42, 2 %), and the prevalent for the haplotype was PX (28, 9%).

Key word: Prevalence-ESRa Polymorphism-Javenese Postmenopausal Women

I. INTRODUCTION

Type 2 Diabetes Mellitus (T2DM) is a disease caused mainly by disrupted homeostasis of glucose with deleterious consequences to many organ including heart, kidney, nervous system, eyes, and vasculare (1). The etiology of T2DM is combination of genetic factors such as polymorphism and mutation and enviromental factors such as diet and life style of low exercises (2,3).

The number of diabetic patients among women are increasing with the increasing age of women especially in menopause and postmenopausal women which known as low level estrogen-associated diabetes type 2 (4). In menopause and postmenopausal women, low level estrogen have associated with several condition or symptom such as vasomotor symptom (hot flash), mood disturbances (loss of control), sleep disorders (insomnia), sexual disfunction and urinary symptom (incontinence), vaginal dryness, cancer, osteoporosis and cardiovascular disease (hypertension) (5,6,7). This condition due to changes of aging itself and changes in endocrine system accompanying natural menopause.

Estrogen with estrogen receptor are becoming new players in diabetes mellitus especially in glucose hemostasis and insulin resistance (8). Estrogen can stimulate liver fatty acid metabolism, suppress hepatic glucose produc- tion, reduce both hyperglycemia and plasma in- sulin levels, protect pancreatic β-cell.
function/survival, and increase GLUT-4 expression and glucose uptake. Estrogen modulates GLUT-4 expression in tissues through its receptors (9). Estrogen modulates insulin secretion, regulates ATP-sensitive potassium channel (K-ATP channel) activity, and regulates calcium signals via plasma membrane estrogen receptors (10).

The physiological effect of estrogen is mediated mainly through estrogen receptors. Currently there are three estrogen receptors, i.e. ESRα, ESRβ and the G protein-coupled ER (GPER) (11,12,13). GPER have been identified in rodent and human β cells. Activation of ESR-α enhances glucose-stimulated insulin biosynthesis, reduces islet toxic lipid accumulation and promotes β-cell survival from proapoptotic stimuli, while activation of ESRβ increases glucose-stimulated insulin secretion, whereas activation of GPER protects β cells from apoptosis, raises glucose-stimulated insulin secretion and lipid homeostasis without affecting insulin biosynthesis (14).

Estrogen receptor alpha (ESRα) function is determined by ESRα gene with various polymorphism such as Pvull and Xbal (Fig.1) in the first intron. The ESR-α gene is large approximately 140 kb of DNA, encompassing 8 exons, encodes protein consisting of 595 amino acids with molecular weight of 66 kDa. The ESRα is located on chromosome 6q25.1 [15].

The aim of this study was to determine the distribution of polymorphism in ESR α gene in diabetes postmenopausal women population. We addressed this question in diabetes Javenese postmenopausal women-based studies.

![Figure 1. Location of ESRα Pvull and Xbal Polymorphism](image)

II. MATERIALS & METHODS

Study Subjects
A total of 121 diabetic subjects with T2DM were recruited in this study by cross sectional design. All the patients were attended during public service program of Faculty of Medicine Islamic University of Indonesia in several places of Kalasan, Condong Catur and Prambanan sub district from April to December 2012. The subjects were selected under the inclusion and exclusion criteria. Diagnosis of type 2 diabetes mellitus was based on WHO 1999 criteria (16). Individuals with fasting blood glucose levels are equal to or greater than 126 mg/dl. Group of individuals are selected as subject of this research in line with
requirements specifically have no history of taking HRT, do not suffer from liver failure and kidney failure and age over 45 years and under 65 years old.

The subjects were recruited only from Javanese ethnic. Then questionnaire were prepared to assess the socio-demographic factors, history and the duration of T2DM.

We have performed physical examination to all subject encompassed blood pressure and anthropometry measurements such as waist circumference, height, weight, BMI, hip circumference and waist circumference.

Sample Collection and Biochemical Analysis

Four-five milliliters of peripheral blood samples were collected and transferred into an EDTA tube by a qualified phlebotomist. Blood samples were collected from the subjects after a 10-12-h fasting. Total cholesterol, HDL cholesterol, and triglyceride levels were determined by standard methods using commercial kits conducted in Kalasan Islamic Hospital Jogjakarta as certified laboratory. Plasma was separated from the blood by centrifuge at 4500 rpm and stored at -20°C until further analysis. Individual weight and height were obtained to calculate body mass index (BMI) using the formula, weight (kg)/ [height (m2)]. To determine the levels of triglycerides (TG), high density lipoprotein cholesterol (HDL-C) and total cholesterol (TC), plasma samples was analyzed using Metrolab 2300 Autoanalyser (Diatron, Argentina) with kits supplied by Clona-test Diagnostics (Linear Chemical, Spain). Low density lipoprotein cholesterol (LDL-C) was calculated using Friedewald formula (17). We have used vectube (Shanghai, China) for blood collection container containing EDTA anticoagulant. In this study triacylglycerol (TAG) examination should be evaluated with serum examination to do check and make certain the result of plasma examination within 10 % of sample. Some literature explained the higher result of TAG in serum sample than plasma sample in range 2.5-4.5%. TAG in non fasting subjects is higher up to 40% than in fasting subjects but for HDL and cholesterol total are not significantly different between non fasting and fasting subjects (18).

Genotyping Methods

Genomic DNA was extracted from peripheral blood using Genomic DNA isolation kit (Nucleo Spin, Macherry Nagel, Hamburg, Germany). The concentration and the purity of extracted DNA were quantified by micro-volume spectrophotometer, using MaestroNano (Maestrogen, China). Isolation of DNA carried out with Nucleo Spin kit method. DNA was isolated from peripheral blood leukocyte cells. Examination of the presence of PvuII and XbaI
polymorphisms in the ESR alpha gene has been performed by PCR-RFLP. By using the forward primer 5'CTGCCACCCCTATCTGTATCTTTCCTTATATTCTCC-3' and reverse primer 5'TCTTTCTCTGCAACCCCCTGGCGATATCTGTA3'. PCR reaction was performed by using a Biometra PCR thermo cycler and reagents intron. PCR reactions using the total volume of 30 μl PCR reaction consisted of 2 μl DNA, 15 μl PCR master mix containing 1 × PCR buffer, 150 mM dNTP and U Tag DNA polymerase, 2 μl primer and 1 μl of each forward and reverse, 11 μl distilled water. Temperature conditions of PCR cycles that initial denaturation for 5 min at 95°C, followed by 35 cycles of PCR with denaturation at 95°C 30 sec, annealing at 62°C 30 sec, extension at 72°C for 30 sec, 2-minute final extension at 72°C and cooling at 4°C (4,9,10).

Polymorphism Analysis
PCR products have been digested by using restriction enzyme of PvuII and XbaI. For each volume 8 μl of PCR products have incubated with 1 unit of XbaI for detecting polymorphism of X/x and with 1 unit PvuII for detecting polymorphism of P/p. The codes of P/p and X/x means that upper case lettering is signifying the absence and the lower case lettering is indicating the presence of the restriction site. Then we have added 1.5 μl of NE buffer 1x, 1.5 μl BSA10x, 3μl distilled water up to 15 μl for each reaction of PvuII and XbaI enzyme. Incubation has conducted for 8 hours at 60°C for both. To distinguish c.454-397 T > C (PvuII) and c.454-351 A>G (XbaI) polymorphism, the amplified PCR fragment of 1372 bp was digested with restriction enzyme XbaI and PvuII separately, followed by electrophoresis on 2% agarose gel. For PvuII, the mutated homozygous variant pp (TT) produced two fragments 982 and 390 bp when heterozygote Pp (CT) produced three fragments of, 1372 and 982 bp and 390. Wild-type P (CC) produced one fragment of 1372 bp. For XbaI the mutated homozygous variant xx (AA) produced two fragments 936 and 436 bp when heterozygote Xx (AG) produced three fragments of 1372, 936, and 436 bp and XX (GG) wild-type produced one fragment of 1372 bp (4,9,10).

Statistics
Statistical analysis was performed with SPSS version 17.0 and THESIAS software version 3.1. Genotype distribution was tested for Hardy-Weinberg equilibrium by χ² to analyze haplotype in Javanese population based on maximum likelihood model and the SEM algorithm (19). A p-value less than 0.05 were considered significant.

Ethics
The study protocol was approved by the Ethical Committee of the Faculty of Medicine and Health Sciences, Universitas Muhammadiyah Yogyakarta (UMY). Ethical committee have issued the Ethical Clearance for this study. Written informed consent was obtained from all the subjects.
III. RESULT AND DISCUSSION

All characteristics are presented in Table 1 as general information of all subjects. The criterion of T2DM is based on fasting glucose levels according to WHO criteria using ≥ 126 mg. For all variables are normal condition in average except glucose.

<table>
<thead>
<tr>
<th>Subject Characteristics</th>
<th>Postmenopausal Women (n=121)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean ± SD</td>
</tr>
<tr>
<td>Age (years)</td>
<td>55.50±6.342</td>
</tr>
<tr>
<td>Systole (mmHg)</td>
<td>126.78±18.57</td>
</tr>
<tr>
<td>Diastole (mmHg)</td>
<td>79.82±9.132</td>
</tr>
<tr>
<td>Height (cm)</td>
<td>152.26±6.12</td>
</tr>
<tr>
<td>Weight (Kg)</td>
<td>54.87±9.67</td>
</tr>
<tr>
<td>BMI</td>
<td>23.12±3.72</td>
</tr>
<tr>
<td>Abdominal Circumference (cm)</td>
<td>85.96±10.60</td>
</tr>
<tr>
<td>Cholesterol (mg/dl)</td>
<td>197.12±48.73</td>
</tr>
<tr>
<td>LDL (mg/dl)</td>
<td>120.43±38.12</td>
</tr>
<tr>
<td>HDL (mg/dl)</td>
<td>55.20±20.01</td>
</tr>
<tr>
<td>TGA (mg/dl)</td>
<td>144.12±73.04</td>
</tr>
<tr>
<td>Fasting-Glucose (GLU) mg/dl</td>
<td>133.39±65.78</td>
</tr>
</tbody>
</table>

Then the subjects have been examined for the genotype to determine the XbaI and PvulI polymorphism. The results of genotype examination have been presented in Table 2. In the population genotyped for PvulI, this polymorphism was distributed as follows: PP 26.3% (n=32), Pp 46.3% (n=56), pp 27.3% (n=33). The frequency of XbaI genotype in the population was XX 42.2% (n=51), Xx 32.2% (n=39), xx 25.6% (n=31). The distribution of genotypes was in Hardy-Weinberg equilibrium for PvulI (\chi^2 p=0.413651) and XbaI (\chi^2 p= 0.091688) calculated by using THESIAS software. Table 2 shows the genotype and allele frequencies of the ESRα intronic polymorphisms PvulI and XbaI in the studied population.

TABLE 2.
DISTRIBUTION OF ESR α PvuII & XbaI POLYMORPHISMS IN JAVANESE POSTMENOPAUSAL WOMEN WITH T2DM

<table>
<thead>
<tr>
<th>Genotype and Allele</th>
<th>Subjects</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>PP</td>
<td>32</td>
<td>26.4</td>
</tr>
<tr>
<td>Pp</td>
<td>56</td>
<td>46.3</td>
</tr>
<tr>
<td>pp</td>
<td>33</td>
<td>27.3</td>
</tr>
<tr>
<td>XX</td>
<td>51</td>
<td>42.2</td>
</tr>
<tr>
<td>Xx</td>
<td>39</td>
<td>32.2</td>
</tr>
<tr>
<td>xx</td>
<td>31</td>
<td>25.6</td>
</tr>
<tr>
<td>P</td>
<td>120</td>
<td>49.6</td>
</tr>
<tr>
<td>p</td>
<td>122</td>
<td>50.4</td>
</tr>
<tr>
<td>X</td>
<td>141</td>
<td>58.3</td>
</tr>
<tr>
<td>x</td>
<td>101</td>
<td>41.7</td>
</tr>
</tbody>
</table>

The study result in Javanese diabetics women have been supported by the result study in Iran presenting the prevalence of ESR polymorphism for PP, Pp, pp and for XX, Xx, xx as follows; 21%, 53%, 26%, 27%, 46%, 27% respectively (Table 3 & 4). Allele frequencies for P and p in Iranian population reported by Golkhui et al are 48% and 52% in diabetics postmenopausal women respectively. Allele frequencies for X and x are 50% each allele (9).

TABLE 3. DISTRIBUTION OF PvuII GENOTYPE IN DIABETICS IN SEVERAL COUNTRIES

<table>
<thead>
<tr>
<th>No</th>
<th>Researchers</th>
<th>Ethnics</th>
<th>pp</th>
<th>Pp</th>
<th>PP</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Qin et al (10)</td>
<td>China</td>
<td>12%</td>
<td>57.6%</td>
<td>30.4%</td>
</tr>
<tr>
<td>2</td>
<td>Jakimiuk et al (11)</td>
<td>Poland</td>
<td>17.2%</td>
<td>50%</td>
<td>32.8%</td>
</tr>
<tr>
<td>3</td>
<td>Golkhui et al (9)</td>
<td>Iran</td>
<td>26%</td>
<td>53%</td>
<td>21%</td>
</tr>
<tr>
<td>4</td>
<td>Yoshihara et al (20)</td>
<td>Japan</td>
<td>31.74%</td>
<td>55.5%</td>
<td>12.69%</td>
</tr>
<tr>
<td>5</td>
<td>Ganasyam S.R. et al (21)</td>
<td>India</td>
<td>39 %</td>
<td>43%</td>
<td>18%</td>
</tr>
<tr>
<td>6</td>
<td>Akhmad, S.A et al (this study)</td>
<td>Indonesia</td>
<td>26.4%</td>
<td>46.3%</td>
<td>27.3%</td>
</tr>
</tbody>
</table>

The result study from China population had different distribution with Javanese population. In comparison, genotype frequencies for PP, Pp and pp in China are 12.1%, 30.4%, 57.5% and for XX, Xx, xx are 11.1%, 39.1%, 49.8% respectively whereas allele frequencies are 40.8%, 59.2%, 36%, 64% for P, p, X, x respectively (10). According to Ganasyam et al, the genotype frequencies for PP, Pp, pp in India postmenopausal women population with diabetics are 18%, 43%, 39% whereas the genotype frequencies for XX, Xx, xx are 75%, 20%, 5% respectively. Allele frequencies for P and p are 41.5% and 63.5% whereas allele frequencies for X and x are 85% and 15% (21). The result of our study Javanese women is not similar with study in China, Iran and India (p=0.000) after evaluating with Chai Square.
TABLE 4. DISTRIBUTION OF Xbal GENOTYPE IN DIABETICS IN SEVERAL COUNTRIES

<table>
<thead>
<tr>
<th>No</th>
<th>Researcher</th>
<th>Ethnics</th>
<th>XX</th>
<th>Xx</th>
<th>xx</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Qin et al (10)</td>
<td>China</td>
<td>11.03%</td>
<td>49.83%</td>
<td>39.13%</td>
</tr>
<tr>
<td>2</td>
<td>Jakimiuk et al (11)</td>
<td>Poland</td>
<td>62.25%</td>
<td>34.4%</td>
<td>59.4%</td>
</tr>
<tr>
<td>3</td>
<td>Golkhu et al (9)</td>
<td>Iran</td>
<td>27%</td>
<td>46%</td>
<td>27%</td>
</tr>
<tr>
<td>4</td>
<td>Akhmad, S.A et al</td>
<td>Indonesia</td>
<td>32.2%</td>
<td>42.2%</td>
<td>25.6%</td>
</tr>
</tbody>
</table>

TABLE 5.
DISTRIBUTION OF HAPLOTYPE ESR α Xbal & Pvull POLYMORPHISM IN DIABETICS JAVANESE MENOPAUSAL WOMEN

<table>
<thead>
<tr>
<th>Haploype</th>
<th>Frequencies</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>PX</td>
<td>118</td>
<td>24.4</td>
</tr>
<tr>
<td>Px</td>
<td>112</td>
<td>23.1</td>
</tr>
<tr>
<td>pX</td>
<td>140</td>
<td>28.9</td>
</tr>
<tr>
<td>px</td>
<td>114</td>
<td>23.6</td>
</tr>
</tbody>
</table>

The frequencies of haplotype in diabetics Javaneses postmenopausal women presented in table 5. In comparison, the frequencies of haplotype in diabetics postmenopausal women is different from other ethnic in non-diabetics postmenopause women presented in table 6. Frequencies of pX is higher in diabetics subject than in no diabetics subject as comparison presented in table 3 and 4. This result is inconsistent with the prior study in Javanese population having frequencies 19.37%, 25.63%, 19.37%, 35.63% respectively for PX, Px, pX, px in more subjects of study (4). In fact, different ethnic populations may partly explain discrepancies among ESRα polymorphism with differential degree of linkage disequilibrium. Haplotype pX was observed in diabetics subject but not observed in the majority of studies in non diabetics subjects. This difference of haplotype frequencies may result from the disequilibrium which is not complete and may be due to recombination occurred at these two polymorphic sites rather than multiple mutation. There are a lot of evidences that ESRα gene polymorphism influence many physiological processes in humans, women in particular, as well as may be the etiopathological factor of various diseases (11).

It is still not understood how the intronic polymorphism of the ESRα gene influences the receptor function. Polymorphisms with its positions in an intron, near the gene
promoter may suggest a possible role in either transcription regulation or mRNA processing and stability. It was recently shown that transition to P allele resulted in a site for myb binding, hence, the presence of this allele possible augments ESRα transcription.

Another explanation to the observations of associations between these SNPs and human illness is a possible linkage disequilibrium between the PvuII and XbaI polymorphisms with other polymorphisms in the ESRα gene (15,22).

**TABEL 6.**

**COMPARISON OF FREQUENCY OF PvuII-XbaI HAPLOTYPES OF THE HUMAN ESTROGEN RECEPTOR A GENE IN SEVERAL ETHNIC IN NON DIABETICS WOMEN**

<table>
<thead>
<tr>
<th>Ethnics Group</th>
<th>Place of study</th>
<th>No.of Subject</th>
<th>Px</th>
<th>PX</th>
<th>Px</th>
<th>pX</th>
</tr>
</thead>
<tbody>
<tr>
<td>Asians</td>
<td>Japan</td>
<td>238</td>
<td>54.9</td>
<td>18.7</td>
<td>26.5</td>
<td>0.3</td>
</tr>
<tr>
<td>Asians</td>
<td>Japan</td>
<td>2238</td>
<td>59.4</td>
<td>18.3</td>
<td>22.3</td>
<td>0</td>
</tr>
<tr>
<td>Asians</td>
<td>Korea</td>
<td>598</td>
<td>57.7</td>
<td>18.5</td>
<td>22.3</td>
<td>2.3</td>
</tr>
<tr>
<td>Africans-</td>
<td>US</td>
<td>19</td>
<td>36.8</td>
<td>50</td>
<td>13.6</td>
<td>0</td>
</tr>
<tr>
<td>Caucasians</td>
<td>UK</td>
<td>206</td>
<td>56.1</td>
<td>33.5</td>
<td>9.2</td>
<td>1.2</td>
</tr>
<tr>
<td>Caucasians</td>
<td>Poland</td>
<td>64</td>
<td>47.4</td>
<td>17.3</td>
<td>24.4</td>
<td>10.9</td>
</tr>
</tbody>
</table>

Source: Jakimiuk et al. (11)

**IV. CONCLUSIONS**

In conclusion, the prevalent gene for ESR-α PvuII was heterozygote Pp (46.3 %) and as for XbaI was homozygote XX (42.2 %), and the prevalent for the haplotype was pX (28.9%). We have found the different distribution of genotype frequencies PvuII and XbaI polymorphisms in diabetics postmenopausal women in Javanese population with other population.

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References

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ICICS 2013
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Present to

Syaefudin Ali Akhmad

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