

ANALYSIS OF MITOCHONDRIAL GENOME VARIATION IN PATIENTS WITH PREMATURE OVARIAN FAILURE USING RESEQUENCING-ARRAY TECHNIQUE

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Purpose: Premature ovarian failure (POF) is the loss of function of ovaries before age 40. It affects 1-2% of female population. Though some cases of POF are associated with genetic defects, such as Turner syndrome and fragile X syndrome, most of cases are idiopathic. Previously, we presented the association between mitochondrial copy number and POF. In this study, we examined whether or not the mitochondrial genome variation is directly related to POF.

Materials and methods: Thirty POF patients and 15 normal controls were examined. Genomic DNAs were extracted from peripheral lymphocytes samples of both patients and controls. Whole mitochondrial genome was sequenced by using the Affymetrix Mitochondrial Resequencing Array 2.0 (Mitochip).

Results: There is no correlation between a specific mitochondrial haplogroup and POF. Sequence variations were found in 395 regions, 107 were in the hypervariable region I and II and 288 were in coding regions. Compare to normal controls, 157 variations were found in only POF patients, 36 were in the hypervariable I and II region and 121 were in coding regions. Out of 121 coding region variations, 34 variations resulted in amino acid change. Eight of them found in genes for NADH dehydrogenase subunit 1, 2, 3, 4, and 5, ATPase6 and cytochrome b were not reported previously.

Conclusion: We identified some mitochondrial genome variations in POF patients. Further studies of the characterization of the sequence alteration in coding region will be required to understand relationship between mitochondrial sequence changes and POF pathogenesis.