



3rd INDERCOS
National Dermatology & Cosmetology Congress
with International Participants

14-17 MARCH, 2018
HILTON ISTANBUL BOSPHORUS HOTEL
ISTANBUL, TURKEY





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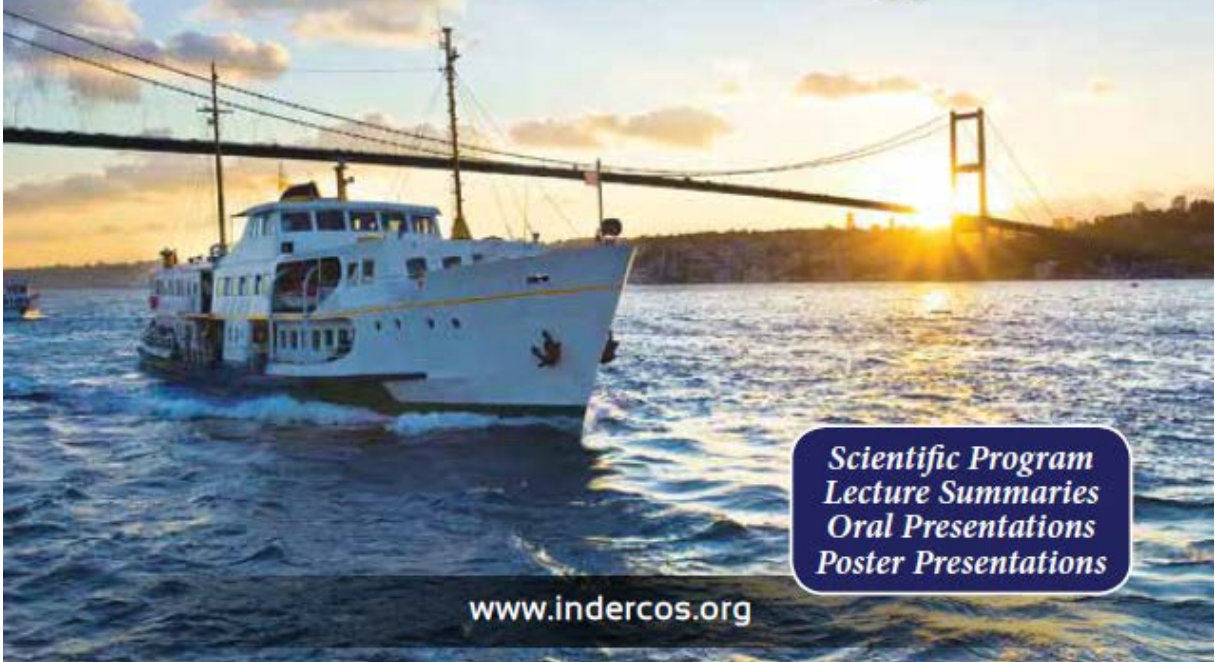
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OP-04

[Genetics]

Investigation of some miRNA expression levels associated with melanogenesis in vitiligo patients

Gurbet Dođru¹, Özlem Izci Ay¹, Mehmet Emin Erdal¹, Mustafa Ertan Ay¹, Merve Türkegün³, Ümit Tursen²

¹Mersin University, Faculty of Medicine Department of Medical Biology and genetic

²Mersin University, Faculty of Medicine Department of Dermatology ³Mersin University, Faculty of Medicine Department of Bioistatistic and Medical Informatics

INTRODUCTION & OBJECTIVES: Vitiligo is the most common depigmenting and acquired chronic disorder of the skin resulting from selective destruction of melanocytes. Vitiligo is characterized by the appearance of patchy discoloration evident in the form of milky white macules. Lesions can change in size and shape over time and can develop at any age, but in approximately half of all cases the disease onset is before the age of twenty. Exact prevalence is difficult to estimate the prevalence of vitiligo is often referred to as 0.5–1% of the world's population. There are many theories about the etiology of vitiligo. Autoimmune theory is the strongest theory in explaining the pathogenesis of the vitiligo. A lot of researches have paid attention to the possibility that miRNAs play a role in the pathogenesis of various human disorders including skin diseases and have a major impact on several physiological and pathological cellular processes including modulation of the innate and the adaptive immune system. The clinical implications of miRNAs are intriguing, both from a diagnostic and a therapeutic perspective. Accordingly, there is emerging evidence for the clinical potential of miRNAs as both biomarkers and possible therapeutic targets in skin diseases.

MATERIALS & METHODS: 56 patients diagnosed as vitiligo in the Department of Dermatology, Mersin University Faculty of Medicine were included in the study. After a detailed history and a careful physical examination of each patient involved in the study, the diagnose was confirmed by a Wood lamp examination. Patients were queried comprehensively about age, gender, the clinical types of the lesions of vitiligo, duration of the disease, family history of vitiligo, presence of any stress factor before the onset of the disease. 56 individuals were included in the study as a control group. Molecular analyses of expressions that belong to hsa-miR-3163, hsa-miR-6783-3p, hsa-miR-1343-3p, hsa-miR-4696, hsa-miR-6824, hsa-miR-5197-3p, hsa-miR-4495, hsa-miR-3680-3p, miR-26b genes, that respectively belong to MITF, SOX 10, TYR, TYRP1, BCL2 genes are performed for each subject using the method of Real-Time PCR, whereafter RNA and cDNA are isolated from blood samples of the patients and control subjects.

RESULTS: Expression levels of hsa-miR-3163, hsa-miR-6783-3p, hsa-miR-1343-3, hsa-miR-4696, hsa-miR-5197-3p, hsa-miR-3680-3p were not significantly different between patient and control groups. A statistically significant relationship between the expression levels of hsa-miR-4495 and hsa-miR-6824 genes and the risk of Vitiligo disease was found ($p < 0.05$). **CONCLUSION:** According to the genetic hypothesis, vitiligo inheritance is multigenic. In conclusion, these data indicate that hsa-miR-6824 which targeting the TYR gene and hsa-miR-4495 which targeting BCL2 gene may play a role in the pathogenesis of vitiligo. This finding has shown that in the future miRNAs may be important molecules in establishing treatment models for vitiligo.

Keywords: Vitiligo, melanogenesis, miRNA expression, Real Time PCR