ABSTRACT BOOK ABSTRACTS



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GENETICS AND GENODERMATOSES

## INTEGRATION OF PROTEIN INTERACTION AND GENE CO-EXPRESSION INFORMATION FOR IDENTIFICATION OF MELANOMA CANDIDATE GENES

Kejia Wu<sup>(1)</sup> - Wenyu Wu<sup>(2)</sup>

King's College London, Medical And Molecular Genetics, London, United Kingdom<sup>(1)</sup> -Huashan Hospital, Dermatology Department, Shanghai, China<sup>(2)</sup>

Introduction: Cutaneous melanoma is an aggressive form of skin cancer leading to death throughout the world. Much has been learned about the molecular basis of melanoma genesis and progression.

Objective: To continue discovering melanoma genes to improve the genetic understanding of this malignancy.

Method: In present study, melanoma candidate genes were identified by analysis of the common network from cancer type-specific RNA-Seq co-expression data and protein-protein interaction profiles. Then an integrated network containing the known melanoma related genes represented as seed genes and the putative genes represented as linker genes was generated by subnetwork extraction algorithm.

Results: According to the network topology property of the putative genes, we selected seven key genes (CREB1, XPO1, SP3, TNFRSF1B, CD40LG, UBR1 and ZNF484) as candidate genes of melanoma. Subsequent analysis showed that six of these genes are melanoma associated genes, and one (ZNF484) is cancer associated gene based on existing literature. A signature comprising these seven key genes was developed and overall survival analysis of 461 cutaneous melanoma cases was performed. This novel signature can accurately determine risk profile for cutaneous melanoma tumors (Logrank p = 3.27E-05).

Conclusion: The presented seven genes might serve as candidates for studying molecular mechanisms and help improve the prognostic risk assessment, which have clinical implications for melanoma patients.

Keywords: Melanoma; Candidate genes; Gene co-expression; Protein-protein interaction; Prognostic signature





