The microRNA landscape of cutaneous squamous cell carcinoma

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Cutaneous squamous cell carcinoma (cSCC) is a keratinocyte-derived skin tumor. It is the second-most-common cancer affecting the Caucasian population and is responsible for >20% of all skin-cancer-related deaths. The estimated incidence of non-melanoma skin cancer in the USA is >1 000 000 cases per year, of which roughly 20–30% are squamous cell carcinoma. To better understand and treat this challenging cancer, current research focuses on development of novel strategies to improve the understanding of tumor biogenesis on an individual basis. microRNAs are becoming important biomarkers in the diagnosis, prognosis and treatment of cSCC. This review describes the current knowledge on miRNA expression in cSCC and its role as a biomarker for personalized medicine.

Introduction

More than 3.5 million cases of non-melanoma skin cancer are diagnosed each year in the USA, with treatment costs reaching US $1.4 billion, making it the fifth-most-costly cancer for the Medicare population [1,2]. It has been estimated that solar ultraviolet (UV) radiation accounts for ~93% of skin cancers [3]. Whereas cutaneous squamous cell carcinoma (cSCC) is strongly related to constant or cumulative sun exposure, malignant melanoma and basal cell carcinoma have been linked to intermittent UV exposure especially at a younger age [1]. cSCC is an epidermal keratinocyte-derived skin tumor that is the second-most-common cancer affecting the Caucasian population [4], it displays a constantly increasing incidence estimated at 200 000 new cases each year in the USA [5,6] and accounts for 20% of all skin-cancer-related deaths [7]. A recently published systematic review of worldwide non-melanoma skin cancer reports that Australia appears to have the highest incidence rates for cSCC at >1000/100 000 population per year [8].

The past few years have been characterized by significant progress in the development of biomarkers in all fields of medicine, including oncology. These specific biomarkers play a crucial part in the understanding of pathomechanisms that drive tumor initiation, progression and metastasis. According to Nalejska *et al.* [9], biomarkers in oncology provide tools to characterize cancer signatures and can be divided into four groups: diagnostic, prognostic, treatment and prevention groups. Diagnostic biomarkers are identified by key mutation and molecular pathways involved in tumor development. Prognostic biomarkers identify somatic germline mutations, dysregulation of microRNA (miRNA) expression, DNA methylation and circulating tumor cells. Treatment and prevention biomarkers guide the individual therapy by estimating different outcome risks. The National Cancer Institute defines biomarkers as a biological molecule found in the blood, other fluids or tissues that is a sign of a normal or abnormal progress of a condition or disease; miRNAs completely fulfill these criteria [10].

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