

REPORT ON SKIN CARE DATABASE

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MEET THE TEAM

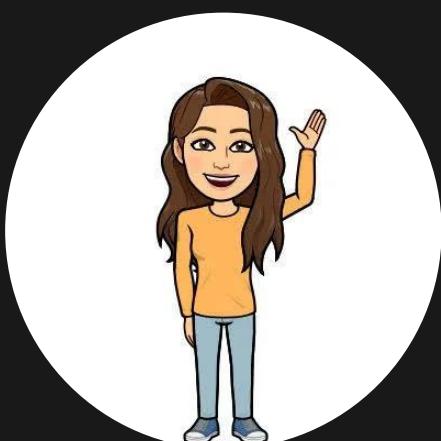
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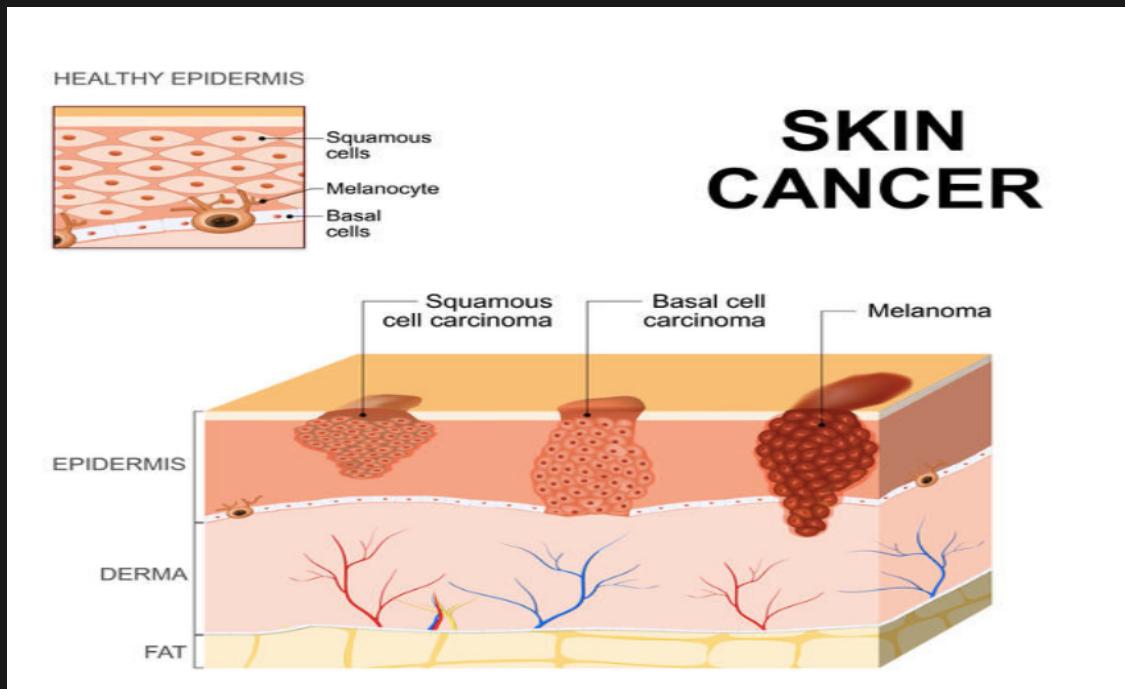


ANANYA ARORA

20BCB0031

INTRODUCTION

Skin cancer is the most common type of cancer. The main types of skin cancer are squamous cell carcinoma, basal cell carcinoma, and melanoma. Melanoma is much less common than the other types but much more likely to invade nearby tissue and spread to other parts of the body. Most deaths from skin cancer are caused by melanoma.



OVERVIEW OF METHODOLOGY

- In this project, sequences will be imported from the Uniprot database. The genes are downloaded from the Cosmic Cancer database from the skin section.
- We will be using specific queries to navigate through the database. The database is created in MySQL by importing the CSV files that were downloaded from the COSMIC cancer database and the database is hosted via Xampp server with the PHPmyadmin host.
- Making a user friendly website where the user just needs to input the Protein name / ID it will be confirmed whether that particular protein is cancerous or not.

The screenshot shows the UniProtKB 2021_04 results page. At the top, there is a search bar with the query "skin cancer". Below the search bar, the main content area displays the results for "UniProtKB 2021_04 results". The results are presented in a table with columns for Entry, Entry name, Protein names, Gene names, Organism, and Length. The table shows 25 of 1,539 results. The first result listed is Folliculin (FLCN_HUMAN). The left sidebar contains filters for "Reviewed (1,420)" (Swiss-Prot), "Unreviewed (119)" (TrEMBL), and "Popular organisms" including Human, Mouse, Bovine, Rat, SALSA, and Other organisms. There are also links for BLAST, Align, Retrieve/ID mapping, Peptide search, SPARQL, Help, and Contact.

Entry	Entry name	Protein names	Gene names	Organism	Length
Q8NFG4	FLCN_HUMAN	Folliculin	FLCN BHD	Homo sapiens (Human)	579
O14519	CDKA1_HUMAN	Cyclin-dependent kinase 2-associate...	CDK2AP1 CDKAP1, DOC1	Homo sapiens (Human)	115
P43355	MAGA1_HUMAN	Melanoma-associated antigen 1	MAGEA1 MAGE1, MAGE1A	Homo sapiens (Human)	309
P43357	MAGA3_HUMAN	Melanoma-associated antigen 3	MAGEA3 MAGE3	Homo sapiens (Human)	314
Q9UGL1	KDM5B_HUMAN	Lysine-specific demethylase 5B	KDM5B JARID1B, PLU1, RBBP2H1	Homo sapiens (Human)	1,544
Q7TM55	ABCG2_MOUSE	Broad substrate specificity ATP-bin...	Abcg2 Abcp, Bcrp1	Mus musculus (Mouse)	657
Q9BPY8	HOP_HUMAN	Homeodomain-only protein	HOPX HOD, HOP, LAGY, NECC1, OB1	Homo sapiens (Human)	73
P63244	RACK1_HUMAN	Receptor of activated protein C	RACK1 GNB2L1, HLC7, PIG21	Homo sapiens	317

LITERATURE REVIEW

PAPER - 1

**Russell W. Jenkins, David E. Fisher,
Treatment of Advanced Melanoma in 2020 and Beyond,
Journal of Investigative Dermatology,
Volume 141, Issue 1,
2021,**

The melanoma field has seen an unprecedented set of clinical advances over the past decade. Therapeutic efficacy for advanced or metastatic melanoma went from being one of the most poorly responsive to one of the more responsive. Perhaps most strikingly, the advances that transformed management of the disease are based upon modern mechanism-based therapeutic strategies. The targeted approaches that primarily suppress the BRAF oncoprotein pathway have a high predictability of efficacy although less optimal depth or durability of response. Immunotherapy is primarily based on blockade of one or two immune checkpoints and has a lower predictability of response but higher fractions of durable remissions. This article reviews the clinical progress in management of advanced melanoma and also discusses the impact of the same therapies on earlier stage disease, where the agents have shown significant promise in treating resectable but high-risk clinical scenarios. Collectively, the progress in melanoma therapeutics has transformed the standard of care for patients, informed new approaches that are increasingly utilized for treatment of other malignancies, and suggest novel strategies to further boost efficacy for the many patients not yet receiving optimal benefit from these approaches.



LITERATURE REVIEW

PAPER - 2

Cutaneous Squamous Cell Carcinoma: From Pathophysiology to Novel Therapeutic Approaches

by Luca Fania 1,*†,Dario Didona 2,†ORCID,Francesca Romana Di Pietro 1,Sofia Verkhovskaya 1,Roberto Morese 1,Giovanni Paolino 3,Michele Donati 4,5,Francesca Ricci 1,Valeria Coco 6,Francesco Ricci 1,Leonora Candi 1,7,Damiano Abeni 1 and Elena Dellambra

Cutaneous squamous cell carcinoma (cSCC), a non-melanoma skin cancer, is a keratinocyte carcinoma representing one of the most common cancers with an increasing incidence. cSCC could be *in situ* (e.g., Bowen's disease) or an invasive form. A significant cSCC risk factor is advanced age, together with cumulative sun exposure, fair skin, prolonged immunosuppression, and previous skin cancer diagnoses. Although most cSCCs can be treated by surgery, a fraction of them recur and metastasize, leading to death. cSCC could arise *de novo* or be the result of a progression of the actinic keratosis, an *in situ* carcinoma. The multistage process of cSCC development and progression is characterized by mutations in the genes involved in epidermal homeostasis and by several alterations, such as epigenetic modifications, viral infections, or microenvironmental changes. Thus, cSCC development is a gradual process with several histological- and pathological-defined stages. Dermoscopy and reflectance confocal microscopy enhanced the diagnostic accuracy of cSCC. Surgical excision is the first-line treatment for invasive cSCC. Moreover, radiotherapy may be considered as a primary treatment in patients not candidates for surgery. Extensive studies of cSCC pathogenic mechanisms identified several pharmaceutical targets and allowed the development of new systemic therapies, including immunotherapy with immune checkpoint inhibitors, such as Cemiplimab, and epidermal growth factor receptor inhibitors for metastatic and locally advanced cSCC. Furthermore, the implementation of prevention measures has been useful in patient management.

LITERATURE REVIEW

PAPER - 3

McDaniel B, Badri T, Steele RB. Basal Cell Carcinoma. [Updated 2021 Sep 20]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2022 Jan



Basal cell carcinoma (BCC), previously known as basal cell epithelioma, is the most common cancer in Humans. BCC mostly arises on sun-damaged skin and rarely develops on the mucous membranes or palms and soles. Basal cell carcinoma is usually a slow-growing tumor for which metastases are rare. Although rarely fatal, BCC can be highly destructive and disfigure local tissues when treatment is inadequate or delayed. On clinical examination, BCC usually appears as flesh- or pink-colored, pearly papules with overlying ulceration or telangiectatic vessels. BCC occurs on the head or neck in the majority of cases, but can involve the trunk and extremities.[1][2]



More than 26 different subtypes of BCC appear in the literature, but the more common, distinctive, clinicopathologic types include: nodular, micronodular, superficial, morpheaform, infiltrative and fibroepithelial (also known as fibroepithelioma of Pinkus). Combinations of these types can occur as well. The majority of BCCs are amelanotic, but variable amounts of melanin may be present within these tumors.

The current mainstay of BCC treatment involves surgical modalities such as excision, electrodesiccation and curettage (EDC), cryosurgery, and Mohs micrographic surgery. Such methods are typically reserved for localized BCC and offer high 5-year cure rates, generally over 95%.

MISCELLANEOUS

TASK COMPLETED:

- Collection of data
- Curated merged and removed redundancy from the CSV file
- Database generation
- Designed the UI for frontend

TASK TO BE COMPLETED:

- Push the data to database
- Connect frontend to backend

SOFTWARE REQUIREMENTS

- Python
- HTML
- CSS
- JavaScript
- Bootstrap
- Django

SCREENSHOTS

A screenshot of Microsoft Excel showing a table of gene information. The table has columns for tax_id, Org_name, GenelD, Symbol, Aliases, description, other_des, map_local, chromosome, start_pos, end_pos, orientation, exon_count, and OMIM. The data includes various genes like CDKN2A, SLC45A2, CDKN1A, IFIH1, MC1R, MCAM, TYR, IL24, MAGEA3, AIM2, PRAME, KISS1, MAGEA1, GPNMB, MIA, and MAGEA4, along with their respective details and OMIM IDs.

tax_id	Org_name	GenelD	Symbol	Aliases	description	other_des	map_local	chromosome	start_pos	end_pos	orientation	exon_count	OMIM
9606	Homo sapiens	1029	CDKN2A	ARF, CDK4 cyclin dependent cyclin-dependent kinase 2, p13.2				9	NC_0000021967752	21995324	minus	8	600160
9606	Homo sapiens	51151	SLC45A2	1A1, AIM1 solute carrier membrane protein 13.2				5	NC_0000033944623	33984693	minus	7	606202
9606	Homo sapiens	1026	CDKN1A	CAP20, CD cyclin dependent cyclin-dependent kinase 2, p21.2				6	NC_0000036676463	36687332	plus	6	116899
9606	Homo sapiens	64135	IFIH1	AGS7, Hccl1, interferon interferon 2q24.2				2	NC_00000162E+08	1.62E+08	minus	16	606951
9606	Homo sapiens	4157	MC1R	CMM5, MC1R, melanocortin 1 receptor, melanocyte 16q24.3				16	NC_00000189918862	89920972	plus	1	155555
9606	Homo sapiens	4162	MCAM	CD146, HE-melanoma cell surface antigen 11q23.3				11	NC_0000011.19E+08	1.19E+08	minus	16	155735
9606	Homo sapiens	7299	TYR	ATN, CMN tyrosinase tyrosinase 11q14.3				11	NC_00000189177565	89295759	plus	6	606933
9606	Homo sapiens	11009	IL24	C49A, FISP, interleukin-24, interleukin-24				1	NC_0000020.07E+08	2.07E+08	plus	7	604136
9606	Homo sapiens	4102	MAGEA3	CT1.3, HIP, MAGE family member 3, Xq28	X			NC_0000021.53E+08	1.53E+08	plus		6	300174
9606	Homo sapiens	9447	AIM2	PYHIN4 absent in interferon 1q23.1-q2				1	NC_000001.159E+08	1.59E+08	minus	11	604578
9606	Homo sapiens	23532	PRAME	CT130, PRAME, PRAME, neurofibromatosis 22q11.22				22	NC_00000222547701	22559294	minus	8	606021
9606	Homo sapiens	3814	KISS1	HH13, KISS-KISS-1, metastasis 1q32.1				1	NC_0000022.04E+08	2.04E+08	minus	3	603286
9606	Homo sapiens	4100	MAGEA1	CT1.1, MA-MAGE family member 1, Xq28	X			NC_0000021.53E+08	1.53E+08	plus		3	300016
9606	Homo sapiens	10457	GPNMB	HGF/N-glycoprotein transmembrane protein 15.3				7	NC_0000023246766	23275110	plus	12	604368
9606	Homo sapiens	8190	MIA	CD-RAP, MIA SH3 domain containing 19q13.2				19	NC_00000140775160	40777490	plus	5	601340
9606	Homo sapiens	4103	MAGEA4	CT1.4, MA-MAGE family member 4, Xq28	X			NC_0000021.52E+08	1.52E+08	plus		11	300175

The Skin Cancer Database homepage features a red-to-white gradient background with the text "Skin Cancer Database" in red. At the top, there are navigation links for HOME, ABOUT US, and CONTACT US. Below the title is a search bar with the placeholder "Enter Protein Id/Name" and a "Search" button.

HOME ABOUT US CONTACT US

Skin Cancer Database

Enter Protein Id/Name Search



THANK YOU!