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Number-needed-to-treat analysis of skin cancers among referrals for suspicious lesions

Nikolai Klebanov, MD, Massachusetts General Hospital; Michael Shaughnessy, BS, Tufts University School of Medicine; Nicole Gunasekera, MD, MBA, Harvard Combined Dermatology Training Program; Sally Tan, MD, MPH, University of California, San Francisco; Hensin Tsao, MD, PhD

Background: Number needed to treat (NNT) is an important outcome measure of skin cancer diagnosis quality. In this study, we aimed to calculate NNT metrics for melanoma and nonmelanoma skin cancer (NMSC) using referral- and biopsy-level data.

Methods: Retrospective review of patients referred to a tertiary medical center dermatology practice for suspicious lesions. We identified 707 unique complete patient visits from 7/2015 to 2/2016. We calculated the number needed to refer (NNR) and biopsy (NNB) for melanoma as the ratio of biopsy-proven melanoma diagnoses among benign and dysplastic nevi, and seborrheic keratoses (SKs). For NMSC, we used the ratio of basal cell and squamous cell carcinoma among actinic keratoses and SKs.

Results: Among 707 referred patients, 327 (46%) were male. Males had mean age 57.5 years, while females were on average 53.5 with a bimodal distribution. The NNR for melanoma was 31.5, and the NNB was 7.5 (4.2-fold difference). The NNR for NMSC was 4.0, and the NNB was 1.5 (2.7-fold difference). Benign nevi were the most common non-cancer diagnosis (28%) among patients younger than the median age of 57, while SKs were the most common (34%) among older patients.

Conclusions: We estimated the NNB for melanoma as 7.5, consistent with NNTs of 6-21 reported in the literature, supporting external validity of the study. Our results show a large reduction in number needed to treat from the referral to the biopsy stage, suggesting that referral-level changes could be targeted for cost-savings in skin cancer management.

Commercial disclosure: None identified.

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Under-representation of dark skin tone in general dermatology textbooks

Fiatsogbe S. Dzuali, BS, Boston Children's Hospital; Connie Zhong, MSc, Joe K. Tung, Ernesto Gonzalez-Martinez, MD, Sotonye Imadojemu, MD, MBE, Joan Y. Reede, MD, Jennifer T. Huang, MD, Boston Children's Hospital

Introduction: A wide representation of skin tones in medical textbooks is necessary to train competent physicians. We report the distribution of skin tone in important chapters from dermatology textbooks to identify areas of disproportionate representation.

Methods: Photographs from 3 best-selling dermatology textbooks were analyzed for skin tone (light, medium, dark) using the Pantone SkinTone Guide by three raters independently. Proportions were analyzed by disease categories including a category of stigmatized conditions that included depictions of sexually transmitted infections, abuse, and psychiatric disease. These proportions were compared with data on skin tone distribution in the US. Comparative statistical analysis was performed using Fisher exact tests.

Results: 2011 images from 62 chapters were included in this study. 80.5% (1619/2011) of images were of light, 11.1% (223/2011) medium, and 8.4% (169/2011) dark skin tone. The interrater reliability was 90.32%. Compared with previous reports of skin tone distribution in the US, light skin tone was over-represented in every disease category. Dark skin tone was underrepresented in every disease category except for stigmatized diseases (17.6% [29/165]). The lowest representation of dark skin tone was in melanoma (2.9% [4/136]), nonmelanoma skin cancer (3.7% [7/188]), bullous diseases (6.3% [9/144]) and non-viral/non-fungal infections (6.9% [14/202]). Representation of dark skin tone was significantly higher in the stigmatized category than in all other categories (17.6% [29/165] vs 7.6% [140/1846], $P < .0001$).

Conclusions: Addressing disproportionate representation of skin tones in dermatology textbooks should be included among the concerted efforts being made to improve diversity in the profession.

Commercial disclosure: None identified.

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The beauty image assessment study: Perspectives of US millennials, generation X, and baby boomers on esthetic treatments

Noëlle Sherber, MD, Sherber + Rad; Jeremy B. Green, MD, Annie Chiu, MD, Edward Lain, MD, MBA, Sabrina G. Fabi, Sanova Dermatology; Deirdre Hooper, MD, Audubon Dermatology; Rod J. Rohrich, MD, Julius Few, MD

Purpose: As esthetic procedures increase in popularity, physicians must understand patient-perceived needs to improve outcomes.

Methods: Adult participants in a global Beauty Image Assessment survey, stratified by age group, were asked about their desired appearance and experience with/interest in esthetic treatments.

Results: Among 3028 participating US adults (70% female), there were 928 millennials (mean age 30 y), 1190 generation Xers (46 y), and 910 baby boomers (61 y). Similar attitudes were noted regarding the importance of looking best for daily activities (range 66%-70%) and consideration of nonsurgical interventions (53%-57%); however, millennials were 2-3 times more likely than baby boomers to want to look like someone else. The most cited barrier preventing respondents across generations from seeking esthetic treatment was financial (45%-50%). All generations were equally concerned about looking unnatural (26%-29%). Millennials were affected nearly twice as often as other generations by barriers such as guilt about modifying their appearance. All generations reported that upper facial line treatment was the most important esthetic intervention (38%-48%); however, millennials and generation Xers considered treatment of crow's feet lines (CFL) as most important, followed by forehead lines. Baby boomers prioritized treating stubborn abdominal fat, followed by CFL. Interestingly, while millennials reported having less discretionary income (13%) versus baby boomers (17%), they reported a greater preparedness to invest in their appearance (82% vs 67%, respectively).

Conclusions: Generational differences exist among adults regarding esthetic goals, barriers, and concerns, which may be insightful for physicians during initial consultations and in shaping ongoing care for individuals in these generations.

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In silico analysis of gamma-secretase complex mutations in hidradenitis suppurativa demonstrates disease-specific substrate recognition and cleavage alterations

John Frew, MBBS, FACD, Kristina Navrazhina, BA, Laboratory of Investigative Dermatology, Rockefeller University

Familial hidradenitis suppurativa and familial Alzheimer disease are both associated with gamma-secretase complex mutations; however, the 2 diseases are not epidemiologically associated. Understanding the molecular differences between the 2 diseases may aid in development of hypotheses for differing pathogenesis and ultimately, targets for detection.

Objective: To characterize the in-silico structural and functional alterations to the gamma-secretase complex in documented mutations in familial hidradenitis suppurativa, along with comparison of downstream substrate recognition and cleavage.

Methods: In silico analysis of publicly available genomic data, assessment of protein structure and binding affinity using Swiss-model and Dynamut was undertaken. Differential expression was expressed using log fold change using the general framework for linear models in R. Differentially expressed genes were defined by fold change ≥ 1.5 or ≤ -1.5 and false discovery rate ≤ 0.05.

Results: 23 of 39 mutations in HS are degraded via nonsense mediated decay with altered substrate and binding affinity of substrates identified in the remaining mutations. Significant differential expression of ErbB4, SCNB1 and Tie1 in lesional skin was specific to hidradenitis suppurativa and EphB2, EPHB4, KCNE1, LRP6, MUSK, SDC3, Sortilin1 in blood specific to familial Alzheimer disease. We present the first in silico evidence as to the impact of documented mutations in familial hidradenitis suppurativa. We also demonstrate unique substrate recognition and cleavage between Hidradenitis Suppurativa and familial Alzheimer disease, providing potential explanations as to why the two diseases do not occur within the same pedigree. These proteomic signatures may be a first step in identifying reliable biomarkers for familial hidradenitis suppurativa.

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