





Challenging cases in patients with multiple nevi

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European Academy of Dermatology and Venereology

What means multiple nevi?







54 years old









ARTICLE

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Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways

David L. Duffy ¹, Gu Zhu¹, Xin Li², Marianna Sanna³, Mark M. Ilex⁴, Leonie C. Jacobs¹, David M. Evans^{6,7}, Seyhan Yazaro ⁶, Jonathan Beesley¹, Matthew H. Law ^{6,1}, Peter Kraft⁹, Alessia Viscontio ³, John C. Taylor ⁴, Fan Lu¹⁰, Margaret J. Wrighto¹, Anjali K. Henders¹¹⁷, Lisa Bowdler¹, Dan Glass², M. Arfan Ikramo¹¹, André G. Utterlinden¹¹³³, Pamela A. Madden¹³, Andrew C. Heath¹⁰, Elliot C. Nelson¹⁵, Adele C. Green ^{6,14}, Stephen Chanock ¹⁵, Jennifer H. Barretto⁴, Matthew A. Brown ⁷, Nicholas K. Hayward¹, Stuart MacGregor ¹⁵, Jennifer H. Barretto⁴, Alex W. Hewitto⁶, Melanoma GWAS Consortum⁴, Manfred Kaysero¹⁰, David J. Hunter⁹, Julia A. Newton Bishop⁴, Timothy D. Spector³, Grant W. Montgomery^{6,137}, David A. Mackey^{6,8}, George Davey Smith⁶, Tamar E. Nijsten⁵, D. Timothy Bishop^{6,4}, Veronique Bataille³, Mario Falchi², Sall Han² & Nicholas G. Martin¹







Fig. 2 Maritudias plot of Produce front meta-analysis conditing mecar and melanama condition

Nevus genes

- SNPs have been significantly associated with increasing (IRF4) or decreasing (PARP1, CDK6 and PLA2G6) naevus count in multivariate shrinkage analyses with all SNPs included in the model; TERT, CDKN1B, MTAP and PARP1 were associated with either globular or reticular dermoscopic patterns (P < 0.05). (Orlow I et al)
- MTAP rs10757257, PLA2G6 rs132985 and IRF4 rs12203592 (Kvaskoff M et al)



Kvaskoff M, Whiteman DC, Zhao ZZ, Montgomery GW, Martin NG, Hayward NK, Duffy DL. Polymorphisms in nevus-associated genes MTAP, PLA2G6, and IRF4 and the risk of invasive cutaneous melanoma. Twin Res Hum Genet. 2011 Oct;14(5):422-32. doi: 10.1375/twin.14.5.422. PMID: 21962134; PMCID: PMC3266856.

Orlow I, Satagopan JM, Berwick M, Enriquez HL, White KA, Cheung K, Dusza SW, Oliveria SA, Marchetti MA, Scope A, Marghoob AA, Halpern AC. Genetic factors associated with naevus count and dermoscopic patterns: preliminary results from the Study of Nevi in Children (SONIC). Br J Dermatol. 2015 Apr;172(4):1081-9.

TRANSLATIONAL RESEARCH	BJD British journal of Dermatology

Common genetic variants associated with melanoma risk or naevus count in patients with wildtype MC1R melanoma

Neus Calbet-Llopart ⁽¹⁾,^{1,2} Marc Combalia ⁽¹⁾, ¹ Anil Kiroglu ⁽¹⁾, ¹ Miriam Potrony ^{(2),2,3} Gemma Tell-Marti ⁽¹⁾,^{1,2} Andrea Combalia ⁽¹⁾, ¹ Albert Brugues ⁽¹⁾, ² Sebastian Podlipnik ⁽¹⁾, ¹ Cristina Carrera ⁽¹⁾,^{1,3} Susana Puig ⁽¹⁾,^{1,2} Josep Malvehy ^{(1),2} and Joan Anton Puig-Butillé ^{(2),4}

- > The rs3798577 ESR1 variant was significantly associated with lower TNC (OR 0.79, 95% CI 0.67–0.92; adjusted P = 0.003).
 - > the association was maintained among women (OR 0.71, 95% CI 0.57–0.88; adjusted P = 0.002)
 - > and not among men (adjusted P = 0.28).







Dermatology Practical & Conceptual

Indications for Digital Monitoring of Patients With Multiple Nevi: Recommendations from the International Dermoscopy Society.

The results of the second round allowed us to propose the following five indications for digital monitoring in the third round:

1. Patients with more than 60 melanocytic nevi.

2. Patients with a CDKN2A mutation or other rarer high-risk melanoma genetic variants.

3. Patients with more than 40 melanocytic nevi and a personal history of melanoma.

4. Patients with more than 40 melanocytic nevi and red hair and/or a MC1R mutation

5. Patients with more than 40 melanocytic nevi and a history of organ transplantation.

Russo T, Piccolo V, Moscarella E, et al. Indications for Digital Monitoring of Patients With Multiple Nevi: Recommendations from the International Dermoscopy Society. Dermatol Pract Concept. 2022 Oct 1;12(4):e2022182.



Figure 1. Patient with more than 60 nevi. Side by side comparison of 3 lesions (A, B, C) during follow structures over time of the first lesion (A) on the left, which was therefore excised and diagnosed as a me

Figure 2. Patient with more than 40 nevi and previous melanoma. Lesion C showed remarkable change in the lesion after 3 months of follow-up and was therefore excised and confirmed to be a melanoma in situ, while lesion A and B did not show significant modifications.

Case 1



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Female, 49 years old, personal history of melanoma and basal cell carcinoma, Atypical Nevus Syndrome.

Pathological diagnosis:

- 06.2006 MM in situ over melanocytic nevus on the left axilla
- 09.2006 MM over melanocytic nevus on the left axilla B 0.6mm
- 2014 Superficial BCC on the neck
- 2017 Melanocytic nevus with moderate atypia on the right arm

















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Case 2





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Case 3

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Visiaalizador de lesiones Driforme

Female, 52 years old, personal history of melanoma in situ on right arm in 2002 (diagnosed in other center) and no familial oncological history.

2021, nodular BCC (scapular region) ; BCC superficial multifocal (lateral right back)

25/10/2021

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Case 4








Case 6







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Vista an sho









Are slow growing melanomas "benign" melanomas?



Case 7







August 2010: after 6 years....

















Sturm RA, Fox C, McClenahan P, Jagirdar K, Ibarrola-Villava M, Banan P, Abbott NC, Ribas G, Gabrielli B, Duffy DL, Peter Soyer H. Phenotypic characterization of nevus and tumor patterns in MITF E318K mutation carrier melanoma patients. J Invest Dermatol. 2014 Jan;134(1):141-149.

Original Investigation

Prevalence of MITF p.E318K in Patients With Melanoma Independent of the Presence of CDKN2A Causative Mutations

Miriam Potrony, MSc; Joan Anton Puig-Butille, PhD; Paula Aguilera, MD; Celia Badenas, PhD; Gemma Tell-Marti, MSc: Cristina Carrera, MD. PhD: Luis Javier del Pozo, MD: Julian Coneio-Mir, MD: Josep Malvehy, MD, PhD: Susana Puig, MD, PhD

IMPORTANCE The main high-penetrance melanoma susceptibility gene is CDKN2A, encoding p16INK4A and p14ARF. The gene MITF variant p.E318K also predisposes to melanoma and renal cell carcinoma. To date, the prevalence of MITF p.E318K and its clinical and phenotypical implications has not been previously assessed in a single cohort of Spanish patients with melanoma or in p16INK4A mutation carriers.

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Supplemental content at iamadermatology.com

OBJECTIVES To evaluate the prevalence of MITF p.E318K in Spanish patients with melanoma and assess the association with clinical and phenotypic features.

DESIGN, SETTING, AND PARTICIPANTS A hospital-based, case-control study was conducted at the Melanoma Unit of Hospital Clinic of Barcelona, with MITF p.E318K genotyped in all patients using TaqMan probes. We included 531 patients: 271 patients with multiple primary melanoma (MPM) without mutations affecting p16INK4A (wild-type p16INK4A): 191 probands from melanoma-prone families with a single melanoma diagnosis and without mutations affecting p16INK4A, and 69 probands from different families carrying CDKN2A mutations affecting p16INK4A. A population-based series of 499 age- and sex-matched cancer-free individuals from the Spanish National Bank of DNA were included as controls. Patients were recruited between January 1, 1992, and June 30, 2014; data analysis was conducted from September 1 to November 30, 2014.

MAIN OUTCOMES AND MEASURES The genetic results of the MITF p.E318K variant were correlated with clinical and phenotypic features.

RESULTS Among the 531 patients, the prevalence of the MITF p.E318K variant was calculated among the different subsets of patients included and was 1.9% (9 of 462) in all melanoma patients with wild-type p16INK4A, 2.6% (7 of 271) in those with MPM, and 2.9% (2 of 69) in the probands of families with p16INK4A mutations. With results reported as odds ratio (95% CI), the MITF p.E318K was associated with an increased melanoma risk (3.3 [1.43-7.43]; P < .01), especially in MPM (4.5 [1.83-11.01]; P < .01) and high nevi count (>200 nevi) (8.4 [2.14-33.19]; P < .01). Two fast-growing melanomas were detected among 2 MITF p.E318K carriers during dermatologic digital follow-up.

CONCLUSIONS AND RELEVANCE In addition to melanoma risk, MITF p.E318K is associated with a high nevi count and could play a role in fast-growing melanomas. Testing for MITF p.E318K should not exclude patients with known mutations in p16INK4A. Strict dermatologic surveillance, periodic self-examination, and renal cell carcinoma surveillance should be encouraged in this context.

JAMA Dermatol. 2016:152(4):405-412. doi:10.1001/iamadermatol.2015.4356 Published online December 9, 2015

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Figure 1. Melanoma

A Clinical image



A fast-growing melanoma developed within 3 weeks and was the fourth to occur in patient M0881-01. Clinical picture of a 4-mm-diameter nodular lesion located on the elbow (A)dermoscopic image of the lesion showing hypopigmentation. asymmetry, unspecific pattern, atypical vessels, and blue-whitish veil (B). Under confocal microscopy, the lesion shows an ulcerated central area (C) with atypical nests in upper dermis with bright roundish nucleated cells in noncohesive nests (D). Histopathologic examination shows an ulcerated nodular melanoma (hematoxylin-eosin. original magnification ×2) (E) and nests of atypical cells and presence of mitosis (hematoxylin-eosin, original magnification ×10) (F).

E Histologic specimen





The back of patient M3879-01 with 2 previous melanomas and more than 200 nevi. Six dermoscopic images show the predominant pattern reticulated dark brown

only 2 fast-growing melanomas identified by dermatologic digieral, the melanoma growth rate is approximately 0.1 mm per tal follow-up in individuals at high risk of melanoma were in month, and slow-growing melanomas usually have a growth rate MITF p.E318K carriers. Fast-growing melanomas are defined by of 0.01 mm per month.³³ Furthermore, a high growth rate is

growing melanomas.^{31,32} Until now in our melanoma unit, the having a growth rate of greater than 0.4 mm per month; in gen-

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Fast growing melanoma in a ptient with 4 primary melanomas carrier of E318K in MITF, MC1R genotype = R/r and p.Gly32Arg in p14arf

Figure 1: Frast growing Amelanotic melanoma from patient E318K in MITF & MC1R genotype = R/r

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Prevalence of the E318K MITF germline mutation in Italian melanoma patients: associations with histological subtypes and family cancer history

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Melanomas in patients with multiple atypical nevi

- 1. They are more difficult to Dx
- 2. They can be slow and fast growing tumours
- 3. Monitoring with TBP +SDD imaging is the Dx best option
- 4. Susceptibility genes are involved in different phenotypes and the risk of MM
- 5. Better phenotyping/genotyping can help to improve strategy for follow-up



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