BACKGROUND

- Acquired melanocytic nevi (AMN) are nearly all stable, but share cutaneous and molecular characteristics with melanoma and may rarely transform.
- Histopathological classification of AMNs is based on the location and proliferation of melanocytic nests (junctional, intradermal, compound) and generally consists of 'benign' or 'dysplastic' classes.
- Dermoscopic classification is used for clinical decision-making, and consists of phenotypic description of lesions (globular, reticular, non-specific).
- Evidence for which of these combinations of classes and patterns of AMNs carry higher risk for transformation is lacking, and mechanisms driving stability of most AMNs are yet unclear.



DNA methylation Figure plays a critical role in the regulation of gene expression, for example at gene promoters by inhibiting transcription.

METHODS

• Methylation-profiling of **32 AMNs** and **32** adjacent normal skin samples from 24 patients using Illumina EPIC array.

Table 1. Nevi Characteristics		
Variable	Subjects	Samples
$\mathbf{C}_{\text{ond}} \mathbf{N} \mathbf{I} \left(0 \right)$	(1N = 24)	(N = 32)
	7 (00 0)	
Female	7 (29.2)	
Male	17 (70.8)	
Age mean (SD)	51.88 (14.36)	
Status N (%)		
Benign		13 (40.6)
Dysplastic		19 (59.4)
Histopath N (%)		
Compound		13 (40.6)
Intradermal		12 (37.5)
Junctional		7 (21.9)
Dermoscopic Pattern N (%)		
Globular		10 (31.2)
Reticular		4 (12.5)
Non-specific (PRG)		10 (31.2)
Non-specific (other)		8 (25.0)
Sun Exposure N (%)		· · · · ·
Exposed		25 (78.1)
Shielded		7 (21.9)
BRAF N (%)		
BRAF V600E		25 (78.1)
BRAF V600K		3 (9.4)
BRAF V600R 1(3)		1 (3.1)
NRAS G12S 1(3)		1 (3.1)
unknown		2 (6.3)

Genome-scale DNA methylation analysis of melanocytic nevi: mechanisms driving stability

Muse ME¹, <u>Bergman DT¹</u>, Salas LA¹, Tom LN², Tan JM², Laino A², Lambie D^{3,4}, Sturm RA², Schaider H^{2,5}, Soyer HP^{2,6}, Christensen BC^{1,7,8}, Stark MS²

¹Department of Epidemiology, Geisel School of Medicine at Dartmouth ²Dermatology Research Centre, Diamantina Institute, The University of Queensland ³IQ Pathology, Brisbane, Australia

⁴Pathology Queensland, Princess Alexandra Hospital, Brisbane, Australia ⁵Department of Dermatology, Sunshine Coast Hospital and Health Service, Birtinya, Australia ⁶Department of Dermatology, Princess Alexandra Hospital, Brisbane, Australia ⁷Department of Molecular & Systems Biology, Geisel School of Medicine at Dartmouth ⁸Department of Community & Family Medicine, Geisel School of Medicine at Dartmouth

Key Points





Methylation profiles of 32 acquired melanocytic nevi

• Tend to be globular (69%) or non-specific (31%) Increased inferred melanocyte proportion • Similar methylation profile to adjacent normal skin Increased Alu/LINE-1 methylation • Tend to be reticular/non-specific (95%) Distinct from adjacent normal skin Increased global methylation in actively transcribed

• Decreased global methylation in enhancer elements

 Similar methylation profile to normal skin • Strongly distinct from normal skin Increased global methylation in actively transcribed

• Decreased global methylation in enhancer elements Strong methylation of tumor suppressor PTEN



Dartmouth GEISEL SCHOOL OF MEDICINE







Figure 2. Benign AMNs have increased genomic stability vs. dysplastic AMNs via increased methylation of LINE-1 and Alu retrotransposons and global methylation.

promoters and decreases in methylation at enhancer regions.