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Article:

Barrett, JH orcid.org/0000-0002-1720-7724 (2016) Telomere length and melanoma - is there a straightforward relationship? *British Journal of Dermatology*, 175 (5). pp. 865-866. ISSN 0007-0963

<https://doi.org/10.1111/bjd.14892>

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Telomere length and melanoma – is there a straightforward relationship?

Telomeres are of major importance to human health, protecting against chromosomal rearrangements and helping to maintain genomic integrity. Telomere length (TL) declines markedly with age, and numerous epidemiological studies have shown an association between shorter telomeres and increased risk of cardiovascular¹ and other chronic disease. However the simple conclusion that longer telomeres are better for human health has been challenged by the observation of a more complex relationship with cancer. Although shorter telomeres are associated with increased risk of some cancers, *longer* telomeres have been associated with increased risk of other cancers², including melanoma³. The reasons for this are not yet well understood; possibly longer telomeres delay senescence of melanocytic naevi, allowing a higher probability of progression to melanoma⁴.

Besides genuine differences of effect, there are many possible reasons for inconsistency in the literature on TL⁵. One problem is that TL is not easy to measure, and there are few large studies. In addition most studies are cross-sectional rather than prospective, and hence may be affected by differences in sample handling or reverse causality. They are also almost always based on measurements of leukocyte TL, relying on this as a proxy for TL in more relevant tissue. However some genetic predictors of leukocyte TL, which have themselves been reliably measured in much larger data sets, also show differences in direction of association between cancers⁶. The genetic studies generally support the evidence for the association between long telomeres and increased risk of melanoma, the strength of the association suggesting telomere genes play a particularly important role in melanoma⁷.

In this issue of the BJD, Menin *et al.*⁸ report on a cross-sectional study of TL in melanoma cases and controls, where they observe a difference in direction of association with familial and sporadic melanoma. They suggest that this heterogeneity may explain inconsistencies in the published findings for melanoma, some of which are based on more familial and some sporadic cases. There is no doubt that melanoma is a heterogeneous disease⁹; the disease may arise through different aetiological pathways, where UV exposure, nevus phenotype, pigmentation and overall genetic predisposition are of differing importance. In addition, given the complex role of telomeres in oncogenesis¹⁰, evidence for different directions of effect in different subtypes of melanoma would not be altogether surprising. That the important subtypes could be simply identified by those with and without a first degree affected relative would perhaps be more of a surprise.

The findings reported by Menin *et al.*⁸ are thus very intriguing, if not totally convincing, based as they are on quite a small sample size. Larger studies are needed to confirm or refute their findings. Understanding the role of telomere length in melanoma could help in understanding disease heterogeneity and also pave the way to providing a useful biomarker of disease risk.

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Acknowledgements

Thanks to Dr Mark Iles for constructive comments on this note.

This research was supported by Cancer Research UK Programme Award C588/A19167.

There are no conflicts of interest.

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