

MEETING ABSTRACTS

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Epigenetic deregulation of *IGF2* and cervical cancer precursors in HIV+ and HIV- patients

Cathrine Hoyo^{1*}, Francine Overcash¹, Zhiqing Huang², Olola Oneko³, Brandi Vaquez⁴, Joseph Obure³, Pendo Mlay³, John Bartlett⁵, Brenda Hernandez⁶, Susan K Murphy²

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Introduction

Early detection and aggressive treatment programs to prevent cervical carcinoma in situ (CIS) and invasive uterine cervical cancer (ICC) have been available for more than 30 years with more than 80% population coverage. Despite this, 11,000 cases of ICC and 40,000 cases of CIS continue to be diagnosed in the United States annually. Women of African descent are at >2-fold higher risk of invasive cervical cancer death compared to other ethnic groups.

Objective

The overarching goal is to develop epigenetic biomarkers that can be used for early identification of aggressive cases likely to result in invasive cervical cancer and death.

Methods

We conducted a hospital-based, case-control study comprising 26 women with ICC, 18 with CIN2/3/HSIL and 41 with normal cytology, at Kilimanjaro Christian Medical Center in Moshi, Tanzania. We analyzed methylation of three regions in the *IGF2/H19* imprinted domain known to regulate the expression of imprinted *IGF2*. Aberrant methylation is associated with *IGF2* deregulation, including changes in expression, loss of imprinting, and neoplasia.

Results

At the *IGF2/H19* imprint center upstream of *H19*, methylation profiles for all women with no evidence of

cervical abnormality or those with CIN2-CIN3 were within normal ranges (40%-60%), while 23% with invasive cancer had hypermethylation. In contrast, 25% of the CIN2/3 cases were abnormally hypomethylated at the *IGF2* DMR in *IGF2* intron 2, and the methylation profile worsened in the invasive cervical cancer cases with 64% having an abnormal methylation profile. A similar trend was found for the regulatory region in *IGF2* intron 6. Stratifying these analyses by HIV status in ICC revealed that aberrant intragenic *IGF2* hypomethylation was observed only among women without HIV. These associations persisted after adjusting for HPV genotype.

Conclusion

Our findings suggest that regulation of *IGF2* is substantially altered in CIN2 or worse via epigenetic alterations. DNA methylation profiles of these regions may be markers of risk of progression especially in HIV- women. The findings support our hypothesis that epigenetic deregulation of this imprinted gene could be useful in discriminating women with dysplasia likely to progress.

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Author details

¹Department of Community and Family Medicine, Duke University, Durham, NC, USA. ²Department of Obstetrics and Gynecology, Duke University, Durham, NC, USA. ³Department of Obstetrics and Gynecology, Kilimanjaro Christian Medical Center, Moshi, Tanzania. ⁴Kilimanjaro Christian Medical Center-Duke Women's Health Collaboration, Moshi, Tanzania and Durham,

*Correspondence: cathrine.hoyo@duke.edu

¹Department of Community and Family Medicine, Duke University, Durham, NC, USA

Full list of author information is available at the end of the article

NC, USA. ⁵Department of Medicine, Duke University, Durham, NC, USA.
⁶Cancer Research Center of Hawaii, University of Hawaii, Honolulu, HI, USA.

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