

# Author's Accepted Manuscript

Circulating tumour DNA for detecting minimal residual disease in multiple myeloma

Trevor J. Pugh



[www.elsevier.com/locate/bios](http://www.elsevier.com/locate/bios)

PII: S0037-1963(18)30018-0

DOI: <https://doi.org/10.1053/j.seminhematol.2018.03.002>

Reference: YSHEM50948

To appear in: *Seminars in Hematology*

Cite this article as: Trevor J. Pugh, Circulating tumour DNA for detecting minimal residual disease in multiple myeloma, *Seminars in Hematology*, doi:10.1053/j.seminhematol.2018.03.002

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting galley proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

**Circulating tumour DNA for detecting minimal residual disease in multiple myeloma**

Trevor J. Pugh, PhD, FACMG<sup>1,2,3</sup>

1. Princess Margaret Cancer Centre, University Health Network, Toronto, Ontario, Canada

2. Department of Medical Biophysics, University of Toronto, Toronto, Ontario, Canada

3. Ontario Institute for Cancer Research, Toronto, Ontario, Canada

**Reported from:**

Princess Margaret Cancer Centre, University Health Network

MaRS Centre, 101 College Street

Princess Margaret Cancer Research Tower, Room 9-305

Toronto, Ontario, Canada M5G 1L7

trevor.pugh@utoronto.ca

416-581-7689

**Supported in part by:**

The Princess Margaret Cancer Foundation

**Financial disclosure:**

Dr. Pugh is an inventor on a patent for hybrid-capture sequencing for determining immune cell clonality (WO2017177308).

**Abstract**

Circulating tumour DNA faithfully recapitulates somatic mutations detected in bone marrow aspirates from patients with newly diagnosed or relapsed/recurrent myeloma. Extending these methods to enable detection of minimal residual disease will require increased sensitivity and breadth of genomic assays to maximize information content from small quantities of cell-free DNA; as well as definition of a clinically-meaningful ctDNA concentration in comparison with conventional bone marrow cell-count thresholds. This review describes the use of cell-free DNA sequencing in myeloma to date, identifies challenges associated with pushing limit of detection of these assays into the realm of detecting minimal residual disease, and describes potential strategies to overcome these challenges.

**Key words**

Cell-free circulating tumour DNA; multiple myeloma; cancer genomics; mutations; epigenetics

Download English Version:

<https://daneshyari.com/en/article/8734810>

Download Persian Version:

<https://daneshyari.com/article/8734810>

[Daneshyari.com](https://daneshyari.com)