

# Abstract #5604: The impact of cause of mismatch repair deficiency and other molecular markers on clinical outcomes with the use of durvalumab in advanced endometrial cancer in phase 2 PHAEDRA trial (ANZGOG1601)

Authors: Daniel D. Buchanan<sup>1</sup>, Khalid Mahmood<sup>1</sup>, Peter Georgeson<sup>1</sup>, Romy Walker<sup>1</sup>, Kristy P. Robledo<sup>2</sup>, Michelle M. Cummins<sup>2</sup>, Amanda B. Spurdle<sup>4</sup>, Deborah Smith<sup>5</sup>, Jihoon E. Joo<sup>1</sup>, Mark Clendenning<sup>1</sup>, Julia Como<sup>1</sup>, Susan Preston<sup>1</sup>, Sonia Yip<sup>2</sup>, John Andrews<sup>2</sup>, Peey-Sei Kok<sup>2</sup>, Yeh Chen Lee<sup>2</sup>, Martin R. Stockler<sup>2,3</sup>, Linda Miles<sup>8,9,10</sup>, Yoland C. Antill<sup>11,12</sup> on behalf of the Australia New Zealand Gynaecological Oncology Group (ANZGOG)

1.University of Melbourne, 2.NHMRC Clinical Trials Centre, 3.The University of Sydney, 4.QIMR Berghofer Medical Research Institute, 5.Mater Pathology, 6.University of Queensland, 7.University Of Sydney, 8.Department of Medical Oncology and the Sir Peter MacCallum Department of Oncology, 9.Peter MacCallum Cancer Centre, 10.University of Melbourne, 11.Cabrini Health, 12.Monash University

## Background:

- The PHAEDRA trial is a single arm, phase 2 trial of durvalumab (1500mg IV Q4W) in women with advanced endometrial cancer (AEC)<sup>1</sup>.
- The objective tumor response (OTR) rate (confirmed CR or PR according to iRECIST) was 47% in mismatch repair deficient (dMMR) compared with 3% in MMR proficient (pMMR) AEC<sup>1</sup>.
- This substudy investigated the cause of dMMR and other genomic tumor features and their correlation with treatment outcomes.

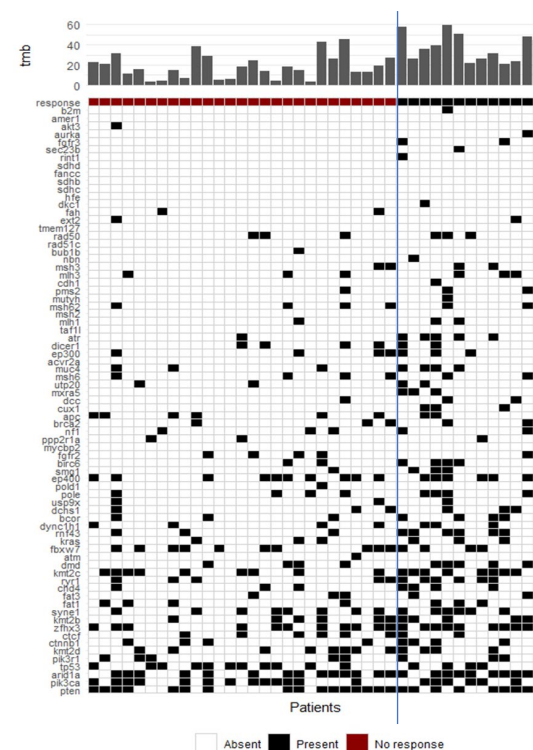
## Methods:

- DNA from formalin-fixed paraffin-embedded tumor tissue for 41/71 (25 dMMR, 16 pMMR) trial participants was sequenced using a custom capture-based 298-gene targeted panel (2.005Mb) and tested for *MLH1* gene promoter methylation.
- Derived genomic features included tumor mutational burden (TMB), COSMIC v.3.2 mutational signatures and insertion/deletion (Indel) somatic mutations.

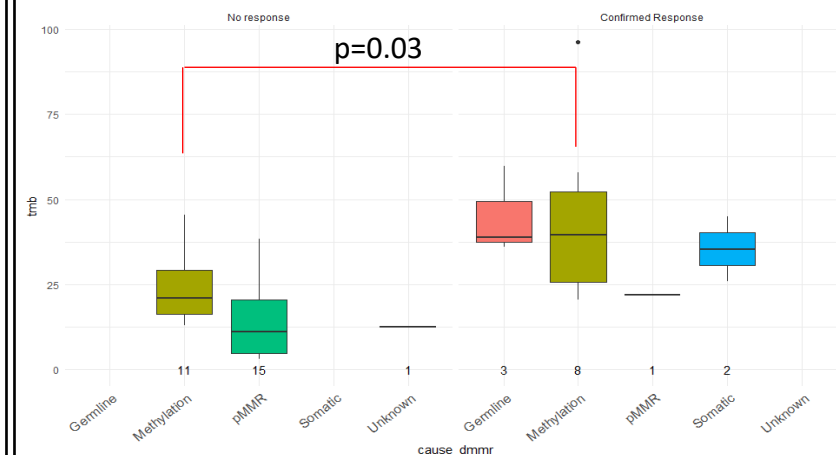
**Results:** **Table 1:** Objective tumor response (OTR= confirmed CR or PR) according to molecular subtype

Molecular subtype	No response, N = 53	OTR, N = 18	OTR rate (95% CI)
dMMR subtype, n (%)			
Germline PV	0 (0)	4 (100)	100% (40-100%)
Somatic MMR	1 (25)	3 (75)	75% (22-99%)
<i>MLH1</i> methylation	15 (60)	10 (40)	40% (22-61%)
pMMR	33 (97)	1 (2.9)	2.9% (0.15-17%)
No treatment	2 (100)	0 (0)	0 (0.0-80%)
Unknown	2 (100)	0 (0)	0 (0.0-80%)

**Figure 1:** Somatic mutated genes in non-responders and responders. Median TMB (assessed in 41/71) was higher in those with a confirmed radiological response (37, IQR:26-50) vs non-responders (16, IQR:9-25;  $p < 0.001$ )



**Figure 2:** MMR subtypes by TMB stratified by response



## Conclusions:

- dMMR-*MLH1* methylated AEC demonstrated greater heterogeneity in OTR to single agent durvalumab than the dMMR-Lynch and dMMR-somatic MMR mutation subtypes.
- Higher TMB was seen in responders, and specifically within dMMR-*MLH1* methylated responders, compared to non-responders.

Author contact: Prof. Yoland Antill (Yoland.Antill@monash.edu)

Funding Acknowledgements: Astra Zeneca Investigator Grant, ANZGOG Fund for New Research, DDB- NHMRC GNT1194896

1. Antill *et al.* Clinical Activity of durvalumab for patients with advanced mismatch repair-deficient and repair-proficient endometrial cancer: a nonrandomized phase 2 clinical trial. *J Immunother Cancer.* 2021 Vol.9 Issue 6. PMID: 34103352