Response to: Correspondence on 'MicroRNA expression as a diagnostic parameter in early endometrial cancer' by Coada et al

We are very glad for Coada and associates' interest in our research, and we greatly appreciate their meaningful and valuable questions.[1] Initially, our article included the molecular classification of endometrial cancer, which was removed based on the reviewer's suggestion. The new International Federation of Gynecology and Obstetrics (FIGO) 2023 staging system[2] was published on June 20, 2023, whereas our article was in the final processing and publication process.[3] For these reasons, a new staging system was not included in our article. Although we are fully aware that a larger sample size and a wide range of endometrial samples with similar clinical and anthropometric parameters could strengthen our results and conclusions, it would be difficult to collect a reasonable number of samples for stronger statistical power, since Serbia is a small country and grade 3 endometrial cancer is extremely rare. Considering these constraints, we had to restrict our study to the presented samples. Furthermore, our initial objective was to explore the expression of biomarkers for distinguishing patients with early endometrial cancer from controls, irrespective of cancer grade. Nevertheless, when three samples with grade 3 endometrial cancer histology were excluded from the statistical analysis, we were still able to find strong significance in microRNA (miRNA) expression between endometrial cancer and control samples (miRNA-200a, p<0.001; miRNA-21, p=0.001; miRNA-210, p=0.008; miRNA-126, p=0.045; and miRNA-130a, p=0.05). Moreover, the selected miRNAs showed similar discriminating power: miRNA-200a, (area under the curve) AUC 0.838; miRNA-21, AUC 0.785; miRNA-210, AUC 0.733; miRNA-126, AUC 0.675; and miRNA-130a, AUC 0.671).

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Contributors SZB: Conceptualization, methodology, validation, formal analysis, investigation, writing - original draft. MGM: Conceptualization, writing - review and editing. DMC: Conceptualization, writing - review and editing, visualization, supervision.

Funding The authors have not declared a specific grant for this research from any funding agency in the public, commercial or not-for-profit sectors.

Competing interests None declared.

Patient consent for publication Not applicable.

Ethics approval Not applicable.

Provenance and peer review Commissioned; internally peer reviewed.

To cite Blagojević S, Milutinović M, Cvetković D. *Int J Gynecol Cancer* Published Online First: [please include Day Month Year]. doi:10.1136/ijgc-2023-005179

Accepted 4 December 2023

► http://dx.doi.org/10.1136/ijgc-2023-005110

► http://dx.doi.org/10.1136/ijgc-2023-004579

Int J Gynecol Cancer 2023;0:1. doi:10.1136/ijgc-2023-005179

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