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## Transcriptomic biomarkers based approach for predicting the risk of heart failure development in postinfarction patients with the use of the ddPCR method



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**Aim:** The aim of our study was to identify distinct biomarkers that correlate with HF development.

**Methodology:** We collected blood samples from AMI patients on admission (1st day of AMI). Clinical evaluation was performed after six months of AMI and patients were divided into HF (n=37), non-HF (n=26) and moderate-HF groups (n=119). Microarrays were used to analyze individual gene expression profiles of the patients. Seven differentially expressed transcripts that best discriminate between HF, non-HF and moderate-HF patients were selected. Microarray results were validated by the ddPCR method using blood RNA. Reference values were obtained for all transcripts and all groups of patients and the HF prognosis risk score was calculated.

**Results & Conclusion:** The obtained results show that the identified gene expression changes at the early phase of AMI allow differentiating patients who developed HF from those who did not and that they may serve as a convenient tool contributing to the prognosis of heart failure.

## **Biography**

Beata Burzynska has completed her PhD from Warsaw University of Life Sciences, Poland. She is a PI at the Department of Genetics, Institute of Biochemistry and Biophysics, Polish Academy of Sciences. She conducted Post-doctoral Training at the Louisiana State University Health Sciences Center. She has published more than 40 papers in SCI journals and has been serving as a Board Member of the Committee on Biotechnology, Polish Academy of Sciences.

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