



**Serbian Biochemical Society  
Tenth Conference**

***"Biochemical Insights into Molecular Mechanisms"***

*Proceedings*

- 12:40-13:00 Milan Dragičević  
Institute for Biological Research "Siniša Stanković", University of Belgrade  
**Arabinogalactan protein mining and diversity - the case of *Centaurium erythraea***
- 13.00-14.00 **Poster session**
- 14.00-15.00 Cocktail / Lunch break
- 15:00-15:20 Miloš Prokopijević  
University of Belgrade - Institute for Multidisciplinary Research  
**Natural polymers: suitable carriers for enzyme immobilization**
- 15:20-15:40 Ana Ninić  
University of Belgrade - Faculty of Pharmacy  
**Link between resistin, low-grade systemic inflammation and obstructive sleep apnea**
- 15:40-16:00 Branka Đorđević  
Faculty of Medicine, University of Niš  
**Blood-retinal barrier breakdown in diabetic retinopathy – the protective role of melatonin**
- 16:00-16:30 Coffee break
- 16:30-17:00 Poster awards and closing ceremony

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# Arabinogalactan protein mining and diversity - the case of *Centaurium erythraea*

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*Centaurium erythraea* (common centaury) is a medicinal plant with extraordinary developmental plasticity *in vitro*, used as a model organism for studying *in vitro* morphogenesis in our lab. Several experimental lines of evidence have identified arabinogalactan proteins (AGPs) as one of the key players involved in centuary morphogenesis; however, the role of specific genes has yet to be determined. AGPs are ubiquitous plant cell surface glycoproteins associated with various physiological functions. AGP sequences are characterized by the presence of non-continuous hydroxyproline residues which serve as O-glycosylation anchor sites for branched arabinogalactans. Due to biased amino acid composition rich in disorder-promoting amino acids, AGP sequences lack a stable structure and consequently have lessened evolutionary constraints. Therefore, homology-based approaches to AGP sequence mining have limited success. We have recently developed a bioinformatics pipeline for AGP sequence mining, *ragp*, which exploits their key feature – the presence of hydroxyprolines<sup>1</sup>. This pipeline combines estimation of proline hydroxylation based on local sequence context by a machine learning model with a flexible motif search. After applying this pipeline to the centaury transcriptome, AGP regions were found to associate with a variety of conserved domains. Here we introduce a streamlined way to train models for prediction of Pro hydroxylation, analyze important protein sequence features determining Pro hydroxylation status, present some of the AGP types found in centaury and discuss model limitations and future prospects.

## Acknowledgements

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## References

1. Dragičević M, Paunović D, Bogdanović M, Todorović S, Simonović A. *ragp*: Pipeline for mining of plant hydroxyproline-rich glycoproteins with implementation in R. *Glycobiology* 2020;30:19–35.

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