specific, in order to understand which outcomes for cardiovascular diseases (CVD) could be translated from animal to human studies.

Introduction: CVD stand as a great cause of morbi-mortality worldwide and polyphenol-rich diets have been associated with improved cardiovascular risk profiles. Although rodent models have been a resourceful means of understanding the CVD mechanisms and possible outcomes of the use of polyphenols in that context, most experimental models do not fully reproduce human CVD.

Methods: Database searching was carried out on PubMed and Google Scholar using specific keywords concerning CVD, retrieving close to 300 publications. After excluding irrelevant results, proteome data was organized in Excel® spreadsheets and the Cytoscape platform, ClueGo + CluePedia and Venny 2.1.0 were used to explore the biological processes influenced by flavonoids in the approached CVD.

Results: This study was mainly focused in the species Rattus norvegicus and Homo sapiens and in flavonoids, a polyphenol subgroup. Only about 5% of the BP influenced by flavonoids were common to both species and they were mostly related to the maintenance of blood pressure and the fatty acid metabolic process. Nevertheless, these effects were accomplished through different proteins/pathways and different subgroups of flavonoids.

Conclusion: Our research highlights the need for a careful translation of the flavonoids' effects observed in rat models to clinical trials, since different proteins and subgroups of flavonoids mediated the observed actions. Though this type of studies can provide insights to help choosing the most adequate polyphenols as preventive approaches or therapies for human CVD, further investigation should be performed to clarify the described effects. Besides, pharmacokinetic aspects of the flavonoids' action should also be considered when planning clinical trials.

http://dx.doi.org/10.1016/j.pbj.2017.07.127

PS167

Affinity of *Listeria* sp. proteins to cAMP and role in virulence

M. Fidalgo [1,2,3,*], J. Moscoso [2,3], S. Sousa [2,3], D. Cabanes [2,3]

[1] *Universidade de Trás-os-Montes e Alto Douro (UTAD), Portugal*
[2] *Instituto de Biologia Molecular e Celular (IBMC), Portugal*
[3] *Instituto de Investigação e Inovação em Saúde (I3S), Portugal*
E-mail address: martafilipafidalgo@gmail.com
(M. Fidalgo).

Aim: The aim of this study was thus to identify Lm proteins capable to bind cAMP.

Introduction: Infectious diseases are still a major cause of death worldwide. To infect a host and survive the environment, bacteria have to sense their surrounding and adjust their behaviour. In this adaptation process, cAMP (cyclic adenosine monophosphate) is known to be an important player in pathogens such as *Pseudomonas* spp., *Vibrio* spp. or *Mycobacterium* spp. The small molecule

cAMP is a cyclic nucleotide that relays information from receptors to one or more effector proteins within a bacterial cell, functioning as a second messenger. To mediate a response, cAMP allosterically interacts with cAMP-binding proteins. Understanding how this happens is fundamental to predict how bacteria will adapt/act to/in a given context.

Methods: We recently showed that the human foodborne pathogen Listeria monocytogenes (Lm) produces cAMP. The aim of this study was thus to identify Lm proteins capable to bind cAMP. To do this, four candidate proteins selected by bioinformatics analyses were expressed, purified and studied biochemically. Three approaches were used: cAMP affinity chromatography; competitive cAMP affinity chromatography; and isothermal titration calometry (ITC).

Results: Among the four tested proteins, CbpA displayed cAMP-binding ability on the three approaches used.

Conclusion: Hence, our preliminary results showed that CbpA binds to cAMP. It is now mandatory to understand the relation between cAMP and CbpA, to determine the function of the protein itself and in complex with cAMP, and to understand the importance of this signalling system for virulence.

http://dx.doi.org/10.1016/j.pbj.2017.07.128

Public Health & Medical Informatics Poster Session
Saturday, September 16th, 10h00

PS044

Assessment of ECG interpretation skills among Polish medical students, nursing, emergency medicine and English Division medical students

Marek Stopa[*], Harison Sevenathan, Mateusz Bogusławski, Izabela Pałasz

Students Scientific Group of Interventional Cardiology at the 2nd Department of Cardiology and Cardiovascular Interventions
E-mail address: mrk.stopa@gmail.com
(M. Stopa).

Aim: The aim of the study was to evaluate ECG interpretation skills among study population, and analyze factors determining their score.

Introduction: The electrocardiogram examination is one of the most frequently performed diagnostic test. Correct interpretation of the ECG, particularly in life-threatening scenarios (LTS) may influence the decisions on appropriate actions and consequently have an impact on the lives and health of patients. It is important for medical, nursing and emergency medicine students to acquire this skill.

Methods: ECG interpretation skills were assessed by self-prepared questionnaire including questions about demographic data and 20 ECG problems with 17 cases. In 6 cases there were LTS. Three questions evaluated basic knowledge about rhythm, heart rate and axis. The survey was conducted via Internet. Study population consist of 551 medical, nursing and emergency medicine students.

Results: The overall score among Polish medical students is 46% which is higher than nursing and emergency medicine students (22% and 37% respectively; $p < 0.001$ in both). English division students scored almost similarly (49%; $p = 0.27$). Polish medical students scored better in LTS than the nursing students (37% vs 23%; $p < 0.001$). Among Polish medical students: Students in year "4–6" scored higher than those from year "1–3" (overall score: 51% vs. 31%; $p < 0.001$, LTS: 41% vs 25%; $p < 0.001$). In addition, members