

## 1) Tomas Otahal

### Corruption in Economic Theory

The aim of the thesis is to explain the corruption problem from the perspective of two different economic theories and to provide a theoretical solution suitable for both 'explanatory or 'theories that will be explained' theories. In the methodological section, the focus is on (?) why the argumentation is built on the principle of methodological individualism followed by deductive analysis supported with evidence from historical examples. Corruption is introduced through the example of bribery.

In the theoretical section, the author explains the historical evolution of agency theory and rent-seeking. The author explains how both the agency theory and rent-seeking understand the problem of corruption and the problems of suggested public policies deduced from both theories. It is argued that while the agency theory lacks the concrete explanation of institutional environment within which the corruption problem occurs, rent-seeking lacks the positive definition of rules determining how corruption should be solved.

In the analytical section, the author suggests the theoretical framework connecting both the agency theory and rent-seeking. The author explains that the suggested theoretical framework applied to historical examples implies that the system of creation of legal rules and the system of their enforcement are crucial for the solution of the corruption problem in every society. More precisely, it is argued that when the system of creation of legal rules is subordinated to the citizens' control and the independent judicial system is subject to competition, the problem of corruption is not so prevalent compared with non-democratic states. The conclusion summarizes and provides an explicit explanation of the author's contribution.

## 2) Jiri Palicka [Title

Although the gene therapy achieved undeniable clinical successes, its use for cancer treatment is still limited by the low efficiency of gene transfer. One of the possibilities for reaching a higher number of affected cancer cells is intercellular spread of the transgene product. Using the known signal sequences responsible for inter- and intracellular trafficking of proteins is the transgene engineered to make its product, the produced protein, capable of being secreted from the affected cells and taken up by the neighboring cells. The aim of this diploma thesis was to improve cellular uptake of the transgene product. The gene for Cre recombinase and the cell line containing a/the reporter cassette allowing detection of the presence of the Cre recombinase in a cell nucleus was chosen as a reporter system. Within this project, the method of bacterial expression and purification of an enzymatically active Cre-fusion protein was established and its capability of entering the reporter cells was assessed. Furthermore, transgenes containing additional protein transduction domain TAT from the HIV virus and an endosomal escape signal from the Influenza virus were constructed. Their activity was not examined in the limited time.

3) Sarka Masova

**"Morphometric and molecular characterization of *Multicaecum heterotis* (Nematoda: Heterocheilidae) from *Heterotis niloticus* (Osteoglossiformes) with determination Key of *Multicaecum* and *Brevimulticaecum* species"**

Ascaridoid nematode species *Brevimulticaecum heterotis* (Petter, Vassiliadès et Marchand, 1979, Khalil, 1984) were recorded from the intestine of the African bonytongue, *Heterotis niloticus* (Cuvier) (Arapaimidae, Osteoglossiformes) from the Mare Simenti in the Niokolo Koba National Park, East Senegal and from Kosti, Sudan. The study includes morphometrical and molecular approaches to identification of the nematode parasite *B. heterotis*. Specimens were examined and redescribed based on light and, for the first time, environmental scanning electron microscopy (ESEM) and SEM. These methods revealed some findings of morphological features such as a dentigerous ridge with small sharp denticles on the upper edge of the lip. On the basis of this feature this taxon belongs back to genus *Multicaecum* (Baylis, 1923). *B. heterotis* differs from a generic diagnosis of *Brevimulticaecum* Mozgovoy (Skrjabin, Shikhobalova et Mozgovoy, 1951) mainly by the presence of dentigerous ridges on lips, location of excretory pores level with or behind the nerve ring, and vulva location in the front half of the body. The study also contains a key for determination of the species from genus *Multicaecum* and *Brevimulticaecum*, and the first published sequence of the species from the genus *Multicaecum*.

4) Khomaini Hasan [TITLE?]

KEYWORDS (?) Mycobacterium tuberculosis H37Rv HALOALKANE DEHALOGENASE (DmbC): BIOCHEMICAL, SUBSTRATE SPECIFICITY, AND STRUCTURAL CHARACTERIZATIONS

Haloalkane dehalogenases (EC. [3.8.1.5](#)) are enzymes which catalyze the hydrolytic conversion of various halogenated compounds to corresponding alcohol and halide ions(?). Because of its broad substrate specificity, haloalkane dehalogenases are promising biocatalysts for bioremediation, biocatalysis, and biosensing. Herein, we report haloalkane dehalogenases DmbC from Mycobacterium tuberculosis H37Rv which demonstrate dehalogenase activity of their translational products. DmbC was produced in the recently developed Mycobacterium smegmatis expression host system. DmbC was purified to homogeneity by nickel affinity chromatography and its characteristics have been investigated covering biochemical, substrate specificities, and secondary structure. DmbC exhibited lower catalytic activity with 30 tested halogenated substrates, but novel specificity towards iodinated and brominated aliphatic compounds. DmbC has temperature and optimum at 40 degrees Celcius and pH optima at 8.3 by using 1,3-diiodobutane as a substrate. The secondary structure of DmbC measured by means of circular dichroism spectroscopy revealed that DmbC is constructed by an alpha/beta-hydrolase family-like structure. Even though the size of the 32.9 kDa monomeric unit of DmbC estimated by SDS PAGE is analogous to other known haloalkane dehalogenases, this enzyme is unique by forming large homo-oligomeric units. The oligomeric state characteristic of DmbC was confirmed by gel filtration, and dynamic and static light scattering. Furthermore, the presence of detergents in purification buffers in the reaction mixture of DmbC showed a clear effect on protein activity. The addition of detergent Tween 80 and DMSO to the protein sample of DmbC results in the formation of a lower oligomeric state and higher catalytic activity.

## 5) Dana Smerdova

The importance, advantages and difficulties in using elements of the Video Interaction Guidance (VIG) method in the preparation of student teachers

This contribution deals with the research which has been realised within the dissertation and aims to express the importance, possibilities and difficulties in the implementation of elements of the Video Interaction Guidance method in the preparation of students of education, and therefore future teachers, in the Faculty of Education. It set itself a task to outline and highlight the close interconnection of the links between communication and interaction at school for the development of the abilities and skills of future teachers and to intentionally create positive psychosocial climate at school as the important precondition for meaningful and effective teaching, where teachers are able to change bad conditions of teaching to be more in tune with human nature and basic human needs, for both pupils and teachers. Further it presents partial findings in student teachers' conception of the educational communication and interaction and ability of student teachers to interpret interaction in the classrooms between teachers and pupils which are alarming in some ways but understandable in the context, and then describes the reasons and advantages of using elements of VIG in student teachers' preparation.

## 6) Zuzana Petrovicova

"Taking Responsibility in Adolescence and its Relationship to Parenting Style"

The aim of the present study was to examine the relationship between components of responsibility-taking among adolescents and perceived parenting style and enabling. Participants were 140 middle (14-16 years of age) and late (16-18 years of age) adolescents and their parents from a midsize town in western Slovakia. Students were equally divided by age and gender. Adolescents completed self-report measures of identity (translated EOMEOS-2), attributional style (shortened version of ASQ), personal and family responsibilities, and well established measures of parenting style. Parents filled in a parenting style questionnaire and an enabling survey.

Correlations and multiple hierarchical regressions were computed. Significant positive correlations were found between parental enabling and autonomy granting ( $r=.50$ ,  $p<.01$  for mothers,  $r=.43$ ,  $p<.01$  for fathers), and between non-enabling and demand-making ( $r=.49$ ,  $p<.01$  for mothers). A relationship between personal responsibilities and paternal positive emotions was found, while family related responsibilities were related to maternal positive emotions. Hierarchical regression revealed that internality was best predicted by parental demand-making and non-enabling. For the purposes of our study, we calculated exploration and commitment scores and regressed them on components of parenting, enabling, and dimension of attributional style. Exploration was best predicted by maternal negative emotions ( $\beta=-.36$ ,  $p<.01$ ), paternal demandingness ( $\beta=.29$ ,  $p<.01$ ), and stability ( $\beta=.24$ ,  $p<.05$ ). Commitment was best predicted by maternal negative emotions ( $\beta=-.45$ ,  $p<.01$ ), accounting for 26% of variance.

The study found a relationship between the autonomy component of parenting and parental enabling, both negatively related to internality. A relationship between identity statuses and components of parenting were also found, supporting the existing theories. Implications for future research will be discussed.

7) Jana Supikova

## FOCUSED MICROARRAY FOR LYMPHOMA DIAGNOSTICS

### Background

Non-Hodgkin lymphomas (NHL) represent a heterogeneous group of lymphoproliferative disorders with highly variable clinical courses and outcomes. In some cases, current diagnostic methods based on histopathology and immunohistochemistry may be insufficient for exact tumor classification and subjectively influenced by a pathologist's experience, especially in Burkitt's lymphoma. Neither do prognostic markers such as the International Prognostic Index (IPI), although highly useful, capture all the variability that affects clinical behaviour of lymphomas. The genome-wide transcriptional profiling was reported to accurately define the biological phenotype of the tumor.

### Aims

The aim of the project was to design a novel focused oligonucleotide microarray directed at molecular diagnostics and prognostication of lymphoproliferative disorders, particularly non-Hodgkin lymphomas, and to test its reliability on a cohort of newly diagnosed lymphoma samples.

### Method

We designed a custom oligonucleotide microarray (Agilent 8x15K custom array) carrying specific probes for approximately 4000 genes. The genes represented on the microarray were selected on the basis of previously published lymphoma/leukemia gene-expression profiling studies. In addition, probes for the genes implicated in crucial cellular processes such as apoptosis or cell cycle control were added. To provide more information, the genes for the majority of CD antigens and „housekeeping“ genes were also included in the microarray design.

67 histologically characterised samples were analysed – 18 Diffuse Large B-cell Lymphomas (DLBCL), 34 Follicular Lymphomas (FL), 3 Burkitt's Lymphomas (BL), 1 MALT Lymphoma, 6 non-malignant lymph-nodes and 3 lymphoma cell lines (SU-DHL-4, WSU-NHL, RAMOS). RNA was obtained either from fresh-frozen lymph-node resections, or from RNA later preserved needle biopsy samples.

### Summary

We demonstrated the benefit of gene expression profiling using novel designed focused microarray for non-Hodgkin lymphoma characterisation. The technology is robust, less expensive compared to whole-genome approach and still capable of retaining important information.

