

CROATIAN INTERNATIONAL PUBLICATIONS

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Baždarić K, Bilić-Zulle L, Brumini G, Petrovečki M. Prevalence of plagiarism in recent submissions to the Croatian Medical Journal. *Sci Eng Ethics*. 2012 Jun;18(2):223-39.

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To assess the prevalence of plagiarism in manuscripts submitted for publication in the Croatian Medical Journal (CMJ). All manuscripts submitted in 2009-2010 were analyzed using plagiarism detection software: eTBLAST, Cross-Check, and WCopyfind. Plagiarism was suspected in manuscripts with more than 10% of the text derived from other sources. These manuscripts were checked against the Déjà vu database and manually verified by investigators. Of 754 submitted manuscripts, 105 (14%) were identified by the software as suspicious of plagiarism. Manual verification confirmed that 85 (11%) manuscripts were plagiarized: 63 (8%) were true plagiarism and 22 (3%) were self-plagiarism. Plagiarized manuscripts were mostly submitted from China (21%), Croatia (14%), and Turkey (19%). There was no significant difference in the text similarity rate between plagiarized and self-plagiarized manuscripts (25% [95% CI 22-27%] vs. 28% [95% CI 20-33%]; $U = 645.50$; $P = 0.634$). Differences in text similarity rate were found between various sections of self-plagiarized manuscripts ($H = 12.65$, $P = 0.013$). The plagiarism rate in the Materials and Methods (61% [95% CI 41-68%]) was higher than in the Results (23% [95% CI 17-36%], $U = 33.50$; $P = 0.009$) or Discussion (25.5 [95% CI 15-35%]; $U = 57.50$; $P < 0.001$) sections. Three authors were identified in the Déjà vu database. Plagiarism detection software combined with manual verification may be used to detect plagiarized manuscripts and

prevent their publication. The prevalence of plagiarized manuscripts submitted to the CMJ, a journal dedicated to promoting research integrity, was 11% in the 2-year period 2009-2010.

Pavic T, Ljubicic N, Stojavljevic S, Krznicaric Z. Nutritional Screening Model in Tertiary Medical Unit in Croatia. *Ann Nutr Metab*. 2012 Jul 24;61(1):65-69.

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Background/Aims: Malnutrition of hospitalized patients is often undetected and untreated due to poor awareness and insufficient knowledge of the attending hospital staff. Nutritional screening has not been part of the daily routine in Croatian hospitals. Our aim was to implement nutritional screening as part of the routine medical examination and to assess the nutritional risk at admission for all hospitalized patients. Methods: All patients hospitalized in departments of internal medicine in tertiary hospitals in Croatia were screened at entry using the Nutrition Risk Screening 2002 (NRS 2002). Results: Between October and December 2010, 1,696 patients were screened and analyzed (948 males and 748 females). 329 (19.4%) had an NRS 2002 score ≥ 3 and were considered to be at nutritional risk. An NRS 2002 score ≥ 3 was identified as a significant predictor of the length of hospital stay (beta coefficient = 0.06, $p = 0.027$) and fatal outcome (OR = 6.18, $p < 0.001$). Only 32.8% of malnourished patients received some nutritional support. Conclusions: Every fifth patient hospitalized in a general medical department in Croatia is at nutritional risk and the majority of them does not receive nutritional support.

More effort is needed to implement nutritional standards in daily clinical practice.

Boban M, Malojčić B, Mimica N, Vuković S, Zrilić I, Hof PR, Simić G. The Reliability and Validity of the Mini-Mental State Examination in the Elderly Croatian Population. *Dement Geriatr Cogn Disord*. 2012 Jul 17;33(6):385-392.

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Aim: The aim of this study was standardization and validation of the Mini-Mental State Examination (MMSE) in the general Croatian aging population. **Methods:** Three-hundred and forty-four participants underwent the MMSE test, 217 cognitively healthy subjects without neurological and psychiatric disorders and 127 patients with mild cognitive impairment (MCI) or dementia. **Results:** The optimal cutoff point for screening of the general Croatian population (cognitively healthy vs. MCI and dementia) is 26/27; in the Croatian population aged ≥ 65 years, the cutoff point is 24/25, whereas for screening of highly educated persons (≥ 14 years of education) aged ≥ 65 years a higher cutoff point should be used (26/27). **Conclusions:** MMSE results when standardized and validated in a certain population might better contribute to recognition of the individuals at risk that should be directed to dementia outpatient clinics.

Vukojevic K, Kero D, Novakovic J, Kalibovic Govorko D, Saraga-Babic M. Cell proliferation and apoptosis in the fusion of human primary and secondary palates. *Eur J Oral Sci*. 2012 Aug;120(4):283-91.

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The markers of cell proliferation (Ki-67) and apoptosis [caspase-3, TdT-mediated biotin-dUTP nick-end labelling (TUNEL)] and the expression of syndecan-1 and heat shock protein 70 (Hsp70) were analyzed immunohistochemically in 11 developing human palates, from developmental weeks 6 to 10. During fusion of the primary palate, the proportion of proliferating cells decreased from 42 to 32% and the proportion of apoptotic cells decreased from 11 to 7% in the medial-edge epithelium. At later stages, the proportions of both types of cells decreased in the ectomesenchyme, except for proliferating cells in its non-condensing part. At developmental weeks 9-10, the epithelial seam in

the secondary palate comprised 28% proliferative cells and 5% apoptotic cells. While condensing ectomesenchyme contained more apoptotic cells than proliferating cells, the opposite was observed for the non-condensing ectomesenchyme. Co-expression of syndecan-1 and Hsp70 was detected in cells budding from the epithelial seam. Our study indicates similar principles for human primary palate and secondary palate fusion, and parallel persistence of proliferation and apoptotic activity. While proliferation enables growth and fusion of different palatal primordia, apoptosis results in the removal of large numbers epithelial cells at the fusion point. The disintegration of seam remnants seems to be executed through the processes of change in protein content and cell migration, probably leading to cell death as their final outcome.

Pevac B, Radulovic Pevac M, Stipic Markovic A, Batista I, Rijavec M, Silar M, Kosnik M, Korosec P. House Dust Mite-Specific Immunotherapy Alters the Basal Expression of T Regulatory and FcεRI Pathway Genes. *Int Arch Allergy Immunol*. 2012 Jun 21;159(3):287-296.

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Background: Regulatory T (Treg) cells and IgE-mediated signaling pathways could play important roles in the induction of allergen tolerance during house dust mite-specific subcutaneous immunotherapy (HDM-SCIT). Our aim was to compare the basal expression levels of Treg, T helper 1 (Th1) and Th2 transcription factors and components involved in IgE-mediated signaling in healthy subjects with those in HDM-allergic patients both untreated and successfully treated with HDM-SCIT. **Methods:** Thirty-nine HDM-allergic patients who completed a 3- to 5-year course of mite extract SCIT, 20 mite-allergic controls and 25 healthy controls participated in this study. The efficacy of SCIT was monitored using skin-prick tests (SPTs), total immunoglobulin E (tIgE), specific IgE (sIgE), sIgG(4), nasal challenge and visual analog scale (VAS) scores at several time points. The mRNA levels of forkhead box protein 3 (FOXP3), T-BET, GATA-3, FcεRI, spleen tyrosine kinase (Syk), phosphatidylinositol 3 kinase (PI3K) and SH2 domain-containing inositol phosphatase (SHIP) were quantified by real-time RT-PCR using nonstimulated whole blood samples. **Results:** Decreased wheal sizes and VAS scores, negative challenges and increased sIgG(4) levels indicated that SCIT was effective in the treated patients. Basal expression levels of FOXP3 and GATA-3 decreased and T-BET levels increased in both treated patients and in healthy controls compared to untreated patients. The IgE-me-

diated pathway kinases Syk and PI3K exhibited reduced expression, whereas SHIP phosphatase levels were elevated in both treated patients and healthy controls relative to untreated patients. The expression levels of FcεRI were not significantly altered. Conclusions: Immunotherapy using HDM extracts results in a modification of the basal expression levels of several IgE-related signaling factors and induces a highly significant upregulation of Th1-response and downregulation of Th2-response transcription factors. Interestingly, this therapy also appears to reduce the basal expression of FOXP3.

Krznařić Z, Vranešić Bender D, Kunović A, Kekez D, Stimac D. Gut microbiota and obesity. Dig Dis. 2012;30(2):196-200.

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The human gut hosts more than 100 trillion microorganisms, encompassing thousands of species. In adults, Bacteroidetes and Firmicutes are the most prevalent phyla. Experimental data in animal and observational studies in obese patients suggest that obesity is associated with substantial changes in the composition and metabolic function of the gut microbiota. The initial findings linked obesity with the decreased relative proportion of Bacteroidetes to Firmicutes. There are some authors who suggest that probiotics and prebiotics can modulate obesity-host metabolism in obesity and obesity-related disorders.

Cepika AM, Soldo Jureša D, Morović Vergles J, Malenica B, Santak M, Kapitanović S, Mayer M, Anić B, Sentić M, Gagro A. Decrease in circulating DNA, IL-10 and BAFF levels in newly-diagnosed SLE patients after corticosteroid and chloroquine treatment. Cell Immunol. 2012;276(1-2):196-203.

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Arsenal of pattern-recognition receptors alongside antibody production machinery make B cells vulnerable to autoimmune response if an autoantigen elicits both pathways in a self-sustained fashion. Systemic lupus erythematosus is an autoimmune disease characterized by autoantibodies to DNA, RNA and related structures. Murine studies demonstrated autoreactive B cell activation upon TLR9 stimulation with DNA-containing immune complexes. This activation could be abolished with chloroquine, a drug used in SLE treatment that also blocks TLR9 signaling. We investigated whether chloroquine modulates TLR9 expression, circulating DNA levels and B cell-related cytokines in newly discovered, untreated SLE patients. TLR9 was measured in peripheral blood B cells by flow cytometry, serum DNA by real-time PCR, and IL-10 and BAFF by ELISA before treatment, after 3 weeks on corticosteroids, and 3 months after introduction of chloroquine. We found that circulating DNA is higher in SLE patients than in controls in every time-point and decreases significantly after chloroquine treatment. Untreated patients had higher serum IL-10 than controls or patients on corticosteroids. Also, corticosteroids decreased and chloroquine completely abolished CpG-mediated CD86 upregulation on B cells and IL-10 secretion in PBMC culture. Providing the TLR9 pathway activation demonstrates its importance in pathogenesis of human SLE, this data supports continuation of chloroquine in SLE treatment protocol. In addition, observed modulation of cytokine and DNA levels after immunomodulatory treatment prompts for inclusion of untreated patients in studies of human immune disorders.