

PRESS RELEASE

Croatian Medical Journal
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Croatian National Biobank launched

The new issue of the Croatian Medical Journal presents the “Croatian National Biobank”, a consortium linking more than 20 research projects from all four Medical Schools in Croatia, several teaching hospitals, and public health institutes. It is coordinated from the recently founded Croatian Centre for Global Health which is based at the University of Split School of Medicine.

The national Biobank aims to develop a resource “10 001 Dalmatians”, a large and internationally recognized study of genetic and environmental determinants of health and disease in genetic-isolate island populations from Dalmatia, Croatia. This effort, aiming to recruit 10 001 examinees, has developed during the recent years in collaboration with the scientists from Scotland, Sweden, The Netherlands, Italy, and Germany. In the period 2001-2007, it already received substantial competitive funding from The Croatian Government, European FP6, UK Medical Research Council, UK Royal Society, The Wellcome Trust, US National Institutes of Health, and The British Council.

This issue of Croatian Medical Journal presents several early results of the field research performed during 2007 in Korcula island, Croatia. The paper by Zemunik et al. used genome-wide association study to confirm the role of SLC2A9 gene in uric acid regulation and CETP

gene in HDL-cholesterol regulation. It also identified some new genes influencing cholesterol levels: KSR2, PKNOX1 and PEMT. The study by Polasek et al. found that the genes ZNF498, SGCD, CRIM1 and ITGA1 are associated with brachial circumference and in some instances hip circumference and weight of Korcula islanders. Vataavuk et al. showed that myocilin gene seems to be the very strong candidate for explaining some of the pathophysiological pathways leading to the development of both glaucoma and high myopia. Finally, Biloglav et al. used demographic data, historic references and population genetic information to show that a historic epidemic from the mid-15th century probably acted as a selection pressure that increased the frequency of the CCR5 Δ 32 mutation in Europe, rather than the major bubonic plague epidemic waves, as previously hypothesized.

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