In 1960 Duncan and Dixon described family whth chronic tubulointerstitial kidney disease associated with juvenile onset of hyperuricemia and gout. Based on combination of these clinical symptoms they named the disease familial juvenile hyperuricemic nephropathy (FJHN) [1]. Disease with very similar clinical presentation but different age of onset and kidney histology was described as a medullary cystic kidney disease (MCKD) in 1977 [2]. Until recently the molecular basis and pathogenesis of this syndrome remained unknown.

The long term aim of our research group is to elucidate the genetic basis of the disease and to solve pathogenetic mechanisms leading to the individual clinical and biochemical symptoms (e.g. hyperuricemia) and kidney damage in general. We systematically identify patients with this disease and healthy family members and collect relevant clinical information and samples for classification (urine, blood, tissue biopsies) and subsequent clinical, biochemical, molecular biology and cell pathology correlations.

We [3, 4] and others [5-7] proved genetic heterogeneity of FJHN and defined four FJHN loci on chromosomes 1q21, 1q41, 16p11.2. and 17q21.3. Further research defined disease causing mutations in three genes - uromodulin (UMOD) [8], hepatonuclear factor 1-beta (HNF-1) [9] and renin (REN) [10], which explain only about 40% of the FJHN cases.

We also found that most of the FJHN cases have altered expression and urinary excretion of UMOD which suggest central role of UMOD protein in development of hyperuricemia and FJHN pathogenesis [11]. Our surprising finding, has been corroborated recently by results of genome-wide association studies (GWAS) showing association of UMOD polymorphisms with development of chronic kidney disease [12, 13]. This is a reason of revived and currently growing interest in still mysterious UMOD biology and function and positioning FJHN as a very hot topic in current nephrology research