SURGICAL TREATMENT OF CARDIAC MYXOMAS – ONE CENTER EXPERIENCE

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INTRODUCTION. Myxoma is the most frequent (40-70%) benign cardiac tumor. The suspicion of myxoma incidence in echocardiography (MRI or MSCT) is the indication for urgent surgery because of possibility of embolism and sudden death. The aim of the study was analysis of early results of surgical treatment of cardiac myxoma in our Department.

MATERIAL AND METHODS. Patients (n=180) undergoing evaluation and surgical treatment for cardiac myxoma in Cracow between 1980 and 2012 year (70% women, average age 57,8 y). Retrospective analysis of medical records was performed. Myxoma was localized in 90,2% in left atrium, in 8,7% in right atrium and in 1,1% in both. Average myxoma size was estimated between 9 cm and 1,8 cm (mean 4,5cm). All patients were operated urgently in mild hypothermia or normothermia using median sternotomy or minitoracotomy and cardiopulmonary bypass (CPB) technique to maintain the circulation of blood and oxygen content. Temporary cessation of cardiac activity and protection against metabolic damage was achieved by crystalloid or blood cardioplegia. Excision of tumor was performed through left or/and right atriotomy. In 16,7% cases additional surgical procedures were performed (ASD closure, CABG, MV-plasty MV-replacement, AV-replacement, TV-plasty). In last 20 cases, cytogenetic analysis (comparative genomic hybridization - CGH) of excised tumors was performed according to standard procedure.

RESULTS. Overall early mortality rate was 4,4% and early morbidity rate was 26,8%. Low output syndrome occurred in 13,8%. Mean intubation time was 18 hours, mean ICU stay was 45 hours and mean hospital stay was 8 days. CGH did not reveal any chromosomal aberrations in analyzed myxomas.

CONCLUSIONS. Urgent operation is the method of choice in treatment for cardiac myxoma. It is associated with acceptable perioperative mortality and morbidity. CGH is a relatively fast screening technique that can point at specific chromosomal regions that might play a role in the tumor pathogenesis. Guided by CGH results, more specific molecular biology techniques like fluorescence *in situ* hybridization, loss of heterozigosity analysis or sequencing can be used to identify oncogenes or tumor suppressor genes in these regions.