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The objective of the study was to evaluate the contribution of chromosomal anomalies to decreased fertility in humans. A total of 782 persons (259 couples, 158 male and 106 female) with different clinical diagnoses of sterility and infertility were analysed cytogenetically. The overall frequency of major chromosomal aberration was 13.1% (103/783), which suggests that fertility or sterility problems in this population are due to chromosomal aberrations. Couples experiencing repeated spontaneous abortions, having malformed children or having sterility problems had chromosomal abnormalities in 18.0% (47/259 couples) of the population studied, and constituted chromosomal disorders occurred in couples seeking IVF and ICSI with prevalence of 22.2% (8/38 couples), especially minor mosaicism of sex chromosomes in the female partners. The prevalence of chromosome abnormalities in infertile men was 17.7% (28/158), and in subfertile females, it was 26.4% (28/106). The results could indicate an increased tendency to mosaic sex chromosome non-disjunction in humans.


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To assess the effectiveness of health services in the city of Osijek during the 1991-1992 war in Croatia, the authors followed the changes in the utilization of health services, morbidity and mortality, and completion of a vaccination plan during the 2 years of the war. They used a retrospective analysis of data from the Osijek Health Center and the Osijek County Institute of Public Health. The organization of health care during the war followed the concept of integrated health care and the instructions of the Ministry of Health. Visits to primary health care physicians decreased considerably, with a concomitant increase in disease and mortality. The plan for mandatory vaccination was not completed because of the evacuation of preschool and school children. The war changed the mode of health care use, the disease and mortality structure, and the implementation of mandatory vaccination. However, timely education and preparation of the health services to the war situation resulted in an adequate provision of health care to the population.


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Thymus tissue was found in a mature cystic teratoma in conjunction with respiratory tissues. Its immunohistochemical pattern of CD99, CD3, CD68 and cytokeratins was that of the normal thymus. The main point raised by this unusual case concerns the origin of its T lymphocytes from either a tumor (parthenogenetic origin) or a secondary colonization of the teratoma from host T cells.


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Expression of neutral glycosphingolipids (GSLs) and gangliosides in normal lymphoid tissues and cells has been studied mostly by biochemical and immunohistochemical analysis of lipid extracts separated by thin-layer chromatography. The authors used specific polyclonal antibodies in immunohistochemistry and flow cytometry to analyze the distribution of globotriaosylceramide (Gb3/Cer), globoside (Gb4/Cer), gangliotriaosylceramide (Gg3/Cer), gangliotetraosylceramide (Gg4/Cer), and gangliosides GM3 and GalNAc-GM1b in the mouse thymus, spleen, and lymph node. Immature thymocytes expressed epitopes recognized by all antibodies, except for anti-Gb4/Cer. Mature thymocytes bound only antibodies to GalNAc-GM1b Gg4Cer, and Gb4Cer. In secondary lymphoid organs, antibodies to globe-series GSLs bound to vascular spaces of secondary lymphoid organs, whereas the ganglio-series GSL antibodies recognized lymphocyte-containing regions. In a Western blotting analysis, only GalNAc-GM1b antibody recognized a specific protein band in all three organs. Flow cytometric analysis of spleen and lymph node cells revealed that B-cells carried epitopes recognized by all antibodies, whereas the T-cell GSL repertoire was mostly oriented to ganglio-series-neutral GSLs and GM1b-type gangliosides. The results of immunohistochemistry and flow cytometry were not always identical, possibly because of cross-reactivity to glycoprotein-linked oligosaccharides and/or differences between cell surface carbohydrate profiles of isolated cells and cells in a tissue environment.


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A genetic perspective of human history in Europe was derived from 22 binary markers of the nonrecombining Y chromosome (NY). Ten lineages account for >95% of the 1007 European Y chromosomes studied. Geographic distribution and age estimates of alleles are compatible with two Paleolithic and one Neolithic migratory episodes that have contributed to the modern European gene pool. A significant correlation between the NRY haplotype data and principal components based on 95 protein markers was observed, indicating the effectiveness of NRY binary polymorphisms in the characterization of human population composition and history.