karyotyping profile in male patients suffering from primary sterility associated with azospermia

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Male infertility was the result of variety of disorders which might or might not be related to each other. In asignificant proportion of cases a genetic factor or chromosome abnormality was found to be responsible.Reviewing historical literatures, chromosomal analysis was not included in tie routine work-up in cases of maleinfertility unless there was unusual clinical findings suggesting genetic problems. However, in phenotypically normal individuals there could be various significant chromosomal abnormalities that might retain over looked unless searched for. In the present study we tried to elucidate the role of genetics in infertility 20 males complaining offaillure to obtain offsprings for more than 2 years were studied. In addition to 10 normal healthy males taken as contro1. The subjects were classified into 2 groups.GROUP 1:- 10 presumably normal males.GROUP 2:- 20 males suffering from primary fertility. Clinical assessment including detailed history, semen analysis to confirm that they are azospermic and chromosomal study. Lymphocyte cultures were processed andthen stained by G-banding stain about 10metaphases were counted for each sample. The metaphases were photographedunder oil immersion objective of the microscope and karyotypes were done for the abnormal cells. Major chromosomal anomalies were detected in 6 out of 20representing 10%. The incidence was 30% in the azoospermic group. Historicalliteratures and our present study ’showed different incidencesof chromosomal anomalies, but most coincides regarding highest percentage of aberrations among the sex chromosomes. Major chromosomal abnormalities were detected in 6 (30%) out of the 20 patients. The 1O.normal0males are free from major aberrations. The aberrations in the 6 cases are KLINFILTER(5% 47,XXY) one RING Ychromosomes(5%), 3 cases (15%) short Y chromosome which could be due to deleted Y and the 6th. case presents ashort 11 and short Y that Y that seems to be deleted, chromosomes. However ,these results has to be confirmed by further investigations using insitu hybridization andmolecular genetics especially the different segments, bands and subbands concerning the Y chromosome and on a larger scale.