dissimilarity index which indicate the percentage of the peak area of the fragment (operational taxonomic unit: OTU) was used.

**Results** Two fecal samples of 1 CC infant and 14 fecal samples of 7 BA infants were obtained. Nine predominant OTUs were detected with Bst I digestion. The microbiota consisted of microbial communities of Bifidobacterium, Lactobacillales, Bacteroides, Prevotella, Clostridium clusters IV, XI, and XVIII, and Clostridium subcluster XIVa. The Bifidobacterium, Bacteroides, and Clostridium clusters were detected predominantly in CC than BA group. Lactobacillales was most predominant group in BA feces.

**Conclusions** Bacterial DNA showed marked differences in the composition of fecal microbiota in CC and BA infants. Molecular analysis of colonic microbiota using 16S rRNA gene libraries and T-RFLP might be useful to differentiate CC from BA.

**734** ASSESSMENT OF DNA DAMAGE USING COMET ASSAY AND DETECTION OF OXIDATIVE STRESS PARAMETERS IN DOWN SYNDROME

**doi:** 10.1136/archdischild-2012-302724.0734

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**Background** Down syndrome is one of the commonest numerical chromosomal aberrations. Recent studies showed that oxidative stress is an important pathological factor in Down syndrome.

**Objective** To estimate the level of oxidative stress and DNA damage in Down syndrome patients.

**Patients** and methods: Fifteen Egyptian patients clinically diagnosed and cytogenetically proven to have Down syndrome. Fifteen Egyptian healthy controls were recruited from the outpatient clinic of Clinical Genetics Department, National Research Centre. Oxidative stress parameters including total antioxidant capacity (TAC), Superoxide dismutase (SOD) enzyme activity and Malondialdehyde (MDA) biomarkers were estimated. DNA damage was determined using the alkaline comet assay.

**Results** The MDA and SOD levels in Down syndrome patients were significantly higher than control group (p<0.000 & 0.01, respectively). Total antioxidants levels were non-significantly higher than control group (p=0.54). Statistical analysis of DNA damage levels in DS patients compared to controls showed significant increased levels (p<0.000). There was a positive correlation of DNA damage levels with age in DS patients but not reaching a significant value (p=0.536). A non-significant positive correlation was detected between DNA damage levels and both MDA and TAC levels (p=0.8 & 0.37, respectively). Also a non-significant negative correlation of DNA damage levels with SOD levels was noticed (p=0.14).

**Conclusion** Oxidative stress plays a major role in DS pathogenesis.

**735** CONTRIBUTION OF ALKYLATED AGENTS IN THE CYTGENOTIC DIAGNOSIS OF FANCONI ANEMIA

**doi:** 10.1136/archdischild-2012-302724.0735

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**Background and Aims** Fanconi Anemia (FA) is an autosomal recessive disease characterized by heterogenous phenotype which includes a bone marrow failure, diverse abnormalities and increased predisposition to develop leukemia. The cytogenetic diagnosis of FA cells to bifunctional alkylating agents, resulting in greatly increased chromosomal breakage and radial stuctures induced by cross-linking agents. To estimate the sensitivity and the specificity of the Mitomycin C (MMC) and the Diepoxylbutan (DEB), two alkylating agents used in the diagnosis of the FA, we studied the chromosomal instability on 22 patients using variable types and concentrations of these alkylating (25 and 40 ng/ml of MMC, 0.1μg/ml of DEB).

**Methods** Heparanized venous blood samples were collected and were processed for the cytogenetic methodology in this study. After culture, 100 of metaphases were analysed to evaluate the frequency of chromosomal aberrations.

**Results** The MMC test at 25ng/ml was High sensitive for FA. The DEB test showed a better specificity. The study of the mitotic segregation of sexual chromosomes by FISH took away any abnormality of the segregation to cells FA.

**Conclusions** A molecular study of the senivity and the specificity of the alkylating agents used according to the group of complementation will come refine the diagnosis of FA by establishing a gold standard.