of *NFI* gene mutation. We also added the relevant literature review regarding the reported similar lesions.

45. GRANULAR CELL TUMOUR – ADENOCARCINOMA COLLISION TUMOUR OF THE OESOPHAGUS: A CASE REPORT

Kais Kasem^{1,2}, Lakshmy Nandakumar¹, Mark Appleyard¹, Mahendra Singh¹

¹Royal Brisbane Hospital, and ²Sullivan Nicolaides Pathology, Australia

We report a case of an unusual oesophageal collision tumour composed of granular cell tumour and adenocarcinoma in a 68-year-old woman. The patient had a history of Barrett's oesophagus and hiatus hernia. A 17 mm distal oesophageal nodule was discovered on endoscopic surveillance. Histologically, the excised nodule comprised an invasive 3mm well-differentiated intramucosal adenocarcinoma which showed permeation of an adjacent 1.8mm granular cell tumour and extended to a radial margin focally. The adenocarcinoma was arising in a background of Barrett's oesophagus with high-grade dysplasia. The patient was followed up closely with multiple endoscopic procedures and biopsies. The patient had no signs of recurrence 5 years after the initial diagnosis. To date, only one such collision tumour has been reported in English literature.

46. PATTERN OF CONCENTRATED HIV EPIDEMIC IN PAKISTAN

Saeed Khan, Fatin Zehra, Maria Zahid, Asif Iqbal, Noorulaine Maqsood

Dow University of Health Sciences, Karachi, Pakistan

Background: Globally the most prevalent HIV subtype is the HIV-1 subtype C. The last two decades have witnessed the concentrated epidemic of HIV in Pakistan in different high risk groups. Bioinformatics is a very useful tool to study the HIV evolutionary dynamics and to understand the route and spread of infection, infer geographical dissemination, genetic diversity and molecular scenario of the HIV epidemic in the region.

Objective: The objective of this study is to observe the Pattern of concentrated epidemic of HIV in Pakistan and to study the possible geographical relation using bioinformatics.

Methodology: Blood samples from 90 HIV infected patients were collected followed by DNA extraction, PCR amplification and sequencing of *gag* gene. We also retrieved 660 Pakistani HIV *gag* sequences from Los Alamos HIV database. The sequences were then aligned with the reference sequences of different subtypes (A to K) using Mega 5. For geographical relationship sequences of the predominant subtype were also aligned with sequences of the same subtype of different countries. Phylogenetic trees were constructed on the basis of *gag* using neighbor joining method using Mega 5 software.

Result: Among the new samples 48 (64%) were subtype A, 18 (24%) subtype C, 7 (11%) subtype G and 1 (1%) were subtype D, while the archived sequences from database showed almost 100% of subtype A-1. Similarly the trees based on geographical relation Pakistani sequences showed close clustering to neighboring countries Afghanistan, India and African countries South Africa, Kenya and Rwanda.

Conclusion: Previous studies show that HIV-1 subtype A is common in our region but our current observation indicates that other subtype beside subtype A, such as C, D and G are also present which is indicating a gradual viral evolution in Pakistan and a possible entry of different subtypes from different regions.

47. DRUG RESISTANT HIV IN PAKISTAN

Saeed Khan, Fatin Zehra, Maria Zahid, Noor-ul-Aine Maqsood
Dow University of Health Sciences, Pakistan

Background: Pakistan has witnessed a transition from low prevalence to a country with concentrated epidemic in high risk group. Antiretroviral therapy has reduced mortality and morbidity of patients infected with HIV-1. Five types of drugs have been found to be effective in antiretroviral therapy namely reverse transcriptase inhibitors, non-reverse transcriptase inhibitors, infusion inhibitors, fusion inhibitors and protease inhibitors. Random mutations mainly of two types, major and minor in HIV genome lead to resistance against these drugs. Application of bio-informatics tools on researches regarding HIV treatment may help in strengthening the anti-retroviral therapy (ART) by enhancing our understanding of HIV drug resistance and its prevention.

Objective: To determine HIV drug resistance in Pakistan using bioinformatics tools.

Method: Reverse transcriptase gene sequences were retrieved from Los Alamos database and were entered into Stanford HIV database from which data for drug resistance and mutations were analyzed.

Results: 93 percent of sequences showed no major or minor mutations hence virus would be sensitive to drugs namely lamivudine, abacavir, zidovudine, stavudine, didanosine, emtricitabine, tenofovir, efavirenz, etravirine, nevirapine, rilpivirine. Rest of the sequences showed a major mutation Y115F that endowed virus with low to intermediate resistance against lamivudine and emtricitabine.

Conclusion: Majority of *rt* sequences retrieved did not have major or minor mutations resulting in a drug sensitive virus. Data suggests that infection is new in the region thus virus is still sensitive to most of the drugs. Although low to intermediate resistance is observed, it is not severe but if infection is not controlled it might result in mild to completely resistant strains.

48. MYCOBACTERIUM TUBERCULOSIS DRUG RESISTANCE IS INCREASING IN PAKISTAN

Saeed Khan, Waleed Yousaf, Uzma Mazahir, Ramsha Khan, M.R. Khanani

Dow University of Health Sciences, Karachi Pakistan

Introduction: Tuberculosis is the most life threatening air born bacterial infection. According to the WHO about 2 billion people worldwide have been infected by Mycobacterium tuberculosis complex. PCR is recognized as rapid, specific and sensitive diagnostic technique as compared to the conventional methods. TB can be controlled through early diagnosis followed by effective treatment. Drugs Rifampicin and Isoniazid are commonly used for treatment, but their excessive use has led to the emergence of mutations in the genome of MTB.