SKIN CANCER (OTHER THAN MELANOMA)

IDENTIFICATION OF IDENTICAL LONG COPY NUMBER VARIATIONS IN MATCHED BLOOD AND SKIN IN MYCOSIS FUNGOIDES AND SEZARY SYNDROME USING SNP ARRAYS

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Introduction: Genome-wide technologies have been increasingly used in cutaneous T cell lymphoma (CTCL) for the detection of driver mutations. However, there is lack consensus in mutations identified, especially in mycosis fungoides (MF) which was thought to be due to the low tumour rate in skin lesions.

Objectives: To identify copy number variations (CNVs) using SNP arrays to understand immunopathogenesis and to make clinicopathological correlation.

Materials and Methods: SNP arrays were performed on 47 stored DNA samples extracted at the time of diagnosis (skin only=25, paired skin+blood) in 36 patients (MF=25, Sezary syndrome(SS)=11) using Infinium Core-24 BeadChip array. Blood stage in the paired samples was B0a=3, B0b=1,B1b=3, B2a=1, B2b=3. Clinicopathological correlation was made following CNV analysis.

Results: Long CNVs were identified in 15/25 skin samples. Sixty per cent of the skin samples with monoclonal TCR had long CNVs whereas none in polyclonal samples (p=0.004).
Amongst 11 paired skin and blood samples, 3 paired samples demonstrated identical long CNVs in paired skin and blood which included two of 4 SS patients tested and one of 7 MF patients (stage IB) who progressed to stage IVA1 at a later stage.

Conclusions: Our study observed identical long CNVs in paired skin and blood samples causing significant defects in genomic function in both SS and one early stage MF patients with B1b class suggesting that the same tumour clones was present in both blood and skin regardless of the clinical stage or level of blood involvement. Paired blood sample has been routinely used as a control to exclude germline mutation in previous exome sequencing

studies in MF and we may have been excluding significant mutations as both were present in blood and skin. Further studies on larger paired samples and using different germline samples will help us to understand the origin and immunopathogenesis of CTCL.