Psoriasis decease

Psoriasis is a chronic, complex, inflammatory, autoimmune condition that causes the rapid build-up of skin cells (epidermal keratinocytes). It affects 2-3% of the population, and the involvement frequently occurs in 5-10% of the patients. Factors such as genetic and environment contribute to the risk of being infected with psoriasis (Constantinides et al., 2014).

This build-up of cells causes scaling on the skin's surface. Inflammation and redness around the scales are fairly common. Typical psoriatic scales are whitish-silver and develop in thick, red patches. Sometimes, these patches will crack and bleed. Psoriasis is the result of a sped-up skin production process. Typically, skin cells grow deep in the skin and slowly rise to the surface. Eventually, they fall off. The typical life cycle of a skin cell is one month. Scalp psoriasis is a common skin disorder that entails the formation of mild, intermittent, scaly, red and patchy lesions on the scalp to the total involvement of the scalp. It can pop up as a single patch or several, and can even affect your entire scalp. It can also spread to your forehead, the back of your neck, or behind and inside your ears. There may be a connection between skin plaques and joint pains which are some of the signs and symptoms of psoriatic arthritis, a condition that can be related to psoriasis.

Psoriasis symptoms differ from person to person and depend on the type of psoriasis. Areas of psoriasis can be as small as a few flakes on the scalp or elbow or cover the majority of the body. The most common symptoms of plaque psoriasis include: red raised inflamed patches of skin, silver-white scales or plaques on the red patches, dry skin that may crack and bleed, soreness around patches, itching and burning sensations around patches, thick pitted nails, painful swollen joints. In a recent study, genetic variances were noted between the normal and skin psoriatic cells in comparison to scalp psoriasis.

They were found similarity in the gene expression of many immunological molecules. In scalp LS genes most significantly up-regulated in scalp LS include S100A12, DEFB4, IL1F9 (coding IL-36?), and IL8 (all >20-fold increased over scalp NL) and all genes regulated by IL-17, such as OASL, KYN4, PI3, CCL20, S100A9, LCN2, CXCL9, IFI27, and OAS1. Within gene comparisons, we found that background NL scalp of psoriasis had gene expressions that were intermediate between LS and N scalp, implying low levels of inflammation in this tissue. In skin psoriasis, many other genes are highly represented in the skin transcriptome. Differences were found in LCN2, KRT6 are all highly up-regulated in psoriasis vulgaris LS, these genes, which show constitutively high expression in scalp NL and N biopsies, are up-regulated to a lesser degree in LS scalp biopsies.

In contrast, scalp tissue had lower expression of CD1A and CD207/langerin (clusters 2 and 3), which are markers of LCs. LCN2 gene encodes lipocalin-2, a protein involved in innate immunity that sequesters iron and consequently limits bacterial growth. Lipocalin-2 is expressed in neutrophils, monocytes, and keratinocytes; its serum levels are increased in patients with psoriasis and correlates with disease severity. KLK6 encodes a serine protease with activity against extracellular matrix proteins, such as fibronectin, laminin, vitronectin, and collagen, and is elevated in both PsA synovial fluids and psoriatic plaques. Thus, genes that are induced by TNFa, IL-17, IL-22, interferons, and other inflammatory cytokines are generally very similar in scalp and skin psoriasis.

However, normalized GSEA enrichment scores of all disease transcriptome genes were slightly higher in skin LS than scalp LS, a finding which may be explained by the constitutive expression of some psoriatic transcriptome genes in the follicular epithelium of NL scalp. To estimate variations in pathway activity in the scalp psoriasis transcriptomes, we performed GSVA. Scalp transcriptomes were particularly enriched with ‘Basal vs upper epidermis’, ‘Melanocytes’, ‘Fibroblasts’ and ‘CD4+ T-cells’ and profiles of keratinocytes activated by INF? or IL-13 and myeloid DCs induced by IL-17. Interestingly, the enrichment of ‘negative regulators’ and ‘epigenetically regulated psoriasis-related genes’ was also observed.

Skin transcriptomes were associated with significant enrichment of gene-sets related to ‘Epidermal Differentiation Complex’, ‘Cornified Envelope’, ‘Keratinocytes’, ‘T-cells’, ‘PBMCs’, ‘Macrophages’, ‘Mature DCs’, ‘Immature DCs’, ‘Th17’, ‘Th22’, and gene-sets related with TNFa/IL-17/IL-22-induced keratinocyte responses. When comparing immune gene-sets by GSEA, scalp psoriasis resembles skin psoriasis and to a much lesser extent the murine models. The STAT3, Tie2, and TGF? transgene models and the imiquimod-induced model represent murine models that express some inflammatory pathways that are present in psoriasis vulgaris, but with lower fidelity in the range of pathways that are expressed in human disease. In our case, IL-23-induced mouse transcriptome showed the greatest resemblance to human skin and scalp psoriasis. Even if the scalp is considered more similar to the skin of animal models, psoriasis remains a disease of the IFL skin even in the scalp. To validate microarray findings, we performed RT-PCR. Expression of IFN-?, IL-23p19, IL-12/23p40, IL-17, and IL-22 was higher in LS compared with NL scalp psoriasis samples, as previously described for LS psoriasis We also analysed IL-20 mRNA, a cytokine produced by inflammatory dendritic cells (iDCs) that affects keratinocyte activation and proliferation and found it to be significantly higher in LS than NL scalp samples. Higher mRNA expression of iNOS, an inducible nitric oxide synthase produced by Tip-DCs, was also observed in LS scalp, similar to previous reports about skin psoriasis. We also analyzed the immune-phenotype profiles of scalp and skin psoriasis compared with AA and AD.

Scalp psoriasis showed a Th1/Th17 activation profile, similar to skin psoriasis, but with more

Th1 and less Th22 activation. We also found significant differences compared to AA, which shows Th1/Th2 and IL-23 polarization and a lack of Th17 or Th22, and AD, which shows a higher expression of Th2/Th22 cytokines These studies have examined scalp psoriasis from a gene level, but information from a protein level is missing even in the light that various proteins and genes are implicated biomarkers for psoriasis. S100A8-S100A9 protein complex mediates psoriasis by regulating the expression of complement factor C3 (Schonthaler HB et al., 2013). It has become apparent that any stimuli that affect the balance between complement activation and repression can cause inflammation (Markiewski&Lambris, 2007). We propose that induction of C3 by S100A8 and S100A9 can lead to 'primed' keratinocytes and subsequently to uncontrolled immune cell activation, angiogenesis, hyperproliferation of keratinocytes, and finally to the chronic inflammation that typifies psoriasis (Schonthaler HB et al.,2013).

Exploration of the differences particularly in a protein level will aid in the generation of specific targeted medication therapy and enhance the efficacy of the therapy process after understanding the underlying pathomechanisms of scalp psoriasis. The immunohistochemistry of S100A8, CD11C, CD83, CD4 and IL-23 especially their roles in the pathways of IL-17 and TNF-a are important biomarkers in the measurement and diagnosis of disease during clinical course. Our aim is to determine the cellular and molecular phenotype of scalp psoriasis by performing a comparative analysis of scalp and skin using lesional and nonlesional samples from 20 Caucasian subjects with untreated moderate to severe psoriasis and significant scalp involvement and 10 control subjects without psoriasis.

Our results suggest that even in the scalp, psoriasis is a disease of the inter-follicular skin. The immune mechanisms that mediate scalp psoriasis were found to be similar to those involved in skin psoriasis. However, the magnitude of dysregulation, the number of differentially expressed genes, and enrichment of the psoriatic genomic fingerprint were more prominent in skin lesions. Furthermore, the scalp transcriptome showed increased modulation of several gene-sets, particularly those induced by interferon-gamma, compared with that of skin psoriasis, which was mainly associated with activation of TNFa/L-17/IL-22-induced keratinocyte response genes. We also detected differences in expression of gene-sets involving negative regulation, epigenetic regulation, epidermal differentiation, and dendritic cell or Th1/Th17/Th22-related T-cell processes.