A04-5 Study for specific gene expressions in keloids lesion: the comparison with adjacent normal dermis

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Aberration of normal wound healing processes is suspected in the pathogenesis of hypertrophic scars and keloids. Numerous treatment options have been described, but there is no single effective therapeutic regimen for the treatment of hypertrophic scars and keloids (Seifert et al., 2009). Furthermore, the molecular mechanisms and characteristic gene expression of keloids remains poorly understood.

To elucidate the molecular alterations and characteristic gene expressions of keloids, we performed the microarray analysis using mRNA extracted from two keloids tissue samples. For their control, we used mRNA extracted from the adjacent normal dermis of each keloids lesion. It revealed the many changes of extracellular matrix protein mRNA in keloids lesion. Many types of collagen—fibronection, laminin, and glycosaminoglycans were up-regulated in the keloids lesion. As we have reported previously (Naitoh et al., 2005), some osteogenesis and chondrogenesis relating factors were up-regulated. We also performed microarray analysis using cultured cells obtained from keloids lesion and adjacent normal skin. Within the molecules showing different expression levels between the tissues of keloids lesion and normal dermis, some molecules did not retain the differences under cultured condition.

We think that ideal controls are tissue samples from identical person and from adjacent area of the keloids lesion. In this context, the result obtained from this study will be great help to elucidate the pathogenesis of keloids.