Background: Epithelial-mesenchymal transition (EMT) is a biological process, in which epithelial cells lose their phenotypic characteristics such as cell polarity and cell-cell contact structures, and acquire mesenchymal traits. Although EMT has been known to play important roles during cutaneous wound healing, and invasion and metastasis of squamous cancer cells, the molecular mechanisms regulating EMT in squamous epithelial cells still remain elusive.

Methods: In this study, we used transforming growth factor (TGF)-β1-induced EMT of human keratinocyte HaCaT cells as an in vitro model. Fluorescence-conjugated phalloidin was used to detect filamentous (F)-actin. We performed quantitative RT-PCR and chromatin immunoprecipitation (ChIP) to analyze the mRNA levels and histone modifications respectively.

Results: HaCaT cells were changed into the elongated fibroblast-like cell morphology at 48 h after TGF-β1 treatment. The formation of actin stress fibers, which is indicative of EMT, was confirmed by F-actin staining. Quantitative RT-PCR analysis revealed that TGF-β1 transcriptionally activated a subset of the EMT transcription factors such as SNAI2 and TWIST1, and partially induced a decrease in the epithelial phenotypic genes and an increase in mesenchymal trait genes. We further found that keratin 13 (KRT13) was drastically suppressed at a relatively late time point after the addition of TGF-β1. ChIP analysis demonstrated that the modification patterns at lysine residues of histone H3 were dynamically changed and the RNA Polymerase II occupancy was reduced in the KRT13 promoter during EMT.

Conclusions: These data indicate that the EMT program induced by TGF-β1 suppresses KRT13 gene expression through modulation of chromatin state at the promoter region in HaCaT cells.