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〈シンポジウム〉

第49回日本香粧品学会（2024）・シンポジウムII「最新技術で皮膚を観る～明日の肌のサイエンス～」

1 細胞解像度で観る皮膚・毛包の発生

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Visualizing the Formation of Skin and Hair Follicles with Single-Cell Resolution

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Abstract

The skin and hair follicles are pioneering model organs in the field of stem cell biology. Due to their unique ability to undergo cyclical regeneration throughout life, stem cells were identified in these tissues early on, thereby contributing significantly to the development of the field. However, the developmental origin and inductive processes that give rise to hair follicle stem cells remain insufficiently explored. To address this, we established a novel, data-driven analytical framework with single-cell resolution that integrates long-term, three-dimensional (3D) live imaging with single-cell transcriptomics. This approach enabled us to reconstruct the complete developmental trajectory of the mouse hair follicle epithelium, capturing dynamic changes in both cell lineage and gene expression with high spatiotemporal resolution. As a result, we established a four-dimensional developmental cell lineage atlas. Our analysis uncovered a previously unrecognized developmental origin of hair follicle stem cells, distinct from conventionally proposed models. Furthermore, we discovered a new mode of hair follicle morphogenesis, which we termed the "telescope model." This model explains how compartmentalization within the organ and stem cell fate specification can occur simultaneously, offering a new perspective on how tissue architecture and stem cell niches form during development. In the presentation, I introduced these findings along with our ongoing efforts to further investigate the mechanisms of hair follicle development and stem cell specification. I also discussed the potential applications of these fundamental discoveries in the context of cosmetic and skincare product development, demonstrating how basic research can inform and inspire innovation in applied fields.

Key words: hair follicle development, stem cell formation, live imaging, single-cell transcriptomics.