AI-ASSISTED INTEGRATIVE TRANSCRIPTOMIC ANALYSIS SUPPORTS MECHANISTIC DELINEATION OF NODULAR AND EXTENSIVE KELOID SUBTYPES WITH THERAPEUTIC IMPLICATIONS

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Running Title
AI-assisted integrative transcriptomic analysis supports mechanistic delineation of nodular and extensive keloid subtypes with therapeutic implications

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BACKGROUND

Keloids are heterogeneous fibrotic skin disorders in which nodular and extensive forms differ in growth behavior, recurrence, and treatment response. While transcriptomic studies have identified subtype-specific signatures, the mechanistic architectures underlying these divergent phenotypes remain unresolved.

OBJECTİVE

To achieve a system-level dissection of nodular and extensive keloids to support subtype-adapted treatment using AI-assisted transcriptomic analysis.

METHODS

We reanalyzed published transcriptomic data from primary dermal fibroblasts of nodular, extensive keloids and healthy skin using OCEAN (Omics-to-Clinical Evidence & Action Navigator), an AI-assisted framework integrating differential expression, pathway enrichment, and protein–protein interaction networks into coherent mechanistic architectures with traceable evidence. Cultured fibroblasts from normal skin biopsies or extensive/nodular keloids were used for biological experiments aimed to validate IA underlined pathways and new pharmacological target molecules.

RESULTS

AI-assisted analysis confirmed known subtype differences, including a dominant extracellular matrix program in nodular keloids and a more inflammatory profile in extensive keloids. System-level integration reconstructed distinct mechanistic architectures: nodular

keloids displayed a compact, self-reinforcing fibrotic network integrating TGF-β signaling, hypoxia adaptation, transcriptional stabilization, and autocrine inflammation, consistent with reduced therapeutic responsiveness. In contrast, extensive keloids showed an adaptive, expansion-oriented program marked by immune responsiveness, stromal plasticity, angiogenic signaling, and metabolic stress adaptation, revealing subtype-specific therapeutic vulnerabilities.

CONCLUSİON

AI-assisted integrative transcriptomics transforms descriptive omics profiles into clinically actionable mechanistic insight, enabling precision stratification and mechanism-informed therapeutic targeting in keloid disease.