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Data Article

Dataset on gene expression profiling of multiple murine hair follicle populations

Anders Patrik Gunnarsson [a,b], Rikke Christensen [a], Jian Li [c,d], Uffe Birk Jensen [a,b,*]

[a] Department of Clinical Genetics, Aarhus University Hospital, 8200 Aarhus, Denmark
[b] Institute of Clinical Medicine, Aarhus University, 8000 Aarhus, Denmark
[c] The Key Laboratory of Developmental Genes and Human Disease, Ministry of Education, Institute of Life Sciences, Southeast University, Nanjing, China
[d] Department of Biomedicine, Aarhus University, 8000 Aarhus, Denmark

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ABSTRACT

The murine hair follicle contains several different keratinocyte progenitor populations within its compartments. By using antibodies against CD34, Itgα6, Sca-1 and Plet-1, we have isolated eight populations and compared their Krt10 and Krt14 expressions using fluorescence microscopy. This improved panel was used in our associated article http://dx.doi.org/10.1016/j.scr.2016.06.002 (A.P. Gunnarsson, R. Christensen, J. Li, U.B. Jensen, 2016) [1] and the present dataset describes the basic controls for the FACS. We also used imaging flow cytometry to visualize the identified populations as control. A more detailed analysis of the global gene expression profiling is presented, focusing on the pilosebaceous unit. Murine whole-mounts were stained for heat shock protein Hspa2, which is exclusively expressed by keratinocytes with low or no expression of the four selection markers (*IRK*). Whole-mount labeling was also conducted to visualize Krt79 and Plet-1 coexpression within the hair follicle and quantification on the distribution of Krt79 positive keratinocytes is presented.

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* Corresponding author at: Department of Clinical Genetics, Aarhus University Hospital, Brendstrupvej 21C, 8200 Aarhus N, Denmark.
E-mail address: uffejens@rm.dk (U.B. Jensen).

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Specifications Table

Subject area	*Biology.*
More specific subject area	*Epidermal stem cells.*
Type of data	*Images (fluorescence microscopy), diagrams.*
How data was acquired	*Images were acquired using confocal LSM 710 and Leica Letiz DMRB microscopes. Venn diagrams were generated using GeneSpring GX (Agilent) from global microarray gene expression profiling.*
Data format	*Raw, merged, filtered and analyzed.*
Experimental factors	*Keratinocytes were isolated from murine dorsal skin after trypsinization for 16 h at* 4 °C. *Murine tail whole-mounts were obtained by keeping the skin in PBS with 5 mM EDTA for 5 h and* 37 °C.
Experimental features	*Murine tail whole-mounts and isolated populations were stained and visualized using fluorescence microscopy. Differently expressed genes were obtained from microarray data using GeneSpring GX software and ANOVA with Benjamin-Hochberg multiple correction (p-value < 0.01).*
Data source location	*AROS Biotechnology (Skejby, Denmark).* *Aarhus University (Aarhus Denmark).*
Data accessibility	*Data is within this article.*

Value of the data

- To give further insight on how the murine hair follicle keratinocytes can be categorized into different populations.
- To deepen the knowledge on how the populations relate to each other by their gene expression profiles.
- To understand where the different hair follicle populations are located.

1. Data

Dorsal keratinocytes were isolated from female C57Bl/6 mice in the age of 7–9 weeks and sorted using flow cytometry. Cells were stained with conjugated antibodies and visualized by fluorescence microscopy. Global microarray data was used to generate Venn diagrams, which show the number of shared differently expressed genes (DEGs) between the different populations and a reference. See Figs. 1–6.

2. Experimental design, materials and methods

2.1. Isolation of murine dorsal keratinocytes

Female 7–9 weeks old C57Bl/6 mice were sacrificed by cervical dislocation. Their backs were shaved using razor machine and the dorsal skin peeled off with sterile forceps and scissors. The dermal fat was scraped away using sterile scalpel and the skin was disinfected in 1% Betadine for 30 s, 70% EtOH for 30 s and washed in PBS. With the epidermal side facing upwards, the skins were kept floating on 0,25% trypsin supplemented with 5 mM EDTA over night at 4 °C. Following day, the epidermal cells were gently scraped away from dermis using sterile scalpels into chilled DMEM with 10% FCS and 100x penicillin-streptomycin, centrifuged at 200 g, 4 °C for 10 min and washed in PBS supplemented with 0.1% Bovine Serum Albumin.