The post-apoptotic fate of RNAs identified through high-throughput sequencing of human hair.

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Authors: Gloria K Lefkowitz, Anandaroop Mukhopadhyay, Christopher Cowing-Zitron, Benjamin D Yu

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Public Summary:
Unlike many tissues, hair regenerates multiple times during the life of an individual. The external hair is composed of dead cells that have undergone a process of differentiation. The linear growth of hair represents different stages of hair development such as the tip of the hair shaft contains the earliest cells that were produced during the new regenerative phase and the base of the hair shaft contains the most recent cells. New RNA-sequencing technologies developed by many California based companies provided us a new way to study these cells. In this study, we discovered that the history of these hair cells could be analyzed using RNA sequencing. The approach allow us to understand what genes are activated in cells which are just beginning regeneration of the hair and which genes are activated when the hair ceases to grow. This discovery may have important implications for understanding hair disease in addition to many systemic diseases that may affect hair.

Scientific Abstract:
The hair of all mammals consists of terminally differentiated cells that undergo a specialized form of apoptosis called cornification. While DNA is destroyed during cornification, the extent to which RNA is lost is unknown. Here we find that multiple types of RNA are incompletely degraded after hair shaft formation in both mouse and human. Notably, mRNAs and short regulatory microRNAs (miRNAs) are stable in the hair as far as 10 cm from the scalp. To better characterize the post-apoptotic RNAs that escape degradation in the hair, we performed sequencing (RNA-seq) on RNA isolated from hair shafts pooled from several individuals. This hair shaft RNA library, which encompasses different hair types, genders, and populations, revealed 7,193 mRNAs, 449 miRNAs and thousands of unannotated transcripts that remain in the post-apoptotic hair. A comparison of the hair shaft RNA library to that of viable keratinocytes revealed surprisingly similar patterns of gene coverage and indicates that degradation of RNA is highly inefficient during apoptosis of hair lineages. The generation of a hair shaft RNA library could be used as months of accumulated transcriptional history useful for retrospective detection of disease, drug response and environmental exposure.