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Label-free screening of niche-to-niche variation in satellite stem cells using functionalized pores MATTHEW R. CHAPMAN, Biophysics Graduate Group, UC Berkeley, KARTHIK BALAKRISHNAN, Dept. Mechanical Engineering, UC Berkeley, MICHAEL J. CONBOY, Dept. Bioengineering, UC Berkeley, SWOMITRA MOHANTY, Dept. Mechanical Engineering, UC Berkeley, ERIC JABART, Dept. Bioengineering, UC Berkeley, HAIYAN HUANG, Dept. Statistics, UC Berkeley, JAMES HACK, Dept. Mechanical Engineering, UC Berkeley, IRINA M. CONBOY, Dept. Bioengineering, UC Berkeley, LYDIA L. SOHN, Dept. Mechanical Engineering, UC Berkeley — Combinations of surface markers are currently used to identify muscle satellite cells. Using pores functionalized with specific antibodies and measuring the transit time of cells passing through these pores, we discovered remarkable heterogeneity in the expression of these markers in muscle (satellite) stem cells that reside in different single myofibers. Microniche-specific variation in stem cells of the same organ has not been previously described, as bulk analysis does not discriminate between separate myofibers or even separate hind-leg muscle groups. We found a significant population of Sca-1+ satellite cells that form myotubes, thereby demonstrating the myogenic potential of Sca-1+ cells, which are currently excluded in bulk sorting. Finally, using our label-free pore screening technique, we have been able to quantify directly surface expression of Notch1 without activation of the Notch pathway. We show for the first time Notch1-expression heterogeneity in unactivated satellite cells. The discovery of fiber-to-fiber variations prompts new research into the reasons for such diversity in muscle stem cells.

Matthew Chapman
Biophysics Graduate Group, UC Berkeley

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