Patterns of gene expression in microgravity

Agnese Po¹, Alessandro Giuliani², Alessandra Cucina^{3,4}, Angela Catizone⁵, Giulia Ricci⁶, Martina Chiacchiarini¹, Marco Tafani⁷, Elisabetta Ferretti⁷, and Mariano Bizzarri^{7,8}

- 1. Department of Molecular Medicine, Sapienza University, Rome, Italy
- 2. Environment and Health Department, Istituto Superiore di Sanità, Rome, Italy
- 3. Department of Surgery "Pietro Valdoni", Sapienza University, Rome, Italy
- 4. Azienda Policlinico Umberto I, Rome, Italy

5. Department of Anatomy, Histology, Forensic-Medicine and Orthopedics, Sapienza University, Rome, Italy

6. Department. of Experimental Medicine, Università degli Studi della Campania "Luigi Vanvitelli", Naples, Italy

7. Department of Experimental Medicine, Sapienza University, Rome, Italy

8. Systems Biology Group Lab, Sapienza University, Rome, Italy

Abstract

Cells growing in microgravity undergo a reversible morphology switch, causing the appearance of two distinct functional and morphological phenotypes in a former homogeneous cell population. Despite the dramatic splitting into an adherent-fusiform and a floating-spherical population, cell transition does not involve a significant change in the gene transcription profile, as highlighted by the substantial invariance of their respective Pearson's correlation coefficients. Morphological and functional changes we observed among the different phenotypes emerging in microgravity are adaptive modifications - as cells promptly recover their native phenotype when placed again into a normal gravity field - and do not alter the internal gene coherence that is highly preserved during microgravityenacted transition. Nonetheless, biophysical constraints are required to drive phenotypic commitment in an appropriate way, given that absence of gravity foster cells to oscillate between different attractor states, thus preventing them to acquire a single, well-defined differentiated phenotype. This is a proof-of-concept of "genome plasticity" that supports even very different phenotypes by adopting a coordinated 'profile preserving' modifications. The existence of a relatively large and stable 'attractor state' governing gene expression allows for the establishing of a potentially very useful metrics to follow gene expression regulation.