**Cell-cell adhesion, ECM topography and propensity of ECM proteolysis dictate the migration pattern of cancer cell collectives**

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Cell migration is associated with many biological processes including morphological devel- opment, tissue formation, wound healing, and disease promoting processes like local invasion of cancer cells, leading to metastasis. As is true for many other biological processes, the cancer metastatic cells utilize various components of cellular machinery and exhibit different invasion patterns while migrating from one place to the other. Extracellular matrix (ECM) associated with the tumour population has been demonstrated to play a significant role in promoting can- cer progression. While several of the studies have proven the role of ECM in influencing various aspects of cancer cell migration, how the topological properties of ECM dictate the cell migra- tion pattern is incompletely understood. Moreover, the combined effect of cell-cell adhesion, as well as motility and proteolytic activity of individual, constituent cells on the invasion pattern of tumour is also debatable. In this work, we present a simple, multi-level, hybrid computational model of migration of cancer cell collectives by integrating several dynamical aspects, including ECM dependent MMP secretion, MMP diffusion, ECM degradation by MMP and active cell motility. The cells are modelled as self-propelled entities with intrinsic motility and polarization. Influence of neighbouring cells on cell polarization and cell-cell adhesion dynamics are also ex- plicitly modelled in this model. The results obtained from this quantitative model suggests that inter-cell signalling, MMP mediated ECM degradation and topology of ECM fibrils collectively dictate the migration pattern of the cancer cells. This work provide new quantitative insights into how the cancer cells choose different migration patterns, including individual migration, collective migration and amoeboid migration under different microenvironmental conditions.