FUNDING PROGRAM FOR NEXT GENERATION WORLD-LEADING RESEARCHERS

Project Title: Identification of the cancer recurrence/metastasis related non-coding RNAs and clarification of their mechanism	
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1. Background of research

Previous studies reported that isolated tumor cells in bone marrow from cancer patients showing EMT and cancer stem cell like phenotype is intimately associated with recurrence or metastasis. Recently, B. Vogelstein et al. reported that clonal population that give rise to distant metastasis are represented within the primary carcinoma, but clones are genetically evolved from the original parental, non-metastatic clones (Nature 2010). Therefore, it is postulated that cancer cells might acquire the genomic alteration (mutation) during metastasis or only clonal population with specific driver mutations might be able to form metastasis.

2. Research objectives

Not all isolated tumor cells in bone marrow can generate metastasis. We will identify driver and passenger mutations existing in cancer cells from recurrence/metastasis (+) patients specifically, and will validate those alterations in another subgroup of GI tract cancers. Then, we will perform comprehensive analysis among mutations in cancer cells from primary site to metastatic site via bone marrow by super-computational analysis.

3. Research characteristics (incl. originality and creativity)

1) we will focus on recurrence related mutations in cancer cells in bone marrow specifically as well as cancer cells from primary and metastatic site by using of NG sequencer. 2) Mutations not only in coding genes but non-coding RNA including lincRNAs will be examined in this study. 3) The super-computational analysis will dissolve the mechanism of metastasis or recurrence comprehensively by using of whole driver and passenger mutations from primary site to metastatic site via bone marrow. 4) Then, we will measure expressions of those genes or ncRNA with mutation for predicting recurrence clinically.

4. Anticipated effects and future applications of research

Genomic mutation is considered to be a robust and a stable alteration in comparison to the transcriptional level examination. Therefore, we will be able to predict the recurrence or metastasis precisely and clinically applicable. While, genomic alterations in host side cells will provide a clew to protect metastasis after the curative operation. The identification of the bona-fide metastasis related driver mutation will allow us to select the high risk patients for recurrence, which reduce the wasted medical expenses and will provide a golden opportunity to have a business chance to develop the molecular target drugs to eradicate cancer metastasis.