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IMPACT OF DEPLOYING A GENETIC APPROACH TO STEM CELLS OPENS-UP NEW FACETS IN THE BLANK SLATES OF OUR BODY

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Since the dawn of the Post-Genomic era (25 years back), applying a genetic approach to solving various intricate problems/issues in research has taken-off even more swiftly than ever before. Spatio-temporal cues defined for certain critical components in a particular developmental pathway (involved in causing/progression of certain disease) provide a firm basis for detecting the order, hierarchy and "switching-off or on" of genes that regulate it. The various time-points, at which genes are switched on/off, clearly determines the fate of what a cell does in terms of being functional or non-functional, due to disruption of that specific pathway. Recent research-work in this area (Bhojwani, 2015) provides strong evidence, toward identifying such components (associated with Wnt-signaling involved in Colorectal Cancer-CRC disease). These crucial elements indeed determined the genetic transformation of a "blank-slate" ("cells of origin" and/or putative "cancer stem cells") or "primitive-state" epithelial cells to an intermediate adenoma/polyp (dyspastic), and later to a proliferative (hyperplastic) or cancerous (neoplastic) state. The idea is to re-iterate the power of genetics, in solving and filling the missing links of any developmental pathway involved in progression of a disease (in this case, CRC). A critical temporal requirement of certain molecules [Caesin-Kinase I (CKI) and Human-Discs-large (hDlg)] was finally established and these proteins were identified as "early" and "late" acting molecules respectively, in a very crucial developmental event, that basically transforms "polyps" to full-fledged "carcinomas" (epithelial cancers) in COLORECTAL tumors. The detection of these genetic and developmental parameters, served as a focal-point and a prominent diagnostic feature, for detection of effects, ie. gain/loss of other components involved during progression of CRC disease. Coincidentally, the chromosomes on which these genes reside have been found to be dense and rich in SNPs (hot-spots), the details of which were published in a separate report (Patidar & Bhojwani, 2013). This work harnessed the potential of Genetics, Developmental Biology and Bio-Informatics tools to solve a long-standing puzzle in pin-pointing some genetic factors that were critically involved in the progression of CRC disease. The report has created enough impact, in terms of authentically suggesting, that it is only when we deploy a combinatorial approach towards certain complicated biological problems, can we successfully unveil the underlying mechanisms in greater details. However, it is now conceived that, at the heart of every tumor lies a rare sub-population of cells (Cancer Stem Cells-CSCs), which give rise to most of the Cancers and are now the targets of investigation. Since no definitive markers or efficient labeling tools are available, this population of cells still remains elusive in both cancer and stem cell biology. Therefore, it would be critical to understand molecular differences between stem cells and cancer cells, which might be helpful in providing novel insights into the mechanism of tumorigenesis as well as potential therapeutic targets, in foreseeable future. We have come a long way in the stem cell advances over time. Very recent breakthroughs include: (a) The tuning and genetic re-programming of stem cells (iPS cells) by a handful of genetic factors (Takahashi et al, 2006, 2007; discussed in Bhojwani, 2008) and; (b) The transformation of cancerous cells to normal cells by reversing the genetic changes involved and also restricting the awry cancerous cells by using microRNAs (http://yournewswire.com/breakthrough-scientists-find-way-to-change-cancer-cells-into-healthy-cells/). My talk would shed light on how we could intelligently utilize these efficient tools together, to attack the "Bad seeds" in ways to cure the myriad diseases, like Cancer.

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