



Exosomes/Microvesicles: Novel Mechanisms of Cell-Cell Communication

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1001 Plasma extracellular vesicles in chronic stress and functional link to epithelial cell migration and wound repair

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Background: Repair after injury or wound and cellular stress response are related processes with poorly understood mechanisms and limited therapies. We hypothesized that circulating extracellular vesicles (EVs) from patients with chronic stress-associated gastro-intestinal dysfunction could transmit stress response signals with functional roles in cell repair.

Methods: Plasma EVs from Irritable Bowel Syndrome patients and controls were isolated (size exclusion chromatography), EV-associated CD9, lysosyme, and integrins were characterized (immunogold electron microscopy). Patients versus controls of differential blood metabolites were used to generate interaction networks. Migration capacity of colon epithelial cells CRI-1790 in response to α -WASP and serum stimulation, with or without lysosyme and CXCR4 ligand CXCL12, was examined (quantitative fluorimetry; scratch wound). Immune response related miRNAs and proteins in cells which survived post injury were quantitated (NanoString).

Results: Plasma EVs from patients and controls contained Lys, Mucin1, Mucin2, and lysosyme. Differential blood metabolites analysis revealed pyridoxal 5 phosphate salvage, cellular movement, assembly and organization of the networks driven by membrane associated, CD9 and CD9. Lysosyme connected to the network via Ubiquitin and Act. Lysosyme and CXCL12 induced CRI-1790 cell migration following injury and stimulation. NanoString analysis of immune miRNAs (172) and proteins (30) from cells which survived post-injury with or without lysosyme revealed links to cell repair and regeneration through miRNAs IL-6, IL-13, miR-141 and protein IC99, N15, PD-1.

Conclusions: Signals for repair and migration in response to injury are associated with plasma EVs from patients with chronic stress.

1003 Adenocarcinomas and their derived lymphovascular emboli contain dual compartmental populations of tumor microvesicles which differ in size and possibly content and function.

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Adenocarcinomas and their associated lymphovascular emboli metastasize as tight aggregates of tumor cells. Using a serigraph model of human, inflammatory breast cancer (M29-30), we characterized lymphovascular emboli, in terms of high density of tumor aggregates (spheroids). *In vitro*, we previously demonstrated that each embol and spheroid are mediated by an intact expressed E-cadherin axis which regulates homotypic tumor cell adhesion. We now report that M29-30 spheroids secrete 5-10 fold higher levels of microvesicles (MVs) than most other carcinoma cell lines. Despite the high density of tumor cells and the strong juxtaposition of tumor cells to each other in the spheroids, intercellular spaces exist which contain numerous MVs. These intracellular MVs are entrapped between the E-cadherin adhesive junctions and can be isolated by dissociating the spheroids in Ca²⁺-free media with EDTA. These EVs compared to the extracellular (ES) MVs found in the conditioned media (CM) comprise a significant (approximately 25%) subpopulation of MVs which persisted for several days in culture (day 3: 0.48 \times 10⁶; day 7: 1.1 \times 10⁶; day 14: 0.64 \times 10⁶ [\pm 3.0 \times 10⁵]). The EVs differed in size compared to the ES MVs. By nanoparticle tracking analysis (NanoSight), EV MV mean volume was 79 nm compared with the ES MV mean volume of 152 nm. These size differences were also confirmed by transmission electron microscopy (TEM), though both were smaller (57 nm v 113 nm). The proteomic profile of the EV MVs can be readily compared with that of the ES MVs found in CM. Cellular target differences between the EV MVs and the ES MVs can also be studied. It would be attractive to hypothesize that EV MVs preferentially function in autocrine signaling whereas ES MVs signal in a paracrine manner.

1002 Mitochondrial Regulation of exosomal microRNA cargo in Vascular Smooth Muscle Cell Proliferation

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MicroRNAs are a class of small non-coding RNA molecules that regulate gene expression at the post-transcriptional level. The expression of microRNAs is regulated by a variety of factors, including transcription factors, signaling pathways, and epigenetic modifications. We have recently shown that mitochondrial dysfunction leads to increased expression of microRNAs, which in turn promotes cellular senescence and apoptosis.

Methods: We have recently shown that mitochondrial dysfunction leads to increased expression of microRNAs, which in turn promotes cellular senescence and apoptosis. We have now shown that mitochondrial dysfunction leads to increased expression of microRNAs, which in turn promotes cellular senescence and apoptosis.

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Conclusions: Mitochondrial dysfunction leads to increased expression of microRNAs, which in turn promotes cellular senescence and apoptosis.

1004 Biopactivity of Exosomal microRNAs in High Immune Responder Cow's Colostrum and Milk

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The expression of bovine host defense proteins in bovine colostrum and milk is regulated by microRNAs. The packaging of microRNAs within milk-derived exosomes ensures their stability and resistance to degradation and allows for shuttling from cell to cell. Notably, immune-related microRNAs are highly expressed in milk, particularly in colostrum, with the potential to regulate gut immunity of newborn calves and humans. While high immune responder (HIR) cows have superior colostrum quality and concentrations of bioactive proteins compared to average (A) and low (L) responders, the expression profiles of colostrum and milk microRNAs and their biological significance remain to be elucidated. The objectives of the study are to test the hypotheses that milk exosomes containing microRNAs are: (1) differentially expressed in HIR cows compared to A and L responders, (2) functionally active at the intestinal epithelial interface, and (3) regulated by differential ultra-centrifugation and their presence was confirmed by immunogold labeling electron microscopy. FISH and CLSM and Western blot. The biopactivity of milk exosomes on healthy and cancerous intestinal epithelial cells is being assessed. Similarly, the role of exosomes containing microRNA released by confluent intestinal epithelial cells on negative cells is being evaluated. Six different methods were compared for optimal isolation of total exosomal RNA containing miRNA. Out of 10 samples, four passed the library generation quality control, sequencing using the Illumina miRNA-RTSeq2000 platform and subjected to bioinformatics analysis. This study is expected to provide new insight into the immunoregulatory role of bovine colostrum and milk microRNAs in humans.