**Advanced Prostate Cancer and Caveolin-1:**

Bone metastasis is the most common complication derived from advanced prostate cancer formation ([Bubendorf *et al.* 2000](#_ENREF_1)). While the primary tumour can be treated and removed efficiently resulting in almost 99% survival, patients inflicted with metastatic prostate cancer possess a reduced 5-year survival rate of 29.3% (SEER 2016). This highlights the necessity to identify therapeutic targets and underlying biological phenomena that induce the metastatic phenotype.

Caveolin-1 has been linked to prostate cancer metastasis and has been a speculated biomarker for cancer progression ([Gumulec *et al.* 2012](#_ENREF_3); [Moon *et al.* 2014](#_ENREF_7); [Hayashi *et al.* 2015](#_ENREF_4)). This protein usually functions as a cholesterol transporter where its interaction with cytoplasmic protein Cavin-1 initiates the formation of specific lipid microdomains on the plasma membrane called Caveolae ([Hill *et al.* 2008](#_ENREF_5); [Moon et al. 2014](#_ENREF_7)). These proteins are co-expressed and co-localised in healthy human tissue, however in the case of many cancer types only caveolin-1 is expressed ([Moumita *et al.* 2015](#_ENREF_8)). Increased proliferation, migration and differentiation are a result of the aberrant caveolin-1 expression, yet, the mechanism that links caveolin to these phenotypes is still actively being investigated. Additionally, ectopic expression of functional cavin-1 in caveolin-1-only expressive cells, such as the PC3 advanced prostate cancer cell line, truncates many of the pro-tumorigenic properties observed by these cells. Similarly, knockdown of caveolin-1 in PC3 cells reduces the oncogenic behaviour, hereby emphasizing its role in metastasis. Amongst the typical signalling abnormalities that describe the link between caveolin and metastatic behaviour, a recent study had linked caveolin-1 overexpression with modifications in the extracellular vesicle content which may also contribute to metastasis.

**Extracellular vesicles and Cancer:**

Secreted membrane-bound vesicles, consisting of exosomes and microvesicles, collectively called extracellular vesicles are important mediators of intercellular communication (Figure 1). Exosomes are defined as 40-100nm diameter extracellular vesicles which are released upon fusion of the multivesicular bodies with the plasma membrane (Gu *et al.* 2014). Whilst similar in function and biochemical markers, microvesicles (≥100nm) differ from exosomes by being released from budding of the plasma membrane (Minciacchi *et al.* 2015). This report focuses on the total mixed population of EVs. EV cargo consists of cytoplasmic material, functional RNA and proteins (Stoorvogel 2015). Secretion and uptake of the extracellular vesicles has been reported to influence a range of biological processes, such as the selective export of cytokines in immunological responses, mediating homeostasis and stress response ([McKechnie *et al.* 2006](#_ENREF_6)). However, recent studies have emerged that determined cancer-derived EVs absorbed into recipient cells are able to induce the establishment of the pre-metastatic niche in cancer progression. Primarily this is attributed to the proteomic EV content being introduced into the endogenous population of the target cell, such as introduction of beta-catenin, epidermal growth factor and major elements of the MAPK pathway. Yet, more intriguing is the discovery that microRNA export may be associated with this function.

**Horizontal Transfer of microRNAs via Extracellular Vesicles:**

MicroRNAs (miRNAs) are small non-coding RNAs found to be involved in most developmental and pathological processes due to its ubiquitous gene regulatory function. The functional miRNA sequences (~19-24 nt) are derived from longer transcripts that undergo processing and shuttling events to give rise to functional mature sequences, known to induce RNA degradation (Ha and Kim 2014). Typically, the mature miRNA sequence interact with the 3’ untranslated region (3’-UTR) of its target transcripts and guides a multi-protein RNA induced silencing complex (RISC) to destine these molecules for degradation or translational inhibition (Djuranovic et al. 2012). A 2009 estimate predicted that approximately 60% of the mammalian genome is able to be directly mediated by the microRNA RISC mechanism where a single miRNA can target hundreds of transcripts. This instigates the necessity of tight temporal and spatial control over miRs to prevent dysregulation of vital pathways. Indeed, this is maintained by the high content of RNases in the extracellular space which would rapidly degrade any miRNAs that attempt translocation across extracellular space. However, EV-bound miRNAs were found to bypass this degradation which allows for the absorption of these molecules into recipient cells, thus evoking their canonical function in a potentially diverse cell type.

Earlier work from our lab utilizes the caveolin-1/cavin-1 system to investigate the role of caveolin-1 in prostate cancer (Inder 2014). Interestingly, the cellular modification inflicted by comparing between PC3 and PC3 cavin-1+ cells modified extracellular vesicle (EV) content, a pathway unrelated to the function of caveolin or cavin-1. In addition to limiting adhesion independent growth, hyper-proliferation and EV protein content of PC3 cells, the ectopic expression of punitive tumour suppressor, cavin-1, modified miRNAs found within EVs; miR-148a and miR-125a. Upon closer investigation, expression of miR-148a in bone marrow was reported to induce osteoclastogenesis by targeting an inhibitory transcription factor, MAFB, of the RANKL-induced osteoclastogenesis pathway, where the inverse was observed upon miR-148a inhibition ([Cheng *et al.* 2013](#_ENREF_2)). Bone fracture, pain and fragility are common co-morbidities associated with the bone metastasis-mediated prostate cancer due to increased bone degradation. Therefore the export of miR-148a from pro-metastatic prostate cancer cell line is consistent with clinical findings and may be one of the main regulators of metastatic progression. However upon comparing miR-148a EV concentration to its cellular levels reveals that the addition of cavin-1 does not modify the cellular expression levels of miR-148a, only the EV content. This suggests that there may be selectivity over the EV exported miRNAs, truncated by cavin-1 expression. Selective EV export of miRNAs had been observed in other studies, some of which links these miRNAs with disease states particularly cancer metastasis. Yet, the mechanism that governs this selectively is mostly unknown.

A recent clue was provided by Villarroya-Beltri et at, who reported that sumoylated ribonucleoprotein, hnRNPA2B1 mediate the transport and subcellular localization of particular miRNAs in T-lymphocytes (Villarroya-Beltri *et al.* 2013). Typically, the hnRNP family are involved in mRNA processing within the nucleus for translational control, mRNA stability and subcellular localisation, yet this is the first reported case of EV localisation occurring from this mechanism and one of the first reports of its ability to bind to miRNAs. Further questions arise due to this finding, such as the use of other hnRNP proteins for this function, how hnRNPs are targeted to the EVs and whether this protein family could be responsible for miRNA EV export in other cell types and stimuli.

**Hypothesis and Aims:**

This project investigated the hypothesis that miRNAs are selectively exported via extracellular vesicles moderated by the expression of cavin-1 to the PC3 model. As cavin-1 cannot directly mediate the export of miRNAs as it is not present within EVs, it is hypothesised that cavin-1 indirectly modulates miRNA escort proteins to the EVs, thereby mediating selective miRNA export. The following aims were devised to address this hypothesis:

1. Assess the microRNA species that are modified by this model
2. Identify candidate export proteins that participate in microRNA EV export.
3. Verify the interaction between candidate protein and microRNA by *in situ* and *ex vivo* experimental methods.

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<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3467054/> Mirs and malignancy

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4016197/> selective mir function example.