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Abbreviations

aMM asymptomatic Multiple Myeloma	89
BM Bone Marrow	88
BMME Bone Marrow Microenvironment	81
BMPC Bone Marrow Plasma Cell	5
BMSC Bone Marrow Stromal Cell	4
CADD Cell Attachment and Detachment Dynamics	iv
CM hMSC-conditioned medium	30
CM-INA6 MSC-Conditioned-Medium-treated INA-6	43
CAM Cell Adhesion Molecule	84
CLI Command Line Interface	63
ECM Extracellular Matrix	85
EMT Epithelial-Mesenchymal Transition	3
FACS Fluorescence-Activated Cell Sorting	76
GUI Graphical User Interface	63
hMSC human Mesenchymal Stromal Cell	80
LLM Large Language Model	63
MA MSC-adhering	38
MACS Magnetic-Activated Cell Sorting	83
MSC Mesenchymal Stromal Cell	81
MGUS Monoclonal Gammopathy of Undetermined Significance	89
MM Multiple Myeloma	87
MMR Multiple Myeloma Relapse	89
MBD Multiple Myeloma related Bone Disease	9
nMA non-MSC-adhering	38
OS Overall Survival	46
PCL Plasma Cell Leukemia	89
PFS Progression-Free Survival	46
SP Solitary Plasmacytoma	2
SASP Senescence-Associated Secretory Phenotype	9
WPSC Well Plate Sandwich Centrifugation	80

Introduction

Aims

This PhD thesis is designed to bridge significant gaps in the understanding and analysis of myeloma cell behavior and the handling of complex biomedical datasets. The specific aims are as follows:

- Develop an *in vitro* model to elucidate the mechanisms of myeloma cell dissemination in interaction with mesenchymal stromal cells (hMSCs), focusing particularly on:
 - Observing and quantifying cell proliferation, attachment, and detachment dynamics using time-lapse microscopy.
 - Isolating and characterizing distinct myeloma subpopulations interacting with hMSCs to understand differential gene expression related to cell adhesion and patient survival.
- Design and implement a Python-based software tool, `plotastic`, to facilitate the analysis of multidimensional datasets generated in biomedical research. This tool will aim to:
 - Streamline the data analysis process, making it more efficient and reproducible.
 - Integrate visualization and statistical analysis capabilities to ensure that data analysis protocols are aligned with the ways in which data is visualized.
 - Provide a case study demonstrating the application of `plotastic` in the analysis of *in vitro* dissemination experiments, emphasizing the tool's ability to handle semi-big data and enhance reproducibility.
- Synthesize the findings from the experimental and software development components to advance the understanding of myeloma dissemination and improve research practices in biomedical data analysis.

These aims are crafted to address both the biological and technical challenges in current cancer research methodologies and data science applications in biomedicine, fostering advancements that could lead to novel therapeutic strategies and more robust scientific inquiries.

Summarising Discussion

The subsequent sections will discuss the chapters presented earlier, focusing on how they fit within current scientific fields and the technical and academic challenges encountered during this project. Given the extensive scope of the topics covered, this discussion is divided into three main sections: Microscopy, Molecular Biology, and Data Analysis. Each section will detail key experiments that led to shifts in understanding and present intermediary conclusions to ensure clarity on broad topics.

Isolating & Quantifying Subpopulations within Cells in Direct Contact with MSCs

This project aimed to develop methodologies for isolating cells after direct contact with human Mesenchymal Stromal Cells (hMSCs). The primary challenge was the scarcity of *in vitro* methods that could effectively separate and isolate adhering cell subpopulations for subsequent molecular analysis. Most available techniques predominantly focus on the quantification of cell adhesion (Khalili & Ahmad, 2015; Kashef & Franz, 2015), and often employ indirect contact setups, complex micromanipulation, or are unsuitable for using live hMSCs as the immobilizing surface. To address the limitations of current adhesion assays, we developed and enhanced innovative methodologies, specifically the Well Plate Sandwich Centrifugation (WPSC) and V-Well adhesion assays.

Variability of Washing Steps: Given the complexity of the requirements, this project first attempts relied on simple and traditional adhesion assays that rely on manual washing steps (Humphries, 2009). Washing involves aspirating the medium, dispensing washing buffer, and potentially repeating these steps multiple times. This introduces variability due to differences in pipetting techniques, which affect the accuracy of volume transfer (Guan et al., 2023; Pushparaj, 2020). However, adhesion assays don't rely on precise volume transfer, but accurate detachment of cells adhering at the well bottom. This introduces a new set of considerations for the pipetting technique, especially since cells are highly sensitive to shear forces applied by fluid flow. From the author's experience with washing experiments and subsequent microscopic evaluations (data not shown), several factors could contribute to the variability of washing steps:

1. The distance of the pipette tip from the well bottom, which decreases during aspiration.
2. The position of the pipette tip relative to the well bottom (center or edge).
3. The angle of the pipette tip.
4. The speed of aspiration.
5. Accidental or intended contact between the pipette tip and the cell layer.
6. The residual volume left after aspiration.
7. *The same considerations apply when dispensing the washing buffer.*

In addition to user-dependent factors, other variables such as the cells' position on the well bottom can significantly impact the outcome. To the author's experience, cells located at the edge of the well don't detach as easily as those in the center, while cells touching the edge are almost impossible to remove. This phenomenon is likely related to the *boundary layer effect*, where fluids slow down near the edges of the well (Weyburne, 2014).

Together, since both user-dependent and independent factors can affect the outcome of washing steps, adhesive assays that replace washing are highly desirable. Still, since washing is straightforward and some variability is alleviated by the disciplined execution of washing protocols, it remains a common method for adhesion assays.

Directly Interacting Cells Contain Unexplored Interaction Scenarios: It is evident that direct and indirect contact to Mesenchymal Stromal Cells (MSCs) have varying effects on myeloma cells. That difference is crucial for understanding changes in the Bone Marrow Microenvironment (BMME) during MM progression (Fairfield et al., 2020; Dziadowicz et al., 2022). These studies utilize well-inserts to co-culture myeloma cells in close—indirect—contact with MSCs. However, such comparison of indirect *vs.* direct co-culturing methods might not fully represent the complexity of intercellular interactions scenarios found in the BMME. This is exemplified by this project, as it relied on the complex growth behavior: INA-6 cells aggregated homotypically in direct proximity to those adhering heterotypically to hMSCs, and detached through cell division. Furthermore, such methods fail to capture the subtle variations in paracrine signaling concentrations, where even a few micrometers of distance could significantly alter cellular responses.

Such knowledge shifted this project’s point of view as well: Initially, our hypothesis focused on direct heterotypic interactions, not expecting a nMA-INA6 population, but rather subpopulations within MA-INA6 cells that are separable by varying adhesion strengths. Hence, our assay employed strict conditions favoring one growth scenario—heterotypic interactions—, with co-cultures providing unlimited hMSC-surface availability causing predominantly heterotypic adhesion, while the short incubation time prevented the formation of aggregates. Despite these measures, our assay still captured cells emerging from recent cell divisions rather than from weak heterotypic adherence as initially hypothesized. This demonstrates the robustness of our method in separating subpopulations that arising from unexpected intercellular interaction scenarios. This can be a major advantage over methods that summarize direct interactions as one population. Analysing the non-adhering subpopulation within directly interacting cells could provide valuable insights not just in multiple myeloma, but also metastasis of other cancer types.

Minimizing Variability: There are innovative adhesion assays that both support the isolation of nonadherent subpopulations from directly interacting cells, and avoid variability introduced by washing steps.

One simple method involves flipping over a 96-well plate, with surface tension preventing medium spills as non-adhering cells fall to the surface for collection (Zepeda-Moreno et al., 2011). However, we found that the medium in fact did spill occasionally (not shown). Other approaches involve sealing the plate, such as with PCR plate seals, and using centrifugation to separate cells (Reyes & García, 2003; Y. Chen et al., 2021). Despite our efforts, we could not consistently avoid air bubbles, which, after flipping, would contact the cell layer and create dry regions during centrifugation.

The V-Well adhesion assay does not flip, but collects non-adhering cells into the nadir of V-shaped wells during centrifugation (Weetall et al., 2001). This work profited greatly from this method, while—to our knowledge—being the first to use cell monolayers as the immobilizing surface. We value this method for its precision, as centrifugation applies a uniform and configurable force, while the

readout remains straightforward, relying on the total fluorescent brightness rather than individual cell counting.

Specializing in Quantifying Adhesion or Isolating Subpopulations: Most adhesion assays primarily focus on quantification rather than isolation. The author attempted to combine both quantification and isolation, but found that the two goals can be mutually exclusive. The author summarizes the key differences between quantification and isolation approaches as such:

- Cell Manipulation for Harvest *vs.* Readout:
 - Isolation methods are designed to manipulate cells for easy harvest. For instance, the WPSC method uses a catching plate to collect non-adherent cells for subsequent analysis.
 - Quantification methods, on the other hand, manipulate cells to simplify the readout process. For example, the V-Well assay, which pellets cells into a single location, allowing for a pooled fluorescence measurement without the need for extensive cell handling.
- Optimization for Subsequent Analysis *vs.* Sample Throughput:
 - Isolation methods are optimized for detailed subsequent analyses, such as RNA or protein analysis. For example, WPSC minimizes the introduction of biases such as those from fluorescent staining, making it suitable for downstream molecular assays.
 - Quantification methods are optimized for high sample throughput. The V-Well assay, as an end-point assay, is designed to efficiently handle multiple treatments simultaneously, providing quick and comparative results with lower cell numbers.
- Handling of Cell Numbers:
 - Isolation methods, such as WPSC, require multiple wells (e.g., 96 wells) to gather a sufficient amount of cells per subpopulation, which is crucial for robust downstream analyses.
 - Quantification methods, exemplified by the V-Well assay, are highly efficient even with low cell numbers.

Thus, this adopted two distinct techniques for isolating and quantifying directly interacting subpopulations, each optimizing for different outcomes, but also supporting the separation of subpopulations within direct intercellular interactions.

Still, it is theoretically possible to insert microscopy steps into the WPSC method to scan the well bottom for later cell counting. Also, this work effectively isolated cell pellets from the V-well plate for subsequent fixation and cell cycle profiling. The process was tedious and required multiple technical replicates to achieve sufficient cell numbers for analysis. It also required removing hMSC from the V-well nadir to prevent contamination during pellet aspiration.

Together, while both methods can combine quantification and isolation, they are optimized towards either of them. Knowing these strengths and weaknesses could help to advance these methods in future studies.

Rationales of the Well Plate Sandwich Centrifugation: Inspired by the principles of both flipping and V-Well adhesion assays, we developed the Well Plate Sandwich Centrifugation (Well Plate Sandwich Centrifugation (WPSC)) method to address the challenges of isolating cell populations. This method innovatively combines elements from both techniques to provide a more reliable approach to cell isolation. One of the key advantages of WPSC is its ability to reduce the variability commonly introduced by manual pipetting. Instead of relying on aspiration, which introduce variability in cell collection and requires touching the well bottom for complete removal of medium, WPSC employs centrifugation to remove non-adhering cells. Medium is then returned by pipetting to repeat the process and maximize non-adhering cell collection, as the number of detachable cells plateau after few rounds of centrifugation. Hence, this approach compromises between minimizing washing variability and isolating larger quantities of cells.

The 96 well plate format has advantages, reducing spilling when flipping the sandwich, as surface tension kept fluids in place. The 96 well plate format also reduces per-well variability by performing the same washing procedure up to 96 times.

The slow centrifugation speeds used during WPSC are also decided after thorough consideration. For this, one has to discuss how exactly non-adhering cells detach during centrifugation. While centrifugal force is an obvious factor, the properties of cell adhesion are unclear under dry conditions during centrifugation. The author assumed that the cells are being pulled along by the medium as it is centrifuged into the catching plate. Hence, the centrifugation speed was chosen as fast enough to transfer the medium, without completely drying the co-culture plate and minimizing overall cell stress.

A significant challenge in WPSC is the dissociation of MA-INA6 from the hMSC monolayer. WPSC employs two distinct techniques to achieve this dissociation. The first technique involves repeated treatment with the gentle digestive enzyme Accutase followed by Magnetic-Activated Cell Sortings (MACSs). MACS, despite being effective, is costly, time-consuming, reduces overall cell yield, and potentially introduces biases due to CD45 antibody selection and the requirement for cold-treatment. The second technique utilizes strong pipetting to physically detach non-adhering cells (termed ‘*Wash*’). It is important to note that these techniques did not affect the protocol on detaching nMA-INA6 from the co-culture, hence providing for a consistent ratio of isolated MA-INA6 to nMA-INA6 across all experiments. Ultimately, we preferred *Wash*, as MACS had to be performed on all samples to ensure comparability, reducing overall cell yield which became limiting for downstream applications, especially for nMA-INA6 cells. Both methods achieved comparable purity of MA-INA6 cells, with few hMSCs per 10^4 MA-INA6 cells (purity assessment not shown). *Wash* probably profited from the highly durable nature of primary hMSC monolayers, whereas *MACS* required dissociation of the co-culture.

Together, WPSC offers a versatile solution for isolating hMSC-interacting myeloma cells. It

successfully balances the need for precision with the ability to handle larger cell quantities. WPSC could be adapted to other cell types that combines monolayer forming and suspension cells.

Key Points: Ultimately, this work established two methodologies that could represent a significant advancement in the field of adhesion assays, providing cost-effective, precise, reliable, and reproducible techniques for both isolating and quantifying subpopulations within co-cultures of directly interacting cell types. They offered valuable insights into the mechanisms of MM detachment and are potentially applicable to other research questions that focus on multicellular interactions and complex growth scenarios.

Constructing a Hypothetical Framework of Dissemination

Until today, a mechanistic understanding of myeloma dissemination is still lacking. Zeissig et al. (2020) has described dissemination as a multistep process along the lifetime of a myeloma cell. However, since evidence is collected mostly for individual steps—each step being very complex itself—the connection of these steps remains unproven and therefore a hypothetical construct. A description of dissemination as a process hence becomes a rough patchwork of *evidence fragments*. In that sense, this work adds further fragments, especially since its validity is limited to the INA-6 cell line. To regain understanding of dissemination as a process, the following sections attempt to integrate the findings of this work with available literature, formulating specific hypotheses to face future experiments. Given that direct observations of *CADD*¹³ have proven insightful, this framework carries the name *Dynamic Adhesion Hypothetical Framework for Myeloma Dissemination*.

Generating Hypotheses from CADD: The following shows examples how hypotheses can be formed after CADD observations: - What predictions can be made from these results for steps of dissemination (retention, release, Extra-/Intravasation, colonization), assuming that INA-6 is representative for all myeloma?

- Retention:

Observation of CADD: INA-6 cells attach fast and strongly to hMSCs and grow into stable aggregates.

Hypothesis: Myeloma cells are retained through strong adhesion to the BM microenvironment and stable homotypic aggregation.

Experiment: Inject INA-6 into mice and make sections of Bone lesions, comparing the growth

¹³*Cell Attachment and Detachment Dynamics (CADD)* (defined in this work): The observation and measurement of time-dependent changes in cell adhesion and detachment events. CADD characterizes the time cells spend attached, migrating or detached and associates these phases with molecular signatures, such as Cell Adhesion Molecule (CAM) expression or cell signaling mediated by CAMs or the microenvironment. CADD expands traditional *cell adhesion* by a time component and implies an intention to predict attachment and detachment events.

pattern to mice co-injected with an ICAM-1 or LFA-1 α /ITGB2 antibody, as that was shown to dissolve homotypic aggregates *in vitro* and prevent INA-6 growth *in vivo* (Kawano et al., 1991; Klausz et al., 2017). If abrogating aggregation leads to a rather diffuse colonization of bone instead of fewer focal lesions, this would support that strong adhesion and aggregation are crucial for retention in the BMME.

- Release:

Observation: INA-6 cells detach from hMSCs through cell division, and external forces can detach single myeloma cells from aggregates.

Hypothesis: Myeloma cells detach from the BM microenvironment through cell division and external force after reaching a minimal aggregate size.

Experiment: This could be tested by injecting INA-6 into mice and comparing the cell cycle profile of circulating cells vs. cells in the BM. If circulating cells are enriched with G1/G0 cells, this would support that detachment is more likely shortly after cell division.

- Intra-/Extravasation: CADD observations in this work did not make predictions, yet it could if MSCs were replaced by endothelial cells.

- Colonization:

Observation: Myeloma cells show quick attachment to MSCs within just 1 h of contact and quick upregulation of a multitude of adhesion factors, including Extracellular Matrix (ECM) factors.

Hypothesis: Quick attachment and fast expression of adhesion factors is a high potential to colonize new niches. This is reasonable especially since INA-6 were isolated from the pleura (Burger, Günther, et al., 2001), suggesting the capability to colonize extramedullary sites.

Experiment: Inject INA-6 into mice and see if they colonize extramedullary sites. Compare that to INA-6 with decreased adaptability,

This shows how CADD observations can lead to testable hypotheses using the results from this work alone. However, since these hypotheses are specialized on INA-6, a more generalized framework is favorable.

Key Hypotheses: The Dynamic Adhesion Hypothetical Framework is structured around four key hypotheses, each addressing fundamental aspects of myeloma cell dissemination based on both literature and the results of this work. These hypotheses are as follows:

1. CADD is adapted in response to different microenvironments faced during dissemination
2. High adaptability of CADD is a hallmark of aggressive myeloma
3. CADD is highly diverse within both patients and cell lines
4. Detachment is caused by multiple cues of varying nature, including external mechanical forces, cell division, loss of CAM expression, or even pure chance.

This framework sets the stage for a detailed exploration of each hypothesis, linking empirical data with theoretical constructs to provide a comprehensive framework of myeloma cell dissemination that can inform both future research to identify commonalities in dissemination and inform the development of targeted therapies.

Hypothesis 1: CADD Adaptations during Dissemination

However, Chapter 1 shows that adhesion factors are lost during MM progression. INA-6 are highly adhesive to hMSCs. This is a contradiction that needs to be resolved.

One explanation is the dynamic change of adhesion factor expression.

- One has to consider that intravasation and/or intra-/extravasation would require a different set of adhesion factors than adhesion to BM or extramedullary environments.

Extravasation: Plasma cells are known to upregulate adhesion factors dynamically once they reach a target tissue (???).

This work showed that INA-6 cells dynamically upregulate adhesion factors when in direct contact with hMSCs. Such adhesion factors are not expressed by INA-6 cells without contact to hMSCs, or by INA-6 cells emerging as daughter cells from MA-INA6 cells. This implies that myeloma cells are capable of rapid changes in adhesion factor expression that are substantially dynamic. Predicting when a myeloma cell starts regulating adhesion factors is a key question in understanding dissemination.

The following paragraphs discuss how the idea of dynamic adhesion factor expression holds up against current knowledge.

What biological implications does CADD adaption have? 1 Location of Myeloma Cells: - Different locations could require different adhesion factors: - Circulating MM cells do not need adhesion, probably losing adhesion factors - BM cells express adhesion factors to adhere to the Bone marrow microenvironment (MSCs, adipocytes, and osteoblasts) - Extravasating/intravasating cells need adhesion factors for endothelium - Extramedullary cells need adhesion factors for respective tissues

Bou Zerdan et al. (2022): "Classically, the BMM has been divided into endosteal and vascular niches"

Overall, cell adhesion play a pivotal role in the attachment/detachment dynamics of myeloma, hence influencing the dissemination of myeloma cells. This is exemplified in this work, where INA-6 cells dynamically upregulate adhesion factors in direct contact with hMSCs. Predicting how and when myeloma cells regulate adhesion activity is a key question in understanding dissemination, since that

Myeloma cells are isolated from patients at a certain stage from a certain location. As summarized by Zeissig et al. (2020), dissemination could be a dynamic process during the lifetime of a myeloma

cell that managed to exit the BMME into blood circulation. This implies that myeloma cells could change their adhesion factors during their course of dissemination to adapt to their current location for specialized tasks like exiting the BMME or intra-/extravasation.

why important?

1 Location: Knowing how an MM cell can change their adhesive properties during its course of dissemination is crucial for understanding the process itself. These changes could be studied by tracking the expression of adhesion factors in MM cells at different locations in mouse models. For humans, designing studies that gather biopsies at different locations from the same patient, e.g. bone marrow and circulating myeloma cells could be a starting point.

How studied? 1 Location: These changes could be studied by tracking the expression of adhesion factors in MM cells at different locations in mouse models. For humans, designing studies that gather biopsies at different locations from the same patient, e.g. bone marrow and circulating myeloma cells could be a starting point.

1 Location of Myeloma Cells

• Other Findings

- The review by Zeissig et al. (2020) could be a starting point. She does not discuss adhesion factors, but seeing dissemination as a multistep process does imply different adhesion factors for different steps.
- Malignant Plasma Cells express different adhesion factors than normal plasma cells (Cook et al., 1997; Bou Zerdan et al., 2022).
- Adhesion molecules have been a popular target for therapy for a decade (Nair et al., 2012)

• Extramedullary Involvement

- Extramedullary involvement: HCAM dramatic upregulation of HCAM
- CXCR4, the homing receptor, mediates production of adhesion factors in extramedullary MM cells (Roccaro et al., 2015)

• Intra-/Extravasation of Myeloma Cells

- Blocking Endothelial Adhesion through JAM-A decreases progression: (Solimando et al., 2020)
- N-Cadherin is upregulated in MM compared to healthy plasma cells, and has been shown to be a potential target for therapy (Mrozik et al., 2015)
- - NONE of Them were shown in Chapter 1 of this study, (except for JAM-B)

• Circulating Myeloma Cells

- This work shows that nMA-INA6 have increased survival during IL-6 deprivation, which could be a mechanism for surviving in circulation.
- Circulating plasma cells are rare, but detectable in peripheral blood (Witzig et al., 1996)
- studies demonstrate that circulating Multiple Myeloma (MM) cells exhibit reduced levels

of integrin $\alpha4\beta1$, in contrast to those located in the Bone Marrow (BM) (Paiva et al., 2013, 2011)

- circulating MM cells were CD138/Syndecan-1 negative (Akhmetzyanova et al., 2020)

- **BM-Resident Myeloma Cells**

- The role of CXCL12—which is highly expressed by MSCs—in inducing adhesion factors in MM is well established
-
-
- THIS WORK: INA-6 cells are highly adhesive to hMSCs, dynamically upregulating adhesion factors when in direct contact with hMSCs, and subsequently losing adhesion factor expression after cell division
- BM-resident MM cells maintain high levels of adhesion molecules to interact with MSCs, adipocytes, and osteoblasts within the BM niche (Bou Zerdan et al., 2022; Burger, Guenther, et al., 2001; Chatterjee et al., 2002).

According to this, this thesis predicts a low expression of adhesion factors in circulating myeloma cells, but a high expression in adhesive cells, e.g. non-circulating, or rather those

This has great implications for targeting adhesion factors for therapy, as it suggests that different adhesion factors should either be antagonized or agonized depending on the function of the adhesion factor. According to this assumption, adhesion factors involved in intra- and extravasation adhesion should be antagonized, while adhesion factors involved in BM adhesion—as identified in Chapter 2—should be agonized. Indeed, Adhesion factors for endothelium were shown to decrease tumour burden in mouse models (Asosingh et al., 2001; Mrozik et al., 2015)

Together, a detailed mapping of the niches available in the bone marrow is required to understand the adhesion factors required for each niche. This is a highly complex task, as the bone marrow is a highly complex organ.

Hypothesis 2: High Adaptability of CADD and Myeloma Aggressiveness

biological implications: 2 Disease Stage: - Higher disease stages imply changes in adhesion factors that favor aggressiveness. - Aggressiveness includes: - Better Colonization of new niches, including extramedullary ones - This implies a more diverse set of available adhesion factors - Faster regulation to adapt to new niches - Better survival in circulation

This assumption dictates that aggressive myeloma cells gain the ability to dynamically express

adhesion factors. It could be that INA-6 has gained the capability to express adhesion factors fast in order to colonize new niches, such as pleura from which they were isolated.

indeed, 3 temporal subtypes have been identified, associating higher risk with faster changes over time (Keats et al., 2012).

Is Disease stage a proxy for tumor aggressiveness?

yes, adhesion has prognostic value: A recent study by Q. Hu et al. (2024) developed a cell adhesion-based prognostic model for MM, calculating an adhesion-related risk score (ARRS) based on expression of only twelve adhesion related genes.

1. Disease Stage

- THIS WORK: Expression decreases during progression from Monoclonal Gammopathy of Undetermined Significance (MGUS) to Multiple Myeloma Relapse (MMR) of adhesion factors involved in hMSC adhesion.
- The idea that MM pathogenesis involves transformative processes has been around for decades (Hallek et al., 1998), but a detailed understanding of changing adhesive properties is still lacking, especially during the progression of MM.
- It is discussed that myeloma cell lines derived from advanced stages show different expression than newly diagnosed patients, discussing that they come from multiply relapsed patients (Sarin et al., 2020). This work also shows that Myeloma cell lines have the lowest expression of adhesion factors compared to all stages of MM and MGUS.
- For B-Cell Chronic Lymphocytic Leukemia, adhesion molecule expression patterns define distinct phenotypes in disease subsets (De Rossi et al., 1993).
- Terpos et al. (2016) reported an increase in adhesion molecule expression of ICAM-1 and VCAM-1 in patients with MM compared to those with MGUS and asymptomatic Multiple Myeloma (aMM).
- However, Pérez-Andrés et al. (2005) reported that CD40 is downregulated in Plasma Cell Leukemia (PCL) patients. Hence, different CAMs could serve ambiguous roles in MM progression.

How could this be studied?

2 Progression: Databases of expression from Myeloma cells gathered from bone marrow MGUS, aMM, MM, MMR already exist Akhmetzyanova et al. (2020); Seckinger et al. (2018). Going through such databases gives a good overview. One could categorize genelists using curated databases, get lists associated with extravasation, intravasation, Bone marrow adhesion. For every gene of these genelists, they could be filtered for significant differences between the stages. Further categorizations of pairwise comparisons of stages are required. but overall, these genelists could be a starting point for This approach is similar to the genelists published in chapter 1, with the difference that the genelists were further filtered by the RNAseq results of *in vitro* experiments.

What new implications do these dimensions have on targeting adhesion factors for therapy?

2 Disease Stages: - Specialized treatment for each stage? - Aggressive MM cells have potential improved control over adhesion factor expression, regulating a more diverse set of adhesion factors faster. This poses further challenges to targeting. It could be smarter to not target effector-molecules, but rather upstream regulators of adhesion. This work shows that NF-kappaB signaling, which by itself is not treatable, but regulators downstream of NF-kappaB were shown to be effective (Adamik et al., 2017, 2018)

Hypothesis 3: CADD is Highly Diverse Within both Patients and Cell Lines

- Describe different cell lines: MM1.S being plastic adhering non-aggregating and moderately MSC-adhering, INA-6 being non adhering aggregate forming and MSC-adhering, U266 being plastic adhering, non-aggregating and non MSC-adhering. - CXCL12 expression varies from QM between QM

One important dimension that is missing here is the genetic background of the myeloma cells. These are based on recurrent patterns of chromosomal aberrations or mutational signatures, defining structural and single nucleotide variants (Kumar & Rajkumar, 2018; Hoang et al., 2019). The prognostic value of genetic variants in MM is well established (Sharma et al., 2021), and their identification is becoming precise and cost-effective using *optical genome mapping*, making progress towards personalized therapies (Zou et al., 2024; Budurlean et al., 2024). The prognostic value of adhesion factor expression is nowhere nearly as advanced, with establishing cell adhesion as a reliable prognostic factor only recently (Q. Hu et al., 2024).

Hypothesis 4: Detachment is Caused by Multiple Cues of Varying Nature

biological implications:

3 Cues or associated processes: - Different cues could trigger different adhesional changes - Soluble signals? - Loss of CD138 (Akhmetzyanova et al., 2020) - Detachment through intercellular effects: cell division, Saturation of hMSC adhesion surface - Detachment with mechanical influence: External forces and instability after aggregate size -

why is this important? 3 The cues that trigger the detachment of MM cells are not well understood.

It could be that MM cells detach due to a combination of factors, such as loss of adhesion factors, changes in the BM microenvironment, or cell division or even completely random. Knowing specific dissemination signals helps preventing dissemination.

Papers like Akhmetzyanova et al. (2020) make it seem as if there is one molecule that decides if a myeloma cell is circulating or not.

It's less about one clear (molecular) mechanism that decides that a myeloma cell decides to become a disseminating cell, but rather a indirect consequence of a combination of many processes. These processes are: - Loss of adhesion factors or dynamic expression of adhesion factors - Loss of dependency from bone marrow microenvironment - asdf

Our thesis postulates that there is no big switch that decides if a myeloma cell detaches from the bone marrow, but rather a prolonged process of continuously downregulating adhesion factors, a dynamic upregulation of adhesion factors when they're needed, but the ultimate event that triggers release is better explained by external mechanical forces intercellular effects (cell division, saturation of adhesive surface and rising instability of aggregates after reaching a minimum size).

Detachment is triggered by external mechanical forces on cell conglomerates previously sensitized by changes in cell adhesion behaviour

1. Cues or Processes

- This work showed that detachment happened mostly mechanically and cell biologically through cell division. - Detachment through intercellular effects: cell division, Saturation of hMSC adhesion surface - Detachment with mechanical influence: External forces and instability after aggregate size.
- Soluble signals within the BM microenvironment, such as cytokines and chemokines, play significant roles in modulating adhesion factor expression in MM cells (Aggarwal et al., 2006; Alsayed et al., 2007).
- CD138 was proposed as a switch between adhesion and migration in MM cells, its blockage triggering migration and intravasation (Akhmetzyanova et al., 2020).

How can this be studied?

3 Cues: Identifying such signals might be challenging without having understood the other two hypotheses about adaptability first.

What new implications do these dimensions have on targeting adhesion factors for therapy?

3 Cues or associated processes: - It could represent a valid strategy to strengthen myeloma adhesion, provided that targeted adhesion molecule is proven to not be involved in other steps of dissemination, such as extravasation. Stimulating adhesion factor expression or activity is harder than inhibition, yet not impossible. For instance, the short polypeptide SP16 can activate the receptor LRP1—its high expression being associated with improved survival of MM patients in this work—,

showing promising results during phase I clinical trial (Wohlford et al., 2021), but could potentially increase survival of MM through PI3K/Akt signaling (Potere et al., 2019; Heinemann et al., 2022) -

- One could also accept that many cues are simply not controllable, and hope for systemic therapies like CAR- T Cells

Outlook: High-Value Research Topics for Myeloma Research Arising from this Work

As an Outlook, the Author lists research topics arising from this work that have great potential for breakthroughs in myeloma research.

Anti tumor effects of MSCs: This thesis has discussed the pro-tumor effects of MSCs. However, MSCs have also been shown to have anti-tumor effects (Galderisi et al., 2015). This work has also shown that primary hMSCs can induce apoptosis in INA-6 cells initially—probably through the action of death domain receptors—, but inhibit apoptosis during prolonged culturing.

This shows that hMSCs could be leveraged as a therapeutic target that could prevent myeloma progression.

Cell Division as a Mechanism for Dissemination Initiation: The author describes how the detachment of daughter cells from the mother cell after a cycle of hMSC-(re)attachment and proliferation could be a key mechanism in myeloma dissemination. This mechanism was shown in other studies of intra-/extravasation. The author sees great potential in this mechanism as a target for future research. It is probably under-researched due to requirement of sophisticated time-lapse equipment, yet the simplicity of detachment through cell division is intriguing through its simplicity. It implies asymmetric cell division. Cancer cells are known to divide asymmetrically, e.g. moving miRNAs to one daughter cell.

Lists of Adhesion Gene Associated With Prolonged Patient Survival: The author lists adhesion genes that are associated with prolonged patient survival. These genes are highly expressed in myeloma samples from patients with longer overall

At this time we could be on the verge of a new era of myeloma therapy, including bi-specific antibodies and cell based approaches (Morè et al., 2023; Engelhardt et al., 2024). Currently, available CAR-T Cell therapies (ide-cel, cilta-cel) are extremely expensive, but show complete remission rates of up to 80 % and a 18-month progression free survival rate of 66 % (Bobin & Leleu, 2022). An affordable “off-the-shelf” CAR-T Cell product could become reality since the problem of deadly graft-versus-host disease during allogeneic transplantation seems to be solvable (Qasim et al., 2017), hence, research groups and biotech companies are racing towards developing a safe allogeneic CAR-T Cell technology (Depil et al., 2020).

the list of genes could be good targets because the BM niche is highly hypoxic, car t cells are not well, but directing them to the BM niche could increase efficacy.

Find MSC and Myeloma crosstalk: Do another GSEA analysis using the list from factors upregulated in Dotterweich et al. (2016), since there, INA-6 and primary hMSC were used as well. Redoing an analysis with the background of the associated processes gained here could reveal insights on the communication between hMSC and INA-6 cells.

Conclusion 3: The Dynamic Adhesion Hypothetical Framework for Myeloma Dissemination

How does limited understanding of one dimension prevent the understanding of the other dimensions?

Location & Progression: If we don't know the expression profile of an MM cell depending on their source, results become incomparable.

Location & Cues: If we don't know the cues that trigger detachment, we can't predict where the MM cells will detach.

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Appendices

A Supplementary Data & Methods

A.1 Figures

A.2 Tables

A.3 Materials & Methods

B Documentation of plotastic