

Short Commentary

Tissue Infiltration of Tumor-Associated Macrophages: Towards the Identification of Therapeutic Targets

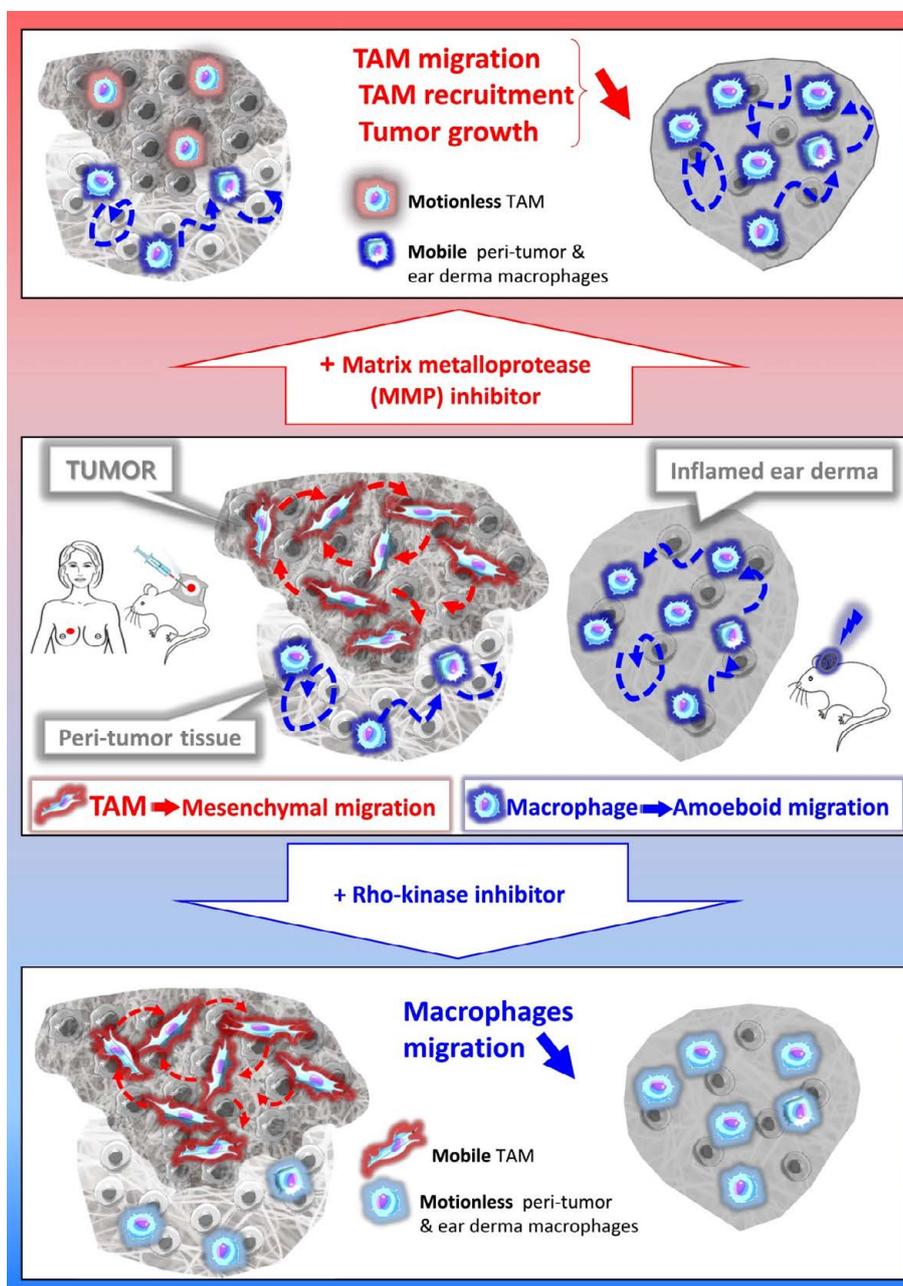
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Macrophages are present in all body tissues. They play a key role in the clearance of pathogens, participate in the immune and inflammatory responses, and partake in tissue repair and homeostasis. However, tissue infiltration of macrophages also exacerbates pathological processes, such as cancers [1-4]. Tumor-associated macrophages (TAMs) mostly originate from blood monocytes [5]. They are recruited to the tumor stroma at all stages of cancer progression [2,6] and can represent more than fifty percent of the tumor mass, thus representing by far the most abundant immune cell of the tumor stroma. Their number positively correlates with poor prognoses in most solid cancers as they are involved in several cancer-promoting events such as angiogenesis, lymphangiogenesis, immunosuppression, metastasis formation and resistance to therapies [7,8]. Therefore, the control of TAM infiltration is a current therapeutic strategy against cancers [9-11]. However, many questions regarding the mechanism of TAM tissue migration remain unresolved, which further hinders the development of novel therapeutic approaches.

Cell migration in tissues occurs in three dimensions (3D) that profoundly differs from 2D migration processes [12,13]. Two main mechanistically distinct migration modes have been described in 3D environments: amoeboid and mesenchymal [14]. The amoeboid movement is characterized by rounded, ellipsoid, or moderately elongated cells that form blebs or generate small actin-rich filopodia [15-17]. These cells do not require adhesion to the extracellular matrix (ECM), but rather use a propulsive and pushing migration mode [16,18,19]. This non-directional motility involves actin-myosin contractions and depends on the Rho-ROCK pathway. Cells migrating through the mesenchymal mode adopt an elongated and protrusive morphology [15,17,18]. The movement is directional, involves cell adhesion to the substratum, and requires proteases to degrade the ECM in order to create paths through dense environments. In macrophages, in contrast to the amoeboid movement, mesenchymal migration is not inhibited, but rather stimulated, by treatment with ROCK inhibitors [20,21]. Unlike lymphocytes, neutrophils and monocytes [3,22,23], macrophages share the capacity with only few cell types including tumor cells or immature dendritic cells (DCs) [17,24,25], to use both amoeboid and mesenchymal migration modes in 3D environments. In vitro studies revealed that macrophages tailor their migration mode to the architecture of the surrounding ECM [20,22,26-35]. In vivo in mouse tumors and ex vivo in human breast cancer explants, macrophages use the two migration modes depending on the tissue they infiltrate. TAMs use the protease-dependent mesenchymal migration mode in mouse fibrosarcoma in vivo or human breast cancers ex vivo [20]. In contrast, in non-tumorous tissues such as the tumor periphery or in inflamed ear derma, macrophages use the amoeboid motility in vivo [20]. A chronic treatment with a broad-spectrum inhibitor of matrix metalloproteinases (MMPs) blocked the mesenchymal migration of macrophages, which correlates with a decrease in both TAM infiltration and tumor growth in vivo [20]. These findings strongly suggest that inhibition of TAM motility could be a way to impede their pro-tumor action and urge to identify specific effectors of the TAM mesenchymal migration as new targets in anti-cancer therapy.

Among effectors of TAM mesenchymal migration, MMPs need

to be considered. MMP inhibitors have already been used to hamper tumor cell invasiveness by impeding tumor stroma remodeling and cancer cell escape from the primary tumor as well as decreasing angiogenesis [36,37]. Anti-tumor action of MMP inhibitors can now be explained by their action on TAM motility. Batimastat as well as its orally bioavailable derivative Marimastat were the first MMP inhibitors to enter clinical trials more than a decade ago [36]. However, clinical trials in patients with pancreatic, brain, lung or renal cancers were disappointing, essentially because these drugs were only tested in patients with advanced diseases despite the fact that studies in animal models had shown a most effective effect in treating early-stage diseases [38]. In addition, the primarily tested broad-spectrum MMP inhibitors were non-specific and did not differentiate between pro-tumor and anti-tumor MMPs depending on the type of cancer [38]. Thus, the recent knowledge on MMP biology and their differential involvement in tumor progression [39] together with the development of new generation MMP inhibitors [40-42] and the involvement of MMP activity on TAM motility stress the need to reassess the use of such inhibitors in early cancer treatment in combination with other anti-cancer molecules.

Another future strategy to identify new potential therapeutic targets consists in identifying new specific effectors of TAM mesenchymal migration. Therefore, exhaustive approaches to reach a comprehensive understanding of this process will be necessary as recently described in a transcriptomic-based analysis [27]. This strategy leads to the identification of a large number of potential targets and the future challenge will be to validate or invalidate all the potential hits as effective actors of macrophage migration both in vitro and in vivo through functional studies. For such large-scale screening approaches, new cellular tools are needed. Many studies use bone marrow-derived macrophages (BMDMs) from wild-type (WT) and knock-out (KO) mice or macrophage cell lines such as murine Raw 264.7 cells or human U937, HL-60 or THP1 cells for this purpose. All these cell models have several drawbacks such as the use of numerous animals, the limited number of cells and the impossibility to generate stable mutants in primary cultures or the fact that macrophage cell lines are usually distantly related to blood-derived macrophages or BMDMs particularly because they are cancer cells. Expansion of murine hematopoietic precursors that were transiently immortalized through a retroviral-delivery of an estrogen-inducible form of the transcription factor Hoxb8 has been described [43] and validated for the study of hematopoietic cell biology [43-52]. The possibility to use the CRISPR/Cas9 technology in this long-term hematopoietic progenitor cell lines has enabled the creation of new genetically modifiable cell models [45]. During the last few years, ectopic expression of Hoxb8 has been used in several studies mainly focused on DC biology [45,47,52-54], but also to generate surrogate macrophages [43,52,55]. This new cellular tool that combines the unlimited proliferative capacity of conditionally Hoxb8-immortalized hematopoietic progenitor cells with the CRISPR/Cas9 technology represents a powerful tool to genetically manipulate macrophages and explore their functionalities in a broad range of applications [55].

In conclusion, the tissue migration of TAMs emerges as a new

therapeutic target to combat cancer diseases and the development of new cellular models to molecularly dissect the mesenchymal migration process should lead to the identification of new leads in anti-cancer therapy in the coming years.

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