Editorial

Blood-Derived Extracellular RNA and Platelet Pathobiology
Adding Pieces to a Complex Circulating Puzzle

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The interaction between blood cells and disease has continued to grow both more complex and increasingly intriguing. Once thought to be static populations, circulating blood cells are now known to interact and communicate in ways far beyond the singular processes historically attributed to each population. A primary example is the platelet, an anucleate cell with a traditional role in hemostasis and thrombosis. The platelets’ defined biological roles have expanded exponentially over the last decade to include immunity, inflammation, and mediation of oncogenesis. Platelets, although anucleate, contain a wealth of transcriptomic information. When viewed from the perspective of a large population analysis, platelets demonstrate wide diversity, important patterns, including association with obesity and diabetes mellitus, and distinct expression profiles as compared with white cells. Platelets’ ability to participate in diverse systemic responses has been elucidated by our growing understanding of their contents and the revelation of their capacity to share these contents. Platelets are now known to horizontally transfer RNA, traffic pathogens, and regulate physiological and pathophysiological processes far beyond hemostasis.

Although there are limited studies available about platelet-specific exosomes or platelet-specific RNA, the field of plasma-derived RNA or extracellular RNAs (exRNAs) has rapidly and greatly expanded. Although few of these studies specifically characterize the cell of origin of these exosomes, the most abundant microparticle subtype in circulation is platelet-derived, suggesting that many exosomes are also platelet-derived. Most plasma exRNA studies have focused primarily on miRNA expression. miRNAs are highly conserved, small noncoding RNAs that regulate protein expression by complementary sequence recognition, binding, and translational repression of protein coding mRNA transcripts. Studies of circulating miRNAs have primarily been conducted to gain a greater understanding of disease processes or identify potential biomarkers, such as in cardiovascular disease. For example, 852 distinct plasma miRNAs were measured in 83 patients presenting for cardiac catheterization. Eight plasma miRNAs were found to have over 2-fold increased expression in patients with significant coronary disease as compared with those with minimal coronary disease or normal coronary arteries. Importantly, cell-specific miRNA profiles are distinct, as demonstrated in patients with

Figure. The connection between plasma and platelet microRNAs (miRNAs). Platelets transfer miRNA and other coding and noncoding RNAs both through direct transfer and via exosome release where it can be detected in the plasma. The transfer of these miRNAs leads to altered vascular cellular phenotypes, including changes in platelet proteins and platelet function (platelet image courtesy of Olga Vitseva). exRNA indicates extracellular RNA.
different types of myocardial infarction, ischemic heart disease, or acute coronary syndromes, who displayed unique miRNA distributions among their plasma, platelets, and leukocytes.7 Finally, the largest study to date, from over 5 thousand people, demonstrated the rich genetic connection of circulating miRNAs with cis-miR-eQTLs that may be associated with complex traits.8

Adding to the exploration of the interaction of circulating exRNAs and platelet processes is the study of Kaudewitz et al examining the association and potential function of plasma miRNAs and platelet activity.9 This group performed sequencing from plasma-derived RNA to identify specific small RNAs, including miRNAs and YRNAs. They then examined a small cohort of patients with a history of acute coronary syndromes and recorded platelet function studies and showed that specific exRNAs correlated with platelet function tests. In a secondary larger population, they demonstrate that circulating plasma platelet protein markers associate with specific exRNAs. They then expand the mechanistic relevance of their findings by demonstrating that inhibition of miR-126 in a murine model reduced platelet aggregation and specific platelet function receptor expression.

The findings of this study are consistent with previous investigations demonstrating an association of plasma miRNAs with cardiovascular disease, as well as studies demonstrating the relevance of platelet miRNA to platelet function.6,7,10 It has been previously shown that platelet miRNAs are able to repress expression of platelet proteins, and consistent with the study by Kaudewitz et al,9 miRNA profiles are associated with and may predict platelet reactivity.10 As suggested by these studies, platelets and their response to antiplatelet therapy may be important to the circulating miRNA pool.11 The strengths of the current study lie in the use of the mechanistic information and the specific insight from the animal model. Although the study by Kaudewitz et al does not demonstrate that miRNA changes in the human populations were specifically derived from platelets, this has been previously shown.12 Specifically, it is known that platelet microparticles, rich in miRNAs, can modify the transcriptome of macrophages and program their function toward a phagocytic phenotype.12 Also consistent with these studies, the importance of platelet activation on the platelet miRNA content has been demonstrated to cause changes in the platelet proteome.13

Although the study by Kaudewitz et al provides intriguing translational insights, like many studies before, it does not definitely define a new biomarker of platelet function. A limitation of this and many of the other circulating exRNA investigations is the small populations used and the limited numbers of miRNA targets studied.14 The issue with such an approach is that it assumes the miRNAs chosen primarily affect a single direct downstream target and ignores the dogma that a single miRNA can result in abundant expression changes because of the combinatorial effect of multiple gene targets. Whether this assumption is correct will likely depend on the setting. Because a single miRNA can target many genes, this cautions that the use of miRNAs as markers of platelet function may be more complex as compared with many classic platelet function assays.

In summary, our understanding of platelet function continues to progress as does our appreciation of their complex regulatory processes. The study by Kaudewitz et al adds to our understanding of the utility of small noncoding RNAs released by platelets into the circulation and how they may reflect platelet processes. They add to these findings by showing functional data linking miRNAs to platelet aggregation. However, as a therapeutic, the use of miRNAs will require thorough analysis examining specificity, toxicity, and human utility. As a biomarker of platelet reactivity, the use of plasma-based exRNA measurements is highly intriguing, but as we have learned from the differences between associative studies and large prospective controlled trials,15 extensive clinical data is needed to infer true utility.

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References


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