Small regulatory RNAs in vascular remodeling and atherosclerosis

Ingen, E. van

Chapter 2

Antisense oligonucleotide inhibition of microRNA-494 halts atherosclerotic plaque progression and promotes plaque stabilization

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Molecular Therapy Nucleic Acids. 2019 Dec 6;18:638-649

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Abstract

We have previously shown that 3rd Generation Antisense (3GA)- inhibition of 14q32 microRNA (miRNA)-494 reduced early development of atherosclerosis. However, patients at risk of atherosclerotic complications generally present with advanced and unstable lesions. Here, we administered 3GAs against 14q32 miRNA-494 (3GA-494), miRNA-329 (3GA-329) or a control (3GA-ctrl) to mice with advanced atherosclerosis. Atherosclerotic plaque formation in $LDLr^{-/-}$ mice was induced by a 10-week high-fat diet and simultaneous carotid artery-collar placement. Parallel to 3GA-treatment, hyperlipidemia was normalized by a diet-switch to regular chow for an additional 5 weeks. We show that, even though plasma cholesterol levels were normalized after diet-switch, carotid artery plaque progression continued in 3GA-ctrl mice. However, treatment with 3GA-494 and, in part, 3GA-329 halted plaque progression. Furthermore, in the aortic root, intra-plaque collagen content was increased in 3GA-494 mice, accompanied by a reduction in the intra-plaque macrophage content. Proatherogenic cells in the circulation, including inflammatory $Ly6C^{hi}$ monocytes, neutrophils and blood platelets were decreased upon miRNA-329 and miRNA-494 inhibition. Taken together, treatment with 3GA-494, and in part with 3GA-329, halts atherosclerotic plaque progression and promotes stabilization of advanced lesions, which is highly relevant for human atherosclerosis.

Introduction

Atherosclerosis is a chronic inflammatory disease characterized by progressive plaque buildup in the arterial wall. Most plaques that develop during one's life remain clinically silent. However, lesion progression and disruption of a vulnerable plaque may result in a cardiovascular event, such as an ischemic stroke or myocardial infarction.[1] Surgical interventions to prevent, for example, ischemic stroke are carotid endarterectomy or stenting, but due to the perioperative risks, these are only performed when a plaque causes a stenosis of the carotid artery of more than 70% or when the plaque is symptomatic, i.e. causing transient ischemic attacks (TIAs).[2]

An established therapeutic strategy is plasma lipid lowering by statins. Lipid-lowering strategies have been shown to contribute to increased plaque stability and reduce the risk of (recurrent) cardiovascular events, including myocardial infarction.[3-5] Independent of lipid lowering, targeting inflammation is also important in reducing the incidence of recurrent cardiovascular events, as was demonstrated in the Canakinumab Anti-Inflammatory Thrombosis Outcome Study (CANTOS) trial.[6] Although current therapeutic strategies contribute to reducing the risk of recurrent cardiovascular events, a clinical need remains for novel noninvasive therapies targeting multiple aspects of atherosclerosis and improving clinical outcome. Therapeutic strategies increasing stabilization of vulnerable plaques, alone or complemented by existing lipid lowering treatments, would be of great clinical value in reducing the risk of thrombotic events in the carotid, coronary and peripheral arteries.

MicroRNAs (miRNAs) are post-transcriptional negative regulators of gene-expression. Because of their ability to fine-tune expression of multiple target genes, miRNAs are promising drug targets for complex diseases, including atherosclerosis.[7] Several studies have focused on the therapeutic potential of miRNA-modulation in atherosclerosis. For example, the miRNA-33 family, including miRNA-33a and miRNA-33b, regulates cholesterol metabolism by targeting cholesterol transporter ABCA1. Inhibition of miRNA-33 resulted in decreased very low-density lipoprotein (VLDL), whereas high-density lipoprotein (HDL) was increased in the plasma.[8-10] More recently, it was shown that miRNA-33 inhibition also promotes cholesterol efflux from arterial macrophages and thereby directly regulates atherosclerotic plaque formation.[11] Inflammation in atherosclerosis was reduced via miRNA-155 inhibition. MiRNA-155 is predominantly expressed in pro-inflammatory macrophages. Inhibition of miRNA-155 resulted in smaller atherosclerotic lesions containing fewer lipid-laden macrophages via increasing expression of its target BCL6, which attenuates pro-inflammatory nuclear factor kB (NF-kB) signaling.[12] Furthermore, plaque stability was shown to increase

upon overexpressing miRNA-210. MiRNA-210 inhibits adenomatous polyposis coli (APC) expression in smooth muscle cells (SMCs) and thereby enhances intra-plaque SMC survival and, thus, intraplaque collagen synthesis.[13] However, as one miRNA can have multiple target genes, single miRNAs also have the potential to target all aspects of atherosclerosis at once. For example, inhibition of miRNAs transcribed from the 14q32 cluster (12F1 in mice), targeted multiple aspects in atherosclerosis, including lipid hemostasis, inflammation and concomitant plaque development, as we have shown previously.[14]

The 14q32 cluster is the largest known miRNA gene cluster in humans and contains more than 50 miRNA genes. We have evaluated the therapeutic inhibition of 14q32 miRNAs in different vascular remodeling processes.[14-17] In two different murine models of vascular remodeling, one for intimal hyperplasia and one for accelerated atherosclerosis, we showed that inhibition of 14q32 miRNAs reduced initial lesion development, increased plaque stability and decreased plasma cholesterol levels.[14, 16] Importantly, inhibition of 14q32 miRNAs reduced macrophage influx in the intima in the intimal hyperplasia model.[16] These studies, however, focused on the effects of 14q32 miRNA inhibition in initial lesion development[14], where most patients present in the clinic with advanced, symptomatic atherosclerotic lesions.

In the current study, we therefore aimed to investigate the effects of 14q32 miRNA inhibition on advanced lesions. We used 3rd Generation Antisense (3GA) to inhibit two different 14q32 miRNAs, miRNA-494 and miRNA-329. Parallel to 3GA-treatment, we included a diet-switch from high-fat high cholesterol to regular chow to normalize hyperlipidemia, in order to closely mimic routine lipid lowering treatment.

First, we show that inhibition of 14q32 miRNAs, particularly miRNA-494, halted atherosclerotic plaque progression and increased plaque stability in mice with advanced atherosclerotic lesions. Second, we show that plasma cholesterol levels show a modest, but further reduction after miRNA-494 and miRNA-329 inhibition. Third, we show that pro-atherogenic cells in the circulation, including inflammatory Ly6C^{hi} monocytes, neutrophils and platelets were decreased upon miRNA-329 and miRNA-494 inhibition, which is highly relevant in further reducing the risk of atherosclerotic complications.

Results

3GA-494 and 3GA-329 treatment reduces plasma cholesterol levels and body weight

The timeline of the study is shown in Sup. Fig. 1. Plasma cholesterol levels showed a clear decrease in all groups after diet-replacement (Fig. 1A). Both 3GA-494 and -329 treated groups showed a further reduction in total plasma cholesterol levels compared to the 3GA-control five weeks after diet switch (3GA-494: 155±6 mg/dL, 3GA-329: 168±11 mg/dL versus 3GA-ctrl: 214±13 mg/dL, P<0.05; Fig. 1B). Similar to as shown previously[18], body weight did not significantly differ after diet switch in the 3GA-ctrl group as compared to baseline, but showed a reduction in 3GA-494 or 3GA-329-treated mice compared to 3GA-ctrl (Fig. 1C). Subsequently, all groups increased in body weight during the remainder of the study, independent of the treatment, but body weight levels of 3GA-494 and 3GA-329-treated mice remained decreased compared to 3GA-ctrl. The size of the spleen was increased in all of the 3GA-494-treated mice and in half of the 3GA-329-treated mice, as is further described below. All other organs appeared normal and mice did not show any pathological changes.

3GA-494 treatment halts plaque progression in the carotid artery

In the carotid arteries, miRNA-494 and miRNA-329 expression were inhibited in both 3GA-494 and 3GA-329, respectively, compared to 3GA-ctrl (Fig. 2A). MiRNA-494 and miRNA-329 target gene expression levels (miRNA-494: IL33, TIMP3 and TLR4; miRNA-329: VEGFA, Mef2A and TLR4), however, were not significantly different compared to the control one week after final 3GA injections (Sup. Fig. 2A, B). 3GA-ctrl-treated mice showed increased carotid artery

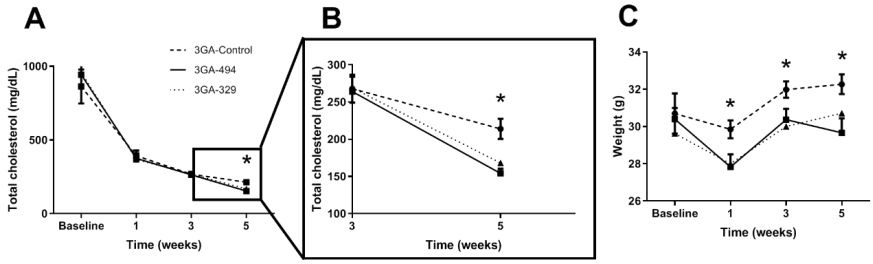

Figure 1. Total cholesterol levels and bodyweight levels of LDLr$^{-/-}$ mice treated with 3GA-ctrl, 3GA-494 or 3GA-329. Mice received 3GA-treatment immediately after (baseline), two and four weeks after diet replacement from high-fat high cholesterol to regular chow. All mice were sacrificed at week five. (A) Total cholesterol (TC) levels in milligrams per decilitre (mg/dL) measured in the serum of 3GA-ctrl, 3GA-494 and 3GA-329 treated mice, quantified by using enzymatic procedures, at baseline and up to five weeks after diet-replacement. (B) Zoomed in graph of TC at week three and five. (C) Bodyweight levels in grams (g) after diet-replacement. A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group at each time point. *P<0.05 compared to 3GA-ctrl. 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8) Data are represented as mean ± SEM.

average plaque size compared to baseline, indicating continued atherogenesis, even after lowering plasma cholesterol levels by diet-replacement (baseline: 18±4*10^3 µm^2 versus 3GA-ctrl: 32±10*10^3 µm^2; Fig. 2B, D). At the site of maximal stenosis, plaque size was increased in 3GA-ctrl compared to baseline (baseline: 30±8*10^3 µm^2 versus 3GA-ctrl: 56±16*10^3 µm^2; Fig. 2C). In 3GA-494 mice, carotid artery plaque size was significantly decreased compared to 3GA-ctrl. In fact, 3GA-494 mice had similar plaque sizes to baseline mice in both average plaque sizes (baseline: 18±4*10^3 µm^2, 3GA-ctrl: 32±10*10^3 µm^2 versus 3GA-494: 13±3*10^3 µm^2, P<0.05; Fig. 2B, D) and at the site of maximal stenosis (baseline: 30±8*10^3 µm^2, 3GA-ctrl: 56±16*10^3 µm^2 versus 3GA-494: 23±7*10^3 µm^2, P<0.05; Fig. 2C). 3GA-329 treated mice showed a trend towards a smaller average plaque size and at the site of maximal stenosis (average: 3GA-329: 15±1*10^3 µm^2 P=0.09, maximal stenosis: 3GA-329: 21±3*10^3 µm^2, P=0.1; Fig. 2B-D). Due to the small size, most plaques showed a fatty streak phenotype rather than an advanced atherosclerotic plaque phenotype. Advanced atherosclerotic plaque features, such as a fibrous cap and necrotic core, were lacking in most plaques and therefore we were unable to quantify and compare this among the groups.

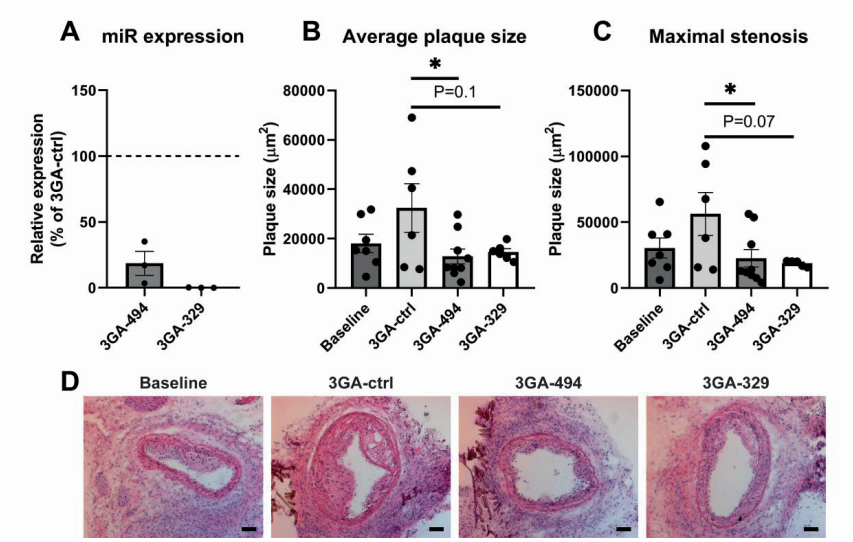

Figure 2. Inhibition of miRNA-494 and miRNA-329 in atherosclerotic lesions in the carotid artery. (A) Levels of miRNA-494 (N=3) and miRNA-329 (N=3) in carotid arteries of LDLr$^{-/-}$ mice one week after the final injection of 3GA-494 and 3GA-329, respectively, normalized to miRNA-494 and miRNA-329 expression in mice treated with 3GA-ctrl (100%; N=3). MiRNA-191 was used as a reference gene. (B) Average plaque size (calculated as the size average of plaque sections taken 100 um apart) in the carotid arteries of baseline (N=7), 3GA-ctrl (N=6), 3GA-494 (N=8) and 3GA-329 mice (N=6) and (C) plaque size at the site of maximal stenosis in µm^2 in the carotid arteries of baseline (N=7), 3GA-ctrl (N=6), 3GA-494 (N=8) and 3GA-329 mice (N=6). (D) Representative images of all groups. Scale bar 100 µm. A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers (α<0.05). *P<0.05 compared to 3GA-ctrl. Data are represented as mean ± SEM.

Inhibition of miRNA-494 increases plaque stability in advanced plaques

In the aortic root, plaque size and necrotic core size did not differ between groups (Fig. 3A, B). Other markers for plaque stability, however, were increased after miRNA-494 and, in part, miRNA-329 inhibition (Fig. 3C, E). Intra-plaque collagen content was strongly increased in 3GA-494 mice compared to the control (3GA-ctrl: 37±3% versus 3GA-494: 55±3%, P<0.0005; Fig. 3C). Treatment with 3GA-329 resulted in four mice in increased collagen content, whereas the other four showed similar collagen content as baseline mice (baseline: 15±2% versus 3GA-329: 34±9%; Fig. 3C). SMCs are the main source of collagen synthesis in atherosclerotic plaques, but the SMC-content was similar in all groups (baseline: 12±1%; 3GA-ctrl: 14±1%; 3GA-494: 11±1%; 3GA-329: 13±1%; Fig. 3D). Relative intra-plaque macrophage area was reduced upon diet switch from diet with high-fat high-cholesterol to regular chow (baseline: 22±2% versus 3GA-ctrl: 17±2%; Fig. 3E). In 3GA-494 mice, a further reduction in intra-plaque macrophage content was shown (3GA-ctrl: 17±2% versus 3GA-494: 12±1%, P<0.05; Fig. 3E), which is another marker of increased plaque stability. For the 3GA-329 treated mice, the relative macrophage area remained similar to control levels (3GA-329: 17±2%; Fig. 3E). Numbers of intra-plaque neutrophils were very small and not different among the groups (data not shown). Plaque necrotic core sizes were not significantly different between groups as well (Fig. 3E).

Blood, spleen and lymph node analyses of LDLr$^{-/-}$ mice treated with 3GA-494, 3GA-329 or 3GA-control

Blood analysis by Sysmex and flow cytometry revealed altered numbers of circulating cells upon 3GA-494 and 3GA-329 treatment compared to 3GA-ctrl (Fig. 4 and Sup. Fig. 3). White blood cells (WBCs) remained similar after miRNA-494 inhibition, but were decreased after miRNA-329 inhibition (Fig. 4A). Myeloid cells, as defined by CD11b^{+} and CD11c^{+}CD11b^{+} were elevated in 3GA-494 mice, whereas CD11b^{+} cells were decreased in 3GA-329 mice (Sup. Fig. 3A, B). More specifically, we observed that neutrophils (Ly6C^{+}Ly6G^{int}), which are part of the myeloid compartment of WBCs, were decreased after miRNA-494 and miRNA-329 inhibition (Fig. 4B, C). Total monocyte count, also part of the myeloid compartment of WBCs, was not significantly altered, although we did observe differences in the pro-inflammatory subset (Ly6C^{+}Ly6G^{-}) quantified by FACS analysis (Fig. 4D, E).

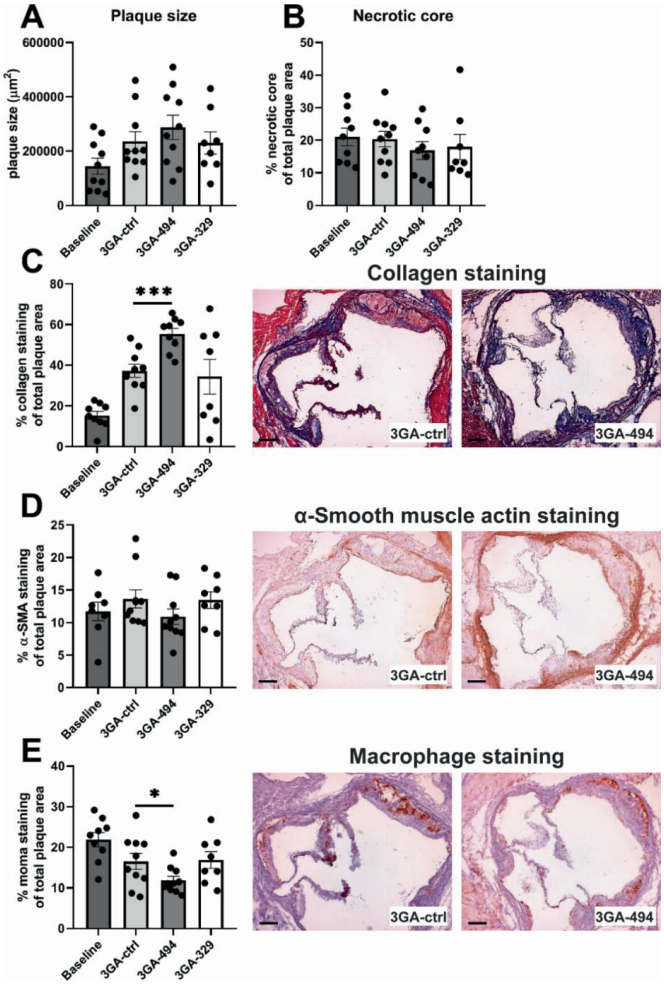

Figure 3. 3GA-494 treatment increased plaque stability in aortic root plaques. (A) Plaque size in µm^2 of aortic root plaques, calculated from at least five 10 µm thick section of the three-valve area. (B) Necrotic core area, defined as an acellular area, measured in the lesions stained with Masson's Trichrome, (C) collagen content, stained with Massons's Trichrome, (D) SMC cell content, stained with an antibody against α-smooth muscle actin (α-SMA), (E) macrophage content, stained with anti-monocyte-macrophage (Moma)-2 antibody. Amount of staining is shown as a percentage of total plaque area quantified in baseline (N=10), 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8). (C-E) Scale bar 250 µm. A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers (α<0.05). *P<0.05, ***P<0.0005 compared to 3GA-ctrl. Data are represented as mean ± SEM.

Although total amounts of lymphocytes were similar, $CD19^+$ B-cells were reduced in 3GA-494 mice and $CD4^+$ and $CD8^+$ T-cells were slightly increased in 3GA-329 mice (Fig. 4F and Sup. Fig. 3C-E). Furthermore, miRNA-494 inhibition decreased red blood cell and, in particular, strongly reduced platelet count (Fig. 4G, H). In the 3GA-329 treated mice, three mice showed reduced platelet counts, whereas platelet counts were normal in the remaining mice (Fig. 4H).

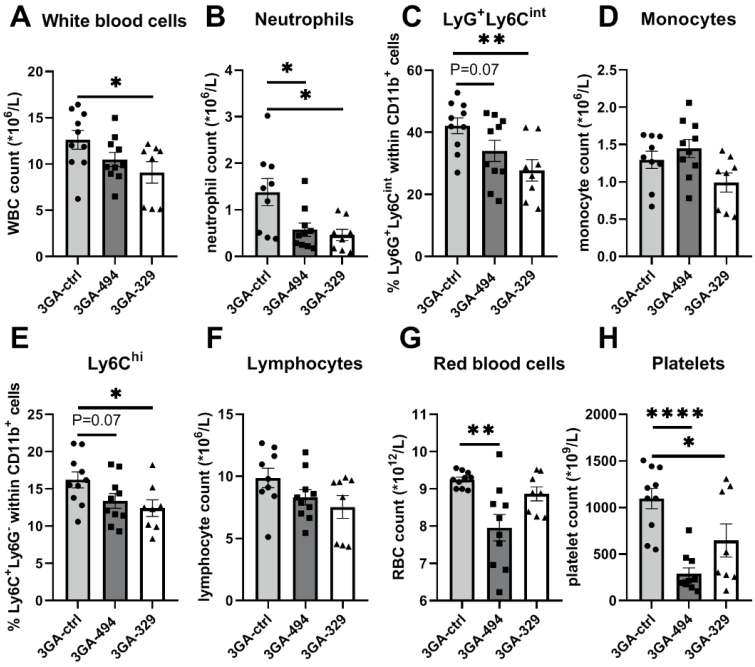

Figure 4. Blood analysis of mice treated with 3GA-494, 3GA-329 or 3GA-ctrl one week after final injection. Amount of circulating (A) white blood cells (WBC; 10^6/L), (B) neutrophils (10^6/L) and (C) neutrophil marker lymphocyte antigen 6 complex, locus G6D ($Ly6G^+$) lymphocyte antigen 6 complex, locus C1 $(Ly6C)^{int}$ cells defined as a percentage within $CD11b^+$ cells, (D) monocytes (10^6/L) and (E) inflammatory subset of monocytes $Ly6G^-Ly6C^{hi}$ cells as a percentage within $CD11b^+$ cells, (F) lymphocytes (10^6/L), (G) red blood cells (RBC; 10^{12}/L) and (H) platelets (10^9/L). (A, C, E-H) Blood cell analysis on whole blood quantified by Sysmex. (C, E) Flow cytometric analysis (FACS) analysis performed on the blood of 3GA-ctrl, 3GA-494 and 3GA-329 mice after red blood cells were removed using lysis buffer. A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers ($\alpha<0.05$). *P<0.05, **P<0.005, ****P<0.0001 compared to 3GA-ctrl. 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8). Data are represented as mean ± SEM.

Percentages of $CD4^+$ and $CD8^+$ T-cells in the spleen were decreased in 3GA-494-treated mice and showed a trend towards a reduction in 3GA-329-treated mice (Sup. Fig. 3F, G). However, since the spleens were enlarged due to proliferation of other cell types, as discussed below, the absolute numbers of $CD4^+$ and $CD8^+$ T-cells may be similar among all groups. $CD4^+$ and $CD8^+$ T-cells in the draining lymph nodes were not different among all groups (Sup. Fig. 3H, I).

Splenic megakaryocyte retention

As mentioned above, all 3GA-494 mice and half of the 3GA-329 mice showed splenomegaly compared to 3GA-ctrl and baseline mice (Fig. 5A, B). Staining for Von Willebrand factor (VWF) revealed strongly elevated numbers of megakaryocytes in the enlarged spleens of 3GA-494 mice compared to 3GA-ctrl, indicating increased megakaryopoiesis (Fig. 5A, C). In 3GA-329 mice, only the mice with low platelet counts showed splenomegaly, accompanied by strongly elevated megakaryocyte numbers (Fig. 5B). Despite the administration of a miRNA-494 inhibitor, splenic expression of miRNA-494 was upregulated one week after the final 3GA-injection (Fig. 5C). Increased expression of megakaryocyte/platelet markers, i.e. glycoprotein Ib platelet subunit alpha (GPIbα) and subunit beta (GpIbβ), both part of the platelet receptor complex for VWF, and integrin subunit beta 3 (Itgb3), in the spleen of 3GA-494 mice confirmed indeed increased megakaryopoiesis (Fig. 5D-F). Megakaryocytes and erythrocytes derive from a bipotent erythrocytic-megakaryocyte progenitor. Transcription factors involved in commitment of erythrocytic-megakaryocyte progenitor cells towards megakaryocyte progenitors and platelet production were also increased upon 3GA-494 treatment (Fig. 5G-I)[19]. Expression of transcription factors involved in hematopoietic stem cell (HSC) proliferation and differentiation, which are putative targets of miRNA-494 and conserved in both human and mice, as was predicted by www.targetscan.org (release 7.2), was similar in both 3GA-494 and 3GA-ctrl treated mice (Sup. Fig. 2C)[20-23]. In the spleen of 3GA-329 mice, no significant differences in megakaryocyte/platelet markers nor transcription factor expression was shown compared to 3GA-ctrl mice (Fig. 5D-I).

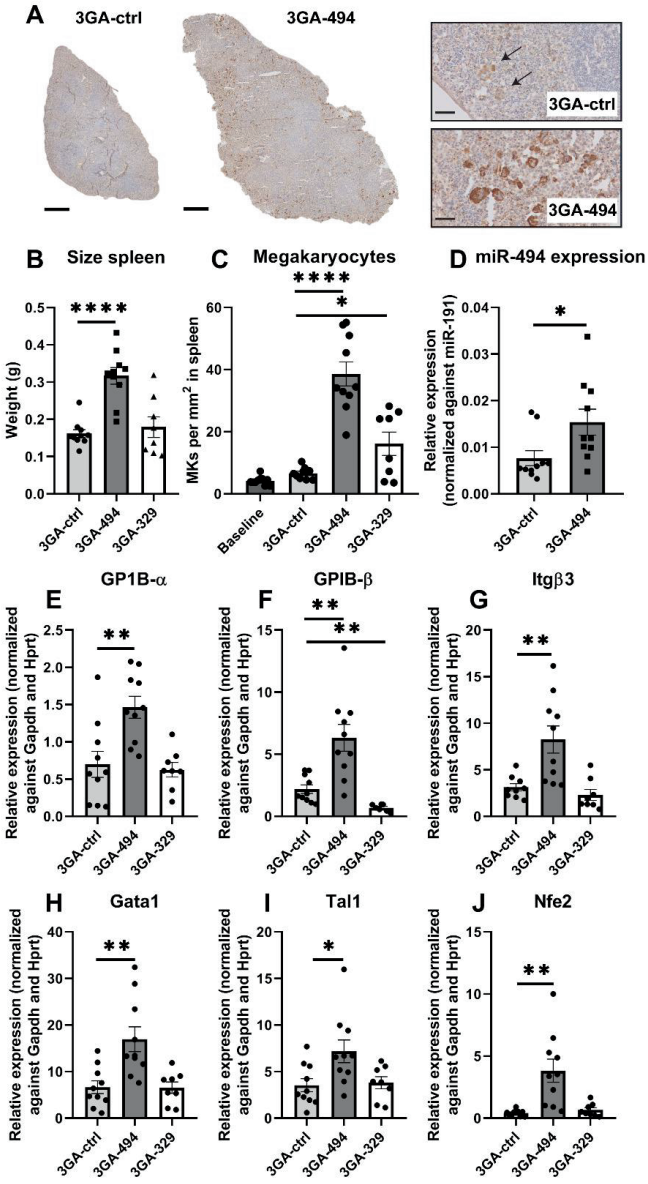

Figure 5. Megakaryocyte accumulation in the spleen upon 3GA-494 and 3GA-329 treatment. (A) Representative images of splenomegaly in 3GA-494 treated mice with megakaryocyte accumulation compared to 3GA-ctrl. Megakaryocytes were stained with an antibody against Von Willebrand factor. Scale bar 500 µm. Zoomed in image scale bar 50 µm. (B) Weight in grams (g) of the spleens of 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 mice (N=8). (C) Amount of megakaryocytes per mm^2 spleen. (D) miRNA-494 expression in the spleen of 3GA-ctrl and 3GA-494 mice, relative to miRNA-191 expression. (E) Three different platelet/ megakaryocyte markers quantified by qPCR in the spleen; Glycoprotein Ib platelet subunit alpha (GP1b-α), (F) beta (GP1b-β) chain and (G) integrin subunit beta

3 (Itgb3) normalized to Gapdh and Hprt. (H-J) Transcription factors involved in megakaryocyte differentiation in the spleen. Gata binding protein 1 (Gata1), TAL bHLH transcription factor 1, erythroid differentiation factor (Tal1), nuclear factor, erythroid 2 (Nfe2). A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers (α<0.05). *P<0.05, **P<0.005, ****P<0.0001 compared to 3GA-ctrl. 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8). Data are represented as mean ± SEM.

A previous study showed that in primary myelofibrosis, overexpression of miRNA-494 in HSCs promotes megakaryopoiesis via downregulation of suppressor of cytokine signaling 6 (SOCS6).[24] We quantified SOCS6 expression in the spleen. However, SOCS6 expression showed a trend towards upregulation compared to 3GA-ctrl instead of downregulation (Sup. Fig. 2D). As the bone marrow is also a source of megakaryopoiesis, we stimulated freshly isolated murine bone marrow cells with either 3GA-ctrl or 3GA-494. Although the miRNA-494 expression was downregulated in bone marrow cells after 3GA-494 treatment, we did not observe differences in SOCS6 expression nor in expression of transcription factors for megakaryocyte commitment and GPIbα and GpIbβ expression (Sup. Fig. 2E, F).

Increased hepatic platelet markers

Platelets can be cleared by hepatocytes and liver macrophages (Kuppfer cells).[25] Expression of miRNA-494 in the liver was similar in both 3GA-494 and 3GA-ctrl mice (Fig. 6A). MiRNA-329 was not expressed at all in the liver of either 3GA-329 or 3GA-ctrl mice (data not shown). Expression levels of platelet markers quantified by qPCR were upregulated in the liver of 3GA-494 treated mice, suggesting increased platelet clearance compared to 3GA-ctrl (Fig. 6B-D). In 3GA-329 mice, only the mice with low platelet counts showed increased expression of platelet markers in the liver (Fig. 6B-D).

Increased expression of platelet receptors upon 3GA-494 treatment

We further investigated whether 3GA-494 treatment could lead to miRNA-494 inhibition in anucleate platelets. Compared to 3GA-ctrl, mature miRNA-494 expression was first downregulated after one hour and then upregulated after four hours of incubation with 3GA-494 (Fig. 7A). As platelets have no transcription, upregulation of miRNA-494 was accompanied by depletion of the primary miRNA-494 transcript, pri-miRNA-494, indicating rapid processing of the pri-miRNA upon miRNA-494 downregulation (Fig. 7B). Changes in the intermediate pre-miRNA-494 were less pronounced (Fig. 7C).

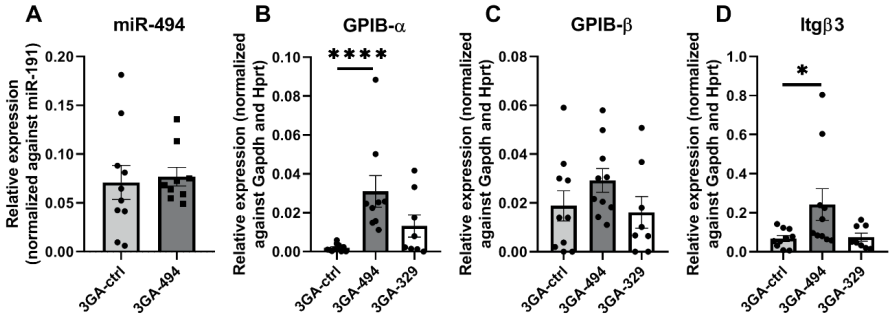

Figure 6. Increased platelet receptor expression in the liver of 3GA-494 mice. (A) MiRNA-494 expression in the liver of mice treated with 3GA-494 (N=9) or 3GA-ctrl (N=10), relative to miRNA-191. (B) Relative expression of three different platelet/megakaryocyte markers quantified by quantitative polymerase chain reaction (qPCR) in the liver of 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8) mice; glycoprotein Ib platelet subunit alpha (GP1b-α), (C), beta chain (GPIb-β) and (D) integrin subunit beta 3 (Itgβ3) normalized to GAPDH and Hprt. (B-D) A Mann-Whitney U test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers (α<0.05). *P<0.05, ****P<0.0001, compared to 3GA-ctrl. Data are represented as mean ± SEM.

Genes that we initially tested as housekeeping genes, including GAPDH, U6 and YWHAE, appeared to be unstable in 3GA-treated platelets (Sup. Fig. 4B-D).[26] Pre-ITGB3 showed stable expression and was, therefore, used as a housekeeping gene (Sup. Fig. 4A). Pro-survival genes BCL2 and MCL1 are putative targets of miRNA-494, as was predicted by www.targetscan.org (release 7.2). Since miRNA-494 was upregulated in platelets, we checked whether BCL2 and MCL1 were downregulated, leading to more apoptosis and subsequently to more clearance. MCL1 appeared downregulated in 3GA-494, but BCL2 did not (Sup. Fig. 4E, F).

Next, we quantified expression of platelet GPIBα and integrin subunit ITGB3, both part of platelet receptors involved in platelet activation, and found upregulation after four hours of 3GA-494 treatment compared to 3GA-ctrl (Fig. 7D-F). Since splicing occurs upon platelet activation, we measured pre-mRNA levels of MCL1, GAPDH and GPIBα.[27, 28] Pre-mRNA levels were declined in 3GA-494 treated platelets compared to 3GA-ctrl, indicating increased splicing and hence increased platelet activation in 3GA-494 treated platelets (Sup. Fig. 4G-I).

Time points from 8 hours on were excluded, since all platelets, independent of their treatment, were hyper-activated in culture.

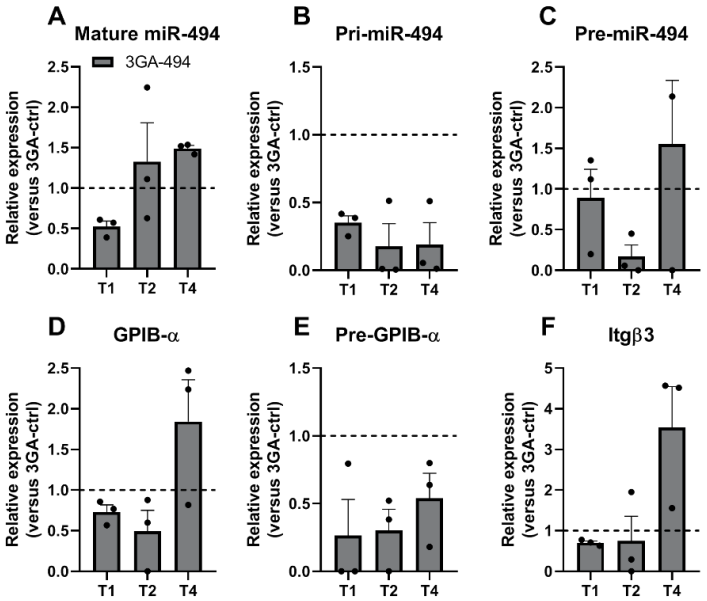

Figure 7. Upregulation of miRNA-494 expression following 3GA-494 treatment led to hyper-activation of platelets. Human platelets were incubated up to four hours in PAS-III buffer with 30-35% plasma with either 3GA-494 or 3GA-ctrl (in triplos). Platelets were kept in an incubator at 22ºC with 5% CO_2 at continuously swirling. (A) Mature miRNA-494 expression, relative to miRNA-126. (B) Pri-miRNA-494 and (C) pre-miRNA-494 relative to pre- integrin subunit beta 3 (Itgβ3) expression. (D) Expression levels of platelet receptors glycoprotein Ib platelet subunit alpha (GP1b-α), (E), beta chain (GPIb-β) and (F) Itgβ3, relative to pre-Itgβ3 expression. All expression levels were normalized to 3GA-ctrl (100%). Data are represented as mean ± SEM.

Discussion

In this study, we first show that inhibition of 14q32 miRNAs, particularly miRNA-494, in mice with advanced atherosclerotic lesions halted carotid atherosclerotic plaque progression and promoted plaque stability in the aortic root of LDLr$^{-/-}$ mice. Second, plasma cholesterol levels were lowered further by 14q32 miRNA inhibition than by diet switch alone. Third, pro-atherogenic cells in the circulation, including pro-inflammatory monocytes (Ly6C^{hi}), neutrophils and platelets were decreased after miRNA-329 and miRNA-494 inhibition.

Even though plasma cholesterol was lowered by diet-switch, plaques in the carotid artery continued to grow in 3GA-ctrl mice. With 3GA-494 treatment and, in part, 3GA-329 treatment, we managed to halt plaque progression in the carotid artery. Although we combined 3GA treatment with plasma lipid lowering, plaque sizes from 3GA-494 and 3GA-329-treated mice were not significantly reduced compared to baseline, indicating that plaque regression did not occur in this setup. Unlike for the carotid artery lesions, neither 3GA-494 treatment, nor 3GA-329 treatment, resulted in reduced plaque sizes in the aortic root compared to 3GA-ctrl treatment. We have previously established that the expression of 14q32 miRNAs differs between sites of lesion development in mice[14] and more recently, we demonstrated that expression of 14q32 miRNAs, including miRNA-494 and miRNA-329 and their targets, varies widely across the human vasculature as well.[29] Differences in response to miRNA inhibition in carotid artery plaques and aortic root plaques are, therefore, likely caused by differences in local miRNA and target gene expression. Although plaque size was not affected in the aortic root, plaque stability was clearly affected and increased after miRNA-494 inhibition, which is particularly relevant in reducing the risk of cardiovascular events. These results indicate that 3GA-494 treatment would be relevant for treating different types of plaques, developing at different sites in the vasculature.

Collagen provides structural support in the fibrotic cap and in our study, particularly miRNA-494 inhibition increased intra-plaque collagen content in advanced lesions. Collagen is synthesized by SMCs, however, we have previously shown that miRNA-494 does not affect collagen synthesis.[14] Furthermore, even though miRNA-494 does affect proliferation of myofibroblasts[15], neither miRNA-494, nor miRNA-329 inhibition affected the intraplaque SMC content, which indicates that another mechanism caused the enhanced collagen deposition. We previously validated tissue inhibitor of metalloproteinases 3 (TIMP3) as a target of miRNA-494.[14] TIMP3 inhibits collagen degradation by matrix metalloproteinases (MMPs) and, therefore, more TIMP3 expression likely contributed to the observed increase in collagen content. Since macrophages produce MMPs, the reduced intra-plaque macrophage content

may also have contributed to the increased collagen content in the plaques. Lipid lowering strategies have been described to contribute to fewer intra-plaque macrophages.[30] Fewer intra-plaque macrophages are associated with a more stable plaque phenotype. In our study, macrophages in advanced plaques of 3GA-ctrl mice were decreased compared with baseline mice, which was likely an effect of plasma lipid lowering by diet-switch and additional treatment with 3GA-494 even further reduced intra-plaque macrophage numbers. Circulating inflammatory monocytes (Ly6C^{hi}) are associated with promoting plaque progression after extravasation into the lesion and here, both miRNA-494 and miRNA-329 inhibition resulted in a reduction in circulating pro-inflammatory Ly6C^{hi} monocytes, which may have caused the reduction in plaque macrophages. In addition, platelets have been described to mediate monocyte activation, recruitment and extravasation into the lesion.[31] Therefore, the strongly reduced blood platelet levels in 3GA-494 mice may also have contributed to a reduction in macrophage extravasation into the lesion.

Particularly 3GA-494 mice showed reduced levels of circulating inflammatory cells, including neutrophils, red blood cells and platelets, all of which originate from a common early myeloid progenitor cell. Decreased expression of miRNA-494 has been reported to drive chronic myeloid leukemia, a stem cell derived malignant disorder in human.[32] We measured whether transcription factors involved in HSC proliferation and differentiation were targeted by increased miRNA-494 expression in the spleen. However, expression levels were not affected, indicating that this was not primary cause of reduced levels of circulating neutrophils, red blood cells and platelets in 3GA-494 mice. Others have also described a role for 14q32 miRNAs, including miRNA-494, in human erythropoiesis and, therefore, proper development of erythrocytes in our murine model may have been targeted by 3GA-494 treatment.[33] Exact mechanisms on how myeloid cells in the circulation are reduced, however, remains to be determined in future research.

In previous studies, we have shown that multiple miRNAs transcribed from the 14q32 cluster are involved in different processes of vascular remodeling.[14-17] Inhibition of 14q32 miRNAs miRNA-494, miRNA-329, miRNA-487b and miRNA-495 improved neovascularization and blood flow recovery in a hindlimb ischemia model.[15] Neovascularization requires a pro-inflammatory response, whereas an anti-inflammatory response is favorable for atherosclerosis. Stimulation of neovascularization often leads to aggravation of atherosclerosis and vice versa.[34] This effect is often referred to as the Janus phenomenon, after the two-faced Roman god.[35] In contrast to the Janus-phenomenon, 14q32 miRNA

inhibition both increases neovascularization and reduces atherosclerosis and, therefore, play a unique role in vascular remodeling.
Strongly increased megakaryocyte content and increased expression of transcription factors in the spleen of 3GA-494 mice clearly showed increased commitment toward the megakaryocyte lineage. Since SOCS6 expression was not affected upon 3GA-494 treatment in either the spleen or bone marrow cells, this indicates that megakaryocyte differentiation was not targeted by 3GA-494 treatment. Increased splenic megakaryocyte differentiation in 3GA-494 mice is, therefore, likely a compensatory mechanism to prevent severe thrombocytopenia. Others have also demonstrated that mice show increased megakaryocyte differentiation as a response to lower platelet counts.[36]

The underlying mechanism of platelet exhaustion may be an increased hepatic clearance. We found increased platelet receptor expression in the liver. Apoptotic platelets are recognized and cleared by the liver.[37] However, pro-survival genes Mcl-1 and Bcl-2 were not clearly affected by miRNA-494 expression in the platelets and were therefore unlikely the key contributors to increased platelet clearance. Activation of the platelet receptor GPIb-IX can also lead rapid hepatic clearance and differential expression of the 14q32 cluster has previously been linked to platelet reactivity.[37-39] Indeed, we found that upregulation of miRNA-494 expression following 3GA-494 treatment led to hyper-activation of platelets. Also, as miRNA-494 expression in the liver itself was not affected by 3GA-494, it is most likely that increased platelet clearance is caused by platelet activation in response to 3GA-494 treatment, rather than by upregulation of clearance pathways in the liver.

A surprising observation in this study is the fact that in both platelets and in the spleen, 3GA-494 treatment resulted in short-term miRNA-494 inhibition followed by a clear miRNA-494 upregulation. The upregulation was accompanied by rapid depletion of miRNA-494 precursors in platelets. RNA binding proteins, which are regulated by miRNAs themselves, are able to regulate miRNA-processing in a cell-specific manner. In a previous study, we have demonstrated post-transcriptional regulation of miRNA-494 by Mef2A, which directly binds to pri-miRNA-494.[17] However, which precise mechanism underlies the cell- and tissue-specific autoregulation of miRNA-494 in LDLr$^{-/-}$ mice remains to be determined.

Since each cell type has its own specific miRNA and target gene expression pattern, single miRNA inhibition has distinct effects in each cell type.[29, 40, 41] Above, we have discussed the effects of miRNA-494 and miRNA-329 inhibition on SMCs and myofibroblasts, on macrophages, and on megakaryocyte cells and platelets, but also the endothelial cell is of

importance in atherosclerosis development and progression. We have shown in the past that inhibition of miRNA-494 had little effect on proliferation of human arterial endothelial cells. Inhibition of miRNA-329, however, increased proliferation of endothelial cells.[15] Whether inhibition of miRNA-329 affects plaque size and composition via increased proliferation of endothelial cells, remains for future research.

In our study, we used a scrambled 3GA as control, and in a previous study we have established that this 3GA-ctrl does not show significant differences as compared to vehicle controls.[15] Non-specific effects of this 3GA-ctrl in this study are thus highly unlikely; however, they cannot be completely excluded. In addition, in this study, we used LDLr$^{-/-}$, which is a strain that allows plasma lipid lowering in response to a diet switch. Previously, we have shown therapeutic effects of 3GA-494 in an ApoE$^{-/-}$ mouse model, in which atherosclerosis develops in response to elevated lipid levels, which cannot be lowered using a diet switch. The data from these two studies may thus not be directly comparable due to strain differences, however in both models 3GA-494 treatment improved lesion size and stability. The most important strength of this study is that we used a murine model with fully established lesions and started 3GA-treatment after advanced plaques had been formed, while most studies focus on initial lesion development. Additionally, we included a lipid lowering strategy by changing the diet from high-fat high cholesterol to regular chow. Since most patients present in the clinic with advanced and unstable atherosclerosis and receive routine lipid lowering treatment, we more closely mimicked the clinical situation in this study.

Conclusions

In conclusion, inhibition of 14q32 miRNAs, and particularly of miRNA-494, halts plaque progression and increases plaque stability in mice with established advanced atherosclerotic lesions. Plasma cholesterol levels were lowered further by 14q32 miRNA inhibition than by diet switch alone. Furthermore, pro-atherogenic cells, including inflammatory Ly6C^{hi} monocytes, neutrophils and platelets, were reduced in the circulation. Inhibition of miRNA-494 would therefore be a potential therapeutic target for stabilizing vulnerable lesions in patients and may even prevent surgical interventions in some cases.

Material and Methods

Mice and experimental design

All animal work was performed conform the guidelines from the Dutch government and the Directive 2010/63/EU of the European Parliament and all experiments were approved by the local animal ethics committee (DEC number 14103). Male LDLr$^{-/-}$ mice, aged 8 to 9 weeks, were obtained from our in-house breeding facility (Gorlaeus Laboratories, Leiden University, Leiden, the Netherlands). Food and water were available *ad libitum*.

The timeline of the study is shown in Sup. Fig. 1. All mice were fed a Western-type diet (WTD) containing 0.25% cholesterol and 15% cacao butter (SDS, Sussex, United Kingdom) for 10 weeks to induce advanced atherosclerotic lesions, as described previously.[42] Four weeks after start of the WTD, mice underwent surgical interventions in order to induce carotid artery plaque formation. As described previously, semi-constrictive collars were placed around both carotid arteries.[14] Mice were anaesthetized by subcutaneous injection of ketamine (60 mg/kg, Eurovet Animal Health, Bladel, The Netherlands), fentanyl citrate and fluanisone (1.26 mg/kg and 2 mg/kg respectively, Janssen Animal Health, Sauderton, UK).

Six weeks after collar placement, mice were age-, cholesterol-, and weight-matched, to ensure an equal distribution over all groups before start of the treatment. At that time-point, a subset of mice (n=10) was sacrificed as baseline control. The remaining mice were placed on a regular chow diet to lower plasma cholesterol levels and 3GAs against miRNA-494 (3GA-494; n=10), miRNA-329 (3GA-329; n=10) or negative control (3GA-ctrl; n=10) were administered via the tail vein (i.v.) at a concentration of 1 mg/mouse. 3GAs were designed with perfect reverse complementary to the mature target miRNA sequence and synthesized by Idera Pharmaceuticals (Cambridge, MA, USA). The same sequences of 3GAs (formerly named Gene Silencing Oligonucleotides; GSOs) against miRNA-494 and miRNA-329 were used as described previously.[15] As a negative control, a scrambled sequence was used, designed not to target any known murine miRNA. Sequences of the miRNAs and 3GAs are shown in Table 1. Second and third injections were given two and four weeks after diet switch. During the experiment, total serum cholesterol levels were quantified by enzymatic procedures using Precipath (Roche Diagnostics GmbH, Mannheim, Germany). One week after the final 3GA injection, mice were anaesthetized by a subcutaneous injection of a cocktail containing ketamine (40 mg/mL), atropine (50 µg/mL), and sedazine (6.25 mg/mL). Mice were subsequently perfused with phosphate-buffered saline (PBS) through the left cardiac ventricle, after which carotid arteries and other organs were collected, frozen and used for

further analysis. At sacrifice, whole blood was analyzed on a Sysmex XT-2000i analyzer (Goffin Meyvis, Etten Leur, The Netherlands).

Flow cytometric analysis

At sacrifice, blood, spleen and the mediastinal lymph nodes near the heart (HLN) were isolated. Single-cell suspensions of spleen and HLN were obtained by squeezing the organs through a 70 µm cell strainer. Red blood cells were removed using Ammonium-Chloride-Potassium (ACK) lysis buffer (0.15 M NH4Cl, 10 mM NaHCO3, 0.1 mM EDTA, pH 7.3). Immune cells were analyzed with flow cytometry: T cells ($CD4^+$, $CD8^+$), B cells ($CD19^+$) neutrophils ($CD11b^+Ly6G^+$) and inflammatory monocytes ($CD11b^+Ly6G^-Ly6C^{high}$). Flow cytometric analysis was performed on a FACSCantoII (BD Biosciences) and data was analyzed with FlowJo software (Treestar).

RNA isolation and RT/qPCR

Frozen tissues were crushed by use of pestle and mortar while immersed in liquid nitrogen. After homogenizing and complete evaporation of the liquid nitrogen, TRIzol (ThermoFisher, Bleiswijk, the Netherlands) was added to the samples. For carotid artery RNA isolation, carotid artery segments from three to four mice were pooled and homogenized with a pellet crusher in TRIzol. Total RNA was isolated by standard TRIzol-chloroform extraction. RNA concentration and purity were measured on the Nanodrop (Nanodrop® Technologies).

For microRNAs, microRNA specific Taqman qPCR kits (ThermoFisher, Bleiswijk, the Netherlands) were used for reversed transcription and quantification by qPCR according to the manufacturers protocol. For mRNA, RNA was reverse transcribed using 'high-capacity RNA to cDNA' kit (ThermoFisher, Bleiswijk, the Netherlands). SybrGreen reagents (Qiagen Benelux, Venlo, the Netherlands) were used for the qPCR. The data was normalized using a stably expressed endogenous control. MiRNA-191 was used for microRNAs and Gapdh and Hprt for mRNA. qPCR was performed on the VIIa7 (Applied Biosystems).

Immunohistochemistry

Frozen sections of carotid arteries (10 µm thick) were fixed with Formal-Fixx (ThermoFisher, Bleiswijk, the Netherlands) for 30 min and subsequently stained with hematoxylin and eosin to determine plaque size. Analysis was performed on sections throughout the atherosclerotic lesion (100 µm apart, resulting in the average plaque size value) and at the site of maximal stenosis, this is the site/section of the plaque that has the largest plaque size, using Leica Qwin software, as described previously.[43] Mice with plaques containing a reorganized thrombus

were excluded from the plaque size analysis (three mice in baseline, four mice in 3GA-ctrl, one mouse in 3GA-494 and one mouse in 3GA-329).

To determine lesion size in the three-valve area, cryosections (10 µm thick) of the aortic root were stained with oil red O and hematoxylin (Sigma-Aldrich, Zwijndrecht, the Netherlands). Lesion size was calculated from at least five 10 µm thick sections of the three-valve area. Masson's trichrome staining was used to visualize collagen and determine necrotic core area. Plaque macrophages were stained using a MOMA-2 antibody at a 1:1000 concentration (rat IgG2b, Serotec Ltd., Kidlington, UK). SMCs were stained with α-smooth muscle actin antibody (Clone 1A4, 1:1000, Abcam, Cambridge, UK). Neutrophils were stained using the Naphthol AS-D Chloroacetate Kit (Sigma-Aldrich, Zwijndrecht, the Netherlands). Collagen, necrotic core size, SMCs, macrophages and neutrophils were defined as percentage of total plaque area using Leica Qwin software.

Frozen cross-sections of spleen and liver were prepared (6 µm thickness) and fixed in ice-cold acetone. An antibody against Von Willebrand factor (A0082, 1:1000, Dako, Santa Clara, CA, USA) was used to visualize megakaryocytes in the spleen. Megakaryocytes were counted manually. ImageJ software was used for area measurements.

Bone marrow cells

To isolate BM cells, femurs and tibias of C57Bl/6 mice were dissected and the bone marrow was flushed with PBS. BM cells were filtered through 70 µm cell strainer, centrifuged at 300g for 15 min, and suspended in RPMI 1640 medium containing L-glutamine supplemented with 10% heat-inactivated fetal calf serum (FCSi) and 1% penicillin/streptomycin (P/S). BM cells were plated at a concentration of 1.8 x 10^6 cells/mL and stimulated with 3GA-494 or 3GA-ctrl at a concentration of 10 ng/µl for 48 hours in an incubator at 37ºC with 5% CO^2. After 48 hours of incubation, cells were washed with PBS and resuspended in TRIzol for subsequent RNA isolations.

Human platelets

Platelets, pooled from five different healthy donors with blood type O and Rh positive, were obtained from a blood bank facility (Sanquin, Amsterdam, the Netherlands). The same conditions as used for storage in platelet transfusion were used in the experiment. Platelets in PAS-III buffer with 30-35% plasma were transferred from the transfusion bag into 6-well plates and kept in an incubator at 22ºC with 5% CO^2 at continuously swirling. Platelet concentration was 0,9-1,3 10^9/ mL and contained <1 10^6 leukocytes. Platelets were untreated

or 3GA-494 or 3GA-ctrl was added at a concentration of 10 ng/µl, and incubated for up to 48 hours. As a quality control, pH was measured at each time point and platelet parameters were measured by Sysmex. To pellet the platelets after treatments, platelets were centrifuged at 800 g for 15 min at room temperature and subsequently resuspended in TRIzol.

Statistical Analyses

Results are expressed as mean ± SEM. A Kolmogorov-SmiRNAnov Test was performed to check normal distribution of values. When values were normally distributed, a two-tailed Student's t-test was used to compare single treatment group with the control group. When values were not normally distributed, a Mann-Whitney U test was performed to compare single treatment with the control group. $P<0.05$ was considered significant. A Grubbs' test was used to identify significant outliers ($\alpha<0.05$).

Acknowledgements

This study was supported by a grant from the Rembrandt Institute of Cardiovascular Science (2016), the Dutch Hart Foundation [grant number 2018T051], the CVON GENIUS II program, the LUMC Johanna Zaaijer Fund (2017) and the Austrian Science Fund FWF [Lise Meitner Grant, grant number M2578-B30]. We acknowledge S. Agrawal, B. Boersma and G. Beerends for their technical support.

Conflicts of Interest

There are no conflicts of interest.

Author Contributions

E.V.I., A.C.F., I.B., A.Y.N. designed the experiments; E.V.I., A.C.F., M.J.K, I.B., A.Y.N. conducted the experiments; E.V.I., A.C.F., I.B., A.Y.N., J.K., P.H.A.Q., wrote, reviewed and edited the paper; I.B. and A.Y.N. acquired funding; I.B., A.Y.N. and P.H.A.Q. supervised.

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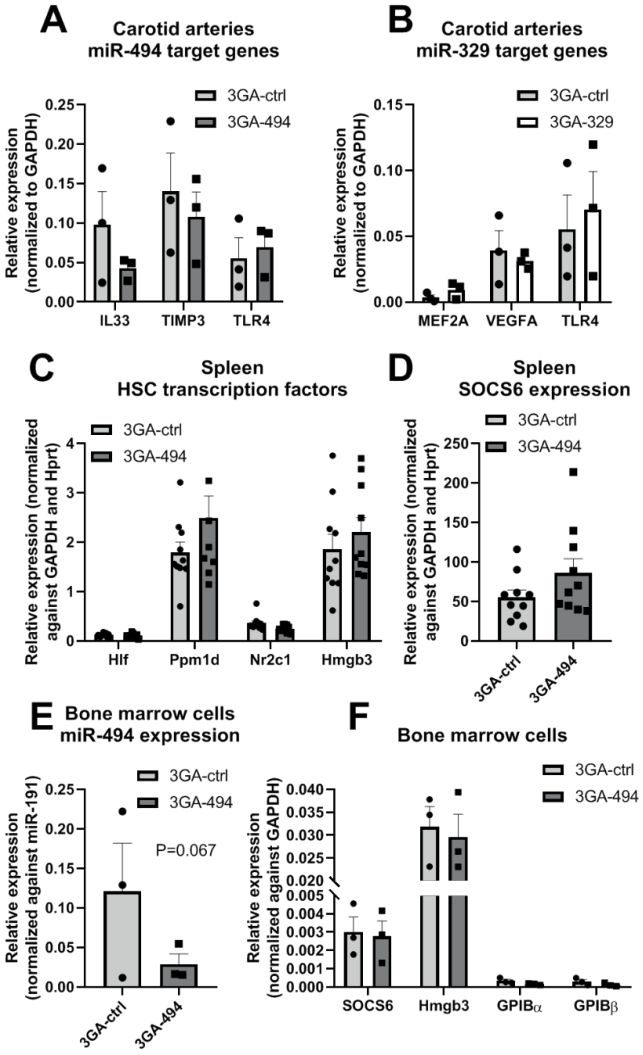
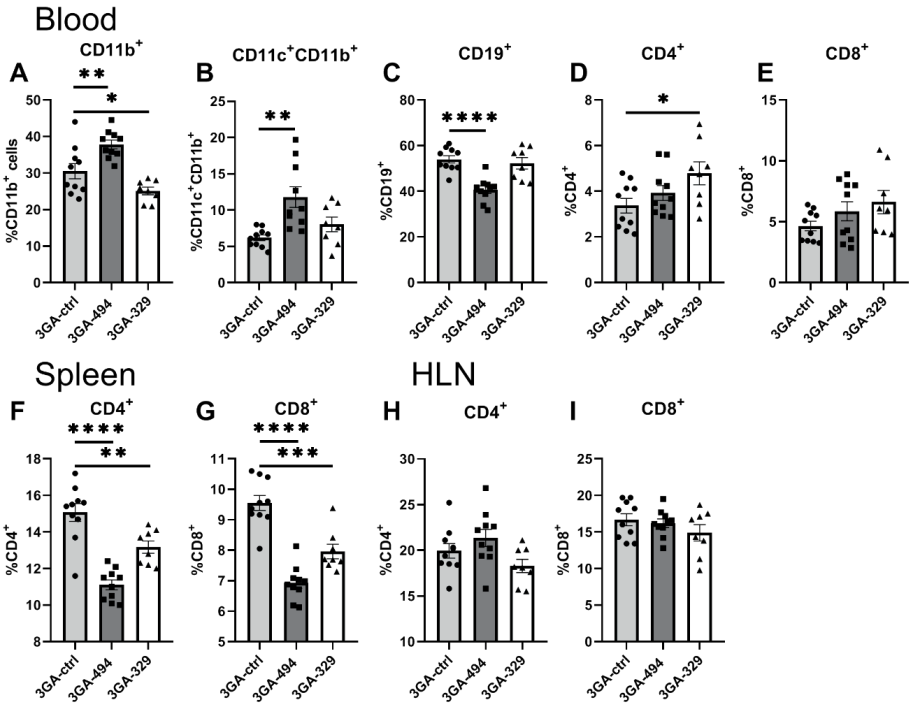
Supplementary data

Supplemental Figure 1. Timeline of the study. All mice were fed a Western type diet for ten weeks to induce atherosclerosis. After four weeks of diet, semi-constrictive collars were placed around both carotid arteries. At week ten, a subset of mice (N=10) was sacrificed as baseline control. The remaining mice were placed on a regular chow diet to normalize plasma cholesterol levels and 3GA treatment against miRNA-494 (3GA-494; N=10), miRNA-329 (3GA-329; N=10) or a scrambled sequence control (3GA-ctrl; N=10) were administered via the tail vein at a concentration of 1 mg/mouse. A second and third injection were given two and four weeks after diet replacement. One week after the final 3GA injection, all mice were sacrificed.

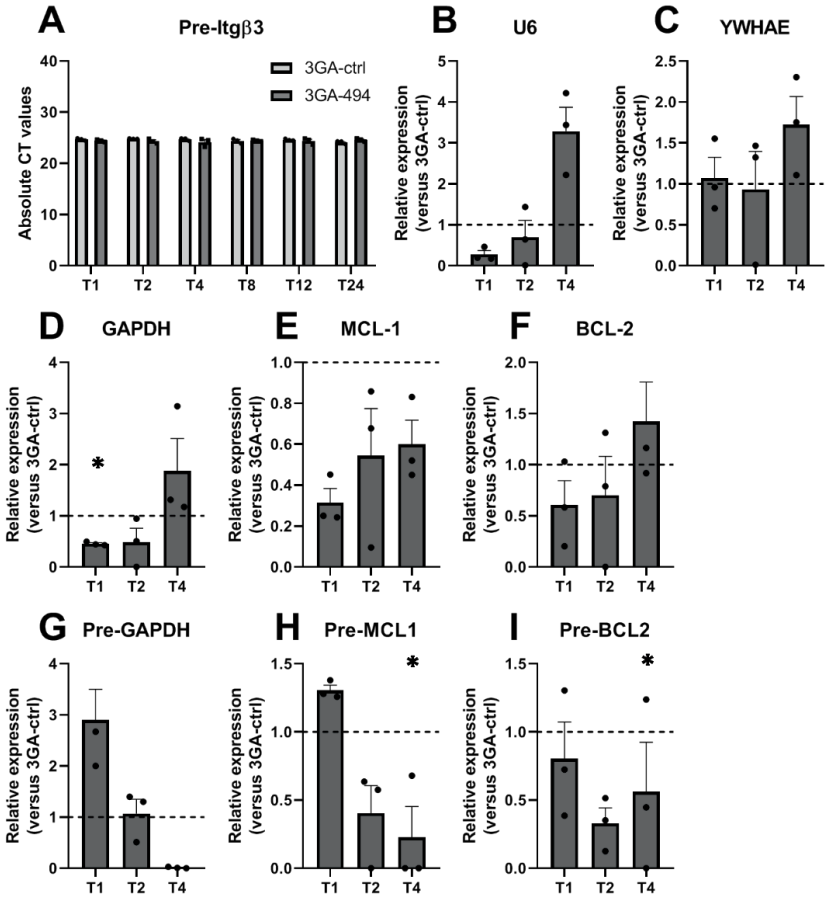


Supplemental Figure 2. MiRNA-494 and miRNA-329 target gene expression in the carotid arteries, spleen and bone marrow cells. (A) Relative expression levels of miRNA-494 and miRNA-329 target genes, interleukin 33 (IL33), TIMP metallopeptidase inhibitor 3 (TIMP3), toll like receptor 4 (TLR4) and myocyte enhancer factor 2A (MEF2A), vascular endothelial growth factor A (VEGFA), TLR4, respectively, one week after the final 3GA injection in the carotid arteries of 3GA-ctrl (N=3) and 3GA-494 mice (N=3). Expression levels were relative to glyceraldehyde-3-phosphate dehydrogenase (GAPDH). (C) Relative expression of transcription factors hepatic leukemia factor (Hlf), protein phosphatase, Mg2+Mn2+ dependent 1D (Ppm1d), nuclear receptor subfamily 2 group C member 1 (Nr2c1) and high mobility group box 3 (Hmgb3), involved in hematopoietic stem cell (HSC) proliferation and differentiation, measured in the spleen of 3GA-ctrl (N=10) and 3GA-494 mice (N=10). Expression is normalized to GAPDH and hypoxanthine guanine phophoribosyl transferase (Hprt). (D) Suppressor of cytokine signalling 6 (SOCS6) expression, normalized to GAPDH and Hprt, in the spleen

of 3GA-ctrl (N=10) and 3GA-494 mice (N=10). (E) Relative miRNA-494 expression in bone marrow (BM) cells treated with 3GA-494 or 3GA-ctrl for 48 hours (in triplo). Expression levels were normalized to miRNA-191. (F) SOCS6, Hmgb3, glycoprotein Ib platelet subunit alpha (GPIBα) and glycoprotein Ib platelet subunit beta (GPIBβ) expression, relative to GAPDH, in BM cells (in triplo). Data are represented as mean ± SEM.



Supplemental Figure 3. Flow cytometric analysis of the blood, spleen and draining lymph nodes of mice treated with 3GA-ctrl, 3GA-494 or 3GA-329 one week after the final 3GA injection. (A) Percentage CD11b$^+$ cells of total input cells from the blood, (B) dendritic cells shown as percentage CD11c$^+$CD11b$^+$ within CD11b+ cells. (C) Percentage CD19$^+$ B cells, (D) CD4 and (E) CD8 T cells of total input cells from the blood. (F) Percentage CD4 and (G) CD8 T cells of total input cells from the spleen. (H) Percentage CD4 and (I) CD8 T cells of total input cells from draining lymph nodes. (A, C-I) Graphs show percentage of total cell input after red blood cell lysis. A two-tailed Student's t-test was performed to compare single treatment to the 3GA-ctrl group. A Grubbs' test was used to identify significant outliers (α<0.05). *P<0.05, **P<0.005, ***P<0.0005, ****P<0.0001 compared to 3GA-ctrl. 3GA-ctrl (N=10), 3GA-494 (N=10) and 3GA-329 (N=8). Data are represented as mean ± SEM.



Supplemental Figure 4. Human platelets treated with 3GA-ctrl or 3GA-494. Human platelets were incubated up to four hours in PAS-III buffer with 30-35% plasma with either 3GA-494 or 3GA-ctrl (in triplos). Platelets were kept in an incubator at 22ºC with 5% CO_2 at continuously swirling. (A) Ct values of pre- integrin subunit beta 3 (ITGβ3) expression in 3GA-ctrl and 3GA-494 treated human platelets, incubated for 1, 2, 4, 8, 12 and 24 hours (in triplos). (B) Relative expression of U6, (C) tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon (YWHAE), (D) glyceraldehyde-3-phosphate dehydrogenase (GAPDH), (E) pro-survival genes and putative targets of miRNA-494 MCL1 apoptosis regulator (MCL1) and (F) BCL2 apoptosis regulator (BCL2), (G) pre-GAPDH, (H) pre-MCL1 and (I) pre-BCL2, relative to pre-ITGβ3 expression and normalized to 3GA-ctrl treated platelets (in triplos) at 1, 2 and 4 hours of incubation. A two-tailed Student's t-test was performed to compare 3GA-494 treatment to the 3GA-ctrl group. *P<0.05 compared to 3GA-ctrl. Data are represented as mean ± SEM.

MiRNA	**Sequence**
hsa/mmu-miRNA-494	5’-UGAAACAUACACGGGAAACCUC-3’
mmu-miRNA-329	5’-AACACACCCAGCUAACCUUUUU-3’
hsa-miRNA-329	5’-AACACACCUGGUUAACCUCUUU-3’
3GA	**Sequence**
hsa/mmu-3GA-494	3’-ACTTTGTATGTGCCCTTTGGAG-X-GAGGTTTCCCGTGTATGTTTCA-3’
mmu-3GA-329	3’-TTGTGTGGGTCGATTGGAAAAA-X-AAAAAGGTTAGCTGGGTGTGTT-3’
hsa-3GA-329	3’-TTGTGTGGACCAATTGGAGAAA-X-AAAGAGGTTAACCAGGTGTGTT-3’
negative control 3GA	3’-TGTACGACTCCATAACGGT-X-TGGCAATACCTCAGCATGT-3’

Table 1. Sequences of miRNAs and 3GAs. ‘X’: Phosphorothioate linker