



HHS Public Access

Author manuscript

Curr Pathobiol Rep. Author manuscript; available in PMC 2016 June 01.

Published in final edited form as:

Curr Pathobiol Rep. 2015 June ; 3(2): 155–161. doi:10.1007/s40139-015-0081-3.

Modeling Disorders of Blood Coagulation in the Zebrafish

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Abstract

Hemostasis, the process of blood clot formation and resolution in response to vascular injury, and thrombosis, the dysregulation of hemostasis leading to pathological clot formation, are widely studied. However, the genetic variability in hemostatic and thrombotic disorders is incompletely understood, suggesting that novel mediators have yet to be uncovered. The zebrafish is developing into a powerful *in vivo* model to study hemostasis, and its features as a model organism are well suited to (a) develop high-throughput screens to identify novel mediators of hemostasis and thrombosis, (b) validate candidate genes identified in human populations, and (c) characterize the structure/function relationship of gene products. In this review, we discuss conservation of the zebrafish hemostatic system, highlight areas for future study, and outline the utility of this model to study blood coagulation and its dysregulation.

Keywords

Zebrafish (*Danio rerio*); Blood coagulation; Thrombocytes; Hemostasis; High-throughput screening

Introduction

Since the first description of the coagulation cascade over a half century ago [1, 2], clinicians have developed the ability to measure various clotting proteins and establish diagnoses in affected patients suffering bleeding or thrombotic diatheses [3]. However, despite these useful tools, genetic variability often complicates the ability to interpret plasma coagulation factor levels [3, 4]. Affected patients with similar clotting *ex vivo* testing profiles may have significantly different clinical manifestations, with high degrees of variable expressivity and incomplete penetrance [3]. Mouse models have been used with

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Compliance with Ethics Guidelines

Human and Animal Rights and Informed Consent

This article does not contain any studies with human subjects performed by any of the authors. With regard to the authors' research cited in this paper, all institutional and national guidelines for the care and use of laboratory animals were followed.

Conflict of Interest

Colin A. Kretz declares no conflict of interest. Jordan A. Shavit has served as a consultant to CSL Behring and Octapharma regarding therapeutic products for patients with bleeding disorders. Angela C. Weyand declares no conflict of interest.

some success to identify genetic modifiers that may underlie this variability, but this approach is time consuming and costly [5–12].

The zebrafish (*Danio rerio*) is a small tropical freshwater fish of the minnow family that has gained popularity as a vertebrate animal model to study human disease [13]. Many of the features that make zebrafish ideal to study in the laboratory are related to husbandry as well as physical and developmental characteristics. First, adults can produce up to 200–300 offspring weekly, which make high-throughput genetic studies in zebrafish particularly robust. Second, embryonic development is external and transparent, allowing detailed observations with as little as a light microscope. Third, zebrafish embryos and larvae during this developmental period [0–7 days post-fertilization (dpf)] are millimeters (mm) in length, and a single 100 mm culture dish can support hundreds of individuals. Compared to other commonly used mammalian animal models, five to tenfold more adults can be housed in equivalent space and at lower costs. These advantages have facilitated massively high-throughput genetic screens for developmental phenotypes in zebrafish [14•]. This has translated into a significant expansion of our knowledge of basic human biology and led to important insights into the pathogenesis and treatment of human diseases. These advantages coupled with emerging genome editing technologies ensure that zebrafish will remain an important model organism. Recently, these tools have facilitated investigation into the processes of hemostasis and the pathogenesis of thrombotic disorders. This field has historically been underrepresented in use of the zebrafish model but is well positioned to take advantage of its unique and powerful capabilities.

Coagulation Factors are Highly Conserved in Zebrafish Genomic Sequence

The zebrafish genome is highly conserved with humans, and 70 % of human genes possess apparent zebrafish orthologs [15•]. Zebrafish experienced a massive genome duplication during evolution with the result that 30–40 % of genes remain duplicated [16•]. As a consequence, some genes have divided their functions between paralogs or acquired new roles. Although the majority of coagulation factors are present as a single copy, a few appear to be duplicated [17]. The blood coagulation system has also been shown to be conserved in other non-mammalian vertebrates, such as the teleost *Fugu rubripes* (Fugu, puffer fish) [18–20]. These data provided an initial foundation suggesting that the zebrafish model would be well suited for blood coagulation research.

Conservation of the Coagulation Cascade in Zebrafish

Zebrafish coagulation factor genes are highly conserved with their corresponding orthologs in humans. To study the impact of targeted gene knockdown, antisense morpholino oligonucleotides (MOs) [21] had been the technology of choice in the preceding decade. Reduction of prothrombin (F2) using MOs demonstrated a dual phenotype [22] with similarity to the mouse *F2* knockout [23, 24]. At 1 dpf, many embryos demonstrated severe growth retardation. This was followed on 2 dpf by bleeding along the trunk, with secondary anemia, compromised circulation, and pericardial edema. Of the embryos that did not exhibit these phenotypes, 5–10 % developed intracerebral hemorrhage and showed a lack of thrombus formation following laser-induced endothelial injury.

Zebrafish factor VII (F7) shares a high degree sequence homology to mammalian factor VII and was also shown to be produced and secreted into the circulation by the liver [25], akin to mammalian factor VII. Immunodepletion of F7 resulted in prolonged fibrin generation upon stimulation using thromboplastin as a source of tissue factor, demonstrating an intact and functionally conserved extrinsic coagulation pathway in zebrafish. Specific MO knockdown of *f7* prolonged the time to occlusion following laser injury in larvae, implying that a zebrafish ortholog to tissue factor can support F7-dependent coagulation in vivo [26]. Although an ortholog to F7-activating protease (Fsap/Habp2) is present in zebrafish, MO knockdown of *fsap* did not affect time to occlusion or activation of F7 [26]. Recent in vitro studies have also called into question the role for FSAP-mediated activation of F7 [27], in support of the findings in zebrafish. However, MO knockdown of the transmembrane serine protease *hepsin* resulted in decreased levels of activated F7, as well as prolongation of the laser-induced time to occlusion [26]. These results are inconsistent with data from the targeted *Hepsin* knockout mouse, which had no abnormalities in various clotting assays [28]. These conflicting data suggest that, despite sequence conservation with human orthologs, Hepsin and Fsap function might not be completely conserved between zebrafish and mammals. Alternative roles for these proteases in zebrafish might be relevant to human biology and warrant continued study.

von Willebrand factor (Vwf) is a critical protein responsible both for adhesion of platelets to the injured vessel wall and as a circulating chaperone for coagulation factor VIII [3, 29]. The human gene is extremely large and consists of 52 exons, with an excessively large exon 28. These features are duplicated in zebrafish, although the overall locus is compressed from 176 to 81 kilobases (kb) [30, 31]. Human VWF has a propeptide and is a target for cleavage by the protease ADAMTS13, features which appear to be conserved based on the *vwf* cDNA sequence [31]. Although the overall protein identity is 46 %, surprisingly the A1 and A2 domains (platelet binding and ADAMTS13 proteolysis, respectively) were the least conserved [31]. RNA in situ hybridization in embryos and larvae showed no signal in endothelial cells [31], although immunostaining with an anti-human VWF antibody detected widespread vascular expression [32]. Depletion of *vwf* by MO knockdown resulted in intracranial and yolk hemorrhage as well as impaired thrombocyte aggregation [32]. Expression of the zebrafish *vwf* cDNA in mammalian cell culture demonstrated assembly of multimers and pseudo-Weibel-Palade body-like organelles [31], both hallmarks of mammalian VWF. These data demonstrate conservation of the most essential roles of zebrafish and human VWF. This suggests that zebrafish may be a useful in vivo model for studying mutations within VWF that cause von Willebrand disease, the most commonly inherited bleeding disorder.

Fibrinogen is a hexamer that is assembled as a homodimer of three polypeptide chains, fibrinogen α , β , and γ (FGA, FGB, and FGG) [3, 33]. Genomic sequencing identified syntenic orthologs on zebrafish chromosome 1 (*fga*, *fgb*, and *fgg*) [15•]. This was also corroborated through cytogenetic in situ hybridization [34], although further study identified some differences. For example, the zebrafish *fgg* locus was noted to be spaced relatively farther from *fga* and *fgb* with two intervening genes, whereas the 3 loci are serially clustered in humans [34]. At the amino acid level, Fgb and Fgg are greater than 50 % identical to their

human orthologs, whereas *Fga* shares only ~34 % identity [34]. As expected, expression of all three chains was detected in hepatic cells through in situ hybridization of larvae, although there was signal in the syncytial layer surrounding the yolk [34, 35], consistent with changes in sites of gene expression during embryonic development. Liver-specific expression of an *fgb-egfp* (enhanced green fluorescent protein) transgene revealed functional conservation, as the expressed fusion protein accumulated in thrombi induced by laser-mediated endothelial injury [35]. Of note, adult transgenics showed occasional signs of external hemorrhage, suggesting functional dysfibrinogenemia due to the presence of the EGFP tag [35], serving as an important caution for modifications to the COOH-terminus of the fibrinogen molecule. Intraventricular and intramuscular hemorrhage were the primary phenotypes observed after individual and combined MO knockdown of the fibrinogen chains, strikingly similar to the symptomatology of patients with hypo- and afibrinogenemia [35].

The discovery and application of genome editing using zinc finger nucleases (ZFNs), TAL effector nucleases (TALENs), and CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats) RNA-guided nucleases to alter target sequences has great potential for rapid and robust gene disruption in zebrafish [36, 37, 38, 39]. These offer an alternative to MO technology, which can be unpredictable and often yields incomplete gene silencing. Recently, a systematic validation study of vascular phenotypes derived from MO knockdown in comparison to targeted genetic mutants derived through genome editing showed poor phenotypic correlation [40]. Although the authors did not test for the potential off target effects of genome editing as an explanation for the discrepancies, the observed biological changes following MO-induced gene silencing are nonetheless called into question, at least for studies of vessel development.

A knockout of *fga* using ZFNs has been described [41], and complete ablation of fibrinogen was demonstrated using a panel of anti-zebrafish fibrinogen antibodies. Overt hemorrhage was observed in adult homozygous mutant fish but not in embryos and larvae suggesting variable roles for fibrinogen during development. The reduced viability observed in the *fga*^{-/-} mutant fish population was incompletely penetrant, which may reflect the known genomic heterozygosity of laboratory zebrafish [15, 42]. In support of this conclusion, *Fga* ablation is variably lethal on different mouse genetic backgrounds [43].

In addition to known procoagulant effectors of the blood clotting system, zebrafish also express conserved natural anticoagulant factors, including antithrombin III (*At3*) [44, 45]. Targeted ablation of *at3* using ZFNs was followed by spontaneous intracardiac thrombi with a variable range of lethality in adulthood [45]. Although the endpoint of pathologic thrombus formation was consistent with the mouse knockout [46] and patient data [3], it occurred at a much later time point than the in utero lethality observed in mammals. Stimulation by laser-induced vascular injury in 3 dpf larvae resulted in the failure to form an occlusive thrombus, a phenotype more consistent with bleeding rather than thrombophilia. Infusion of plasma-derived human fibrinogen restored the ability to develop induced thrombi, suggestive of a consumptive coagulopathy in *at3*^{-/-} mutant fish. Injection of fluorescently labeled human fibrinogen into larvae resulted in widespread fluorescence accumulation in the circulatory system of unprovoked *at3*^{-/-} mutants. This would be expected in the syndrome of disseminated intravascular coagulation (DIC), a disorder

resulting from loss of regulation of the coagulation system [47]. Importantly, larval DIC was reversed by expression of human *AT3*, which was leveraged as an in vivo platform to study the impact of previously described *AT3* mutations [45••]. Mutations in the *AT3* P1 arginine eliminated the capacity to rescue this phenotype, whereas disruption of the *AT3* heparin binding site had no effect. These data highlight the power of coupling zebrafish and genome editing tools to study human diseases. Whole genome sequencing of human disease populations regularly uncovers genome sequence variants of unknown biological importance. As this technology is increasingly applied to the clinic, there is a recognized need for rapid and robust tools for evaluating the impact of gene sequence variants on protein function. Zebrafish may offer the unique capacity to rapidly characterize sequence variants in an in vivo setting.

Defining the Role of Thrombocytes in Hemostasis and Thrombosis

The closest equivalent to the platelet in zebrafish is the thrombocyte, a nucleated cell also found in birds [48], and evidence continues to support a functional correlation to mammalian platelets. Previous studies in trout (*Oncorhynchus mykiss*) established that like platelets thrombocytes respond to either thrombin or a thromboxane mimetic (U-46619), by forming aggregates [49]. Furthermore, other canonical platelet agonists (including collagen, ADP, ristocetin, and arachidonic acid) cause zebrafish thrombocytes to aggregate, and many receptors have been found to be conserved (P2Y₁₂, Gp6, Gp1b, and Tbx2r, respectively) [50]. Thrombocyte aggregation can be inhibited by an RGDS tetra-peptide, suggesting a role for an integrin-like fibrinogen receptor during thrombocyte accumulation at sites of injury [51]. Although ultrastructure analysis has identified vesicles within thrombocytes that resemble platelet granules [50], more direct evidence for a fully functional open canalicular system is still needed.

Zebrafish lack an analog to the polyploid megakaryocyte, and thrombocyte production remains incompletely understood. Thrombopoietin (Tpo) and its receptor (Mpl) are conserved and MO knockdown of the latter decreased mobilization of a thrombocyte/erythroid precursor cell population (TEPs) from the extravascular compartment between the dorsal aorta and caudal vein [52]. Recently, TEPs were identified and isolated from zebrafish, and stimulation by zebrafish Tpo promoted thrombocyte differentiation, whereas stimulation by erythropoietin promoted erythroid differentiation [53]. The high-throughput screening capacity of zebrafish could provide a unique opportunity to identify novel mediators of thrombocyte development. Study of zebrafish thrombocytes has led to novel insights into platelet function (reviewed elsewhere [54, 55]), suggesting that results from thrombocyte production screens in zebrafish may be relevant to human biology.

Zebrafish Screens from Hematology to Hemostasis

The use of zebrafish as a model to study hematopoiesis is well established and serves as a proof-of-principle for guiding future discoveries in hemostasis. Forward genetic screens employing large-scale mutagenesis led to the identification of novel genes that regulate blood development [56, 57]. Furthermore, this approach has identified key mediators of human diseases, such as the link between ferroportin and hemochromatosis [58, 59]. The

first genetic screen in blood clotting employed laser-induced endothelial injury to produce thrombi in larvae, uncovering a mutation linked to the prothrombin (*f2*) locus [60]. These studies are facilitated by the highly fecund nature of zebrafish and the accessibility of their circulatory system to observation, features that are critical to hemostasis research.

Zebrafish also have been utilized for small molecule screens in both embryos and larvae [61]. For example, a stable derivative of prostaglandin E₂ (PGE₂) was shown to enhance hematopoietic stem cell engraftment in zebrafish embryos and mice [62]. This discovery was extended into nonhuman primates [63], followed by a small human clinical trial with umbilical cord blood transplantation [64]. This example proves the feasibility of translating chemical screens performed in zebrafish into treatments for human diseases.

In hemostasis, recent experimentation testing the safety of cationic PAMAM dendrimers, an emerging basis for nanoparticles in biomedical applications, revealed substantial thrombocyte and fibrinogen aggregation akin to disseminated intravascular coagulation (DIC) [65]. This important toxicity result detected in zebrafish urges caution in moving forward to human trials for applications using this nanoparticle. With the conservation of the major components of the blood coagulation pathway, zebrafish are particularly well suited for screening small molecules that may evolve into the next generation of anticoagulants. Such a screen can readily be optimized to focus on targeting thrombosis-related pathologies while limiting the complication of bleeding that plagues the majority of traditional and new oral anticoagulants [66, 67].

Dissection of Human Coagulation and Associated Disorders Using Zebrafish

Blood coagulation requires well-timed orchestration of soluble plasma proteins with hematopoietic and vessel wall cellular mediators. As demonstrated for At3, zebrafish are uniquely poised to rapidly screen novel human sequence variants in an *in vivo* setting where the complexity of the entire circulatory systems comes to bear. This feature may be particularly useful in human genetics where validation of a genomic sequence variant linked to a particular disease is a major bottleneck. Zebrafish have assisted this process in a number of fields, including thrombocytopenia and associated disorders, as biochemical or cellular approaches are not always sufficient for such complex systems. Human familial autosomal-dominant thrombocytopenia was linked to a locus on chromosome 10p, and a missense mutation in microtubule-associated serine/threonine-like kinase (*MASTL*) was identified as a potential candidate gene. MO knockdown of the zebrafish ortholog of *MASTL* recapitulated clinical features, including thrombocyte deficiency and reduction of *itga2b* and *mpl* expression, consistent with a *MASTL*-dependent thrombocytopenia [68]. Similar experiments in zebrafish larvae also confirmed *NBEAL2* and *RBM8A* as the mutated loci in the gray platelet and thrombocytopenia with absent radii syndromes, respectively [69, 70].

Thrombosis models have been widely used in mice to study blood coagulation in an *in vivo* setting; however, these techniques are technically cumbersome and low throughput [71]. Induced thrombosis in zebrafish larvae offers many advantages and has been used to validate targets identified via systems biology. Targeted screening in zebrafish of five

predicted thrombocyte-expressed genes uncovered a previously unappreciated role for BAMBI (bone morphogenic protein and activin membrane-bound inhibitor) in laser-induced thrombus formation [72]. Subsequent studies in mice validated these results and determined that BAMBI expressed on the vessel wall, and not platelets, supports thrombus stability following laser-induced injury [73]. Zebrafish have also been used to validate potential mediators of thrombus formation identified from platelet mRNA expression profiling or genome-wide association studies (GWAS). These studies identified *COMMD7* and *LRRFIP1* as genes that contribute to thrombus formation [74]. Furthermore, zebrafish were successfully used to validate hits identified via GWAS meta-analyses for platelet count and mean platelet volume [75], providing a highly tractable system for validation of genomic signals from human populations.

Conclusion

Over the last two decades, the zebrafish has been established as a vertebrate organism with significant benefits beyond traditional mammalian models. The work summarized above demonstrates that it is a useful tool for the study of hemostasis. However, success in these endeavors will depend on continued delineation of the conservation among the key mediators of the blood clotting system. Such conservation provides the rationale for employing some of the most powerful high-throughput screening tools available to the zebrafish investigator. Zebrafish are particularly well suited for small molecule screens [13] that may identify novel anticoagulants. Forward genetic screening may uncover previously unknown mediators of thrombosis and thus possible new targets for future anticoagulant therapy. Furthermore, combined with emerging genome editing approaches, zebrafish are a convenient model to test hypotheses uncovered by systems biology pipelines, validate candidate disease genes, and study structure/function relationships for proteins in an in vivo setting. Leveraging the power of zebrafish offers the opportunity to enhance future research into the regulation of hemostasis and pathogenesis of thrombotic disorders that may ultimately improve the quality of diagnosis and treatment of important human diseases.

Acknowledgments

This work was supported by the National Hemophilia Foundation Judith Graham Pool Fellowship (C.A.K.), NHLBI HL007622 (A.C.W.), American Heart Association #14IRG18840066, the Bayer Hemophilia Awards Program, and the National Hemophilia Foundation/Novo Nordisk Career Development Award (J.A.S.). J.A.S. is the Diane and Larry Johnson Family Scholar of Pediatrics and Communicable Diseases.

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