

Review

The coagulation of insect hemolymph

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Abstract. In contrast to both vertebrates and non-insect arthropods, little is known about the coagulation of hemolymph (hemostasis) in insects. We discuss the integration of the hemostatic response with other branches of the insect immune system. We also describe the present stage in the characterization of both soluble and cellular factors that contribute to hemostasis in insects. The factors of the well-characterized clotting cascades of vertebrates,

primitive chelicerates and crustaceans are used to assess the implications of sequencing the whole *Drosophila* genome for searching candidate genes involved in hemostasis. Some striking similarities between blood clotting in vertebrates and the reaction of insect cells involved in hemolymph coagulation have implications for a phylogenetic comparison of hemostasis between divergent animal classes.

Key words. Insect immunity; blood clotting; phosphatidylserine; phenoloxidase; coagulogen; transglutaminase; *Drosophila melanogaster*.

The role of coagulation in insect immunity

Much of the evolutionary success of insects and other arthropods has been attributed to their efficient immune system. Like vertebrates, insects rely on both soluble factors and immune-competent cells to defend themselves against foreign intruders [1–6]. In contrast to vertebrates, there is little evidence for adaptive changes of the immune response during the individual's life [2]. Nevertheless, there is strong induction of gene expression for a number of immune components following the first encounter of the foreign antigen, including components of the signal transduction machinery and effector molecules [7]. Induction by microbial elicitors has been used successfully as a hallmark to identify immune molecules and differential expression screens as a method of isolating the corresponding complementary DNAs (cDNAs) and genes [8–12].

In addition to de novo induction of immune components, there are a number of reactions that take place immediately after an insect has been wounded (the so-called wound response) and are often the basis for subsequent immune responses involving microbe-specific reactions [13–18]. A large fraction of these initial responses serve to seal a wound in order to avoid loss of body fluid and at the same time restrict the movement of microbes [17, 19]. The activities that contribute to stopping loss of body fluids are collectively called the hemostatic system. The formation of a clot, which seals the wound, is achieved in arthropods as in vertebrates through the activity of clotting systems [19, 20]. Many arthropods contain enzyme cascades, which result in the formation of a clot by protein cross-linking. Since arthropods have an open circulatory system, they use clot formation much more extensively than vertebrates without the potential danger of thromboses. One of the cascades leading to cross-linking is the clotting (or coagulation) system, which ultimately

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leads to deposition of specialized clottable proteins, a number of which have been isolated ([19, 21], and below). The second is the PPO activating cascade, which leads to the (mostly enzymatic) activation of phenoloxidase (PO) [22]. PO has a number of activities, including immune functions as well as developmental functions, for example the hardening of the insect cuticle [23]; a function of PO during the wound response has been suggested as well [24, 25]. Most of the recent investigations on the PPO-activating cascade have focused on its immune function, in particular its activation by microbial elicitors. Here, we discuss both cascades in a number of invertebrate species and speculate on the implications for insects, where less is known about the physiology of coagulation, but genomic (*Drosophila melanogaster* [26]) and biochemical data are available.

Coagulation in non-insect species

Most of the research on arthropod clotting systems has been performed in non-insect species, including crustaceans and two ancient chelicerates, the horseshoe crabs *Limulus polyphemus* and *Tachypleus tridentatus*. Since there are a number of excellent reviews on clotting in horseshoe crabs [20, 27], we summarize only those aspects that might have implications for the insect clotting system, in particular the domain structure of the proteins involved. The LPS-activated clotting system in the horseshoe crab comprises three proteases (factor C, factor B and proclotting enzyme) which activate each other sequentially in a proteolytic cascade, leading finally to the precipitation of the clottable protein coagulogen into insoluble coagulin. In addition to a serine protease domain, the clotting factors contain a number of domains, including epidermal growth factor (EGF)-like domains; sushi domains, which are also found in mammalian complement factors; C-type lectin domains and clip (or disulfide-knotted) domains. The latter domain shows similarities to antibacterial peptides (big defensin) and may be released during the activation process of the cascade. It was speculated that this and other peptides released during the activation of the cascade have antibacterial activity, adding to the efficiency of the clotting cascade, which leads to both immobilization and killing of bacteria. Antibacterial activity was recently shown for the clip domain of the PPO-activating enzyme from crayfish [28]. Gelation in horseshoe crabs does not seem to involve cross-linking through the activity of a transglutaminase as observed in other arthropods (see below), although transglutaminase activity has been found in horseshoe crab hemocytes (summarized in [20]). A second activation pathway, which is initiated by the fungal elicitor β -glucan, involves the heterodimeric factor G, which contains some additional domains worth mentioning. The α sub-

unit is composed of several regions with similarities to bacterial enzymes involved in carbohydrate degradation (glucanases and xylanases). Since some of the functionally essential amino acids of the active sites are missing in these domains, they are likely to act as lectins, which retain substrate specificity of the enzymes but lack their activity. A mechanism to keep the coagulation reaction localized may involve a tight regulation by serpins (serine protease inhibitors). An important feature of the horseshoe crab clotting system is the recognition of microbial elicitors, which bind to factor C (in the case of lipopolysaccharide, LPS) or factor G (in the case of β -glucan). The sensitivity of horseshoe crab hemolymph towards LPS is in fact the basis for the so-called *Limulus* test, which is used in the clinical field. To our knowledge, there are no reports showing activation of the system in the absence of microbial components, even though the effective closure of epidermal lesions is an essential requirement in aquatic organisms.

In crustaceans, clotting has been shown to depend on the activity of the calcium-dependent enzyme transglutaminase, which has cross-linking activity. Transglutaminase is released by hemocytes or muscle cells upon wounding and cross-links clottable hemolymph proteins. Clotting proteins have been isolated from a number of crustacean species, including a crayfish [21, 29], shrimp [30] and sand crayfish [31]. They are often large (~200 kDa) lipoproteins with similarity to vitellogenins [21]. As in the horseshoe crab, the blood clotting system in vertebrates is dependent on the activity of a proteolytic cascade (including the protease thrombin) leading ultimately to the precipitation of fibrin. It also involves a thrombin-activated transglutaminase (blood coagulation factor XIIIa), which stabilizes fibrin aggregates through cross-linking. Although both horseshoe crabs and vertebrates employ proteolytic cascades to achieve hemostasis, there is little similarity in the primary structure of the proteins involved in both reactions. Although sequence similarity might be rare, protein domains are shared between members of protein cascades from different animal groups [32]. The best-studied example is the von Willebrand factor (vWF), which plays a central role in blood clotting. Domains with similarity to vWF are present in at least one insect protein that is involved in hemolymph clotting [33]. One protein that does show high similarity between arthropods and vertebrates is in fact transglutaminase, which is involved in clotting reactions in both crayfish and vertebrates (see above).

The PPO-activating cascade

The PPO activating system is a proteolytic cascade that is activated by a number of microbial elicitors. A concept of immune recognition that has emerged in recent years is

that microbial elicitors (pathogen-associated molecular patterns, PAMPs) are recognized by specialized binding proteins (the so-called pattern recognition proteins, PRPs), leading to the activation of a range of immune functions [2, 34]. Such immune functions include phagocytosis, the PPO-activating cascade and the production of antibacterial peptides. The PPO-activating cascade consists of a number of proteins, including several proteases, which ultimately activate PO. The activated PO is involved in several reactions, including melanin formation, production of reactive oxygen species [35] and to some extent sclerotization as part of the formation of the cuticle, capsule formation and wound healing. The concept of pattern recognition has gained strong support through the identification of a number of proteins that recognize microbial elicitors and subsequently activate the PPO-activating cascade [36–39]. Together with some older findings, the PPO-activating cascade is usually discussed as an integral part of innate immunity, which is activated in the presence of PAMPs and not as part of the hemostatic system. While this picture is certainly true, there are some additional aspects of the PPO-activating cascade that might link PO activity to other functions, including hemolymph clotting. A link between both systems has been suggested by others as well [40]. Some of these aspects include:

- the presence of multiple PO genes in several species, which may differ in their enzymatic activity and substrate specificity. For example, *Drosophila* contains three and *Anopheles* at least six different PPO genes (see also below the specific aspects of the *Drosophila* genes);
- the possible activity of regulatory proteins within the PPO-activating cascade, including dopachrome-converting enzyme and quinone isomerase [41]. Shifts in the relative concentration of key metabolites of the PPO-activating cascade are expected to influence PO activity, leading in some cases to an increase of sclerotization at the expense of the production of antibacterial quinoid intermediates of melanin biosynthesis [35];
- early findings that PPO can also be activated by non-microbial elicitors like denaturing agents or denatured proteins, which may indicate a role for PO in house-keeping functions to be activated in the absence of microbial elicitors. Alternative nonmicrobial elicitors include certain phospholipids, which are released from damaged cells [41], and denatured lipophorin [42];
- an unsolved issue is the mechanism by which PO is transported into hemolymph and to the cuticle [24] in the absence of any signal peptide in the primary sequences, which code for PPOs [43–46]. There have been recent reports of a mechanism which allows transport of proteins across membranes independent

of the presence of a signal peptide in the primary sequence [47, 48]. One of these proteins (the engrailed homeoprotein) associates with specialized membrane structures, so-called microdomains, before getting access to a compartment which is involved in secretion [49]. It remains to be determined whether this mechanism also applies to PO, or other proteins, which are apparently secreted in a nonclassical pathway [50, 51].

Although the PPO-activating cascade has recently been discussed foremost as an independent part of humoral immunity, it is likely that PO cooperates with other branches of the immune system, including the clotting system. By binding to the clot, it might enhance the cross-linking activity and/or add antibacterial activity to other immune mechanisms that are localized there [52] and aid in wound healing [53].

The coagulation cascade in insects

In contrast to other arthropods, little is known about the clotting system in insects. Similar to the situation in vertebrates and non-insect arthropods, hemolymph coagulation in most insects involves cellular and humoral components which are inactive on their own [19]. Full clotting activity has been shown to depend on both cellular and humoral procoagulant activity in a number of species. Much of the early work has been on the morphological characterization of the cellular reactions that are found in different insect species [19], leading to a classification of four different types of coagulation patterns [54]. At present, the molecular characterization of the proteins involved in hemolymph clotting is lagging behind the detailed morphological characterization of the cell types involved.

Humoral procoagulant activity

When the sequencing of the *Drosophila* genome reached completion, there was hope that *Drosophila* homologues could be identified for many of the known immune molecules from other systems, including components of the clotting cascade. But as mentioned above, only a few arthropod proteins involved in hemolymph clotting can be considered true orthologues of vertebrate clotting factors. Even comparison among different classes of arthropods shows that different proteins are utilized for establishing a functional clot. Therefore, it is not surprising that sequence searches for most members of the hemostatic system of crustaceans, chelicerates or humans fail to detect any orthologues in the *Drosophila* genome. One of the genes that can be positively identified by performing sequence comparisons is, just like in crustaceans, the

enzyme transglutaminase (or factor XIIIa in vertebrates), for which there is high similarity to a protein in the *Drosophila* genome (CG7356). No obvious similarities between *Drosophila* proteins and crayfish clotting protein or the horseshoe crab coagulogen can be found. Although vitellogenin also exists in insects, its function in the clotting system may be different from crustaceans, since a vitellogenin-like protein has recently been implied in the melanization reaction [55]. Nevertheless, in a number of insect species one coagulogen has been identified as a lipid-carrying protein called lipophorin [56–59]. Lipophorin is a multifunctional protein in insects that consists of three subunits, all of which have been also implied in immunity. In addition, there has been a report on a 22-kDa protein from *Manduca sexta* (hemofibrin), which forms a fibrous clot that can be visualized using electron microscopy [60].

A surprisingly high number of protease genes are present in the *Drosophila* genome, including a number of proteases with clip domains, which are present in protease members of the PPO-activating cascade in other insects [61] and crustaceans [62]. Some of these proteases might be involved in digestion and others in proteolytic cascades during developmental processes, but some may be involved in immune functions. A number of observations show that members of proteolytic cascades can be involved in both development and immunity [2, 63]. This suggests that it might be necessary to reconsider some of the proteases that have been identified due to their developmental phenotype as multifunctional proteases with both developmental and immune functions. Included in this class of proteins may be gene products which show high similarity to certain proteases but lack some of the amino acids known to be necessary for catalytic activity. One such protein is the *masquerade* gene product, which has been identified as a developmentally important protein in *Drosophila* [64] and shows similarity to proteins with immune function in crayfish [62, 65] and insects [66].

There are a number of proteins from other insects, which have been implied in induction of coagulation reactions, including M13 [67] and scolexin [68] from *M. sexta* as well as hemocytin, a multidomain protein from *Bombyx mori*, which has significant similarity to vWF [69].

Although true homologues of proteins involved in clotting in other species are somewhat difficult to identify in the *Drosophila* genome [32, 70], there are a number of annotated genes which might turn out to play an important role in hemolymph clotting or related processes. Here we provide a list of some examples, which is far from being complete but points towards some potentially interesting genes and their products. There are a number of predicted gene products which contain domains known to exist in clotting factors from other species. These domains include the immunoglobulin fold, the EGF-like do-

main, domains with similarity to vWF, sushi domains, clip domains and C-type lectin domains [26, 71, 72]. In most cases the functional importance of these domains has still to be confirmed. One also has to keep in mind that the annotation of many genes is preliminary and might change in years to come. Nevertheless, there are some predicted genes with unique combinations of domains that seem worthy of further functional analysis:

- a protein with similarity to *Bombyx* hemocytin exists in the *Drosophila* genome (CG7002) and will most likely turn out to be involved in immune reactions;
- three genes coding for POs, one of which seems to be expressed in SL2 cells, as there are at least two ESTs (expressed sequence tags) which have been derived from these cells. SL2 cells are usually used as a negative control to assay PO activity, opening the possibility that traditional PO assays may leave some PO-like activity undetected;
- a number of *Drosophila* homologues of a gene for dopachrome conversion enzyme from *Aedes aegypti*, which can be found in GenBank [AF288384, unpublished]. One of these homologues is the *yellow* gene, mutants of which show defects in melanization. Homologues from other species include a gene for a protein from royal jelly (RJP57-1, [73]);
- members of the pentraxin family in *Drosophila*. Pentraxins include C-reactive protein (CRP) and a CRP-related protein from horseshoe crab, which are involved in the activation of the complement system, and the clotting system respectively;
- in addition to PO activity there is a laccase-like activity which can be identified in the insect cuticle [74]. Since to our knowledge no laccases have been cloned from insects, we used plant laccase genes to search the *Drosophila* genome and identified four genes with significant similarity (CG7871, CG3759, CG19408, CG5959). Interestingly, one of these (CG3759) displays additional similarity to the type C domain of vWF. It remains to be investigated in which tissues these genes for laccase-like proteins are expressed.

Cellular aspects of the coagulation cascade

In contrast to the humoral part of the clotting system, which shows little similarity between vertebrates and insects, there are a number of similarities on a cellular basis between the reaction of hemocytes in insects and platelets in vertebrates. This includes the mechanisms that contribute to clot formation in insects. They comprise the release of granular components [13] as well as the formation of membranous vesicles, so-called microparticles, which are released from blood cells [54]. Most prominent among the biochemical similarities is the exposure of negatively charged phospholipids (visualized

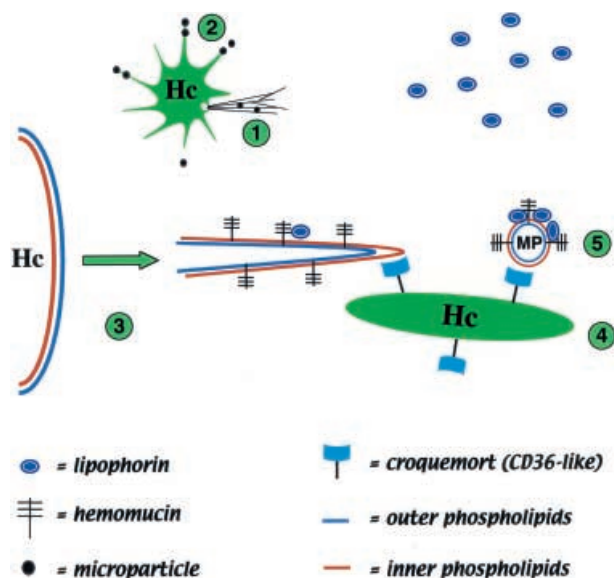


Figure 1. Scheme of hemolymph coagulation in insects. Coagulation of insect hemolymph comprises the activation of both hemocyte and hemolymph coagulogen activity. Hemocytes (Hc) show two reactions, namely degranulation (1), and the formation of microparticles (2). Microparticle (MP) formation is accompanied by a reversal in membrane polarity, leading to the exposure of (mostly negatively charged) lipids from the inner leaflet of the membrane lipid bilayer on the cell surface (3). These lipids can be recognized by receptors like the *Drosophila* croquemort protein or other CD36-like proteins on hemocytes, which are not involved in clot formation during subsequent wound healing (4). The hemocyte coagulogen attracts hemolymph coagulogen, comprising lipophorin (5) and possibly other factors. See text for further details.

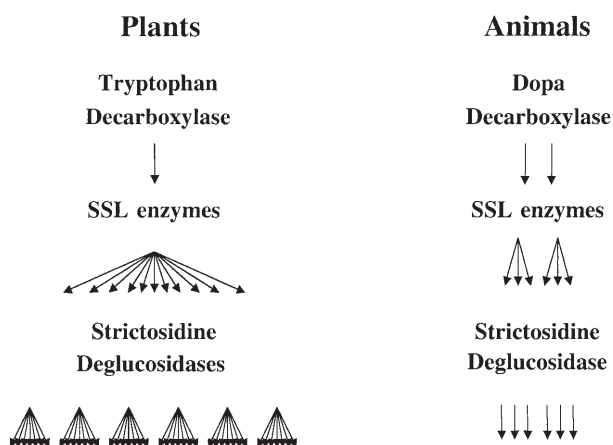


Figure 2. Biosynthetic pathway involving strictosidine synthase-like (SSL) enzymes in plants and animals. The pathway has diversified at least at two levels in plants, leading to a multitude of isoforms of SSL enzymes and strictosidine deglucosidases. The resulting branched pathway might be involved in the production of different alkaloids. In contrast, there are only few members of the two enzyme families in animals pointing towards a more restricted function.

by annexin V labeling), during clotting. These phospholipids are usually confined to the inner leaflet of the cell membrane but become exposed both during vertebrate blood clotting [75] and hemolymph coagulation in insects [76]. The rearrangement of phospholipids is achieved through the activity of scramblases [77, 78]. There are two annotated genes with similarity to vertebrate scramblases in the *Drosophila* genome (CG6590 and CG1893). It is believed that the negatively charged phospholipids play a role in the elimination of cells during wound healing. Scavenger receptors with affinity for these lipids have been identified in both vertebrates [79–81] and insects [4]. In *Drosophila*, the *croquemort* gene product belongs to the scavenger receptor family [82]. This protein has mostly been discussed as an important scavenger receptor for apoptotic cells, which share exposure of aminophospholipids with cells that are involved in clotting [83]. A possible role for croquemort in wound healing remains to be studied.

Blood clotting in vertebrates similarly involves the production of membrane vesicles which are released from platelets and also show strong annexin V staining [84, 85]. The formation of microparticles is dependent on calcium [84]. In insects, similar structures have been described [54, 86]. More recently, the formation of these ‘insect microparticles’ could also be shown to depend on calcium, and positive labeling of insect microparticles with annexin V was observed as well [76].

It should be mentioned that the exposure of negatively charged phospholipids is a feature that apoptotic cells and cells involved in coagulation share with bacteria [87, 88]. Although the exact mechanism for how antibacterial peptides act on the bacterial membrane remains to be determined in many cases, a common feature seems to be the affinity of these – mostly basic – peptides for the negative charge on the bacterial surface [88]. Thus, it is expected that many antibacterial peptides should also bind to cells which expose a negative charge and act in helping to solubilize cellular lipids and clean up cellular debris. The activity of some antibacterial peptides against tumor cells might be explained in a similar way, since a number of them expose negative charge on their surface [89, 90], a possibility which would impact on the choice and design of potential peptides with antitumor activity [91].

The strictosidine-synthase family

Similar to their vertebrate counterparts, insect microparticles are enriched in certain proteins, one of which is hemomucin, a protein that comprises a typical mucin domain as well as a domain with similarity to strictosidine synthase (SS, [92]), a plant enzyme involved in the production of monoterpene indole alkaloids [93, 94]. A number of these alkaloids are used for treatments of neu-

rological disorders [95]. This includes reserpine, which interferes with dopaminergic signal transduction [96]. Hemomucin shares similarity to SS with a number of similar proteins from other insects [76, 97] as well as zebrafish, mouse and humans. Interestingly, the human member of the gene family is strongly expressed in the brain, the very organ many of the plant alkaloids act upon [98].

The function of hemomucin and the other animal members of the SSL family remains to be established, but data so far point towards a role in the coagulation process, at least for the *Drosophila* members [76]. Because the substrates of the plant members of this family belong to the biogenic amines, it is tempting to speculate that the insect members also metabolize such derivatives. A number of biogenic amines are in fact known to play a role in sclerotization reactions [99] and the regulation of hemocyte activity [86, 100]. In addition, dopamine-like substances are induced during bacterial infections of insects [101]. When we searched for possible animal homologues of additional members of the plant pathway involved in the production of indole alkaloids, we identified two possible homologues from *Drosophila* of the next enzyme upstream. They include a dopa decarboxylase, which has been isolated from mutants due to a defect in learning behavior [102, 103]. A dual function in both the immune and nervous system might therefore turn out to be a common feature of members of this biosynthetic pathway.

In the search for new strategies to identify proteins involved in hemolymph coagulation, we have chosen two approaches:

- 1) Based on previous findings that hemocytes release highly glycosylated proteins during coagulation reactions [17, 54], we have used lectin affinity purification to identify and purify novel factors of the coagulation cascade.
- 2) By performing an in vitro coagulation reaction and using the cross-linked clot for immunizing rabbits, we obtained an antiserum with specificity for clot components. Since PO activity was not inhibited, we expected to isolate components of both the clotting cascade and the PPO-activating cascade. The antiserum has been used successfully to isolate cDNAs from an expression library [D. Li et al. unpublished].

These approaches allowed us to identify candidates for novel proteins which are involved in coagulation as well as previously known components of both the PPO-activating cascade and the clotting reaction, like lipophorin and PO. cDNAs coding for novel candidate clotting factors include a distant relative of the α -crystallin/small heat-shock protein family [104, 105]. Members of this family are known to have a tendency to aggregate and are substrates for transglutaminases, both features which suit a protein involved in clotting [104]. One of the emerging

themes of this work seems to be the dual expression of proteins in both the salivary glands and in hemocytes, which has been previously shown for hemomucin [106] but now also for a lepidopteran silk protein and a product of the *Drosophila* 71E puff [unpublished results]. The latter protein is a relative of the salivary gland glue proteins ([107], M. Fabbri et al. unpublished). One may speculate that a tendency for proteins to precipitate and form a coagulum upon contact with air predisposes them for a dual use as part of salivary secretions and of the hemocyte coagulum.

Outlook

In recent years, a concept for the recognition of molecular patterns has emerged from a number of investigations trying to explain how immune responses are activated. As mentioned before, according to this idea, the innate immune system uses evolutionarily conserved molecular patterns that are characteristic for pathogens as distinctive features to activate immune responses [34]. These PAMPs are recognized by specialized receptors, many of which have been isolated [2].

While we agree that this concept applies to essential activation processes in the hemostatic response, wounds nevertheless have to be sealed even in the absence of microbial elicitors. Therefore, other signals have to be recruited for activation of clotting cascades [16, 108]. These may include physical signals such as an oxidizing environment, which has been shown to induce immune responses [109], or biochemical clues such as intracellular components, which are released upon wounding [110]. As a framework, concepts of vertebrate immunity, which focus more on the internal regulation of immune responses, seem more fruitful in this context. One such concept is the idea that immune reactions rely on so-called danger signals, which are produced by cells that have undergone damage, for their activation [110–112]. Such signals may include nucleic acids, typical intracellular proteins or immature proteins. Wounding may also lead to changes in hemolymph and fat body [109] proteins, which could potentially be used as activating signals. While these signals might activate mostly the clotting system, there is also evidence that under certain circumstances, the PPO-activating cascade relies on such signals for its activation [113]. PPO has in fact been shown to be activated at a low calcium concentration and in the absence of microbial elicitors [114].

There is also recent evidence for cooperation between the clotting system and the PPO-activating cascade [115]. These studies were performed in chelicerates, where the PO activity resides in a member of the hexamerin family, a situation that is different from insects. This protein is hemocyanin, normally the oxygen transporter in the he-

molymph of chelicerates, which can be activated to perform PO activity. This activation can also be achieved by nonenzymatic means [116]. Likewise, in the horseshoe crab, where the focus has been on activation by microbial elicitors, there is evidence indicating that the clotting system is linked to the activation of hemocyanin through a nonenzymatic activity of clottable protein [115, 116]. Studies on the PPO-activating system and on hemolymph coagulation in arthropods are thus expected to further add to an integrated view of the innate immune system.

A number of recently developed or refined techniques used in functional genomics are also expected to add substantially to our understanding of hemolymph clotting. Genes that have recently been found to be induced during immune reactions using microarrays include a laccase, an annexin and the yellow gene [Bruno Lemaître, personal communication], findings that are compatible with the ideas proposed here.

Note added in proof. The *Drosophila* hemacytin homologue: Goto A., Kumagai T., Kumagai C., Hirose J., Narita H. et al. (2001) A *Drosophila* haemocyte-specific protein, hemolactin, similar to human von Willebrand factor. *J. Biochem.* **359**: 99–108.

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