PERSPECTIVE

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The Possibility and Molecular Mechanisms of Cell Pyroptosis After Cerebral Ischemia

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Introduction

Stroke is an important disease that is prevalent worldwide [1-3]. Ischemic stroke accounts for 80% of stroke cases. Currently, evidence-based effective treatments for ischemic stroke are limited, and only intravenous thrombolysis with Alteplase (a commercially available thrombolytic agent) within 4.5 h of stroke onset and thrombectomy and arterial thrombolysis within 6-24 h of onset are effective [4, 5]. However, because these two treatments have strict indications and certain risks (reperfusion injury and bleeding) [5-8], there is an urgent need to develop new treatment methods. Thus, comprehensive elucidation of the molecular mechanisms underlying ischemic brain damage and the search for key signaling pathways and protein molecules are important for guiding the clinical treatment of ischemic stroke.

The inflammatory reaction is an important pathophysiological mechanism underlying cerebral ischemic injury. The inflammatory reaction after cerebral ischemia influences the development of ischemic injury and is considered to be a key element related to lesion progression. Both

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permanent ischemia and reperfusion after transient ischemia have been shown to induce inflammatory reactions in cerebral tissues [9]. However, the pathophysiological processes of these two ischemic conditions are different [10], and the severity of the inflammatory reactions also differ. An inflammatory reaction can be initiated within several hours of stroke onset and can last for several days or even longer [11]. Therefore, treatments targeting the inflammatory reactions have a longer time window and excellent prospects for clinical application.

Cells in the ischemic core undergo necrosis within a short time after cerebral artery occlusion, whereas cells in the surrounding area (ischemic penumbra) can survive for several hours [12]. Restoration of blood flow within this time window may allow cells to survive but may also result in irreversible cell death (reperfusion injury) [12]. For several minutes to several hours during cerebral ischemia, dead cells release danger signals, such as purines, high mobility group box 1 protein, heat shock proteins, and peroxiredoxin family proteins [13]. These danger signals bind to the receptors in the cell membrane or intracellular receptors of adjacent cells to initiate innate immune responses, resulting in inflammatory reactions [13]. These endogenous danger signaling molecules are known as damage-associated molecular patterns (DAMPs). The receptors that recognize DAMPs are known as pattern recognition receptors (PRRs) and mainly include families such as the Toll-like receptors and Nod-like receptors (NLRs) [14]. DAMPs released by necrotic cells in the ischemic core are the source of signals that initiate inflammatory reactions. However, the sources of the danger signals that promote further development of the inflammatory reactions and how they exert their functions are still unclear. Cells in the ischemic penumbra are thought to undergo apoptosis, which can last for several weeks [15].

However, during apoptosis, the cell membrane is intact, and there is no spillover of cytoplasmic components [16]. Hence, apoptosis is unlikely to be the primary instigator of inflammation during brain ischemia.

Pyroptosis is a special form of programmed cell death with strong pro-inflammatory effects. Previous research has shown that the upstream molecules of pyroptosis are highly expressed in the ischemic penumbra. Therefore, we speculated that pyroptosis might occur in the ischemic penumbra and play an important role in the inflammatory injury of cerebral ischemia. In this article, we discuss the possible development of pyroptosis after cerebral ischemia and hypothesize the possible molecular mechanisms.

Discovery of Cell Pyroptosis

For many years, the forms of cell death were divided into apoptosis and necrosis. Apoptosis is gene-regulated programmed cell death, whereas necrosis is accidental cell death. However, recent studies have shown that necrosis can also be gene-regulated programmed cell death which is called programmed necrosis [17]. Pyroptosis is a form of programmed necrosis in which significant research progress has been made in recent years. The phenomenon of pyroptosis was first discovered in 1992 during a study of macrophages infected with Shigella flexneri [18]. Subsequently, cytoplasmic vacuolization, DNA fragmentation, chromatin condensation, and caspase-1 activation were also observed in macrophages infected with the mouse Salmonella typhimurium strain [19, 20]. Researchers at that time considered caspase-dependent activation to be a specific feature of apoptosis and mistook this type of cell death as apoptosis. With in-depth studies and technological development, researchers have found that pyroptosis is mainly mediated by caspase-1 rather than the traditional apoptosis-related reactive molecule caspase-3 [21]. Therefore, this process was proposed as a form of programmed cell death that differs from apoptosis, and the concept of pyroptosis was formally proposed in 2000 [22]. Pyroptosis does not only occur during infectious diseases. Recent studies have shown that pyroptosis is also present in sterile inflammation, including diabetic atherosclerosis [23], acute liver injury [24], alcoholic hepatitis [25], diabetic cardiomyopathy [26], diabetic nephropathy [27], benign prostatic hyperplasia [28], Alzheimer's disease [29], temporal lobe epilepsy [30], renal ischemia/reperfusion [31], traumatic brain injury [32], ethanol-induced brain injury [33], and myocardial ischemia/reperfusion [34].

Characteristics of Pyroptosis

Pyroptosis differs from other forms of cell death. (1) The most distinctive morphological feature is that the cell

membrane has pores with diameters of 10-20 nm during pyroptosis [35-40]. After the pores form in the plasma membrane, water influx is driven by intracellular non-ionic osmolytes and causes swelling, membrane rupture, and the release of cellular contents. Nuclear chromatin condensation and DNA cleavage and fragmentation also occur, similar to apoptosis. However, the nuclear membrane is intact, unlike apoptosis [41, 42]. (2) The most distinctive biochemical feature is that the development of pyroptosis mainly depends on the activation of inflammatory caspases (including caspase-1 or caspase-4/5/11). Caspase-1 is present in both humans and rodents, while caspase-11 is present only in rodents but is homologous with caspase-4 and caspase-5, which are present only in humans. Caspase-1 activation usually occurs in a multi-protein complex called the inflammasome. The inflammasome generally contains the following 3 components: receptors-PRRs in the cytoplasm that mainly include NLRs (such as NLRP1, NLRP3, and NLRC4) and absent in melanoma 2 (AIM2); effectors-the caspase-1 precursor (pro-caspase-1); and apoptosis-associated speck-like protein containing a CARD (ASC), which is an adaptor protein connecting PRRs and pro-caspase-1. Caspase-1 gene-knockout mice do not develop pyroptosis [43, 44], so the Nomenclature Committee on Cell Death 2012 recommended defining pyroptosis as a form of caspase-1-dependent cell death [44]. However, studies have shown that caspase-1 gene-knockout in mice also results in caspase-11 inactivation. In addition, studies on bacteria-induced cell death reported that the bacterial component lipopolysaccharide (LPS) directly activates caspase-11 (rodent-derived) or caspase-4/ 5 (human-derived), resulting in pyroptosis in infected cells [45]. The two different pyroptosis pathways (caspase-1 and caspase-4/5/11) are called the canonical and the noncanonical inflammasome pathways, respectively (Fig. 1).

Necroptosis is another form of programmed cell death with a common feature of plasma membrane rupture. Unlike pyroptosis, necroptosis is initiated by a ligand binding to death receptors, including tumor necrosis factor receptor 1 [46]. The rupture in necroptosis is explosion-like and it is known that the execution of necroptosis is mediated by mixed lineage kinase domain-like oligomers in the plasma membrane [17, 38, 46].

Pro-inflammatory Function of Pyroptosis

Necrotic cells release various cell components (DAMPs) under many pathological conditions. These DAMPs act on cell membranes or intracellular receptors (PRRs) in adjacent cells to cause inflammasome formation and caspase-1 or caspase-11 activation. Consequentially, pyroptosis occurs, and the inflammatory factors IL-1 β and IL-18 are released. Further, these DAMPs induce PRR

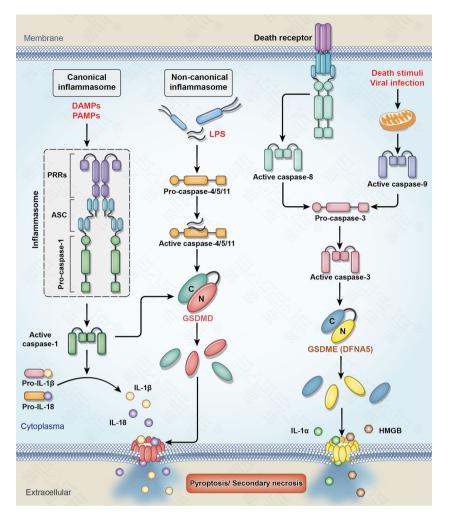


Fig. 1 Pyroptosis pathways. In the canonical inflammasome pathway, microbial pathogens (PAMPs) or sterile inflammatory substances (DAMPs) are detected by various cytosolic sensor proteins (PRRs) which leads to caspase-1 activation through an inflammasome complex. Active caspase-1 converts the precursors of IL-1 β and IL-18 to their mature forms, which are released from cells by pyroptosis. In the non-canonical pathway, LPS in the cytosol of cells infected by bacteria binds to precursor caspase-4/5/11, which leads to the activation of caspase-4/5/11. Both caspase-1 and caspase-4/5/11 process GSDMD, which results in the release of the N-terminal fragment of GSDMD (GSDMD-N). GSDMD-N forms pores in the

activation in other adjacent cells, resulting in pyroptosis and the release of inflammatory factors [47]. This cascade amplifies the inflammatory reactions to aggravate injury. Recent studies have shown that NLRP3 and ASC are released outside of the cells after pyroptosis. After extracellular NLRP3 and ASC undergo recombination and polymerization or ASC undergoes self-aggregation, they continue to activate caspase-1 and promote IL-1 β maturation. In addition, after engulfment of NLRP3 and ASC by macrophages, the above process can occur in cells to amplify the inflammatory reactions [47, 48]. Therefore, pyroptosis not only participates in the initiation of

plasma membrane that induce pyroptosis. The other pathway of pyroptosis is caspase-3/GSDME (DFNA5). Caspase-3 can be activated by the mitochondrial pathway and the death receptor pathway. Activated caspase-3 in turn cleaves GSDME to generate the GSDME-N fragment that forms pores in the plasma membrane and induces secondary necrosis/pyroptosis [1]. *PAMPs* pathogen-associated molecular patterns; *DAMPs* danger-associated molecular patterns; *PRRs* pattern recognition receptors; *ASC* apoptosis-associated speck-like protein containing a CARD; *LPS* lipopolysaccharide; *GSDMD* gasdermin D; *GSDME* (DFNA5), gasdermin E (deafness autosomal dominant type 5).

inflammatory reactions but also plays a critical role in spreading inflammatory signals and amplifying inflammatory reactions.

Induction of Pyroptosis by Gasdermin Proteins

Studies on the mechanisms of pyroptosis have made major breakthroughs in the last two years. The gasdermin protein family has been found to be the direct executor of pyroptosis. This family includes gasdermins A (GSDMA), B (GSDMB), C (GSDMC), D (GSDMD), E (GSDME, also known as DFNA5), and DFNB59. GSDMD and GSDME are the proteins most studied in pyroptosis.

Three articles published in 2015 in journals such as Nature showed that GSDMD is the common substrate of all inflammatory caspases (caspase-1 and caspase-4/5/11) [49–51]. These activated caspases cleave GSDMD between the N-terminal and C-terminal domains. The N-terminal domain of GSDMD (GSDMD-N) has pyroptosis-inducing activity and plays a decisive role in IL-1ß and IL-18 secretion. The C-terminal domain of GSDMD (GSDMD-C) does not have these functions but inhibits the N-terminal domain when cells are in a quiescent state to maintain GSDMD in an inactivate state. Five research articles published in 2016 elucidated the process of the direct involvement of GSDMD-N in membrane pore formation during pyroptosis [35-39]. GSDMD-N specifically interacts with phospholipid molecules on the cell membrane and results in pore formation to change the cellular osmotic pressure, eventually leading to cell membrane lysis and pyroptosis. Studies also showed that the N-terminal domains of almost all gasdermin family proteins have pyroptosis-inducing function. However, aside from GSDMD, the other family members are not substrates of the inflammatory caspases.

Recent studies have shown that caspase-3, which has long been considered an apoptosis marker, can also induce secondary necrosis (pyroptosis) through activation of GSDME [52–54]. These results broke with the classic concept that caspase-3 activation necessarily leads to apoptosis. One caspase-3 cleavage site is present between the N-terminal and C-terminal domains of GSDME. The N-terminal fragment of GSDME (GSDME-N) produced by activated caspase-3 cleavage is similar to GSDMD-N, leading to pore formation in the cell membrane and inducing pyroptosis. Therefore, GSDME is a key factor mediating the conversion of apoptosis (induced by the activation of caspase-3) into pyroptosis (Fig. 1).

Possibility of Pyroptosis After Cerebral Ischemia

Many studies using rodent models of focal cerebral ischemia/reperfusion have shown that the formation of the NLRP1, NLRP3, AIM2, and NLRC4 inflammasomes and caspase-1 activation occur in ischemic cerebral tissues. In addition, an increase in the NLRP1 or NLRP3 inflammasome or caspase-1 expression has been reported in neurons, microglia, astrocytes, vascular endothelial cells, and infiltrated white blood cells from the peripheral blood. Gene knockout of these inflammasomes or caspase-1, or inhibition of their activity, can relieve ischemic injury (see review by Allan *et al.* for details) [55]. Up-regulation of NLRP1, NLRP3, ASC, and caspase-1 expression has also been found in cortical neurons from human cerebral

infarction tissues [56]. In addition, *in vivo* and *in vitro* studies in mice have shown that caspase-11 is activated in ischemic cortical neurons [56]. Therefore, the above studies confirm that the expression of pyroptosis-related proteins is up-regulated in neurovascular cells after cerebral ischemia and aggravates ischemic injury. These results strongly suggest that pyroptosis occurs after cerebral ischemia to aggravate tissue injury. However, these studies did not search for direct evidence of pyroptosis since these studies only observed the upstream molecules of pyroptosis in ischemic cells and did not further observe whether these cells possess the morphological feature or biochemical markers of pyroptosis.

As noted above, previous studies have confirmed that inflammasomes, caspase-1, and caspase-11 expression is up-regulated after cerebral ischemia. Since these proteins are all upstream molecules of the GSDMD protein [55, 56], we hypothesized that two inflammatory caspase-mediated signaling pathways of pyroptosis, the inflammasome/caspase-1/GSDMD pathway and the caspase-11/GSDMD pathway, can both be activated after cerebral ischemia, although the activation levels might differ. Caspase-11 expression is up-regulated in ischemic cortical neurons [56], but the current literature reports that the induction of pyroptosis by caspase-11 is limited in infectious diseases. Whether sterile inflammation has the same mechanisms requires further confirmation. We suggest that cerebral ischemia mainly activates the inflammasome/caspase-1/ GSDMD pathway.

Many studies have shown that caspase-3 is activated in ischemic cerebral tissues and cells (generally considered to indicate apoptosis). Recent studies have shown that caspase-3 induces pyroptosis through activation of GSDME [52–54]. Previous studies on apoptosis in cerebral ischemia usually used terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) and Annexin V staining to show DNA damage and phosphatidylserine expression on the cell membrane, respectively [15]. However, these two staining methods can both be positive in pyroptotic cells. Therefore, part of the apoptosis observed might actually be pyroptosis. We speculate that the caspase-3/GSDME pathway might also be partially activated after cerebral ischemia to induce pyroptosis.

The cell type(s) undergoing pyroptosis after ischemia remains unclear. Neuronal, microglial, and astroglial pyroptosis have been reported in some pathological states without ischemia. However, all these cells undergo caspase-1-dependent pyroptosis [29, 30, 32, 33, 57]. Microglia are macrophages located in the brain and are the major executors of inflammatory reactions in the brain. Microglial activation is a key element of inflammation following ischemic stroke [9, 11]. Therefore, we speculate that microglial may be the major cell type involved in

inflammatory caspase-mediated pyroptosis after cerebral ischemia and play a critical role in the pyroptosis-mediated spread of inflammation. Furthermore, since caspase-3 is mainly activated in neurons after cerebral ischemia [58], caspase-3-mediated pyroptosis may mainly occur in neurons.

The pathophysiological states differ during the different stages after cerebral ischemia. The presence of inflammation precedes apoptosis, and the time frame of apoptosis lasts longer. Therefore, we speculate that the signaling pathways that induce pyroptosis at different stages after cerebral ischemia might be different, with the inflammatory caspase/GSDMD pathway serving as the major pathway in the early stage, and the caspase-3/GSDME pathway serving as the major pathway in the late stage. Furthermore, the inflammatory reaction after cerebral ischemia/reperfusion is more severe than the reaction in sustained cerebral ischemia. Therefore, the development of pyroptosis and the activation of its signaling pathways may also be more intense after cerebral ischemia/reperfusion.

In summary, the GSDMD and GSDME signaling pathways (inflammasome/caspase-1/GSDMD, caspase-11/ GSDMD, and caspase-3/GSDME) can be activated after cerebral ischemia to induce pyroptosis. However, the levels of activation of these pathways and the degree of pyroptosis may differ under different ischemic conditions (permanent ischemia or ischemia/reperfusion), during different ischemic stages (early or late stage), and in different cell types.

Conclusions

Previous studies on cerebral ischemia have shown upregulation of the expression of pyroptosis-related signaling proteins, indicating the possible role of pyroptosis in neurovascular cells after cerebral ischemia. Recent studies have shown that GSDMD and GSDME are the executors of pyroptosis and that their upstream molecules are the inflammatory caspases and caspase-3, respectively. Therefore, we speculated that the microglial inflammasome/caspase-1/GSDMD pathway and the neuronal caspase-3/ GSDME signaling pathway are the major molecular mechanisms underlying pyroptosis after cerebral ischemia. In-depth studies of pyroptosis and its mechanisms will further elucidate the mechanisms underlying the inflammatory injury of cerebral ischemia and provide new drug targets for the treatment of ischemic stroke.

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Compliance with Ethical Standards

Conflict of interest The authors claim no conflicts of interest.

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