Rapid intracellular acidification is a novel plant defense response countered by the brown planthopper

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Abstract

The brown planthopper (BPH; *Nilaparvata lugens*) is the most destructive insect pest in rice. Through a stylet, BPH secrets a plethora of salivary proteins into rice phloem cells as a crucial step of infestation. However, how various salivary proteins function in rice cells to promote insect infestation is poorly understood. Among them, one of the salivary proteins is predicted to be a carbonic anhydrase (NlCA). The survival rate of the *NlCA*-RNA interference (RNAi) BPH insects was extremely low on rice, indicating a vital role of this salivary protein in BPH infestation. We generated *NlCA* transgenic rice plants and found that *NlCA* expressed in rice plants could restore the ability of *NlCA*-RNAi BPH to survive on rice. Next, we produced rice plants expressing the ratiometric pH sensor pHusion and found that *NlCA*-RNAi BPH induced rapid intracellular acidification of rice cells during feeding. Further analysis revealed that both *NlCA*-RNAi BPH feeding and artificial of lowering intracellular pH activated plant defense responses, and that NICA-mediated intracellular pH stabilization is linked to diminished defense responses, including reduced callose deposition at the phloem sieve plates and suppressed defense gene expression. Given the importance of pH homeostasis across the kingdoms of life, discovery of NICA-mediated intracellular pH modulation uncovered a new dimension in the interaction between plants and piecing/sucking insect pests. The crucial role of NICA for BPH infestation of rice suggests that NICA is a promising target for chemical or trans-kingdom RNAi-based inactivation for BPH control strategies in plants.

Introduction

The brown planthopper (BPH; *Nilaparvata lugens* Stål, Hemiptera, Delphacidae) is a monophagous insect pest of rice (*Oryza sativa* L.) found in all rice-growing Asian countries. The BPH sucks rice phloem sap via its stylet, causing leaf yellowing and wilting, stunted plant growth, reduced photosynthesis and ultimately death of rice plant [1]. During severe BPH outbreaks, tens of thousands of insects swarm on a rice field, resulting in the 'hopperburn' phenomenon, which is characterized by large-scale wilting, yellowing and lethal drying of rice plants [2]. Besides direct damages, the BPH may also indirectly damage rice plants by oviposition and transmitting viral disease agents [3,4].

Application of chemical insecticides has been a main strategy for controlling BPH. Although it has the advantages of having rapid effects on killing insects and low costs, use of insecticides leads to environmental pollution and resistance of BPH to pesticides. In recent decades, breeding rice resistant varieties to control BPH has attracted increasing attention. To date, more than 30 resistance genes have been found in the rice genome [5]. However, BPH often quickly evolves new

biological types that evade rice resistant genes. Therefore, additional BPH controlling methods need to be developed to complement the current control measures toward long-term solutions of achieving durable BPH resistance in rice. One method could be based on disruption of key steps of BPH's natural infestation process. However, development of such methods will require a comprehensive understanding of the basic biology of the BPH-rice interaction.

A critical step in BPH infestation of rice is secreting bioactive substances into the plant tissues through the stylet [6-8]. Specifically, during feeding, BPH secretes both colloidal and watery saliva [9,10]. The main function of the colloidal saliva is to form a saliva sheath around the piercing-sucking mouthparts, stabilizing the overall feeding apparatus. The composition and function of watery saliva is more complex, and it contains salivary proteins that are believed, in most cases, to regulate various pathways in plant cells to enhance BPH feeding and survival in rice plants. For example, NlEG1, a salivary endo-b-1,4-glucanase, degrades plant celluloses to help the BPH's stylet reach to the phloem [11]. NlSEF1, an EF-hand Ca^{2+}-binding protein, interferes with calcium signaling and H_2O_2 production during BPH feeding [12]. Salivary protein 7 is required for normal feeding behavior and for countering accumulation of a defense compound, tricin [13]. On the other hand, mucin-like protein (NlMLP) triggers defense responses in rice cells, including cell death, callose deposition and up-regulation of pathogen-responsive genes [14,15].

Carbonic anhydrases (CAs) (EC 4.2.1.1) are zinc metalloenzymes that function as catalysts in the bidirectional conversion of CO_2 and water into bicarbonate and protons [16]. There are at least five distinct CA families (α-, β-, γ-, δ-, and ε-CAs) and three of them (α-, β-, and γ-CAs) are ubiquitously distributed among animal, plant, and bacterial species. The widespread distribution and adequate abundance of these CA families underline their evolutionary importance throughout the kingdoms of life. CAs participate in a wide range of biological processes, such as pH regulation, CO_2 homeostasis, stomatal aperture, and plant defense [17-21]. NlCA belongs to the α-CA subfamily. Our previous study showed that *NlCA* expressed in BPH salivary glands [6]. Surprisingly, however, RNA interference (RNAi) of the *NlCA* transcript in BPH insects affects neither pH maintenance within the salivary gland, watery saliva or gut, nor insect feeding behavior or honeydew excretion, but greatly reduced survival of BPH on rice plants, suggesting a critical function *in planta* via an unknown mechanism [6].

Here, we report that *NlCA*-RNAi BPH feeding results in rapid intracellular acidification of rice cells. We found that NlCA is secreted into the rice tissues and functions as an effector that stabilizes host cell intracellular pH, accompanied by suppression of defense responses, during BPH feeding. Thus, we have uncovered intracellular pH homeostasis is a previously uncharacterized battleground in plant-insect interactions.

Results

NlCA is detected in rice sheath tissues during BPH feeding. NlCA was previously found to be highly expressed in salivary glands and present in the watery saliva of BPH fed on artificial diet [6]. We conducted a more detailed characterization of *NlCA* expression in this study. RNA *in situ* hybridization showed that the expression level of *NlCA* was detectable throughout the principal glands (PGs) and accessory glands (AGs), but not in A-follicle of the principal gland (APG) (Fig. 1a), which further raised the possibility that NlCA may be one of the "effector proteins" secreted into the rice tissue during BPH feeding on rice plants. To test this possibility, we compared protein profiles in the leaf sheaths of Nipponbare rice plants before and after BPH feeding using liquid chromatograph-mass spectrometer (LC-MS). We found 8 NlCA-specific peptides in BPH-fed leaf sheath tissue (Fig. 1b*;* Supplementary Fig. 1), confirming that NlCA is secreted into the host tissues during BPH feeding.

Transgenic expression of *NlCA* in rice rescues the ability of *NlCA*-silenced BPH to feed and survive. To further clarify the site of function (i.e., in insect vs. in plant) of NlCA in the BPH-rice interaction, we produced transgenic Nipponbare plants expressing *NlCA* (see Methods). A total of 26 lines were produced and 6 lines were found to robustly express the *NlCA* transcript. *NlCA*-expressing plants exhibited no noticeable changes in appearance compared to Nipponbare plants (Supplementary Fig. 2). *NlCA*-expressing plant lines were propagated to T3 generation, and 3 lines were subjected to further characterization, including BPH feeding. For BPH feeding assay, double-stranded RNA (dsRNA) of *NlCA* (ds*NlCA*) or the control green fluorescent protein gene (ds*GFP*) was injected into 3rd instar BPH nymphs to initiate RNAi of the *NlCA* transcript [22]. The sequence of *NlCA* used for RNAi treatment is expected to be specific to BPH (Supplementary Fig. 3). Quantitative real-time PCR analysis confirmed that the transcript levels of the *NlCA* gene were reduced by 99% and 97%, respectively, in tested individuals when compared with non-RNAi control and ds*GFP*-treated insects (Figure 2a). There were no significant differences in survival rates between ds*GFP* and ds*NlCA* BPH when fed on the artificial diet, indicating that silencing *NlCA* expression has no obvious impact on the basic physiology of BPH (Fig. 2b). However, we found that the survival rate of ds*NlCA* BPH was sharply decreased, starting at day 9 post-infestation, to ~40% at day 14, whereas the control ds*GFP* BPH survived normally on wild-type Nipponbare plants (Fig. 2c). This result is consistent with previous results conducted in the *japonica* cultivar Xiushui134 rice plants [6], suggesting that the requirement of NlCA for BPH survival is not specific to a specific rice genotype. Strikingly, *NlCA* transgenic plants almost fully restored the survival of *NlCA*-silenced BPH insects (Fig. 2c; Supplementary Fig. 4), demonstrating that *Nl*CA expressed in the host tissue can complement the infestation defect of *NlCA*-silenced BPH insects.

The conserved catalytic site amino acids of *Nl*CA are critical to its function in rice. NlCA contains several conserved amino acid residues predicted to be at the catalytic site of carbonic anhydrases (Fig. 2d). We asked if some of these conserved active site residues are critical to the function of *Nl*CA in the rice-BPH interaction. Accordingly, we expressed three different *NlCA* mutants in Nipponbare plants. "*NlCA-m1*" plants contain a *NlCA* transgene in which His^{159} and His^{161} were mutated to Ala; "*NlCA-m2*" plants contain a *NlCA* transgene in which Glu^{182} and His^{184} were replaced by Ala; and "*NlCA-m3*" plants carry a *NlCA* transgene in which all seven conserved active site residues, His^{159}, His^{161}, Glu^{171}, Glu^{182}, His^{184}, Thr^{269} and Phe^{279}, were changed to Ala. Like *NlCA* transgenic plants, transgenic plants expressing these *NlCA*-mutants exhibited no noticeable changes in appearance (Supplementary Fig. 2). We conducted BPH survival assay and found that, in contrast to plants expressing wild-type *NlCA*, the *NlCA-m2* and *NlCA-m3* plants could not fully rescue the infestation defect of *NlCA*-silenced BPH insects. The *NlCA-m1* plants, on the other hand, could recover the infestation defect of ds*NlCA* BPH (Fig. 2e and f; Supplementary Fig. 5). Thus, several conservative residues at the predicted catalytic site are indispensable for the function of *Nl*CA inside the plant cell.

After having demonstrated the requirement of catalytic site residues for the function of NlCA in rice, we next investigated the subcellular localization of NlCA in both *Nicotiana benthamiana* leaf cells and rice leaf protoplasts transiently expressing *NlCA:CFP*. In both cases, NlCA:CFP showed a nonuniform distribution of CFP signal in the cell. Further colocalization studies with YFP signal revealed that NlCA was colocalized in the cytoplasm but not in the nucleus (Fig. 1c; Supplementary Fig. 6).

NlCA counters rapid intracellular acidification during BPH feeding of rice. BPH feeding on rice plants can be divided into two phases based on the electropenetrography (EPG) waveforms [23]. The first phase involves BPH's stylet penetrates the plant through the cell walls and cell membranes of various epidermal and mesophyll cells until the stylet reaches the phloem sieve cells inside the vascular system. In Nipponbare, the time to reach the phloem sieve cells can be around 1.2 h before sustained phloem sap ingestion occurs at 3.8 h [23]. Our finding of the site of NlCA action in the plant prompted us to test the hypothesis that NlCA might modulate rice cell pH changes during BPH feeding. To directly test this hypothesis, we constructed a rice transgenic line expressed a cytoplasmic ratiometric pH sensor, cyto-pHusion. Cyto-pHusion consists of the tandem concatenation of enhanced green fluorescent protein (EGFP) and a monomeric red fluorescent protein 1 (mRFP1) [24]. EGFP is highly sensitive to pH variation with the brightest EGFP signal emitted at a pH of 7-8. EGFP fluorescence is gradually quenched at lower pH values and totally quenched at pH values < 5. In contrast, mRFP1 is insensitive to pH changes in the physiologically relevant range and serves as an internal reference. We placed 5th instar BPH

nymphs on the leaf sheath of cyto-pHusion-expressing rice plants and recorded GFP and RFP signals of the feeding sites under microscopic observation at different time points with a 12 h test period. As shown in the Fig. 3b-e, ds*GFP* BPH feeding did not elicit an obvious intracellular pH change in rice cells during this period. In contrast, ds*NlCA* BPH feeding induced a significant pH decrease at 4 h and 8 h (Fig. 3c and d). The decreased ratio of EGFP: mRFP was caused by the quenched EGFP signals after ds*NlCA* BPH feeding, while the internal control, mRFP, kept at a stable level (Supplementary Fig. 7). These results uncovered a previously uncharacterized plant cellular response, rapid intracellular acidification, during the early stage of ds*NlCA* BPH feeding and demonstrated that BPH has evolved a critical virulence effector, NlCA, to counter this novel plant cellular response.

Because extracellular pH change is associated with plant responses to biotic stress [25,26], we speculated that rapid intracellular acidification of ds*NlCA* BPH feeding might induce defense gene expression. To test this possibility, Nipponbare plants infested by ds*GFP* and ds*NlCA* BPH were examined for defense gene expression. We found that expression of defense response genes (e.g., *OsNH1*, *OsNH2*, *OsWRKY45*, *OsWRKY13*) was significantly induced at a higher level by ds*NlCA* BPH infestation than by dsGFP BPH control at 4 h and 8 h (Fig. 3f-i), which is consistent with the intracellular pH change at 4 h and 8 h (Fig. 3c-d). Taken together, these results indicate that intercellular acidification is linked to rice defense activation.

Ectopic intracellular acidification causes defense gene expression in rice plants. Because plant defense responses are important for limiting BPH survival in rice [27-30], we conducted experiments to determine if intracellular acidification would trigger defense gene expression. Rice is normally grown in Yoshida medium, pH of 4 [31]. To test if medium pH changes can modulate defense responses in rice, we first grew rice seedlings in Yoshida medium until they reached the 5-leaf stage and then placed them to fresh Yoshida medium with pH adjusted to 2, 3, 4, 5, 6 and 7, respectively, for 48 hours. Interestingly, drastically increased expression of defense response genes (e.g., *OsNH1*, *OsNH2*, *OsWRKY45*, *OsPBZ1*) was observed in Nipponbare plants at acidic pH of 2 (Supplementary Fig. 8-9). The pHusion sensor plants exposed to external pH of 2 showed significant intracellular acidification (Fig. 3j-k). Survival rates of BPH insects were lower in Nipponbare plants growing in media with pH of 2, compared to those growing in media with pH of 4 (Fig. 3l) These results suggest that cellular acidification is sufficient to induce defense gene expression in rice and to reduce BPH's ability to survive on rice.

Rice defense responses are inhibited by NlCA. As NICA stabilizes intracellular pH during WT BPH feeding (Fig. 3a-d) and both ds*NlCA* BPH feeding and ectopic intracellular acidification causes activation of defense gene expression (Fig. 3f-i; Supplementary Fig. 8-9), we next tested

the hypothesis that a major function of NICA-mediated stabilization of intracellular pH may be to prevent over-stimulation of downstream rice defense responses during feeding. Callose deposition in the phloem sieve tubes is a classical defense response that is associated with feeding of piercing-sucking insects [32]. We examined this response using aniline blue to stain callose in the phloem sieve cells. Indeed, we found that fewer and smaller callose deposition was found in the sieve plates of *NlCA*-expressing leaf sheaths compared to those found in the sieve plates of Nipponbare fed by BPH (Fig. 4a-f), demonstrating that *Nl*CA suppresses callose deposition in sieve cell pates. Interestingly, the transcript levels of callose biosynthesis genes, such as *OsGSL1*, *OsGSL3*, *OsGSL5* and *OsGns5,* were expressed at lower levels in *NlCA* transgenic plants compared to Nipponbare plants (Fig. 4g-j). We also measured the transcript levels of defense marker genes (e.g., *OsNH1, OsNH2, OsWRKY45* and *OsWRKY13*) in Nipponbare and *NlCA*-expressing plants fed by ds*GFP* and ds*NlCA* BPH. As shown in Fig. 4k-n, induced expression of *OsNH1, OsNH2, OsWRKY13* and *OsWRKY45* by ds*NlCA* BPH was suppressed in *NlCA* transgenic plants compared to those in Nipponbare plants. Collectively, these results showed that NICA-mediated intracellular acidification is linked to downregulation of callose deposition in phloem sieve cells as well as defense gene expression in rice plants.

Discussion

In this study, we provided evidence that intracellular acidification is a previously unrecognized plant defense response that occurs during BPH feeding on rice. This finding was facilitated by our attempt to understand the role of NICA in the rice-BPH interaction. We found that the *NlCA* transcript is detected mainly in the salivary glands (Fig. 1a) and that the NICA protein is found in rice tissues fed by BPH (Fig. 1b). *NlCA*-silenced (ds*NlCA*) insect survived very poorly on at least two independent cultivars of rice plants, Xiushui134 and Nipponbare ([6], Fig. 2), whereas *NlCA* expressing rice plants can restore the normal survival of *NlCA*-silenced (ds*NlCA*) insects (Fig. 2; Supplementary Fig. 4), suggesting that NlCA functions in plant cells. Using the cytoplasm pH sensor, we found that NlCA is required for BPH to maintain a normal plant cytoplasm pH during BPH feeding (Fig. 3a-d). Pathogen/insect-derived effectors can be powerful molecular probes to discovering novel plant regulators/responses to biotic attacks. Although other piercing/sucking herbivores derived effectors, such as Btfer1, LsPDI1, LsSP1, Mp55, DNase II and BISP, have been reported as defense-suppressive effectors [33-38], our discovery of intracellular acidification as a plant defense response and our finding that brown planthopper (BPH) secretes NICA as a counter-defense measure illustrates host cell pH homeostasis as a novel battlefield that has not been revealed in any plant-biotic interactions.

Extracellular alkalinization of culture plant cells has long been recognized as a canonical plant response to microbial elicitors as well as endogenous plant signals [26]. Extracellular alkalinization caused by plant endogenous RAPID ALKALINIZATION FACTOR (RALF) peptides, for example, are perceived by the FERONIA-family receptors [39,40]. There is evidence that this perception causes phosphorylation of PM-localized H(+)-ATPase 2, resulting in the inhibition of proton transport across the PM [41]. Notably, extracellular alkalinization has recently been shown to inhibit or promote growth- or immunity-associated cell surface receptor functions through specific pH-sensitive amino acid sensors [26]. In contrast, intracellular pH changes have so far escaped the discovery by researchers until this study. Our demonstration of a link between intracellular acidification and defense activation has laid a foundation for future discovery of potentially diverse pH-sensitive intracellular regulators of defense responses, which could add a new dimension in the study of plant-biotic interactions.

Because cellular pH alterations could potentially affect multiple biomolecules and, hence, multiple cellular processes, future research should comprehensively define all cellular processes that are affected by intracellular pH acidification. In this study, we found that this pH change is linked to activation of callose deposition at phloem sieve cells and expression of defense response genes, such as *OsNH1, OsNH2, OsPBZ1* and *OsWRKY45* (Fig. 3; and Supplementary Fig. 8-9). In reverse, NICA-mediated intracellular pH stabilization dampens these defense responses (Fig. 4). Callose deposition in phloem sieve cells, in particular, is a classical defense response to a variety of sucking/piecing insects and is thought to limit nutrient flow during insect feeding [32,42-45]. Together, these results suggest that a major effect of NICA-mediated pH stabilization is to prevent overactivation of defense responses during BPH feeding.

The mechanism by which NICA counters intracellular acidification is likely inherent to its reversible inter-conversion of carbon dioxide and water into carbonic acid, protons and bicarbonate ions. CAs are universally present in all organisms (Supplementary Fig. 10); other piecing/sucking insects may use CAs or another mechanism to manipulate host intracellular pH as part of their infestation strategy. Indeed, CA has been reported as a protein component of saliva in rice green leafhopper, *Nephotettix cincticeps* [46] and aphid *Myzus persicae* [47]. In the case of *M. persicae,* CA-II was shown to increase viral transmission via plant apoplastic acidification-mediated acceleration of intracellular vesicular trafficking [47]. However, because NICA plays a critical role in BPH's survival on rice plants *per se* (i.e., in the absence of viral infection), as shown in this study, it is more likely that insect-secreted CAs constitute play a primary role in facilitating insect survival by countering intracellular acidification-associated defense activation. In fact, future research should examine if CA-mediated increase in viral transmission may be a

secondary consequence of defense suppression, which was not examined in the previous study [47].

Discovering the role of pH regulation during plant response to biotic and abiotic stresses and characterizing the impact of such pH alterations could be an important area for future research. Because maintaining proper external and internal pH is critical for all forms of life, prokaryotic and eukaryotic organisms, alike, have evolved mechanisms to achieve pH homeostasis. Facing the fluctuating external pH, prokaryotes have evolved diverse mechanisms for sensing external pH. For instance, the bimodal sensing of pH is employed by *Bacillus subtilis* and *Escherichia coli* [48]. Fungi employ a conserved pathway, mediated by Rim101 and PacC, to sense external pH [49]. It has been reported that different subcellular compartments within the plant cell maintain different pH values, presumably as part of carrying out their unique physiological functions [50]. The demonstrated ability of NICA to counter stimulus-dependent pH changes in plant cells could make NICA a useful molecular tool to modulate and broadly understand the effects of pH stabilization on plant signaling and metabolic pathways in different cell types, organelles, and tissues in plants by, for example, targeting NICA expression in specific tissues, cells, or organelles. Additionally, the crucial role of NICA for BPH infestation of rice suggests that NICA is an important target for chemical or trans-kingdom RNAi-based inactivation for the development of novel BPH control strategies in plants.

Methods

Plant materials and insects. *Oryza sativa* ssp. Japonica cv. Nipponbare was used as the wild type and for generating transgenic plants. The *Nilaparvata lugens* population used in this study was originally derived from a rice field on the Huajiachi Campus of Zhejiang University, Hangzhou (30° 16’ N, 120° 11’ E), China, in 2008, and artificially propagated for many generations until now. BPH insects were reared in environmentally controlled growth chambers on a susceptible cultivar rice variety Xiushui 134 at 27 ± 0.5°C and 50 ± 0.5% relative humidity under a 16-h light and 8-h dark photoperiod in a modified Yoshida solution (in which ammonium nitrate was replaced by 1.06 M carbamide) with pH of 4.

Transgenic rice. The *NlCA* coding sequence was amplified from BPH. Several *NlCA* mutants (*NlCA-m1, NlCA-m2, and NlCA-m3*) were made by site-directed mutagenesis. The *NlCA-m1*, *NlCA-m2* and *NlCA-m3* PCR products encoding proteins in which His159 and His161 were mutated to Ala, Glu182 and His184 were replaced by Ala, and all seven conserved active site residues, His159, His161, Glu171, Glu182, His184, Thr269 and Phe279, were changed to Ala, respectively. The WT and mutant *NlCA* PCR products were recombined into the intermediate vector pDonor207 using the BP recombination kit (Invitrogen), and then recombined into the

destination vector pEarleygate104 using the LR recombination kit (Invitrogen) to generate *P_{35S}::NlCA-YFP* and *P_{35S}::mutant NlCA-YFP* expression vectors. The transgenic rice plants were generated by Agrobacterium-mediated transformation at BIOGLE GeneTech (Hangzhou Biogle Co., LTD.) where rice plants were reared in a greenhouse at 27 ± 0.5°C and 60 ± 0.5% relative humidity under a 16-h light and 8-h dark photoperiod.

***In situ* mRNA hybridization analysis.** Fresh salivary tissues were isolated from 100 5th instar BPH and washed 3 times before being placed in the 4% paraformaldehyde (PFA) fix solution (Servicebio, G1113) at 4°C overnight, dehydrated and embedded in paraffin. Ten μM-thick sections were cut on glass slides, dewaxed and digested by Protease K (Servicebio, G1205) at 37°C for 15 min. After three washes in phosphate buffered saline (PBS) buffer (Servicebio, G0020), the sections were incubated in pre-hybridization solution at 37°C for 1 h and then in hybridization solution containing the *NlCA* probe (1μM) at 42°C overnight. The PCR primer for generating the probe was 5'-GGTTCTGTGATTGAGTGTTTGGATCTCCCTGCG-3' with a single-end CY3 tag generated using the DIG RNA Labeling Kit (Roche Applied Science, Penzberg, Germany) based on the manufacturer's instructions. The slides were stained with DAPI for 8 min in the dark after being washed in saline sodium citrate (SSC) buffer (Servicebio, G3016-4) for three times (2 × SSC, 10 min; 1 × SSC, 2×5 min; 0.5 × SSC, 10 min). Sections hybridized with sense probe was used as a negative control and antisense probe was used to detect the target mRNA. All steps were performed at 37°C and sections were examined under a Nikon fluorescence microscope with a 40 × lens (330 nm – 380 nm for DAPI, 510 nm-560 nm for CY3).

Rice sheath sample preparation for LC-MS. Three independent sets of Nipponbare rice sheath protein samples (three biological replicates) were collected after feeding by 5th instar nymphs as follows. Ten 6-leaf-stage rice plants were individually placed into a breathable transparent plastic bottle (5 cm in diameter, 30 cm in height) containing Yoshida medium, pH=4, and then fed by ~500 fifth instar BPH for 72 h. Next, the two outermost layers of leaf sheath surrounding the stem were cut into small pieces, rinsed with ultrapure water for three times and ground to powder in liquid nitrogen. Total protein was extracted in a buffer containing 60 mM Tris-HCl (pH=7.6), 2.5% Glycerol, 6% SDS, 0.1 M DL-Dithiothreitol (DTT), 1x Protein inhibitor cocktail and 1 mM phenylmethanesulfonyl fluoride. Protein samples were concentrated using 3-kDa filtration units and shipped on dry ice to Shanghai Hoogen Biotech for shot-gun LC-MS analysis. Briefly, protein samples digested by trypsin for 16 h at 37°C. The hydrolysates were then loaded into Zorbax 300SB-C18 peptide traps (Agilent Technologies, Wilmington, DE) and analyzed by a Q Exactive mass spectrometer (Thermo Fisher). The raw LC-MS data were searched against the BPH protein database (NCBI Accession No. PRJNA669454) using software MaxQuant 1.5.5.1.

Peptides with a high confidence score was extracted, and the database search was conducted with false discovery rate (FDR) under 0.01.

RNA interference (RNAi). The nucleotide sequence (around 500 bp long) specific to the *NlCA* coding region was cloned into the pMD 19-T vector (TAKARA). The double-stranded RNA was synthesized through PCR amplification by using the Mega script T7 High Yield RNA Transcription Kit (Vazyme, Nanjing, China), following the manufacturer's instructions. The procedure for gene knockdown by RNAi was described previously [22]. Briefly, the 2nd and 5th instar BPH nymphs in an insect rearing growth chamber were anaesthetized with carbon dioxide for ~10 s. Approximately 50-250 ng of dsRNA was injected into BPH mesothorax using FemtoJet (Eppendorf-Netheler-Hinz, Hamburg, Germany). The efficiency of RNA interference was assessed 48 h after injection. RNA from 30 nymphs was extracted using the RNAiso Plus kit (TaKaRa) according to the manufacturer's instructions as one biological replicate. The relative level of the *NlCA* transcript was quantified using a CFX96TM Real-Time PCR Detection System (Bio-Rad, Hercules, CA, USA) with primers shown in Supplementary Table 1. The Aequorea Victoria green fluorescent protein (*GFP*) gene sequence was used as the control template in RNAi experiments. Four biological replicates (30 individual insects pooled for each biological replicate) were conducted.

BPH survival test on artificial diet. The 5th instar BPH nymphs injected with ds*GFP* or ds*NlCA* were immediately placed on one-week-old rice seedlings (1-leaf-stage) for recovery in the small breathable transparent plastic bottle for 3 days. Fifty normal-appearing BPH adults were gently transferred into a shaded black plastic bottle of 5 cm in diameter and 15 cm in height, with translucent double-layer parafilm loaded with fresh artificial diet. The first layer of parafilm closed to BPH was needled 40 holes by a 1 ml syringe and fresh artificial diet AADM, pH of 6.0, was filtered through a 0.22 micrometer needle-type bacterial filter (Sangon Biotech, F513142-0001). Fresh artificial diet was replaced every 24 hours. The second layer of parafilm wrapped the artificial diet to isolate the diet from bacteria in the air. Dead BPHs were separated from live BPHs daily and mucus adhering to the inner wall of the black plastic bottle was cleaned daily to eliminate possible impact on live BPHs. and the pH was changed from 6.8 to 6. There were three biological replicates for each treatment, and each biological replicate includes 50 BPH adults. Experiments were repeated three times with similar trends.

BPH survival test on rice. BPH nymphs with verified *NlCA* knockdown by RNAi were placed into a small breathable transparent plastic bottle of 10 cm in diameter and 9 cm in height containing one-week-old rice seedlings (1-leaf-stage) for 12 h to recover. About 20 healthy-appearing 2nd

instar nymphs were gently transferred into a longer breathable transparent plastic bottle of 5 cm in diameter and 30 cm in height containing four-week-old rice plants (4- to 5-leaf-stage) and observed for up to 15 days. The feeding space for BPH in each plastic bottle was around 200 cm3 divided by two sponges of 5 cm in diameter and 2 cm in thickness. The number of surviving BPHs were counted daily on each plant. ds*GFP* BPH were used as control. The average of survival rate on each seedling was calculated.

For BPH survival test on normal and acidic media growing rice plants, the early 5th instar BPH nymphs inoculated ds*GFP* and ds*NlCA* fed on one-week-old rice seedlings (1-leaf-stage) were recovered in the small breathable transparent plastic bottle for 24 hours. The Nipponbare rice plants (5-leaf stage) growing on normal liquid media (pH = 4) was transferred into fresh liquid media with pH of 4 and 2 for 24 hours, respectively, before conducting BPH survival test. There were five biological replicates for every treatment, and one biological replicate is one rice plant fed by 20 BPHs. Experiments were repeated three times with similar trends.

pH assay. Transgenic rice plants expressing the cyto-pHusion pH sensor were grown in the modified Yoshida medium as described above. Each 5-leaf-stage seedlings were fed by 30 5th instar BPH, which were starved in the breathable plastic tubes for 3 h before feeding. No BPH treatment was included as control. The microscopic images were taken from the phloem of rice leaf sheaths that were fed by BPH for 1.5 h, 4 h, 8h and 12 h using an Olympus FV3000 with a 40.0 x objective. EGFP was imaged with λEm = 540 nm and the detection wavelength at 500-540 nm. mRFP was imaged with λEm = 570 nm and detection wavelength wat 570 to 620 nm. EGFP fluorescence data and EGFP:mRFP ratio data were obtained using 64-bit professional edition Fiji ImageJ2. Each treatment includes > 24 circular areas of leaf sheath with a diameter of 100 μm each, including the feeding site at the center.

RNA isolation and quantitative real-time PCR (qRT-PCR). The total RNA was extracted using the TRIzol reagent kit (Invitrogen), and then treated with Rnase-free Dnase I (Invitrogen) according to the manufacturer's protocol. The RNA was reverse-transcribed using a cDNA synthesis kit (TaKaRa) and one μg of each RNA samples was reverse transcribed. qRT-PCR was performed from cDNA using SYBR Green qPCR mix (TaKaRa, RR601A) following the manufacturer's instructions using the LightCycler 480 system (Roche Diagnostics). Fold changes were calculated using the ΔCt method. Each assay was replicated at least three times, each with three biological replicates (independent RNA preparations). The rice Actin gene (*LOC_Os03g50885*) and the BPH 18S rRNA (*LOC_111047943*) gene were used as a reference. Sequences of qRT-PCR primers are given in Supplementary Table 1.

Callose deposition in rice sheath. For counting callose deposition, four-leaf-stage rice plants were infested with ~15 fifth instar BPH. The two outermost rice leaf sheaths were collected before and after BPH feeding for 72 h and fixed in FAA solution as described by Guo et al. [29], dehydrated and embedded in paraffin. The sections were cut to 5 um thickness on glass slides, dewaxed and stained with 0.1 % aniline blue in 0.1 % 5 M K_2PHO4 for 10 min, and examined under Zeiss confocal microscope with a 40× oil objective lens. The total area and number of callose deposition in the rice sieve pores were counted. Each treatment has at least 400 cross sections and 12 biological replicates.

Data Availability.

All data are presented within this paper.

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Author Contributions: S.Y.H., C.X.Z., Y.J.J. and X.Y.Z. conceptualized and designed this study; Y.J.J., X.Y.Z., S.Q.L., Y.C.X., X.M.L., Y.P.Y., Z.Y.P., L.Z., J.B.L., and H.J.H. performed experiments and analyzed data; C.X.Z. and S.Y.H. analyzed data. Y.J.J., X.Y.Z., C.X.Z. and S.Y.H. wrote the paper with all authors approved the final article.

Competing Interest Statement: The authors declare no competing interest.

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Figures

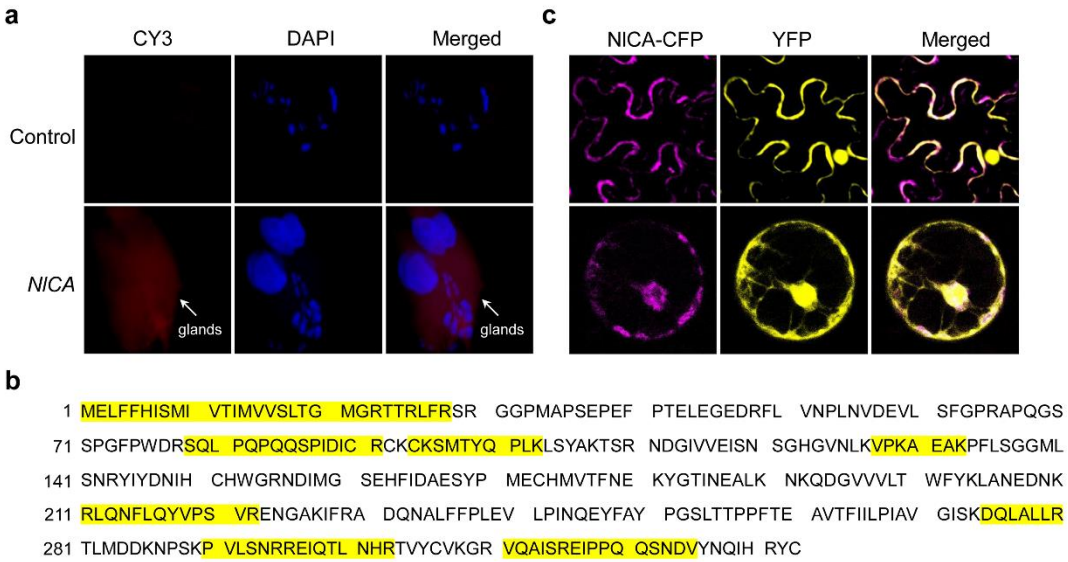

Fig. 1| Initial characterization of *Nilaparvata lugens* carbonic anhydrase (NlCA). a, *in situ* RNA hybridisation of salivary glands in 5-instar BPHs (lower row) using antisense NlCA sequence as a probe. Sense *NlCA* probe was used as a negative control (upper row). White arrows indicate glands. Nuclei are stained blue by 4',6-diamidino-2-phenylindole (DAPI). **b**, The amino acid sequence of NlCA. The highlighted amino acid residues indicate the peptides detected in BPH-infested rice sheath tissue by LC-MS analysis. **c**, NlCA is colocalized with the YFP signals in *N. benthamiana* (upper row) and rice cells (lower row). YFP and NlCA-CFP fusion proteins were co-expressed in *N. benthamiana* leaf cells for 48 h using the *Agrobacterium*-mediated transient expression method. YFP and NlCA-CFP fusion proteins were co-expressed in rice protoplasts 16 h after the corresponding DNA constructs were introduced into rice protoplasts via polyethylene glycol-mediated transformation. Experiments were repeated three times with similar trends.

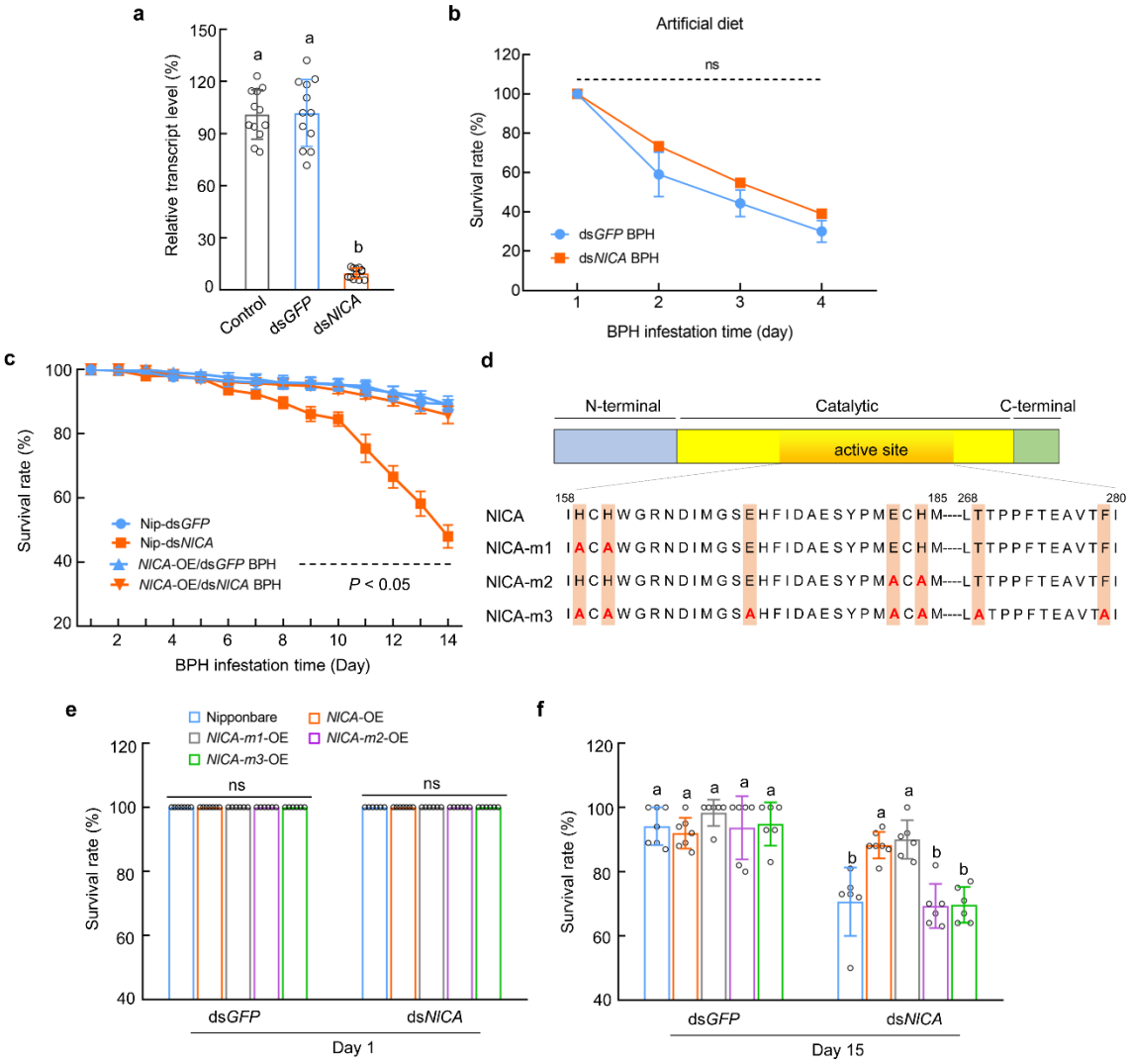

Fig. 2| Effects of *NICA* RNAi on BPH survival on rice cultivar Nipponbare. a, The *NICA* transcript levels in BPH at 3 dpi post-injection of ds*GFP* or ds*NICA* were determined by qRT-PCR (displayed as % of the *NICA* transcript abundance in control BPH). Values are displayed as mean ± SEM of 4 experimental replicates (Two-way ANOVA; 3 biological replicates in each experiment and 30 individual insects pooled for each biological replicate). **b**, The daily survival rates of ds*NICA*-injected BPH insects feeding on artificial diet. Values are displayed as mean ± SEM of 3 biological replicates (one biological replicate includes 50 individual BPH adults fed on artificial diet in a lucifugal plastic bottle). **c**, The daily survival rates of ds*NICA*-injected BPH insects feeding on Nipponbare and NICA-expressing line 1. Values are displayed as mean ± SEM of 8 biological replicates (Two-way ANOVA; 20 individual 2nd BPH nymphs per rice plant for each biological replicate). The black dashed line indicates significant differences ($P < 0.05$) in survival rates start day 9 between ds*NICA* BPH on Nipponbare (Nip) and other treatments. **d**, Schematic display of

the NlCA protein with the N-terminus displayed in bule, the C-terminus in green and the central catalytic domain in yellow/orange. The amino acid sequence (158 - 280 aa) of the putative active site is showed. Amino acid substitutions in NlCA-m1, NlCA-m2 and NlCA-m3 are indicated in red. **e-f**, The survival rates of 20 ds*GFP* and ds*NlCA* BPH insects in Nipponbare and *NlCA* transgenic plants after 1- and 15-days post-infestation. Values are displayed as mean ± SEM (n ≥ 6 biological replicates; 20 individual 2nd BPH nymphs per rice plant for each biological replicate). ns indicates no significant difference between treatments (Two-way ANOVA). Different letters indicate statistically significant differences analyzed by two-way ANOVA (Tukey test, $P < 0.05$). Experiments were repeated three times with similar trends.

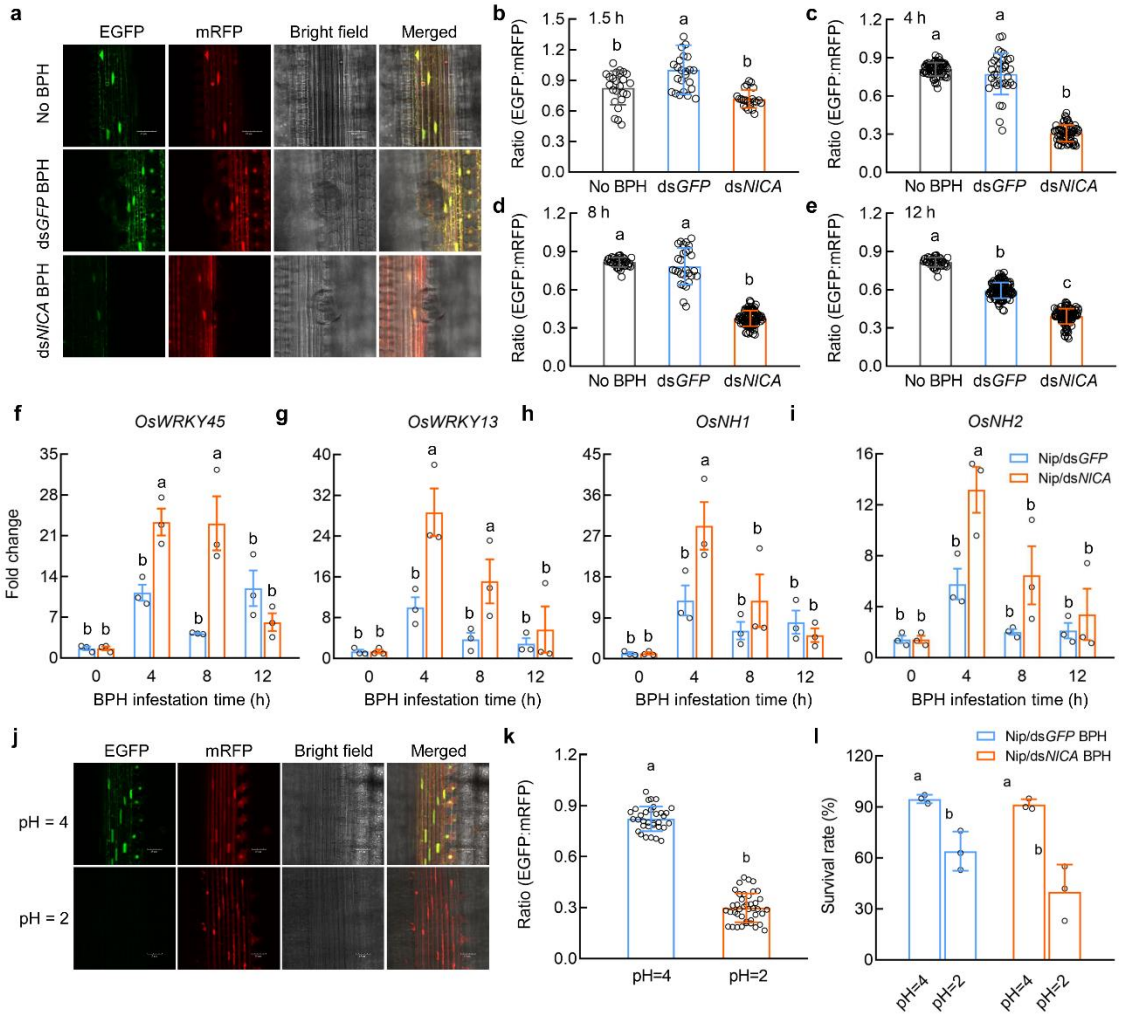

Fig. 3| Role of NICA in maintaining intracellular pH of rice cells. a, Confocal microscopic images at BPH feeding sites in Nipponbare plants expressing a ratiometric cytoplasmic pH sensor (Cyto-pHusion) 4 h after placing 30 5th-instar BPH nymphs on each plant. Confocal images from plants with no BPH feeding served as the control. **b-e**, EGFP:mRFP signal ratios at 1.5 h (a), 4 h (c), 8 h (d) and 12 h (e) of ds*GFP* or ds*NICA* BPH treatment compared with no BPH control. EGFP was imaged at λ_{Ex} = 500 nm and λ_{Em} = 540 nm. mRFP was imaged at λ_{Ex} = 570 nm and λ_{Em} = 620 nm. Values are displayed as mean ± SEM (n ≥ 24 circular areas of leaf sheath phloem with a diameter of 100 μm with the feeding site at the center). **f-i**, Expression of defense response genes, *OsWRKY45*, *OsWRKY13*, *OsNH1* and *OsNH2*, in Nipponbare plants infested by ds*GFP* or ds*NICA* BPH. Values are displayed as mean ± SEM of three biological replicates. Each biological replicate represents pooled leaf sheaths from three individual rice plants fed by 20 5th instar BPH nymphs per plant. **j**, Confocal microscopic images of Nipponbare plants expressing a ratiometric cytoplasmic pH sensor (Cyto-pHusion) at 12 h after being transferred to Yoshida

medium at pH of 2. Confocal images from plants grown in Yoshida medium with pH of 4 served as the control. **k**, EGFP:mRFP signal ratios. EGFP was imaged at λ_{Ex} = 500 nm and λ_{Em} = 540 nm. mRFP was imaged at λ_{Ex} = 570 nm and λ_{Em} = 620 nm. Values are displayed as mean ± SEM (n ≥ 33 calculation area per condition). **l**, The 7th-day survival rates of ds*GFP*- and ds*NlCA*-injected BPH insects feeding on Nipponbare growing in media with different pHs. Values are displayed as mean ± SEM of 3 biological replicates (20 individual insects per each biological replicate). Different letters indicate statistically significant differences analyzed by two-way ANOVA (Tukey test, $P < 0.05$). Experiments were repeated at least three times with similar trends in this figure.

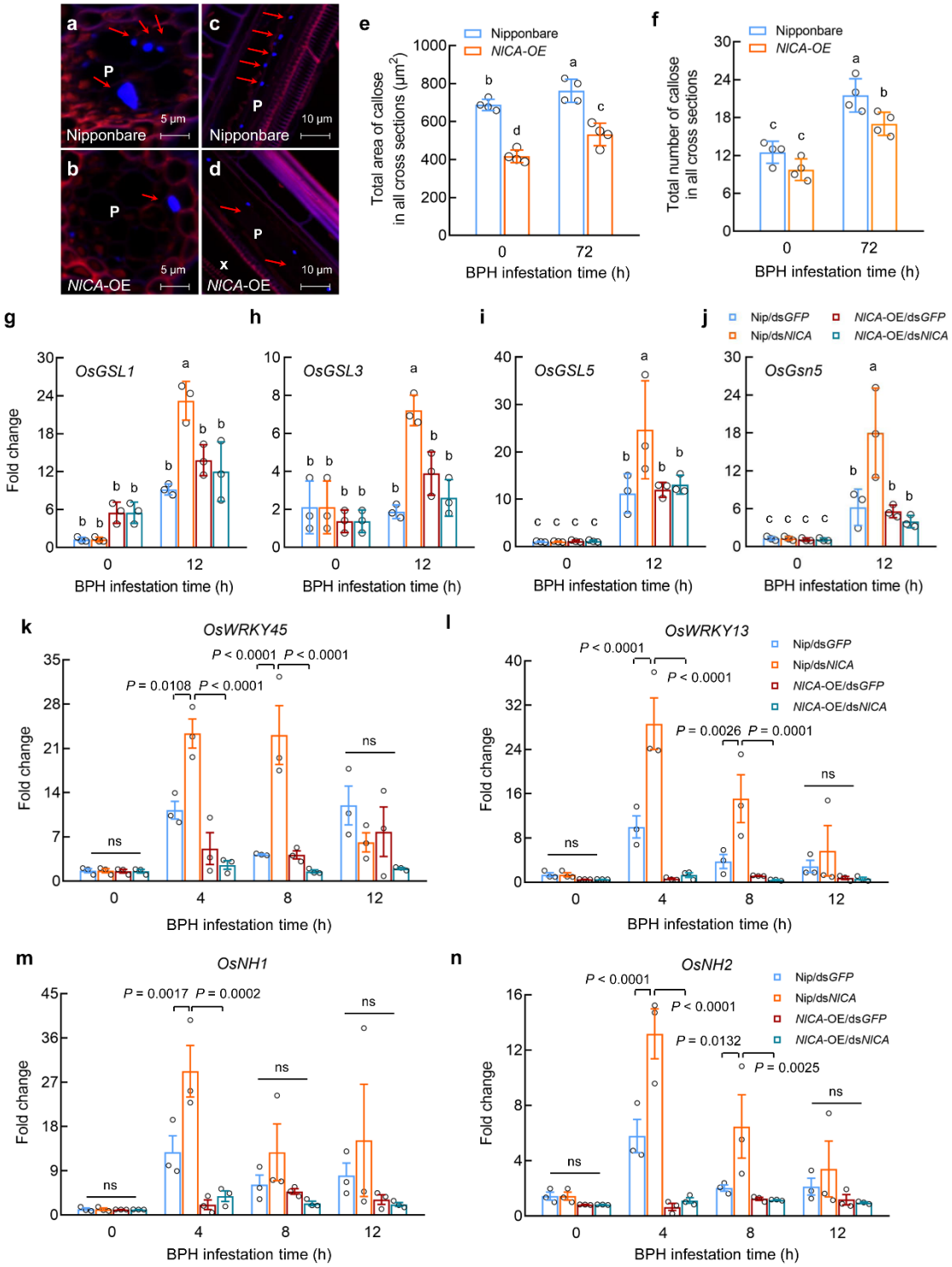

Fig. 4| NICA dampens callose deposition and defense gene expression. a-d, Callose accumulation (bright blue fluorescence indicated by red arrows) on the sieve plates of Nipponbare leaf sheaths (a and c) and *NICA-OE* leaf sheaths (b and d) plants before and 72 h

after BPH feeding. P, phloem; X, xylem. The pictures were taken under a Zeiss Microscope. (a-b) Cross-sections. (c-d) Longitudinal sections. **e**, Total areas of callose deposition in BPH-infested leaf sheaths of Nipponbare and *NlCA*-OE. Each data point represents the total areas of callose deposition found in 300 cross-sections of each experiment. Values are displayed as mean ± SEM of four experiments. **f**, Total number of callose deposits in BPH-infested leaf sheaths of Nipponbare and *NlCA*-OE. Each data point represents the total number of callose deposits found in 300 cross-sections of each experiment. Values are displayed as mean ± SEM of four experiments. **g-j**, Relative expression levels of the callose synthase gene *OsGSL1* (g), *OsGSL3* (h), *OsGSL5* (i) and *OsGns5* (j) in response to BPH feeding. Values are displayed as mean ± SEM of 3 biological replicates. Each biological replicate represents pooled leaf sheath form three individual rice plants fed by 20 5th instar BPH nymphs per plant. **k-n**, Expression of defense marker gene *OsWRKY45* (k), *OsWRKY13* (l), *OsNH1* (m) and *OsNH1* (n) in response to BPH feeding. Values are displayed as mean ± SEM of 3 biological replicates. Each biological replicate represents pooled leaf sheaths from three individual rice plants fed by 20 5th instar BPH nymphs per plant. ns indicates no significant difference between treatments (Two-way ANOVA). Different letters indicate statistically significant differences analyzed by two-way ANOVA (Tukey test, $P < 0.05$). Experiments were repeated three times with similar trends.