


Harnessing the functional diversity of plant cystatins to design inhibitor variants highly active against herbivorous arthropod digestive proteases

Jonathan Tremblay¹, Marie-Claire Goulet¹, Juan Vorster², Charles Goulet¹ and Dominique Michaud¹ 

¹ Département de phytologie, Centre de recherche et d'innovation sur les végétaux, Université Laval, Québec, Québec, Canada

² Department of Plant and Soil Sciences, The University of Pretoria, Pretoria, South Africa

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Correspondence

D. Michaud, Centre de recherche et d'innovation sur les végétaux, Département de phytologie, Université Laval, Québec G1A 0A6, Québec, Canada
 Tel: +1 (418) 656-2131
 E-mail: dominique.michaud@fsaa.ulaval.ca

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Protein engineering approaches have been proposed to improve the inhibitory properties of plant cystatins against herbivorous arthropod digestive proteases, generally involving the site-directed mutagenesis of functionally relevant amino acids or the selection of improved inhibitor variants by phage display approaches. Here, we propose a novel approach where the function-related structural elements of a cystatin are substituted by the corresponding elements of an alternative cystatin. Inhibitory assays were first performed with 20 representative plant cystatins and model Cys proteases, including arthropod proteases, to appreciate the extent of functional variability among the plant cystatin family. The most, and less, potent of these cystatins were then used as ‘donors’ of structural elements to create hybrids of tomato cystatin SICYS8 used as a model ‘recipient’ inhibitor. In brief, inhibitory activities against Cys proteases strongly differed from one plant cystatin to another, with K_i (papain) values diverging by more than 30-fold and inhibitory rates against arthropod proteases varying by up to 50-fold depending on the enzymes assessed. In line with theoretical assumptions from docking models generated for different Cys protease–cystatin combinations, structural element substitutions had a strong impact on the activity of recipient cystatin SICYS8, positive or negative depending on the basic inhibitory potency of the donor cystatin. Our data confirm the wide variety of cystatin inhibitory profiles among plant taxa. They also demonstrate the usefulness of these proteins as a pool of discrete structural elements for the design of cystatin variants with improved potency against herbivorous pest digestive Cys proteases.

Introduction

Protease inhibitors of the cystatin protein superfamily play various roles in plants, from the regulation of Cys proteases in seeds and senescent organs to the inhibition of exogenous digestive proteases upon arthropod herbivory or pathogenic infection [1,2].

Cystatins act as reversible pseudosubstrate inhibitors to hinder the active site of target proteases and block their catalytic action on the peptide bonds of protein substrates [3]. The inhibitory function of these proteins relies on two structural elements, a central hairpin

Abbreviations

CsCYS, *Cucumis sativa* (cucumber) cystatin; CV, coefficient of variation; GST, glutathione *S*-transferase; LRD, loop replacement design; MCA, methylcoumarin; PpCYS, *Physcomitrella patens* (moss) cystatin; SE, structural element; SICYS8, eighth inhibitory domain of tomato multicystatin; StCYS5, fifth inhibitory domain of potato multicystatin.

loop with the conserved pentapeptide motif Gln–X–Val–X–Gly (where X is any amino acid) and a second hairpin loop in the C-terminal region with a conserved Trp residue, which physically interact with amino acid residues in the active site cleft of the target enzyme. A third structural element is also involved, consisting of a flexible, N-terminal amino acid string presenting a conserved Gly–Gly dipeptide motif [2]. This third element, referred to as the N-terminal trunk, interacts with surface residues on the target enzyme to strongly influence the inhibitory potency and specificity of the cystatin towards different protease isoforms [4].

An increasing body of knowledge about the properties and physiological roles of plant cystatins has triggered the development of various biotechnological applications over the years [5]. Studies have shown the potential of these proteins as ectopic regulators of endogenous Cys proteases to regulate storage protein deposition and degradation in reproductive organs [6,7], to restore fertility in Cys protease-induced male sterile plants [8] or to avoid the detrimental action of endogenous Cys proteases on heterologous proteins in plants used as bio-factories for clinically relevant proteins [9–12]. Other studies have shown their potential to implement drought, cold or salt tolerance in different crops [13–16], associated with the induction of abiotic stress-related genes upon recombinant cystatin expression [17,18]. Most importantly, numerous studies have described the potential of plant cystatins to protect plants from microbial pathogens, root parasitic nematodes and phytophagous arthropods (reviewed in [19–22]). Cystatins inhibit digestive Cys proteases secreted in the extracellular milieu of microbial cells or digestive tract of herbivorous arthropods, to cause amino acid shortage, growth delays and eventual death of the pathogenic or herbivorous enemy [20,23].

From a physiological standpoint, the actual ability of a cystatin to protect the plant from herbivory is determined by its relative abundance compared to Cys proteases in the target herbivore midgut, by its inhibitory range towards these enzymes, and by any compensatory response induced in the herbivore after ingestion [24]. Herbivorous insects have developed effective strategies to avoid the negative effects of dietary protease inhibitors, including the secretion of digestive proteases from different functional classes, the overexpression of proteases following inhibitor uptake, and the production of protease isoforms weakly sensitive to inhibition [25]. A well-documented example is the coleopteran insect pest Colorado potato beetle (*Leptinotarsa decemlineata*), which uses an array of positively selected digestive Cys protease isoforms to process leaf proteins [26]. Divergent, if not

contradictory, effects have been reported for transgenic potato lines engineered to express cystatins, ranging from major developmental delays and mortality [24,27,28] to compensatory growth and hypertrophic behaviour sustained by Cys protease overexpression [28–30]. Possible explanations for such discrepancy among studies include differential expression levels of the recombinant cystatin in leaf tissue, varying stability of this protein in different potato cultivars, distinct inhibitory ranges towards the insect Cys proteases and experimental biases influencing insect fitness. Together, these observations stress the need for a better understanding of complex interactions between wound-inducible cystatins and Cys proteases in plant–insect systems. They also underline the relevance of rational strategies for the molecular improvement of recombinant cystatin inhibitory profiles towards Cys proteases.

Three main approaches are generally adopted for the molecular improvement of plant cystatins [5,31,32]. The first approach involves site-directed substitution at functionally relevant amino acid sites, the second approach the generation of improved inhibitory variants using phage display or DNA shuffling artificial evolution procedures and the third approach the design of bi- or multifunctional translational fusions integrating one or more cystatin inhibitory domains. In this study, we explored the potential of a fourth approach based on the substitution of one or more function-related structural elements (SE's) of the cystatin by the corresponding element(s) of an alternative cystatin. Our goal was to assess the usefulness of potent cystatins from different plant taxa as SE “donors” to generate functional variability among the structural hybrids of a “recipient” cystatin. The idea was to translate the concept of ‘loop replacement design’ (LRD), as described for the engineering of multimeric mammalian antibodies [33], to the improvement of single-domain cystatins. Amino acid substitutions in the N-terminal trunk or the inhibitory loops of plant cystatins have proved useful to enhance the inhibitory potency or change the affinity profile of these proteins towards insect or nematode Cys proteases [4,34–36]. We hypothesized that an LRD-like scheme by which the function-related elements of a protein are changed for the corresponding elements of a related protein would represent a welcome complement to site-directed mutagenesis as it would allow conformational changes in the cystatin on a length scale beyond that accessible to single mutations [33].

Cystatins are well suited to protein engineering and polypeptide grafting, as illustrated by their stability in fusion with different protein partners [5,31,37], the structural stability of model tomato cystatin SICYS8

bearing a poly-His tag for protein purification in a non-inhibitory loop of the protein scaffold [38], the ability of SICYS8 to stabilize a human protein translational fusion partner *in planta* [9], the structural assessment of natural cystatins as a guide for *de novo* protein design [39] and the use of a consensus plant cystatin scaffold to design Affimer binding proteins for a variety of imaging, diagnostic and therapeutic purposes [40,41]. Here, we confirm the usefulness of plant cystatins as a reservoir of discrete structural elements for cystatin engineering, and the potential of SE substitutions as a novel approach to create cystatins with improved inhibitory potency against arthropod Cys proteases.

Results

Variable contributions of the N-terminal trunk and two inhibitory loops to the protease binding strength of plant cystatins

Docking simulations were performed *in silico* with three protease models to gain preliminary indication of the functional variability of plant cystatins and relative contributions of their function-related SE's to the enzyme-inhibitor complex. Five plant cystatins and the three model Cys proteases papain, human cathepsin L and Colorado potato beetle intestain D4 (IntD4) [26] were selected for the simulations, for a total of 15 protease-cystatin complexes and 45 protease-SE interactions (Table 1). Structural models were first built for the proteases and the cystatins by homology modelling with the solved structures of human cathepsin L [42] and oryzacystatin I (OsCYS1) [43] respectively. Protease-cystatin interactions were then simulated using the Z-Dock algorithm of Chen *et al.* [44], by homology to the solved structure of papain in complex with human stefin B (Protein Data Bank Accession No. 1STF). In line with variable sequences in the functional regions of both the cystatins and the proteases, amino acid residues predicted to contribute to the binding process differed from one cystatin to another for a given protease, and from one protease to another for a given cystatin (Fig. 1). Accordingly, total binding energies differed for the 15 protease-cystatin complexes, from an inferred total energy value of $-544 \text{ kcal}\cdot\text{mol}^{-1}$ for maize ZmCYS1 interacting with papain to an energy value of $-1234 \text{ kcal}\cdot\text{mol}^{-1}$ indicating a stronger interaction between the same cystatin and cathepsin L (Table 1 and Table S1).

In accordance with previously described models indicating variable contributions of the N-terminal trunk and two inhibitory loops to the protease binding

Table 1. Binding energies inferred *in silico* for Cys proteases papain, human cathepsin L and *L. decemlineata* Intestain D4 interacting with different plant cystatins^a

Cystatin/Protease	Interaction energy ($\text{kcal}\cdot\text{mol}^{-1}$)			
	N-ter trunk	Loop 1	Loop 2	Total
SICYS8				
. Papain	-141.0	-105.9	-385.6	-632.5
. Cathepsin L	-386.6	-133.5	-408.8	-928.9
. Intestain D4	-333.2	-84.4	-240.1	-657.7
SICYS9				
. Papain	-133.6	-180.1	-401.6	-715.3
. Cathepsin L	-389.0	-327.3	-274.5	-990.8
. Intestain D4	-302.2	-92.1	-271.7	-666.0
OsCYS1				
. Papain	-151.1	-170.0	-317.9	-639.0
. Cathepsin L	-419.7	-273.3	-290.8	-983.8
. Intestain D4	-341.1	-104.0	-289.1	-734.2
GmCYS2				
. Papain	-333.8	-188.7	-483.5	-1006.0
. Cathepsin L	-412.8	-303.6	-218.0	-934.4
. Intestain D4	-346.6	-165.8	-192.6	-705.0
ZmCYS1				
. Papain	-131.9	-136.4	-276.0	-544.3
. Cathepsin L	-591.2	-322.5	-320.4	-1234.1
. Intestain D4	-326.4	-76.8	-202.7	-605.9

^aData are the sum of binding energy values inferred for the complement of protease-cystatin interacting residues associated with the N-terminal trunk (N-ter), the first inhibitory loop (Loop 1), the second inhibitory loop (Loop 2) or the whole cystatin (Total) (Table S1 for binding energy values at the amino acid level). Cystatin interacting residues are identified in Fig. 1 for the three model proteases.

process [45,46], binding energies assigned to the three structural elements differed depending on the cystatin or the protease considered (Table 1). For instance, a binding energy value of $-334 \text{ kcal}\cdot\text{mol}^{-1}$ accounting for 33% of the complex total binding energy was inferred for the N-terminal trunk of soybean GmCYS2 interacting with papain, compared to weaker energy values and relative contributions of less than 25% for the N-terminal trunks of tomato SICYS8 and SICYS9, OsCYS1 and ZmCYS1 interacting with the same enzyme (Fig. 2). Likewise, an energy value of $-402 \text{ kcal}\cdot\text{mol}^{-1}$ accounting for 56% of the total was calculated for the second inhibitory loop of tomato SICYS9 interacting with papain, compared to weaker binding energies (and smaller relative contributions) of $-275 \text{ kcal}\cdot\text{mol}^{-1}$ (28%) and $-272 \text{ kcal}\cdot\text{mol}^{-1}$ (41%) for the same cystatin interacting with cathepsin L and IntD4 respectively (Table 1). These numbers suggesting SE-specific interactions between plant cystatins and their target proteases, together with heterogeneous binding energy values inferred for the 15 protease-cystatin

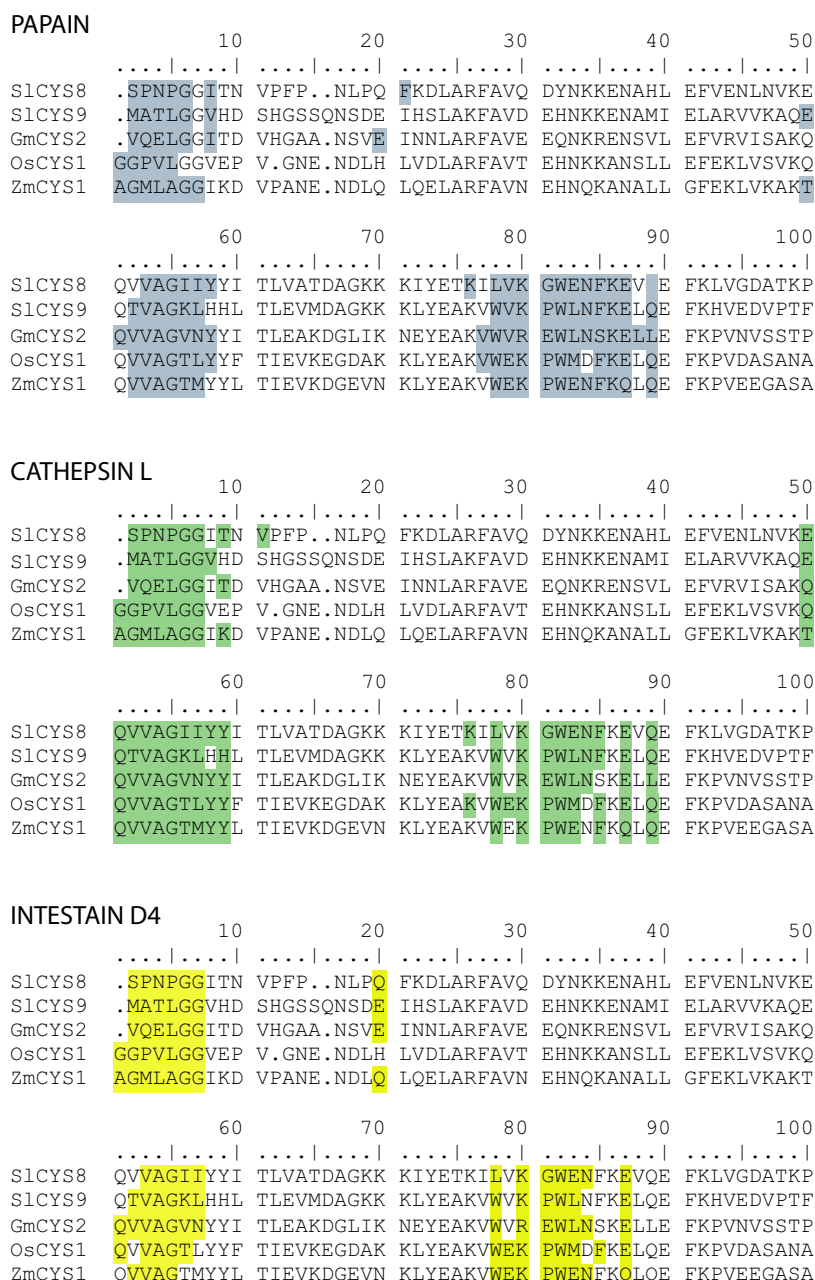


Fig. 1. Amino acid sequence alignments highlighting the residues of tomato cystatins SICYS8 (GenBank Accession No. [AF198390](#)) and SICYS9 (GenBank [NP001275067](#)), soybean cystatin GmCYS2 (GenBank [AAA97906](#)), rice cystatin OsCYS1 (oryzacystatin I) (GenBank [NP001044550](#)) and corn cystatin ZmCYS1 (GenBank [NP001105295](#)) predicted to interact with papain (PDB Accession No. [9PAP](#)) (in blue), human cathepsin L (PDB [1SC8](#)) (in green) and *L. decemlineata* IntD4 (GenBank [EF154436](#)) (in yellow). Sequence alignments were generated using the MultAlin algorithm (<http://multalin.toulouse.inra.fr>). Structural models for IntD4 and the plant cystatins were generated with Modeller, v. 9.7 (<https://salilab.org/modeller/>), using the crystal structure of human cathepsin L (PDB [1SC8](#)) as a template for IntD4 and the NMR structure of oryzacystatin I (PDB [1EQK](#)) as a template for the cystatins. Protease–cystatin interactions were simulated using the Z-Dock algorithm of Discovery Studio (ACCELRYS Software Inc.) as detailed in Materials and Methods, by homology to the solved structure of papain in complex with human stefin B (PDB [1STF](#)).

complexes, provided preliminary evidence for a certain functional variability among plant cystatin family members, likely explained by differential contributions of their N-terminal trunk and two inhibitory loops to the protease binding process.

Functional variability among plant cystatin protein family members

In vitro protease inhibitory assays were conducted with cystatins of different plant taxa to empirically support

these *in silico* assumptions suggesting functional variability among plant cystatins, to confirm the potential of these proteins as a source of SE's for cystatin improvement, and to identify potent cystatin donors for the SE substitution experiments. A multiple sequence alignment was generated with 262 cystatin primary sequences available in the National Centre for Biotechnology Information (NCBI) database, using tomato SICYS8 as a reference [36]. Double-stranded DNA fragments, or 'g-blocks', were then produced for 30 of the cystatins, chosen based on their distribution

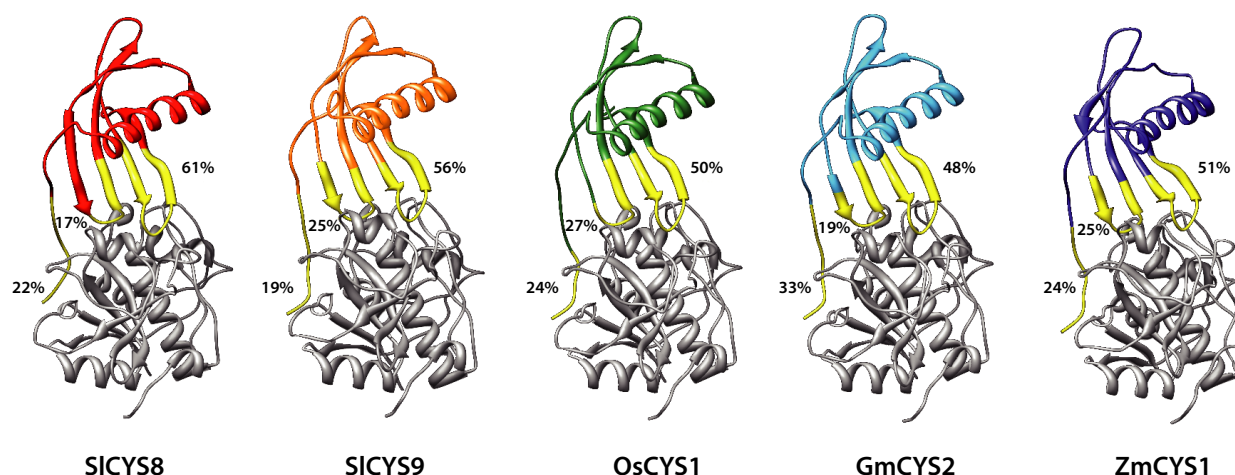


Fig. 2. Docking models for plant cystatins SICYS8, SICYS9, OsCYS1, GmCYS2 and ZmCYS1 interacting with papain (in grey). Cystatin residues physically interacting with the target enzyme are highlighted in yellow (Fig. 1 for details). Numbers indicate relative contributions of the N-terminal trunk, first inhibitory loop and second inhibitory loop to the binding process, as inferred from Table 1 (total = 100%). The cystatin models were generated using Modeller, v. 9.7 (<https://salilab.org/modeller/>) based on the NMR spatial coordinates of rice cystatin OsCYS1 (PDB Accession No. 1EQK). Docking simulations were inferred using the Z-Dock algorithm of Discovery Studio (ACCELRYS Software).

in different branches of the resulting phylogenetic tree (Fig. S1) and their belonging to different subgroups of the plant cystatin family [2]. The DNA fragments were used as coding gene templates for heterologous expression in *E. coli* and affinity purification using the glutathione *S*-transferase (GST) gene fusion [38]. A total of 20 cystatins or cystatin domains deemed representative of the plant cystatin protein family (Fig. S1) were recovered under a stable form and used as test inhibitors for the protease assays (Table 2).

In agreement with our *in silico* models indicating variable binding energies for SICYS8 and other plant cystatins interacting with papain (Table 1), inhibition constant (K_i) values against papain ($K_{i(\text{papain})}$) differed by more than one order of magnitude from one cystatin to another, from 1.2 nM for *Physcomitrella patens* C-tailed cystatin domain PpCYS or 2.7 nM for tomato multicystatin domain SICYS7, to 38.2 nM for soybean GmCYSB or even no measurable inhibitory activity for Arabidopsis AtCYS6B (Table 2). Similarly, the 20 cystatins showed variable inhibitory potency against midgut cathepsin L-like (Z-Phe-Arg-MCA hydrolysing) Cys proteases of *L. decemlineata* and the acarid herbivore generalist two-spotted spider mite, *Tetranychus urticae* (Fig. 3). For instance, *P. patens* cystatin PpCYS and potato multicystatin domain StCYS5 showed strong inhibitory activity against these proteases at low (20 nM) concentration, in sharp contrast with cucumber cystatin CsCYS and barley cystatin HaCYS3 showing negligible activity. Not surprisingly given the high specificity of Cys protease–cystatin

interactions at the submolecular level, several cystatins showed variable effects depending on the protease tested (Table 2 and Fig. 3). This was observed, for instance, with AtCYS6B showing weak activity against papain and *L. decemlineata* cathepsin L-like enzymes but easily measurable activity against *T. urticae* cathepsin L-like enzymes, or with *Glycine soja* GsCYS efficiently inhibiting papain and *T. urticae* proteases but showing weaker activity against the *L. decemlineata* enzymes. Together, these observations confirmed the occurrence of functional variability among plant cystatin family members and the eventual potential of these proteins as a source of SE's to design improved cystatins.

A generic scheme for plant cystatin SE substitutions

An SE substitution strategy was designed to determine whether the variable inhibitory effects of plant cystatins against Cys proteases could be formally associated with the primary structures of their N-terminal trunk and inhibitory loops as suggested by our docking inferences, and whether plant cystatins as a group would represent a useful pool of discrete SE's for the design of cystatin variants with improved inhibitory potency against herbivorous pest digestive Cys proteases. Tomato SICYS8 was used as a recipient protein model for hybrid design given its reported suitability for protein engineering [9,36–38] and moderate activity against Cys proteases compared to other plant

Table 2. Plant cystatins selected for the functional studies and their calculated K_i values for model Cys protease papain

Cystatin code	Source species	Accession No.	K_i (papain) (nM)
One-domain cystatins			
.CsCYS	<i>Cucumis sativus</i>	KGN48310.1	14.4
.GmCYSB	<i>Glycine max</i>	XP_003538534.1	38.2
.GsCYS	<i>Glycine soja</i>	KHN18133.1	4.3
.JcCYS	<i>Jatropha curcas</i>	ADB02894.1	7.0
.KsCYS	<i>Knorringia sibirica</i>	ADD69946.1	7.5
.MsCYS	<i>Medicago sativa</i>	AAZ98791.1	7.1
.PsCYS	<i>Picea sitchensis</i>	ABK23108.1	4.8
.SiCYS	<i>Sesamum indicum</i>	XP_011090213.1	5.5
.TcCYSB	<i>Theobroma cacao</i>	XP_007015329.1	5.6
.ThCYS	<i>Tarenaya hassleriana</i>	XP_010536153.1	14.0
C-tailed cystatins			
.AtCYS6B	<i>Arabidopsis thaliana</i>	NP_850570.2	n.i.
.EgCYS	<i>Elaeis guineensis</i>	XP_010906414.1	6.4
.LjCYS	<i>Lotus japonicus</i>	AFK41721.1	13.5
.PpCYS	<i>Physcomitrella patens</i>	XP_001778431.1	1.2
.SiCYS9	<i>Solanum lycopersicum</i>	NP_001275067.1	13.3
.ZmCYSB	<i>Zea mays</i>	ACG33316.1	4.8
Multicystatin domains			
.HaCYS3	<i>Helianthus annuus</i>	BAA95416.1	15.4
.SiCYS7	<i>S. lycopersicum</i>	XP_004253396.2	2.7
.SiCYS8	<i>S. lycopersicum</i>	XP_004253396.2	14.7
.StCYS5	<i>Solanum tuberosum</i>	P37842.1	6.0

cystatins (Table 2 and Fig. 3). *P. patens* PpCYS and potato StCYS5 were used as donors given their strong inhibitory potency against *L. decemlineata* proteases, and hence, the expected potential of their function-related structural elements for SiCYS8 improvement. Cucumber CsCYS, weakly active against the arthropod cathepsin L-like enzymes (Fig. 3), was selected as a 'flawed', negative control donor to further confirm the potential of inherently efficient inhibitors, such as PpCYS and StCYS5, as loop donors to generate potent cystatins.

The SE hybrids were designed *in silico* by substituting the sequence(s) of SiCYS8 N-terminal trunk, first inhibitory loop (L1) and/or second inhibitory loop (L2) by the corresponding element(s) of PpCYS, StCYS5 or CsCYS (Fig. 4). The N- and C-terminal boundaries of each structural element were defined based on their distance relative to conserved amino acid motifs essential for activity in the transferred element, in such a way as to also include all amino acids assumed to physically interact with amino acid residues of the target enzyme [26] (Fig. 4). More specifically, the N-terminal trunks were devised based on the Gly–Gly (–GG–) motif characteristic of the N-terminal region of plant cystatins, the first inhibitory loops based on the conserved pentapeptide motif Gln–X–

Val–X–Gly (–QxVxG–) interacting with specific residues in the active site of the target protease, and the second inhibitory loops based on the conserved Trp residue also interacting with specific residues in the active site cleft [2]. Twenty-one cystatin variants were designed overall, including all seven structural element combinations possible for each of the three cystatin donors (Table 3 and Table S2). DNA g-blocks were produced for the 21 hybrids and used as templates for bacterial expression and affinity purification using the GST gene fusion. As for the original cystatins above, some hybrids could not be properly expressed under our experimental conditions, likely due to deficient stability in a foreign cellular environment during heterologous expression. Overall, 16 hybrids were produced in a form suitable for protease inhibitory assays with papain and the arthropod proteases (Table 3), a large enough number of variants to draw conclusive trends about the potential of SE substitutions for cystatin engineering.

SE substitutions for the molecular improvement of tomato SiCYS8

Papain inhibitory assays were conducted to measure the impact of N-terminal trunk and inhibitory loop substitutions on the inhibitory activity of SiCYS8. In line with the variable efficiencies of SiCYS8 and donor cystatins against papain, K_i values for this enzyme differed from one hybrid to another (Fig. 5). The most potent hybrids were hybrids P-1 and P-N1, both including the first loop of PpCYS. The less potent hybrid was hybrid C-N12, with the three functional elements of CsCYS. Overall, most substitutions involving the structural elements of StCYS5 and PpCYS, both more potent than SiCYS8 and CsCYS against papain (Table 2), showed decreased K_i values for this enzyme compared to the original inhibitor, unlike substitutions with the structural elements of CsCYS giving a more contrasted picture.

Similar trends were observed with the two arthropod proteases (Figs. 6 and 7). Most substitutions for the structural elements of StCYS5 and PpCYS, two potent inhibitors of *L. decemlineata* cathepsin L-like enzymes, strongly improved the inhibitory potency of SiCYS8 against these proteases, unlike substitutions for structural elements of CsCYS having a general negative impact (Fig. 6, upper panel). This was illustrated, for instance, by an anti-cathepsin L activity of SiCYS8 increased by ten times following the substitution of its two inhibitory loops by the two loops of StCYS5 (Hybrid S-12) or those of PpCYS (Hybrid P-12), in sharp contrast with the systematic low inhibitory

Fig. 3. Inhibition of *L. decemlineata* and *T. urticae* Z-Phe-Arg-MCA-hydrolysing (cathepsin L-like) enzymes by 20 representative members of the plant cystatin protein family (as identified in Table 2). Data are expressed as relative inhibitory rates compared to the inhibitory rate measured with E-64 (100%), a broad-spectrum diagnostic inhibitor for Cys proteases of the C1A (papain) family. Inhibitory assays were conducted with limiting (20 nM) or excess (200 nM) concentrations of cystatin. Each bar is the mean of three independent replicates \pm SE.

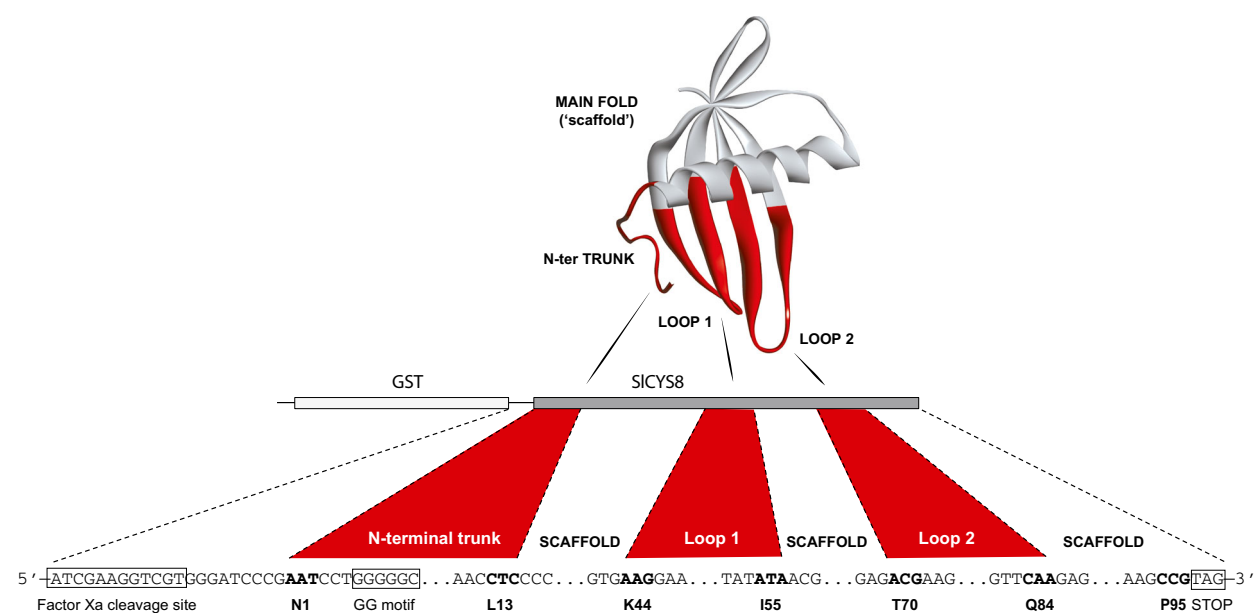
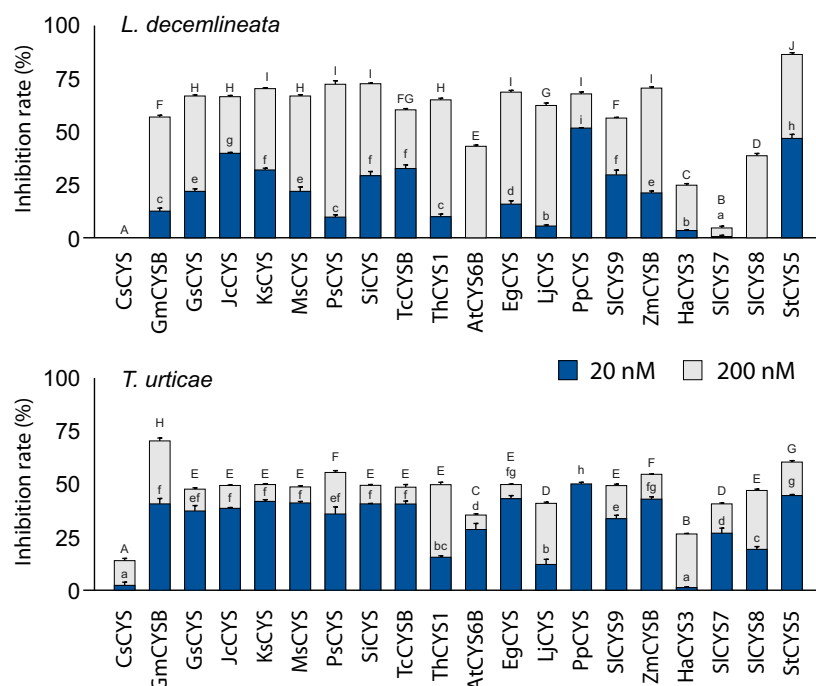


Fig. 4. A generic scheme for plant cystatin SE substitutions. The cystatin hybrids were first designed *in silico* by substituting the N-terminal trunk, first inhibitory loop [Loop 1] and/or second inhibitory loop [Loop 2] (in red) of tomato SICY8 used as a recipient (or scaffold) by the corresponding element(s) of potato StCYS5, *P. patens* PpCYS or cucumber CsCYS used as donors. DNA g-blocks synthesized for the resulting hybrids were then inserted in a modified pGEX-3X vector, downstream of a GST tag coding sequence, for heterologous expression in *E. coli* and affinity purification. Numbered amino acids under the gene sequence correspond to the N- and C-terminal amino acids of the three substituted elements. The structure model for SICY8 was generated using Modeller, v. 9.7 (<https://salilab.org/modeller/>) based on the NMR spatial coordinates of rice cystatin OsCYS1 (PDB Accession No. 1EQK).

potency of hybrids bearing the N-terminal trunk and/or inhibitory loop(s) of cucumber CsCYS (Hybrids C-N, C-2, C-N2 and C-N12). Changing the structural

elements of SICY8 by those of StCYS5 or PpCYS had little impact overall for the acarid proteases (Fig. 7), likely explained by the roughly similar

Table 3. SICYS8 hybrids designed for the functional assays using the N-terminal trunk and/or inhibitory loops of potato cystatin domain StCYS5, *P. patens* cystatin PpCYS or cucumber cystatin CsCYS

SICYS8 hybrid	Transferred structural elements (•)		
	N-ter trunk	Loop 1	Loop 2
StCYS5 elements			
. S-N ^a	•		
. S-1		•	
. S-2			•
. S-N1	•	•	
. S-N2	•		•
. S-12		•	•
. S-N12 ^b	•	•	•
PpCYS elements			
. P-N	•		
. P-1		•	
. P-2			•
. P-N1	•	•	
. P-N2	•		•
. P-12		•	•
. P-N12 ^b	•	•	•
CsCYS elements			
. C-N	•		
. C-1 ^b		•	
. C-2			•
. C-N1 ^b	•	•	
. C-N2	•		•
. C-12 ^b		•	•
. C-N12	•	•	•

^aS, P and C stand for StCYS5, PpCYS and CsCYS respectively; N, 1 and 2 for the N-terminal trunk, first inhibitory loop and second inhibitory loop of the donor cystatin; ^bUnsuccessfully produced in *E. coli* and not considered further for the functional assays.

inhibitory efficiencies of SICYS8, StCYS5 and PpCYS against *T. urticae* cathepsin L-like enzymes (Fig. 3). By comparison, substitutions for the structural elements of CsCYS had a general negative impact, in accordance with the weak activity of this cystatin against *T. urticae* cathepsin L enzymes compared to SICYS8 and the other two donor cystatins. Most interestingly, grafting the N-terminal trunk and first inhibitory loop of StCYS5 to SICYS8 (Hybrid S-N1) increased its inhibitory potency by more than 20 times against *L. decemlineata* cathepsin B-like enzymes (Fig. 6, lower panel). This improved inhibitory rate was more than three times the inhibitory rate observed for StCYS5 used at low concentration, suggesting the potential of SE substitutions not only to improve the inhibitory potency of a cystatin against its natural protease targets but also to broaden its inhibitory range to other Cys proteases.

K_i (papain) distribution maps were drawn to compare the overall impact of our SE substitutions strategy on SICYS8 inhibitory activities with the impact of our site-directed mutagenesis approach involving single substitutions at functionally relevant, positively selected amino acid sites [35] (Fig. 8). An overall coefficient of variation (CV) of 53% was calculated for the relative K_i (papain) values of a previously described collection of 24 SICYS8 single mutants bearing an alternative amino acid at positively selected sites Pro-2 (P2) or Thr-6 (T6) in the N-terminal trunk [36]. By comparison, CV values of 104% and 73% were calculated for the here tested 20 original (natural) cystatins and 16 SE hybrids respectively. More specifically, K_i (papain)

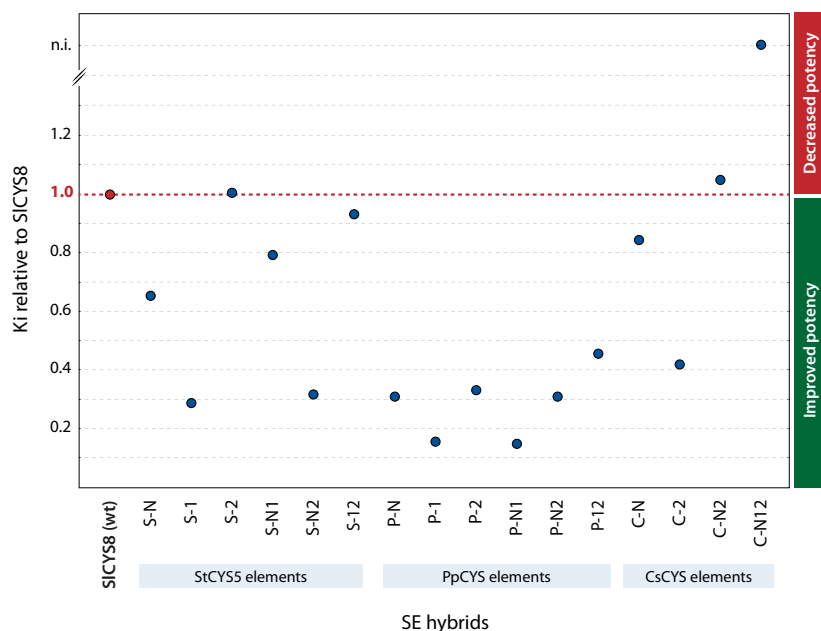
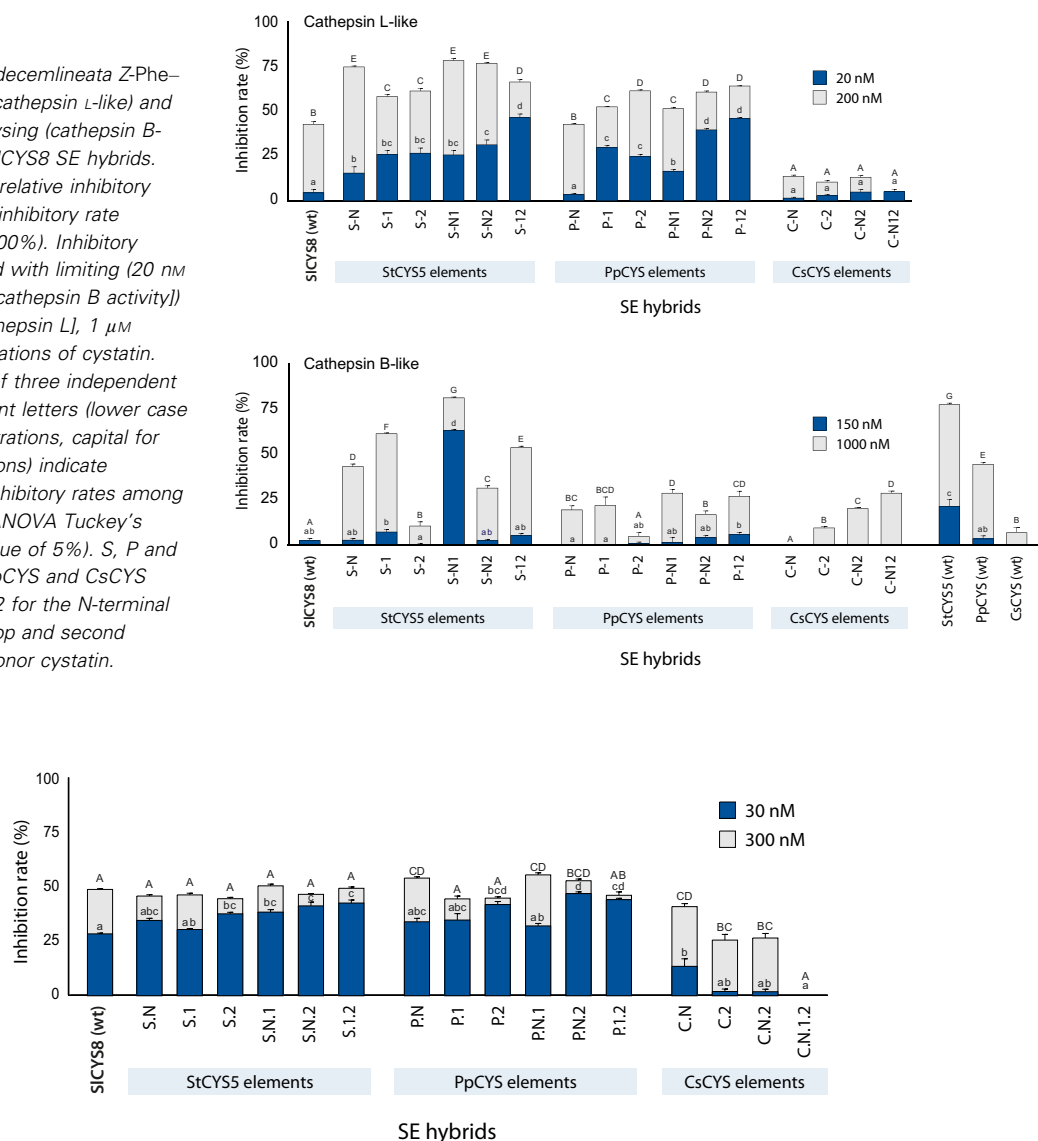
**Fig. 5.** K_i (papain) values for the SICYS8 SE hybrids, relative to the K_i (papain) value for wild-type SICYS8. A ratio greater than 1.0 indicates a negative impact, and a ratio lower than 1.0 a positive impact, of the element substitution(s) on papain inhibitory activity. S, P and C stand for StCYS5, PpCYS and CsCYS respectively; N, 1 and 2 for the N-terminal trunk, first inhibitory loop and second inhibitory loop of the donor cystatin. n.i., no inhibition.

Fig. 6. Inhibition of *L. decemlineata* Z-Phe-Arg-MCA-hydrolysing (cathepsin L-like) and Z-Arg-Arg-MCA-hydrolysing (cathepsin B-like) enzymes by the SICYS8 SE hybrids. Data are expressed as relative inhibitory rates compared to the inhibitory rate measured with E-64 (100%). Inhibitory assays were conducted with limiting (20 nM [cathepsin L], 150 nM [cathepsin B activity]) or excess (200 nM [cathepsin L], 1 μ M [cathepsin B]) concentrations of cystatin. Each bar is the mean of three independent replicates \pm SE. Different letters (lower case for the limiting concentrations, capital for the excess concentrations) indicate significantly different inhibitory rates among cystatin hybrids (post-ANOVA Tukey's tests, with an alpha value of 5%). S, P and C stand for StCYS5, PpCYS and CsCYS respectively; N, 1 and 2 for the N-terminal trunk, first inhibitory loop and second inhibitory loop of the donor cystatin.



values for the single mutants were improved by 31% overall relative to wild-type SICYS8, smaller than the average improvement rate of 154% observed for the SE hybrids (post-ANOVA Fisher's LSD test, $P = 0.02$). These observations confirmed the potential of our new SE substitution approach to implement functional diversity among a relatively small set of recombinant cystatin variants eventually useful in plant protection.

Discussion

Protein engineering approaches have been proposed by several groups to improve the inhibitory properties of plant cystatins against herbivorous pest digestive Cys proteases [5,32]. These strategies typically involve point mutations at functionally relevant amino acid sites or phage display procedures to select improved variants produced by random mutagenesis in the inhibitory

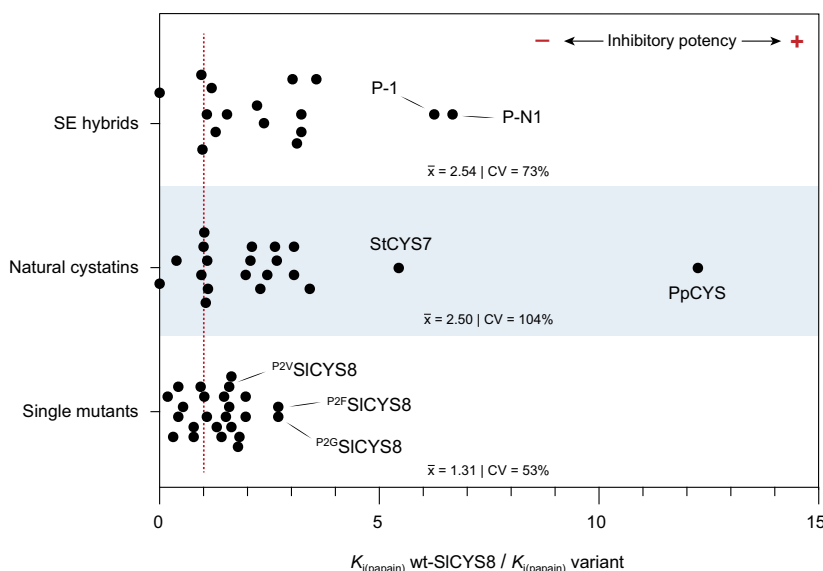


Fig. 8. Functional variability among populations of SICYS8 variants produced by site-directed mutagenesis at positively selected amino acid sites [36], SICYS8 SE hybrids produced by SE substitution(s) using the N-terminal trunk and/or inhibitory loops of StCYS5, PpCYS or CsCYS, or *E. coli*-produced cystatins representative of the plant cystatin protein family (this study). Data are expressed as K_i (papain) values for wild-type SICYS8 relative to K_i (papain) values for the different cystatins or cystatin hybrids. K_i ratios were inferred from Table 1 of ref. [36] (single mutants); Fig. 5, this study (SE hybrids); and Table 2, this study (original cystatins). The red line highlights a reference K_i (papain) ratio of 1 for wild-type SICYS8. SE, structural element; CV, coefficient of variation.

loops. Here, we explored the potential of SE substitutions as a novel approach for cystatin design, using tomato SICYS8 and the digestive Cys cathepsins of *L. decemlineata* as a protease–inhibitor model system. Our data confirm the usefulness of natural cystatins among plant taxa as a pool of discrete function-related structural elements for the design of stable and active cystatin variants. They also confirm the potential of SE substitutions to improve the inhibitory efficiency of SICYS8 against Cys proteases, in line with the reported robustness of plant cystatin structures and the usefulness of these proteins as translational fusion partners or scaffolds for different applications of biotechnological value [9,38,41].

Our underlying assumption for this work was that substituting the N-terminal trunk and/or inhibitory loops of a cystatin would represent a useful alternative to current protein engineering approaches by allowing conformational changes on a length scale beyond that accessible to single mutations [33]. Supporting this, SE substitutions as here implemented had a much greater impact on SICYS8 inhibitory activities than our previously described approach involving single substitutions at positively selected amino acid sites (Fig. 8). Much interestingly, SE hybrids showed average K_i (papain) values improved by 150% overall relative to wild-type SICYS8, five times higher than the overall improvement rate observed with the site-directed mutagenesis approach. Likewise, potent single mutants such as P2L, P2M and P2F produced earlier exhibited inhibitory activity rates increased by – i.e. IC_{50} values decreased by – two- to threefold against *L. decemlineata* cathepsin L-like enzymes compared to wild-type SICYS8 [36]. By comparison, most SE variants bearing

one or two elements of StCYS5 or PpCYS here showed five- to tenfold inhibitory rate increases against these enzymes in non-saturating conditions (Fig. 6). Overall, these observations point to the potential of SE substitutions as an effective way to derive functionally diverse cystatin variants from a plant cystatin template, and hence the potential of this approach as a valuable complement to current protein engineering strategies for cystatin design.

An unsolved question at this point is the actual relevance of our new approach in practice considering the functional variability already observed among plant cystatin family members and the high inhibitory efficiency here measured for some of them. For instance, the inhibitory effect of potent SE hybrids like P-N1 or P-1 against papain was much stronger than the anti-papain activity of wild-type SICYS8 but comparable to the inhibitory activity of PpCYS used as a donor cystatin for the two variants (Fig. 5 and Table 2). Similarly, StCYS5 and PpCYS both showed inhibitory values 10 times higher than SICYS8 against *L. decemlineata* cathepsin L enzymes, comparable to the inhibitory values observed for the two most potent SE hybrids, S-12 and P-12, bearing the inhibitory loops of these donor cystatins (Figs. 3 and 6). On the other hand, hybrid S-N1, with the N-terminal trunk and first inhibitory loop of StCYS5, exhibited very strong inhibitory activity against *L. decemlineata* cathepsin B-like enzymes, more than 15 times higher than, and approximately three times higher than, the inhibitory activities of SICYS8 and StCYS5 respectively (Fig. 6). These data, while leaving open the question of a comparative plus-value for the SE substitutions strategy to produce potent inhibitors of cathepsin L-like enzymes,

suggest the potential of this approach to generate broad-spectrum cystatins that also inhibit alternative proteases naturally recalcitrant to cystatin inhibition [25], such as those upregulated in *L. decemlineata* to sustain leaf consumption and larval growth [24].

Additional studies will be welcome in forthcoming years to compare the plant protective effects of potent SE variants like hybrids S-N1, S-12 and P-12 with the protective effects of potent natural cystatins like StCYS5 and PpCYS or with those of SICYS8 single variant ^{P2V}SICYS8, an improved but still moderately efficient inhibitor (Fig. 8) reported to protect genetically modified potato lines from *L. decemlineata* feeding [24]. Studies will also be welcome to assess the inhibitory potential of SE hybrids integrating N-terminal trunk and inhibitory loop(s) of different cystatin donors, given the specific contributions of these structural elements to the Cys protease–cystatin complex. Studies will be welcome, finally, to measure the impact of a fourth ‘structural element’, the central fold supporting the N-terminal trunk and two inhibitory loops, on the inhibitory activity of plant cystatins. The strong inhibitory potency of hybrid S-N1 against *L. decemlineata* cathepsin B-like enzymes compared to wild-type StCYS5 used as a donor, or the occurrence of positively selected amino acids presumably influencing protease inhibition in the α -helix and inter-loop region of plant cystatins [35], point to a possible impact of this non-functional element on the inhibitory efficiency of the protein. The central fold of cystatins is not directly involved in protease inhibition but still might represent a valuable target for plant cystatin engineering given its possible effects on the spatial orientation and stability of the three functional elements.

Materials and methods

Cys protease–cystatin docking simulations

Enzyme–inhibitor docking simulations were performed for tomato cystatins SICYS8 (GenBank Accession No. AF198390) and SICYS9 (GenBank NP001275067), soybean cystatin GmCYS2 (GenBank AAA97906), rice cystatin OsCYS1 (GenBank NP001044550) and corn cystatin ZmCYS1 (GenBank NP001105295) interacting with papain, human cathepsin L and *L. decemlineata* IntD4 (GenBank EF154436) considered as target Cys proteases. Simulations were performed using the Z-Dock algorithm of Discovery Studio (ACCELRYS Software, San Diego CA, U.S.A.) after inferring structure homology models for IntD4 and the five plant cystatins. Twenty tentative models were built using Modeller, v. 9.7 [47,48], with the crystal structure of human cathepsin L (PDB 1SC8) as a template for the insect protease

[46] and the NMR structure of oryzacystatin I (PDB 1EQK) [43] as a template for the cystatins. Stereochemical quality of the models was compared to their template structures with the Procheck program, v.3.5.4 (<http://www.ebi.ac.uk/thornton-srv/software/PROCHECK/>) [49] and the best models were selected for further analyses. Docking simulations with models of the five cystatins were produced for papain (PDB 9PAP), cathepsin L (1SC8) and IntD4 [26] using the Z-Dock algorithm to generate 2000 tentative poses for the resulting complexes. Top-ranking poses, based on the Z-score [44], were compared with the solved crystal structure of human stefin B in complex with papain (PDB 1STF) to confirm the relative binding positions and orientations of the proteins in the predicted complexes. Five tentative complexes were chosen for each protease–cystatin combination and refined through energy minimization using the R-Dock algorithm [50]. Interacting residues and interaction (binding) energies were inferred for the top-ranking models. Normal distribution tests were performed on calculated data using the Shapiro–Wilk test of normality [51], followed by a *F*-test to compare the variances of two samples structural element combinations (N-terminal trunk vs the first inhibitory loop; N-terminal trunk vs the second inhibitory loop; and first loop vs the second loop) from normal populations. An alpha threshold of 5% was used for statistical significance.

Representative plant cystatins

Phylogenetic inferences were performed with the MEGA6 software, v.6.06 [52], using plant cystatin sequences available in the NCBI protein database (<http://ncbi.nlm.nih.gov/>). Non-redundant cystatin sequences were retrieved from the Viridiplantae domain of the database using the in-built Protein Blast tool, with the sequence of tomato SICYS8 as a query sequence (GenBank Accession No. AF198390.1; gi|6671196). Amino acid sequences including at least 90% of a full cystatin, here corresponding to 262 non-redundant NCBI accessions, were used as a starting point. A multiple sequence alignment was generated using the MUSCLE algorithm [53], from which a maximum likelihood tree was calculated based on the “JTT” amino acid substitution model [54] (Fig. S1). Fifty-seven ‘representative’ cystatins were identified by restricting the selection (a) to one sequence among highly similar sequences (>95% identity), and (b) to one cystatin per branch of the phylogenetic tree. A subset of 30 cystatins was taken from this sample for the functional analyses, in such a way as to maximize sequence variability among the selected cystatins at amino acid positions expected to physically interact with the target proteases [26].

Recombinant cystatins

All cystatins were produced in *E. coli*, strain BL21 as described previously [36], using the GST gene fusion system

for heterologous expression and affinity purification (Fisher Scientific, Nepean ON, Canada). DNA templates for the cystatins were synthesized as g-blocks (IDT), including GoldenGate BSAI cloning sites on both sides of the cystatin coding region [46]. DNA coding sequences for the original cystatins corresponded to those sequences reported in GenBank (as listed in Table 2). DNA sequences for the SE hybrids were designed as described in the Results (Fig. 4), with structural elements from donor cystatins potato StCYS5, *P. patens* PpCYS or cucumber CsCYS replacing the N-terminal trunk (amino acids 1–13, StCYS8-numbering), first inhibitory loop (amino acids 44–55) and/or second inhibitory loop (amino acid 70–84) of tomato StCYS8 (Table S2). G-blocks were inserted in a modified version of the pGEX-3X expression vector (Fisher Scientific) using the Golden Gate DNA shuffling method of Engler *et al.* [55], downstream of a ‘GST-factor X_a cleavage site’ coding sequence [46]. The GST tag was removed by cleavage with bovine factor X_a, according to the manufacturer’s specifications (Fisher Scientific). Cystatin products showing fragmentation, as assessed by 15% (w/v) SDS/PAGE, were not considered further for the functional analyses. The purified cystatins were quantified by densitometric analysis of Coomassie blue-stained polyacrylamide slab gels following 15% (w/v) SDS/PAGE, using three technical replicates and bovine serum albumin (Sigma-Aldrich, Oakville ON, Canada) as a protein standard.

Test proteases

Papain (E.C.3.4.22.2, from papaya latex) was purchased from Sigma-Aldrich. Colorado potato beetle (*L. decemlineata*) proteases were extracted from the midgut of fourth instars reared on greenhouse-grown potato plants, cv. Norland, as described previously [36]. Two-spotted spider mite (*T. urticae*) proteases were obtained from a laboratory colony reared in greenhouse on common bean (*Phaseolus vulgaris*). Whole mites were ground in liquid nitrogen, the resulting powder kept on ice for 10 min after resuspension in 50 mM Tris-HCl buffer, pH 7.0, and the whole mixture centrifuged at 4 °C for 10 min at 20 000 g. The pellet was discarded, and the supernatant used as a source of digestive proteases for the protease inhibitory assays. Papain and soluble proteins in the arthropod crude extracts were assayed according to Bradford [56], with bovine serum albumin as a protein standard.

K_i (papain) value determinations

K_i (papain) values for the cystatin variants were determined by the monitoring of substrate hydrolysis progress curves [57], based on the linear equation of Henderson [58]. Papain activity was monitored in 50 mM Tris-HCl, pH 7.0, using the synthetic peptide substrate Z-Phe-Arg-methylcoumarin (MCA) (Sigma-Aldrich). Hydrolysis was allowed to proceed at 25 °C

in reduced conditions (10 mM L-cysteine) with the substrate in large excess, after adding (or not) recombinant cystatins dissolved in a minimal volume of reaction buffer. Papain activity was monitored using a BioTek Synergy H1 fluorimeter (Agilent Technologies, Mississauga ON, Canada), using an excitation filter of 360 nm and an emission filter of 450 nm. K_i values were calculated using experimentally determined K_i (app) and K_m values, based on the following equation: $K_i = K_{i\text{(app)}} / (1 + [S]/K_m)$. A K_m value of 93.6 μM was determined for papain under our assay conditions.

Arthropod protease assays

Cys cathepsin activities in the arthropod protein extracts were assayed in 0.2 M NaH₂PO₄/0.2 M Na₂HPO₄ phosphate buffer, pH 6.5, using the synthetic peptide substrates Z-Phe-Arg-MCA for cathepsin L-like activities and Z-Arg-Arg-MCA for cathepsin B-like activities. Hydrolysis was allowed to proceed in reduced conditions (10 mM L-cysteine) for 10 min at 25 °C, with ~ 5–6 ng of arthropod protein per μL in the reaction mixture and the peptide substrate added in large excess. Cystatins dissolved in a minimal volume of reaction buffer were added to the reaction mixture for the inhibitory assays. Proteolytic activity was monitored using a BioTek Synergy H1 fluorimeter (Agilent Technologies), with excitation and emission filters of 360 nm and 450 nm respectively.

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Conflict of interest

The authors declare no conflict of interest.

Author contributions

JT, CG and DM conceived the new approach and the experiments. JT and JV performed the modelling inferences. JT and MCG performed the *in vitro* experiments and analysed the data. JT, MCG and DM wrote the manuscript. All authors read and approved the manuscript for publication.

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Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Fig. S1. Maximum likelihood phylogenetic tree generated for 262 plant cystatin amino acid sequences available in the NCBI protein database.

Table S1. Complement to Table 1: Interaction binding energies inferred *in silico* for model Cys proteases papain, human cathepsin L and *L. decemlineata* IntD4 interacting with N-terminal trunk, Loop 1 and Loop 2 amino acids of tomato cystatins SlCYS8 and SlCYS9, rice cystatin OsCYS1, soybean cystatin GmCYS2 and corn cystatin ZmCYS1.

Table S2. Primary sequences of recipient cystatin SlCYS8, donor cystatins StCYS5, PpCYS and CsCYS and SlCYS8 SE hybrids bearing one, two or three structural elements of StCYS5, PpCYS or CsCYS.