

Overexpression of Pepper Capsaicinoid Pathway Genes in Tomato

Department of Biology, University of Louisiana at Lafayette, Lafayette, LA 70504, USA

In this study we attempted to overexpress three pepper genes in tomato to produce spicy fruits. The three genes, BCAT (branched-chain amino acid aminotransferase), Kas (ketoacyl-ACP synthase) and CS/AT (Capsaicin synthase/acyltransferase), were separated by P2Am and T2Am sequences in a tricistronic cassette driven by the 35S promoter. The genes were expressed in transgenic tomato although tomato fruits were not spicy based on two-

Capaicinoid pathway gene; Overexpression; Pepper; Tomato

The pungency of hot peppers is the result of accumulation of groups of alkaloids called capsaicinoids, the major pungent capsaicin and dihydrocapsaicin [1]. The heat of capsaicinoids is due to the presence of the capsaicinamide moiety, which means 'hot' [2]. Capsaicinoids are synthesized in pepper from phenylalanine in the pathway of phenylalanine ammonia-lyase, which produces 8-methyl-6-nonenic acid, which is then converted to capsaicin and other capsaicinoids by the action of capsaicin synthase (CS) [3]. The capsaicin synthase (CS) gene combines with the capsaicin synthase (CS) gene to produce capsaicin and other capsaicinoids [2].

Chili peppers are an important crop and a basic ingredient in a variety of cuisines worldwide, the nutritional value of capsaicin is high and is considered an antioxidant of amines, A, B-complex and E along with minerals like molybdenum, manganese, folate, potassium, and histamine [4]. The pungency of capsaicin is the result of capsaicinoids. A medicine is mainly used to relieve pain in rheumatoid arthritis, headache, and non-steroidal anti-inflammatory drugs [5]. The plant has been used as a folk remedy for rheumatoid arthritis, headache, and non-steroidal anti-inflammatory drugs [6]. All the essential ingredients in capsaicinoids are beneficial for health and hot peppers should be considered a functional food [7].

Unlike other domesticated members of Solanaceae family, such as tomato, potato, and tobacco, capsaicinoids are not naturally found in the wild and are the result of genetic modification through a series of mutations [3]. Environmental factors such as high temperature, high CO₂ levels, and excessive nitrogen can all affect the plant growth, yield and incidence of capsaicinoids in the plant [8]. Seed yield and germination are highly dependent on moisture, temperature, light, and planting density [9]. Even if all the agronomic conditions are optimized, the high pungent capsaicinoids in the heat-tolerant lines are not necessarily the result of the problem in the control of pungency production in pepper [10].

Classical breeding and modern genetic manipulation can both be used for improvement and control of pungency in pepper. Breeding has been identified as the best way to increase capsaicinoids [11]. Agrobacterium-mediated genetic transformation is a

non-invasive method for capsaicinoid production. Commercial capsaicinoids are produced by genetic engineering and high genetic dependence [12,13]. Gene manipulation is not a suitable option for pepper improvement [3]. Engineering and model plant production of capsaicinoids could be a complementary approach for production of the second generation [14].

Economically, tomato (*Solanum lycopersicum*) is the most important vegetable crop, and its yield is only second to potato in the world [15]. Despite the wide distribution of capsaicinoids in the tomato genome [16], genome of capsaicinoids and tomato are well studied, the basic chromosome number of $2n=12$ in both species and major economic traits are well understood [17]. Tomato being a self-pollinating model with high amenability to biotechnological manipulation and high productivity in the cropping cycle [18] can be used as a capsaicinoid biofactory model plant [19]. Phylogenetic analysis of gene families involved in capsaicinoid biosynthesis in pepper and other Solanaceae species, potato and Arabidopsis identified 51 gene families and of these 13 gene families had independent pepper-specific duplications (such as ACL1, AT3, b-CT, C3H, CAD, CCR, KAI and PAL genes) [17]. Comparison of an capsicum analysis revealed a gene in capsaicin biosynthesis pathway has high diversity in pepper and tomato. Functional analysis of the capsaicin biosynthesis pathway genes along with other genes necessary for capsaicinoid biosynthesis, such as the capsaicin synthase gene in tomato pathway (BCAT, Kas and CS) are analyzed and expressed in fruiting stage [2]. Comparison of pepper diversity in non-pungent pepper pungent pepper and hot peppers in CS gene is not observed for the capsaicinoid pathway genes. The results of the analysis indicate a change in the gene expression of BCAT, Kas and CS/AT enabled capsaicinoid biosynthesis in hot peppers [20,21]. Mutagenesis is

Yi-Hong Wang, Department of Biology, University of Louisiana at Lafayette, Lafayette, LA 70504, USA, E-mail: yihong.wang@louisiana.edu

08-Nov-2023, Manuscript No. jpgb-23-119545; 10-Nov-2023, PreQC No. jpgb-23-119545 (PQ); 18-Nov-2023, QC No. jpgb-23-119545, 23-Nov-2023, Manuscript No. jpgb-23-119545 (R); 30-Nov-2023, DOI: 10.4172/jpgb.1000176

Prakash CS, Wang YH (2023) Overexpression of Pepper Capsaicinoid Pathway Genes in Tomato. J Plant Genet Breed 7: 176.

© 2023 Prakash CS, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

in hot pepper also revealed loss of function in diene gene, a cyclic hydroperoxide diene. Peroxidase in pepper, however, appears to be under an epigenetic control and is directly linked to high capsaicinoid levels of capsaicinoid biosynthesis gene in the placental epimorphogenesis [21,22]. Compared to chili pepper, in tomato some genes have the level of expression (PAL, CH, ACL, AMT), others have the level of expression in the epimorphogenesis (COMT, FaTA) and fewer are expressed (Ka, BCAT and CS) [2].

Based on the genetic information on both pepper and tomato, it is theoretically possible to create capsaicinoid pathway in tomato. Genome engineering strategies could be used for this endeavor. One is use of an epigenetic activator like TALE (CRISPR/Cas9) for multiple activation of genes in pepper [23-25]. Second strategy is use of targeted promoter replacement through genome engineering for activation of inactive genes in tomato [26,27]. And third would be in the overexpression of the pepper genes (Ka, BCAT and CS) in tomato through Agrobacterium mediated transformation of tomato.

For our study, we employed Agrobacterium mediated transformation of tomato and overexpressed the hot pepper genes isolated in capsaicin biosynthesis pathway, namely BCAT, Ka and CS/AT. To determine the expression of the 35 promoters and one specific E8 promoter. All these genes were included in single cloning vector for transformation (more in method). All these genes are involved in capsaicin biosynthesis through branched chain fatty acid pathway. BCAT (branched-chain amino acid aminotransferase) condenses α -keto acid, Ka (ketoacyl-CoA synthase) along with ACL (acyl carrier protein) involved in fatty acid synthesis through β -CoA to 8-methyl-6-nonenic acid and CS/AT/PUN1 (Capsaicin synthase) condenses aniline from phenylpropanoid pathway through 8-methyl-6-nonenic-CoA from branched chain fatty acid pathway to form capsaicin [2].

pCAMBIA1301 vector was used in transformation of overexpression gene construct in the cloning vector of hot pepper genes arranged as shown in Figure 1A. The genes were expressed by P2Ap and T2Ap promoters (Figure 1B) from Oboon MJ [28]. The promoters were cloned into DNA template (P2A and T2A in Figure 1B) and optimized for plant (Arabidopsis) using JCa [29] promoter. The P2Am and T2Am (Figure 1B) used in Figure 1A. The cassette (Figure 1C) was transformed by BioBac (Amherst, NY, USA) and ligated into pCAMBIA1301 at digestion sites NcoI and B-EII.

Tomato seed (*Solanum lycopersicum*) cv Mic o-Tom and Mic o-Tina from Tomato Gene Supply Company, Fort Meade, FL were surface sterilized in 40 ml of 25% bleach in 2 d of 15 min and in ed 5-7 times in distilled water before planting in seed germination medium (MS salt 4.3 g l⁻¹, Nicotinic acid 1 ml l⁻¹, cobalt 30 g l⁻¹ and agar 6 g l⁻¹, pH 5.8). Hypocotyl and cotyledon leaves of 7-10 day old seedling were used for transformation. The *Agrobacterium* culture was added in 20 ml LB medium supplemented with 50 mg l⁻¹ kanamycin. A day before transformation, hypocotyl and cotyledon leaves were cut from seedling at the petiole and at the tip using sterile razor on the cocliation media (MS salt 4.3 g l⁻¹, hiamine-HCL 0.4 mg l⁻¹, misoninol 100 mg l⁻¹, cobalt 30 g l⁻¹, 2,4-D 0.2 mg l⁻¹, agar 6 g l⁻¹ and kine in 0.1 mg l⁻¹) in the sterile paper laid on the surface. Bacteria from LB broth are harvested centrifugation and resuspended in cocliation media (in the agar). Leaves from overnight incubation were capped and mixed in bacteria and incubated at room temperature for 30 min in the occasional mixing. Bacterial suspension was diluted, leaves were dried on sterile paper and embedded in cocliation media in the paper on the surface. The explants were sealed in micropore tape and incubated in dark at room temperature for 3 days. Following 3 days of cocliation leaves were placed on regeneration medium (MS salt 4.3 g l⁻¹, Nicotinic acid 1 ml l⁻¹, cobalt 30 g l⁻¹, Zea in 1.5 mg l⁻¹, IAA 0.2 mg l⁻¹, ca benicillin 400 mg l⁻¹, hygromycin 30 mg l⁻¹, agar 6 g l⁻¹ and pH 5.8) and incubated under natural day/night cycle for 3-8 weeks in the media change every 3 weeks. Shoots were identified in the period. Regenerated shoots were transferred to rooting medium (MS salt 4.3 g l⁻¹, Nicotinic acid 1 ml l⁻¹, cobalt 30 g l⁻¹, IBA 0.5 mg l⁻¹, ca benicillin 400 mg l⁻¹, hygromycin 30 mg l⁻¹, agar 6 g l⁻¹ and pH 5.8) for further growth and rooting. Then transferred to soil and acclimatization for few days.

Transformation and insertion of a gene a construct plan gene a ion on hygromycin containing gene a ion media then PCR using hygromycin primer (forward: GATGTTGGCGACCTCGTATT and reverse: GATGTAGGAGGGCGTGGATA) on DNA from an genetic plant.

From T0 an genetic plant, RNA was extracted for RT-PCR. Leaf sample from young an genetic plant were collected in the RNA. Fresh 50-100 mg of leaf tissue was frozen in liquid N₂ and ground in powder in mortar and pestle. One ml of TRIzol reagent was added to homogenize 50-100 mg of tissue. After 5 min of incubation, 0.2 ml of chloroform was added to the sample and the incubation for 3 min at room temperature was centrifuged at 4 C for 15 min. The supernatant was transferred to a new tube and mixed with 0.5 ml of isopropanol and incubated for 10 min. After centrifugation at 4 C for 5 min, the supernatant was discarded and RNA pellet was mixed with 1 ml of 75% ethanol and centrifuged for 5 min at 4 C, the supernatant was discarded, and pellet was dried in a vacuum oven for 10 min. A 0.25-0.30 of DNA/RNA free acetone was added to dissolve the RNA. Aliquot of the RNA was added in the DNase I at 37 C for 10 min. The isolated phenol: chloroform extraction in isopropanol precipitates a ion and 75% ethanol wash. The precipitates of RNA was added in the DNase I and an isolated in Nanodrop. Sample in the 260/280 ratio were been 1.9-2.1 were used for the analysis.

Semi quantitative RT-PCR was done to confirm the expression of the Scip XLT One-Step RT-PCR kit from Qiagen Applied Biosystems in the 2720 thermocycler. Manufacturer's guidelines were followed for reaction setup and the thermocycler protocol. In short, RT-PCR was done for RNA of both an genetic and control plant in 10 l volume. All the reagents, RNA and primer were heated in ice for 15 min and the reaction was pre-on ice. For each 10 l reaction, 5 l One-Step To Go Mi (20X), 0.2 l each of forward and reverse primer, 0.4 l of Scip XLT One-Step enzyme and cypase (25X), 2.2 l of nuclease free water and 2 l of RNA were added and mixed. PCR plate was then pre-heated to 95 C for 2 min and collected the content in the bottom of the well. In the thermocycler, RT-PCR was programmed as follows: cDNA denaturation at 48 C for 20 min, initial denaturation at 94 C for 3 min, 35 cycle of denaturation at 94 C for 20 s, annealing at 56 C for 30 s and extension at 72 C for 1 min. The final extension was followed by 72 C for 5 min and 4 C for 5 min. PCR products were run on 1% agarose gel along with loading dye to visualize the presence of a gene in RNA.

Transgenic tomato were generated and checked for any phenotypic change in the fruit shape, color and on the fruit size of the mature age. Ripened tomato of fruit were analyzed for capsaicin by people in lab.

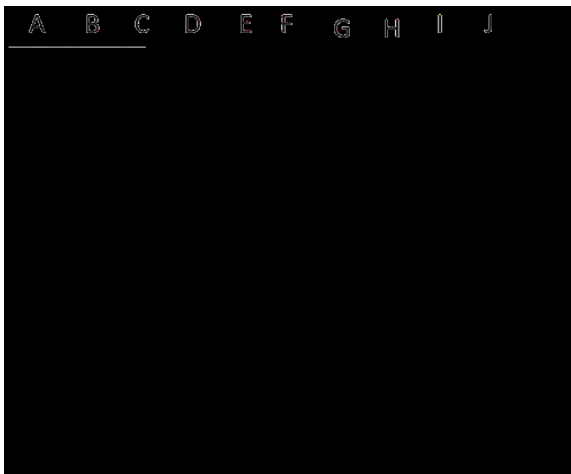
To determine the inheritance of the gene in the transgenic tomato line (Mic o-Tina and Mic o-Tom) were used for the transformation. The control in the 35S promoter was added to the an form Mic o-Tina and control in the E8 promoter was added to the an form Mic o-Tom. Although the number of infected leaves was not considered, regeneration of callus from leaves was a viable for both Mic o-Tina and Mic o-Tom line. Mic o-Tom homozygous had an age in the germination, fragrance and compound of Mic o-Tina (data not collected). During callus regeneration a taken to place the leaves in the agar plate to increase the chance of regeneration. Callus taken in the 0.5% agar plate and the plant were established in 2 weeks. Once callus was established in the hoo, the regenerated plant was transferred to Magenta Biotec in the greenhouse and grown in the pot for plant propagation. In total 30 an genetic plant from 35S vector and 35 an genetic line from E8 vector were generated.

Genomic DNA was extracted from the leaves of an genetic and control tomato plant for PCR. Hygromycin primer were used to confirm the presence of a gene in T0 generation of an genetic plant (Figure 2). Hygromycin band was observed in both Mic o-Tina and Mic o-Tom an genetic line but were absent from control plant confirming the insertion of a gene in the tomato genome.

Expression of a gene a construct semi quantitative RT-PCR using pepper gene specific primer. For each primer, once the primer was designed, the primer was tested again to ensure no cross-reactivity with other tomato. For each of the gene one specific primer was designed. RT-PCR was done using the primer on RNA deionized from control and an genetic plant. Gel electrophoresis of the RT-PCR products showed the gene band for all the target gene.



line 1; C- transgenic line 2; D-Micro-Tina control; E-Micro-Tom control and F-PCR negative control.



Gene expression in transgenic plants. Lanes A-ladder; B, C, D-control for AT, BCAT and Kas gene; E, F, G-transgenic line 1 for AT, BCAT and Kas; H, I, J-transgenic line 2 for AT, BCAT and Kas.

(AT, BCAT and Ka) in bo h an genic line e ed hile he con ol plan did no ha e an an gene e pe ion (Fig e 3). i ho all h ee peppe gene e e in eg a ed in oma o genome and e e being e pe ed.

T an genic plan e e ob e ed fo an pheno pic cal change in plan a ell in fi e e e e no o e helming change ha e econ i en ho gho all an genic line , ome an genic oma o plan , ho e e , did p od cef i h peppe like o gh kin.

Ripened an genic oma of i e e a ed fo hin of ho ne . T o people a ed he j ice fom he ame fi o de mine he he he e i an ho ne in i e e a con en , none of an genic oma of i ca ied an picine on hem. Al ho gh o e l fom RT-PCR gge ed he e pe ion of all h ee gene in an genic plan , lack of ho ne in fi gge ei he he e i no de ec able inc ea e in cap acin p od c ion, o he bio n he ic pa h a e i e mo e han 3 gene o be o e e pe ed.

Toma o a a biofac o fo p od c ion of econda me aboli e i no a ne concep , i ha been demon a ed oma o can be ed in ch p po e [30] e e able o e oma o p od ce be alain (food colo). O he die ha e ed oma oe o inc ea e he p od c ion of a io a onoid [31], phenip opanoid compo nd like e e a ol and geni in [32]. Toma of i a e ich in me aboli e ch a c o e, he o e , ci a e, mala e and a co bic acid a ell a econda me aboli e ch a ca o enoid , phenip opoid and e penoid i ome e en [33]. e pe ence of ch compo nd gge he pe ence of ba ic bio n he ic pa h a fo each in oma o. e pe ence of he e bio n he ic pa h a ha led man o belie e oma o can be ed a cha i o p od ce a io economically a ell a pha macological impo an me aboli e ch a e inol (Vi amin A) h o gh B-ca o ene bio n he i [34] and dio cin h o gh e oidal glycoalkaloid p od c ion [35].

e pe ence of def nc cap acinoid bio n he i pa h a in oma oe o e an oppo ni o p od ce cap acin in oma oe . i ill alle ia e he p oblem a ocia ed i h peppe fa ming ch a a ing le el of p ngend en i onmen al di e , lo eed ge mina ion and long-life ccle a ell a high le el of oil bo ne di ea e and nema ode infec ion [3]. Bo h peppe and oma o being he membe of ame nigh hade famil (Solanaceae) ha e majo con e ed n en i h ba ic ch omo ome n mbe of =12 in bo h pecie and ha e man ai be een hem [18]. Compa i e genomic e ealed pe ence of all nece a cap acinoid gene in oma o i h a ing e pe ion [2]. O e e pe ion of ho ele e pe ed gene in oma oe ho ld in heo make oma of i pic.

B in e ing h ee cap acinoid gene (BCAT, Ka and AT) e in ended o ac i a e he cap acinoid pa h a in oma o. Ag obac e i m media ed an fo ma ion me hod a cce f l in deli e of all h ee gene a e idenced b e gene a ion of h g om cin e i an an genic plan and e pe ion of h ee peppe gene a een in RT-PCR. i , ho e e , did no e l in an inc ea e in cap acin n he i o acc m la ion in oma of i . e gene a ion of an genic oma o plan e pe ing peppe gene, ho e e , i a igni can ep o a d he gene a ion of pic oma o e e co ld be man ea on h o plan e e no p od cing pic fi . I co ld be ha oo li le cap acin o be de ec ed b a ing, o he h ee gene migh no be eno gh o ac i a e hole cap acin bio n he i pa h a a i comp i e mo e han 51 gene familie [18]. Gene d plica ion d ing cap ic m e ol ion mean bio n he i pa h a ha p o 13 peppe peci c d plica ion compa ed o oma o [18], al o i e peci c and de elopmen al e pe ion of gene in ol ed in cap acinoid bio n he i co ld pla ole in making oma o pic.

Wi h pheno pic anal i e did no nd an igni can change be een an genic and con ol oma oe . T an genic oma oe in ome ca e , ho e e , did ha e long inge in ea age of f i de elopmen and p od ced o gh kin nlike moo h kin of con ol plan e e cha ce e e no pe alen . We did no nece a ill e pec an genic oma oe o ha e a e ed hape o i e, b he e e e ome in e e ing ob e a ion .

Cap acin i an impo an econda me aboli e ha ha been a cen al elemen in c lina and pha macological ac i i e in man con ie and c l e e demand fo ch a al able p od c ill likel inc ea e in coming sea . I i ideal e ha e a l e na e a of ge ing cap acin i ho nece a ill depending on n eliable and labo -in en i e peppe fa ming. Toma oe being clo e ela i e of

pepper and having defined capsacin biosynthetic pathway could be an effective way to be a leading in the area of biofactory model for economic benefit.

ACKNOWLEDGMENTS

CSP thank the Graduate Student Organization (GSO) for their support. This project was supported in part by the University of Louisiana at Lafayette. The authors thank each did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

CONFLICT OF INTEREST

CSP performed all the experiments and wrote the manuscript; YHW conceived the project and finalized the manuscript. All authors have read and approved the manuscript for submission.

REFERENCES

- None declared.
- None declared.
- Aza-González C, Nunez-Palenius HG, Ochoa-Alejo N (2011) Molecular biology of capsaicinoid biosynthesis in chili pepper (*Capsicum* spp.). *Plant Cell Rep* 30: 695-706.
 - Kim S, Park M, Yeom SI, Kim YM, Lee JM, et al. (2014) Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species. *Nat Genet* 46: 270-278.
 - Naves ER, Silva L De A, Sulpice R, Araujo WL, Nunes-Nesi A, et al. (2019) Capsaicinoids: Pungency beyond *Capsicum*. *Trends Plant Sci* 24: 109-120.
 - Simonne AH, Simonne EH, Eitenmiller RR, Mill HA, Green NR, et al. (1997) Ascorbic acid and pro-vitamin A contents in unusually colored bell peppers (*Capsicum annuum* L.). *J Food Comp Anal* 10: 299-311.
 - Kothari SL, Joshi A, Kachhwaha S, Ochoa-Alejo N (2010) Chilli pepper - A review on tissue culture and transgenesis. *Biotechnol Adv* 28: 35-48.
 - Ravishankar GA, Suresh B, Giridhar P, Rao SR, Johnson TS, et al. (2003) Biotechnological studies on *Capsicum* metabolite production and plant improvements. *Capsicum: the genus Capsicum*. London: CRC Press.
 - Hardy G (2000) Nutraceuticals and functional foods: introduction and meaning. *Nutrition* 16: 688-689.
 - Lee SG, Kim SK, Lee HJ, Lee HS, Lee JH, et al. (2018) Impact of moderate and extreme climate change scenarios of growth, morphological features, photosynthesis, and fruit production of hot pepper. *Ecol Evol* 8: 197-206.
 - Demir I, Ellis RH (1992) Development of pepper (*Capsicum annuum*) seed quality. *Ann App Biol* 121: 385-399.
 - Zewdie Y, Bosland PW (2000) Evaluation of genotype, environment, and the genotype-by-environment interaction for capsaicinoids in *Capsicum annuum* L. *Euphytica* 111: 185-190.