

Genome-wide identification of Receptor-Like Kinase gene families in three different plants: Tomato, Broccoli, and Maize

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Abstract

Background: Receptor-like kinases (RLKs) play a crucial role in plants' primary defense against pathogens. Studying the gene structures of these RLKs can enhance our understanding of their functions.

Methods: In order to conduct this study, conserved blocks of RLK sequences were identified in three different plants: tomato (*Solanum lycopersicum*), broccoli (*Brassica oleracea*), and maize (*Zea mays*). The goal was to determine promising sequences for resistance to common biotic stresses.

Results: The results revealed that motifs 1 and 2, were clustered together more closely than the other motifs, indicating their importance in the RLKs receptor sequences. Furthermore, the synteny of gene blocks encoding RLKs receptors and their homologs showed a higher density of lineages between the two LTK1 and LTK2 genes, leading to a higher level of observed similarity. The most significant disparities in the receptor genes of *Brassica oleracea* and *Zea mays* are the presence of bulb-type lectins (B lectin) and leucine-rich repeat sequences (LRR), respectively. These domains play a vital role in innate immunity.

Conclusion: In the interactions among the domains within the LePRK gene, the STIG1 domain had the highest score and played the most significant functional role in the growth of the pollen tube within this network.

Keywords: Conserved domain. Genome-wide analyses. Gene block relationships. Receptor-Like kinase (RLK).

Introduction

Cellular signalling is the foundation for both extracellular and intracellular communication. Various signal recognition receptors and signal transduction pathways have been identified to regulate cellular functions, metabolism, and development. Furthermore, these pathways are essential for cellular dynamics and build a highly regulated cellular signalling network (Schlossmann 2013).

The success in the response of plants to environmental stressors depends on the regulatory networks that connect plant perception and plant response (Hernandez and Martinez 2022).

In the past three decades, more than a dozen families of Receptor-like kinases (RLKs) have been described (Dievart et al. 2020). However, there is still a lack of a systematic and automatic pipeline for classifying the RLKome. The study of RLK receptors, which regulate signaling pathways in plants, has sparked a heated debate today.

Since these receptors play an important role in the primary defense of plants against pathogens, studying their gene structure will enhance our understanding of their analysis and function.

The purpose of conducting a bioinformatics assessment is to gain insights into the structural differences and similarities of these receptors. This information serves as a foundation for further research on biotic stress, with a particular focus on the hypersensitivity reaction.

It has been reported that Leukocyte tyrosine kinase (LTK) is a receptor that shares high homology with the anaplastic lymphoma kinase (ALK) (Centonze et al. 2019).

Maize cDNAs are transcribed from a small gene family that encodes a novel group of RLKs. The distinctive extracellular domain of these novel RLKs includes a unique number and arrangement of leucine-rich repeats (LRRs), a proline-rich region (PRR), a putative protein degradation target sequence (PEST), and a serine-rich region (SRR).

Unlike LTK1 transcripts, which were consistently observed in all tested maize tissues, LTK2 transcripts were only detected in the endosperm. Two of the three LRR-type LTK proteins may play a role in endosperm development, one of the two LRR-type SERK proteins is thought to be involved in reproductive events. Generally, these results indicate that members of the LTK gene family mediate signals related to seed growth and maturation (Abdel-Sabour et al. 2005).

According to a study, pollen-specific kinase genes, which are potential signal transduction components of pollen-pistil interactions, were screened. Two structurally related RLKs were isolated from tomato and named LePRK1 and LePRK2.

These kinases are similar to a pollen-expressed RLK from petunia, but they are expressed later during pollen development than the petunia RLK. The abundance of LePRK2 increases when pollen germinates, but LePRK1 remains constant. Both LePRK1 and LePRK2 are localized to the plasma membrane/cell wall of growing pollen tubes.

*LePRK1 and LePRK2 are two pollen-specific RLKs from *Solanum lycopersicum* that are involved in signaling during pollen-pistil communication (Tamara et al. 2012).*

A Receptor-like kinase, SRK, has been implicated in the auto incompatible response that leads to the rejection of self-pollen in Brassica plants.

SRK is encoded by one member of a multigene family, which includes several RLK genes. These genes have patterns of expression that are very different from that of SRK but their function remains unknown.

Recently, the characterization of the Brassica S gene family, SFR2, has been characterized and reported.

Based on the research, SFR1 transcripts were only accumulated in response to bacterial infection and their abundance was not significantly affected by wounding.

The accumulation of SFR2 mRNA in response to wounding and pathogen invasion is a characteristic feature of a gene involved in the plant's defense responses (Pastuglia et al. 2002).

Brassica S gene family receptor 1 (SFR1) and SFR2 are both SRK-like genes, and their expression is increased by plant wounding and pathogen challenge (Shiu et al. 2001).

The rapid accumulation of SFR2 mRNA suggests that SFR2 playing a role in the signal transduction pathway leading to the induction of plant defense proteins, such as pathogenesis-related proteins or enzymes involved in phenylpropanoid metabolism.

Materials and Methods

*In this research, the gene sequences encoding the kinase receptor in three plants; *Solanum lycopersicum*, *Brassica oleracea*, and *Zea mays*, were obtained from the NCBI database. In this search, the homologous sequences related to the gene clusters LePRK1, LePRK2, SFR1, SFR2, LTK1, and LTK2 were identified using the Tblastx tool among the conserved sequences in these three plants.*

All sequences have an E-value less than 0.05, indicating a high degree of alignment randomness.

To categorize and examine the evolutionary relationships of genes related to RLKs receptors in the three mentioned plants, the MEGA X software was utilized with the neighbor-joining method.

In order to identify some characteristics of protein sequences related to receptor-like kinases in the studied plants, online platform Expasy was used at <https://web.expasy.org/protparam>

*All protein sequences obtained were checked in the STRING database (<http://www.string-db.org>) to confirm the presence of domains for the LePRK1 and LePRK2 genes. The Pfam and SMART programs were used to identify protein domains for RLKs receptor genes in the three plants mentioned. Additionally, five motifs with high similarity were identified to assess the function of RLKs receptors in *Solanum lycopersicum*, *Brassica oleracea*, and *Zea mays*. The exon and intron structure of RLKs receptor genes along with their protein-coding sequences (CDS) were depicted using GSDS software. To investigate the relationship between the gene blocks among the homologues of LePRK1, LePRK2, SFR1, SFR2, LTK1, and LTK2 genes and their genomic sequences, synteny*

analysis was performed using Circoletto software. Circoletto is innovative in combining BLAST and Circos (Krzyszowski et al. 2008), a visually appealing visualization suite written in Perl, that offers rich and flexible features. As the name implies, Circos is based on a circular organization of information.

Results and Discussion

Phylogeny analysis of homologous genes

Investigations of this phylogenetic tree reveal that the sequences of 6 RLKs receptors are divided into four categories. The results showed that all homologous sequences of the *sfr1* gene, except for the sequence with the accession number EH417489.1, (which is in the green clade), are placed in the same group.

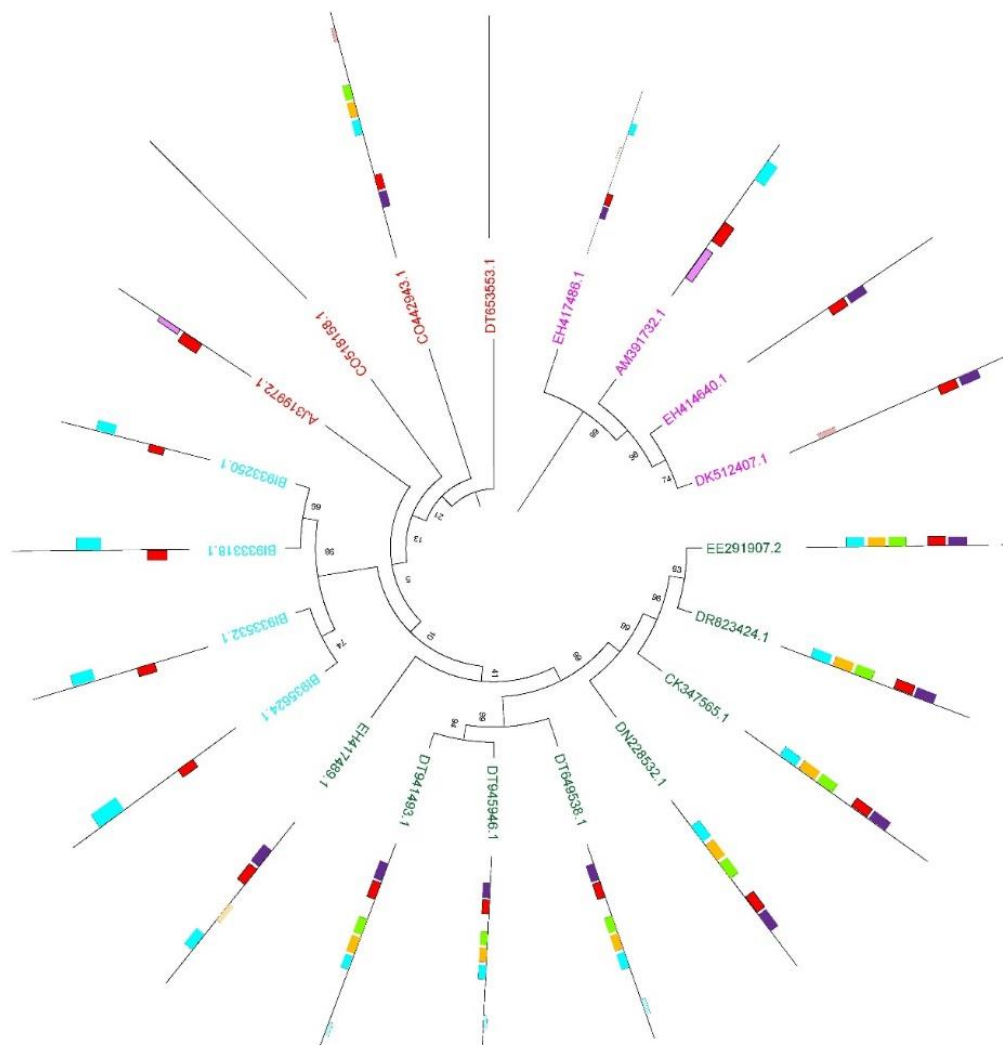
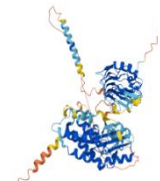


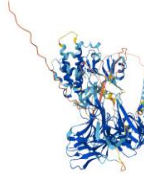
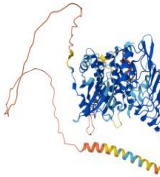
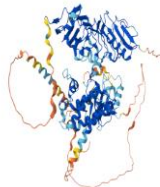
Figure 1- Phylogeny analysis of homologous genes including *LePRK1*, *LePRK2*, *SFR1*, *SFR2*, *LTK1*, and *LTK2*, in *Lycopersicon esculentum*, *Brassica oleracea*, and *Zea mays* respectively. The percentage of bootstrap values is provided in the branches. The motif location for 20 homologous sequences in 4 genes encoding receptor-like kinase (RLK) receptors.

Each gene encoding RLKs receptor is unique in its location on the chromosome. For example, LePRK1 is located on chromosome 5 in tomatoes, while another gene with the same function, LePRK2, is located on chromosome 7. Additionally, the RLK type SFR gene belongs to the S domain type, distinguishing it from the genes studied in *Lycopersicum esculentum* and *Zea mays*. Also, the highest number of amino acids belongs to the SFR1 gene, and another gene with the same function (SFR2) has higher values in terms of isoelectric point and molecular weight than the other genes studied. (Table 1). Generally, the isoelectric point provides important information about the interactions of proteins with their surroundings and how they regulate their structure and function (Lehninger 2004). A comparative genomic analysis was conducted on the TIFY gene family comparing 48 genes from tomato (*Solanum lycopersicum*, a dicot) with 26 genes from maize (*Zea mays*, a monocot). The analysis focused on sequence structure, phylogenetic, expression, and regulatory systems. The identified TIFY protein interactions were grouped into four subfamilies named TIFY-S, JAZ, ZML, and PPD. The PPD subfamily was identified only in tomato (Heidari et al. 2021). Based on research, the availability of the whole genome sequence of *B. oleracea* creates an opportunity to perform in silico analysis of Hsf genes in *B. oleracea*. Thirty-five putative genes encoding Hsf proteins were identified and classified into classes A, B and C. These Hsfs are transcription factors that play an important role in various stresses (Lohani et al. 2019). A comprehensive study of the PRK1 gene family in bread wheat (*Triticum aestivum*) has not been reported. Therefore, we have reported the characteristics and expression patterns of the PRK1 gene family in wheat across the entire genome. The results confirmed 15 PRK1 genes, which were mainly classified into three subclasses based on the phylogenetic tree. PRK1 genes were mapped on chromosomes 1-3 in the respective A, B and D genomes (Rahim et al. 2022).

Table 1. Annotation of genes encoding receptor-like kinase (RLK) in *Lycopersicum esculentum*, *Brassica oleracea*, and *Zea mays*

Gene	Organism	Chromosome	MW ¹ (Da)	PI ²	Protein Length	RLK type	Function	3D Structure
LePRK1	<i>Lycopersicum esculentum</i>	5	74883.69	8.03	669	LRR	Pullen tube-specific expression	
LePRK2	<i>Lycopersicum esculentum</i>	7	71466.84	7.58	642	LRR	Pullen tube-specific expression	
SFR1	<i>Brassica oleracea</i>	4	96321.25	8.51	849	S domain	Inducible by wound and bacteria	

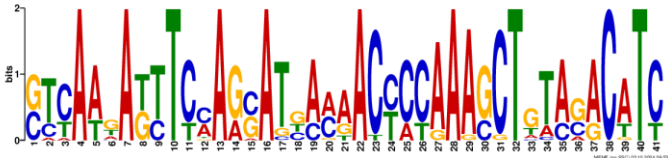
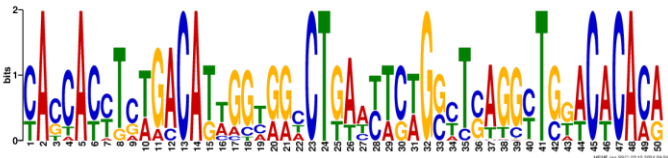
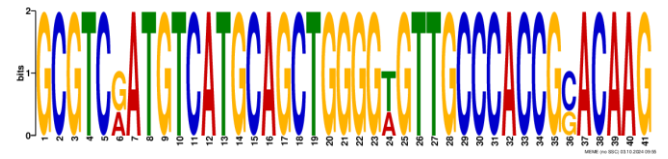
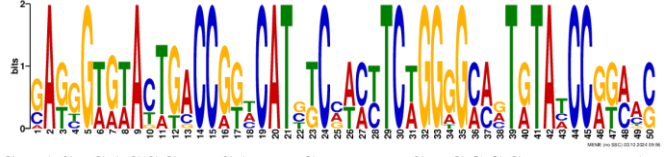
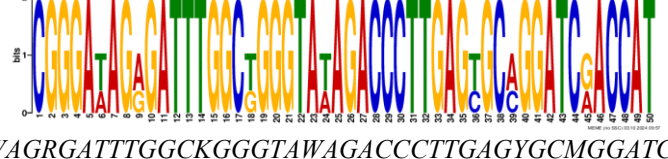
1- Molecular weight
2- Isoelectric Point

<i>SFR2</i>	<i>Brassica oleracea</i>	1	99634.22	7.69	883	<i>S domain</i>	Inducible by wound and bacteria	
<i>LTK1</i>	<i>Zea mays</i>	1	80246.68	6.26	736	<i>LRR</i>	Expressed in all tissues	
<i>LTK2</i>	<i>Zea mays</i>	9	79161.27	5.55	725	<i>LRR</i>	Endosperm-specific expression	

Motif identification and their location

The E-value indicates that the High Scoring Pairs (HSPs) were generated by chance. Therefore, the lower the E-value, the more significant the motifs found. The E-value is an estimate of the expected number of motifs with the given log-likelihood ratio (or higher), and with the same width and site count, that one would find in a similarly sized set of random sequences (sequences where each position is independent and letters are chosen according to the background letter frequencies) (Nobel and Bailey 2014).

Table 2. Discovered motif for 20 homologous sequences in 4 genes encoding receptor-like kinase (RLK) receptors

Lego motif / sequence motif	E-value	site	width	Color
 STCAAKAKTTCMAGSATBAMAACYCCAAAGCTGTASACATC	7.2e-136	18	41	Red
 CACCACYTCWGACATWGGYGGHCTGAWYTCWGSYTSAGGYTGKACACACA	1.8e-131	15	50	blue
 GCGTCRATGTCATGCAGCTGGGGWGTGCCCACCGSACAAG	5.6e-096	8	41	green
 GAKGGWGWACTGACCGKHCATBKCVMYTCWGGGGMMVTRTAHCCRKMAS	6.0e-112	12	50	purple
 CGGGAWAGRGATTGGCKGGGTAWAGACCCTTGAGYGCMGGATCRACCAT	3.2e-111	8	50	yellow

Each motif describes a fixed-width pattern, with no gaps allowed in MEME motifs. Areas with long columns and capital letters indicate positions where the sequences are highly conserved. These regions likely play important biological roles. Shorter columns and smaller letters indicate greater variation at that position. These regions may experience less selective pressure. The height of each letter in the sequence logo is proportional to the frequency of that base at that position (Shultzaberger et al. 2012) and larger letters indicate a greater abundance. The total height of each column in the logo indicates the amount of information for that position. This value is measured in bits and shows the level of conservation for that position in motif conservation.

According to Figure 1 and Table 2, the degree of conservation of motif number 3 is evident due to the high density of capital letters. These regions have likely experienced less change throughout evolution. Motif number one has the lowest E-value. This demonstrates the significance of the discovered motif and justifies its functional and biological role compared to other motifs. In a study, 20 non-redundant maize MAPK genes (ZmMPKs) were investigated and identified through a genome-wide survey. ZmMPKs in the same class exhibited similar domains, motifs and genomic structures (Sun et al. 2015).

A motif is an approximate sequence pattern that occurs repeatedly in a group of related sequences. This figure represents motifs as position-dependent letter-probability matrices that describe the probability of each possible

letter at each position in the pattern (Dinka and Milkesa 2020) Individual motifs do not contain gaps. Patterns with variable-length gaps are split by MEME into two or more separate motifs. The results showed that motifs No. 1 and 2 with widths of 41 and 50, respectively, had much lower E-values than other motifs in all identified homologous sequences for genes encoding RLKs receptors. These motifs are co-located. These two motifs are likely to be very important for studies on biotic stress. Also, motif number 4 with a width of 50 is located in the LTK1, LTK2, and Sfr1 genes.

Checking exon-intron structure

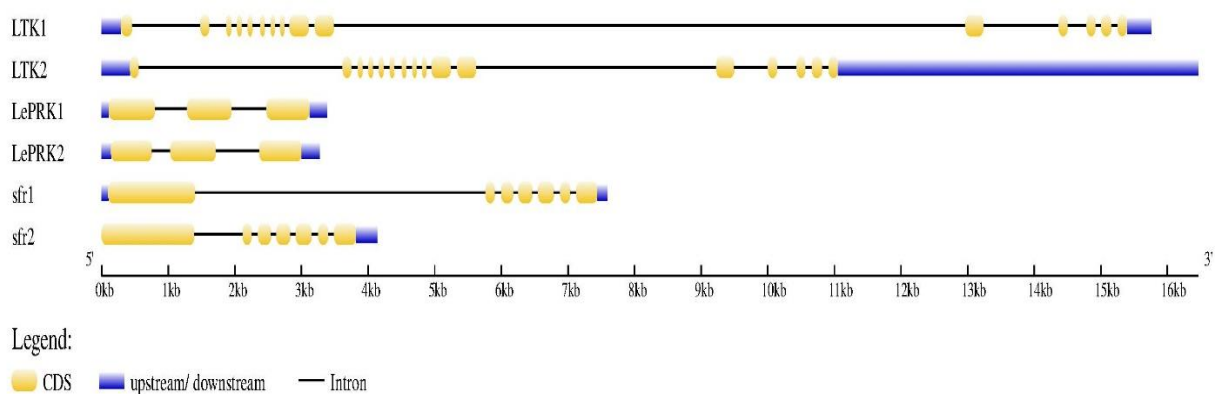


Figure 2- The exon-intron structure of receptor-like kinase genes (RLK) in *Lycopersicum esculentum*, *Brassica oleracea*, and *Zea mays*. Yellow and blue colors are used to represent gene exon and introns, respectively.

According to Figure 2, we can observe the abundance of introns in the LTK1 genomic sequence as well as its overall structure. In contrast, genomic sequences such as SFR and LePRK, have longer lengths than the CDS sequence. Additionally, the genomic regions in the LTK2 sequence are longer than those in other sequences exceeding 16 kb.

Checking Domain structure

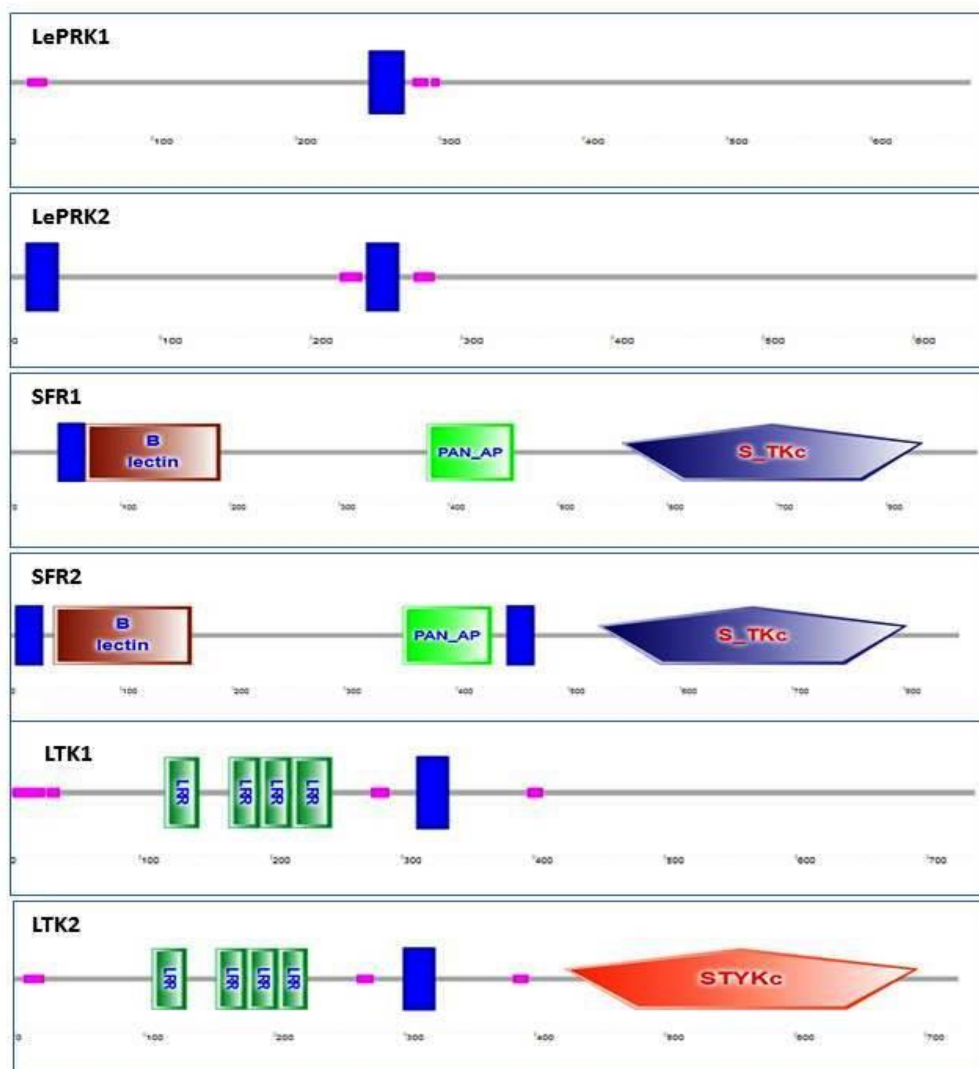


Figure 3- Domain structure of receptor-like kinase (RLKs) sequences in *Lycopersicon esculentum*, *Brassica oleracea*, and *Zea mays*. Different domains are marked with different colors. Schematic diagram for the domain structure was plotted using the SMART program algorithm.

The bulb-type lectins (B lectin), shown in brown, are proteins consisting of three sequential beta-sheet subdomains that bind to specific carbohydrates in order to carry out specific biological functions. This domain typically binds to mannose, but in the presence of a protein called curculin, it appears to lack mannose-binding activity. (Zhao et al. 2017).

The serine/threonine-specific protein kinases (STKs) are important for cell survival, proliferation, differentiation, and apoptosis. In B cells, these kinases play indispensable roles in regulating important cellular functions. Multiple studies on human and other animal cells have shown that multiple STKs are involved in different stages of B cell development and antibody production. Serine/threonine-specific protein kinases (STKs) are a family of kinases that phosphorylate the hydroxyl (OH) groups on serine or threonine residues of proteins. (Han et al. 2024). The Plasminogen-Apple (PAN) domain present in G-type lectin RLKs is essential for immunosuppression in plants. Defense pathways involving jasmonic acid and ethylene are critical for plant immunity against microbes, necrotrophic pathogens, parasites, and insects (De et al. 2023). These domains are exclusively located within the gene that encodes the RLKs in *Brassica oleracea*, specifically within the amino acid region 380 to 459.

The leucine-rich repeats (LRR)-containing domain is evolutionarily conserved in many proteins associated with innate immunity in plants, invertebrates and vertebrates. The innate immune response serves as the first line of defense and is initiated by sensing pathogen-associated molecular patterns (PAMPs) (Ng and Xavier 2011). This sequence, which plays an important role in identifying the interaction between the plant and the pathogen, was found only in Zea mays' LTK1 and LTK2 genes. The only difference between these two genes is their location. Leukocyte tyrosine kinase (LTK) is an endoplasmic reticulum-resident receptor tyrosine kinase. Depletion of LTK as well as its pharmacologic inhibition reduces the number of ER exit sites and slows ER-to-Golgi transport (Shultzaberger et al. 2012). Research has led to the isolation of two new members of the receptor protein kinase (RLK) family from maize embryos. These new members show homology to ZmPK1, which was the first RLK identified in the plant kingdom. PK8-a and PK8-b share 88% sequence identity and code for inferred proteins with molecular masses of 57.3 and 56.6 kDa, respectively (Abdel-Sabour et al. 2005). The catalytic domain of STAYKc is located between amino acids 423 and 694 in the ltk2 gene. This domain has not been identified in the structure of the ltk1 gene.

Synteny analysis

Biologists studying organismal evolution often investigate syntenic relationships among orthologous gene clusters using comparative genomic approaches (Daniel et al. 2016). The number of genes within a gene family can vary among species. This analysis helps us understand the evolutionary relationships between genes and different species.

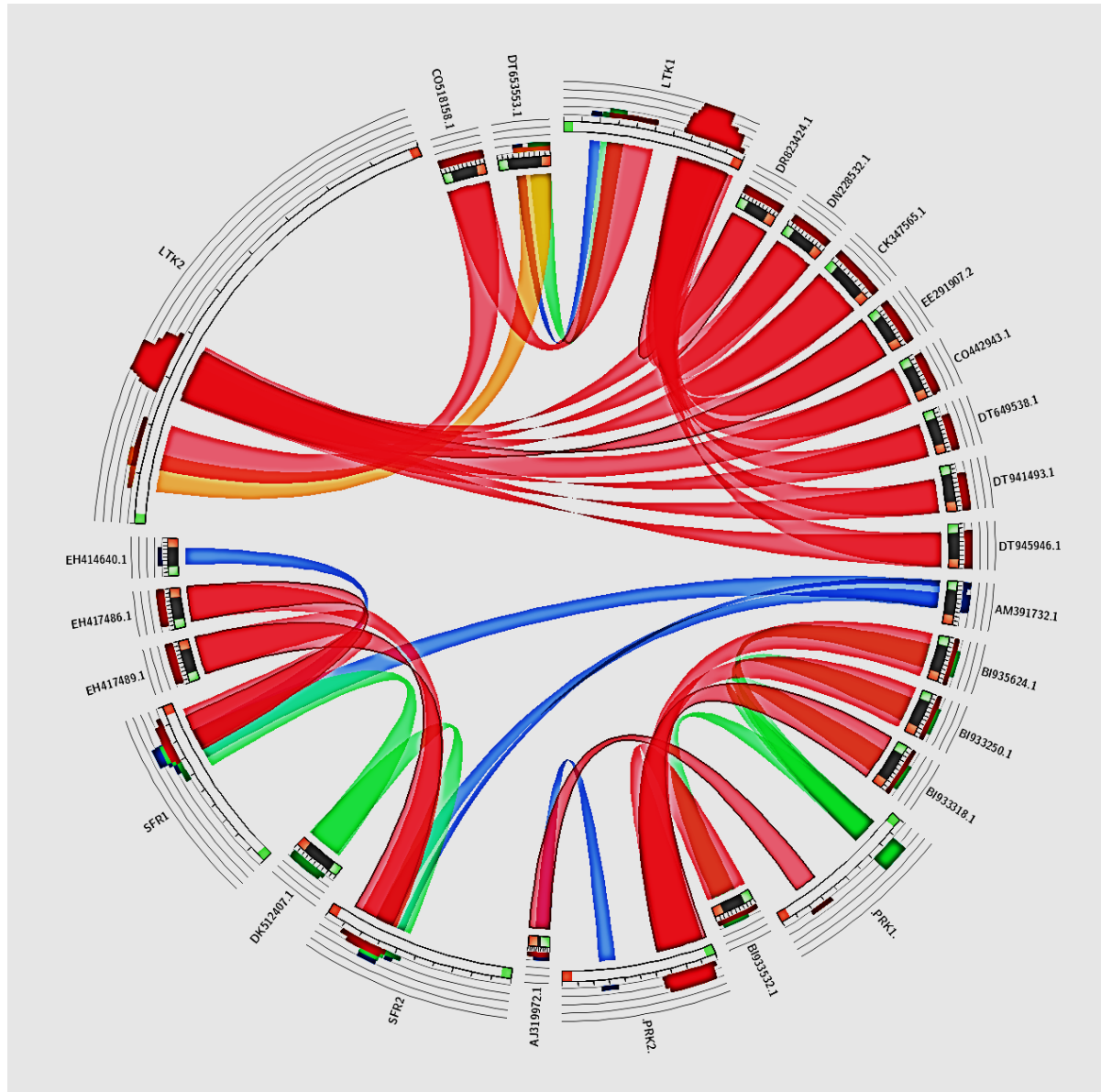


Figure 4- Synteny analysis of the receptor-like kinase gene family (RLKs) in *Solanum lycopersicum*, *Brassica oleracea*, and *Zea mays*. The percentage identity of the syntenic block is shown on the color spectrum, with red representing high identity and blue representing low identity. Identity color key: blue ≤ 0.25 ; green ≤ 0.50 ; orange ≤ 0.75 ; red > 0.75 .

In the output of this software, linear blocks with a low score and in blue color were also observed. This indicates the presence of weak synteny for these genes in this homologous sequence. Orthologous genes among different species often share similar functions. Therefore, studying evolutionary genomics can help us better understand gene functions. The synteny analysis of genes encoding RLKs in *Brassica oleracea* revealed a difference between the SFR1 and SFR2 genes in the conservation of nucleotide bases within the sequence EH414640.1. Considerable synteny is indicated between the LTK1 and LTK2 gene blocks by the density of the lines representing the similarity of their genomic regions. Research describes the characteristics of three proteins that interact with the cytosolic domain of SRK kinase. A homolog of the Arabidopsis kinase-related protein phosphatase was discovered in *B. oleracea*. This protein was found to interact with and phosphorylate SRK and was also phosphorylated by SRK

(Vanoosthuyse et al. 2003). Researchers conducted an analytical study to understand the biosynthetic pathway of carotenoid biosynthesis genes (CBGs) in Brassica species. In this study, synteny analysis (CBGs) showed that these genes are divided into three subgenomes: LF, MF1, and MF2. Among the 58 syntenic homologous genes, 27 are present in LF, 17 in MF1, and 14 in MF2. Additionally, a linear relationship was observed between Brassica oleracea and Brassica rapa (Cao et al. 2021). A receptor in tomato called systemin SYR1 (an LRR-RLK) has been identified. This receptor is not essential for local and systemic wound responses but it is crucial for defense against insect herbivory (Wang et al. 2018).

Table 3. Synteny of receptor-like kinase gene (RLK) blocks and their homologues detailed

Gene	Syntenic sequences	Bits score	E-value
<i>LePKR1</i>	AJ319972.1	640	0.0
	BI935624.1	216	3e-58
	BI933532.1	216	3e-58
	BI933318.1	216	3e-58
	BI933250.1	216	3e-58
<i>LePKR2</i>	BI933318.1	1411	0.0
	BI935624.1	1368	0.0
	BI933250.1	1345	0.0
	BI933532.1	1236	0.0
	AJ319972.1	161	7e-42
<i>SFR1</i>	EH417489.1	700	0.0
	EH417486.1	681	0.0
	DK512407.1	173	4e-45
	AM391732.1	153	4e-39
	EH414640.1	136	3e-34
<i>SFR2</i>	EH417489.1	666	0.0
	EH417486.1	636	0.0
	DK512407.1	241	1e-65
	AM391732.1	144	2e-36
<i>LTK1</i>	CK347565.1	1574	0.0
	EE291907.2	1325	0.0
	DN228532.1	1261	0.0
	CO518158.1	1227	0.0
	DR823424.1	1222	0.0
	CO442943.1	1222	0.0
	DT945946.1	623	0.0
	DT941493.1	610	5e-177
	DT649538.1	595	4e-172
	DT653553.1	294	2e-81
<i>LTK2</i>	CK347565.1	1157	0.0
	CO518158.1	1123	0.0
	CO442943.1	1013	0.0
	EE291907.2	984	0.0
	DN228532.1	925	0.0
	DR823424.1	892	0.0
	DT945946.1	562	6e-142
	DT941493.1	549	4e-158
	DT649538.1	534	3e-153
	DT653553.1	463	5e-132

checking protein interactions

In the STRING database, each protein interaction is annotated with a score. The important thing to note is that these scores do not necessarily reflect the strength or characteristics of the interaction. Rather they are simply indicators of confidence levels. In other words, the probability that these interactions are accurate is high. Scores are measured on a scale from zero to one, with one representing the highest possible score.

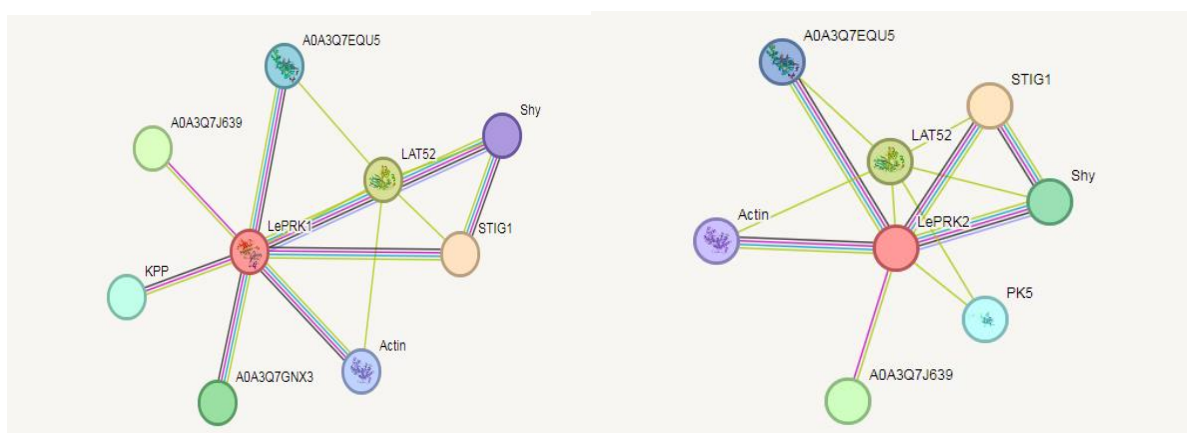


Figure 5- Functional protein network for LePRK1 and LePRK2 genes.

Table 4. Annotation of interactions between the corresponding domains of LePRK1 and LePRK2 genes. The corresponding score is written next to each domain.

Domain	Function	score	Domain	function	score
STIG1	Promote pollen tube growth	0.950	STIG1	Promote pollen tube growth	0.973
LAT52	May play a role germination or early tube growth	0.941	LAT52	May play a role germination or early tube growth	0.966
AOA3Q7J639	SEC7 domain-containing protein	0.648	AOA3Q7J639	SEC7 domain-containing protein	0.649
AOA3Q7GNX3	Uncharacterized protein	0.588	Shy	LRRNT-2 domain-containing protein	0.541
KPP	PRONE domain-containing protein	0.551	PK5	Protein kinase domain-containing protein	0.528
AOA3Q7EQU5	Uncharacterized protein	0.419	AOA3Q7EQU5	Uncharacterized protein	0.489
Actin	Uncharacterized protein	0.419	Actin	Uncharacterized protein	0.489
Shy	LRRNT-2 domain-containing protein	0.411			

In the STRING database, every protein interaction is annotated with a score. It's important to note that these scores do not indicate the strength or characteristics of the interaction; instead, they represent levels of confidence.

In other words, the accuracy of these interactions is represented by scores measured on a scale from zero to one, with one indicating the highest level of accuracy.

In this research, the STIG1 domain has the highest score of 0.973 for the LePRK1 gene and 0.950 for the LePRK2 gene. The speed of pollen tube growth is a major determinant of reproductive success in flowering plants. Tomato (*Solanum lycopersicum*) STIGMA-SPECIFIC PROTEIN1 (STIG1), a small Cys-rich protein from the pistil, was previously identified as a binding partner of the pollen receptor kinase LePRK2 and shown to promote pollen tube growth in vitro. However, the in vivo function of STIG1 and the underlying mechanism of its stimulatory effect remain unknown (Huang et al. 2014). In Figure 5, each node represents domains produced by a single protein-coding gene source. The connecting line between them represents proteins that share a common function. This does not necessarily mean that they are only physically connected to each other.

Conclusion

The receptors in plants are a crucial component of the plant's interaction with its environment. They transduce information and make the plant aware of its surroundings. The mechanisms of response to biotic stresses, which often result in the alkalization of the intercellular space in plants and ultimately trigger a hypersensitivity reaction, are mediated by RLKs receptors that are typically associated with a set of conserved sequences. The study of the functional regions and structural differences and similarities of these receptors revealed significant synteny between the homologues of the LTK1 and LTK2 receptors. Despite their larger genome, they have longer intron than the kinase receptors in *Brassica oleracea* and *Lycopersicum esculentum*. Motif numbers 1 and 2 in the homologous sequences of this receptor with a low E-value indicate a high degree of conservation during evolution. These regions are particularly important because they have a similar function in resisting biotic stresses.

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آنالیز گسترده ژنومی خانواده ژنی گیرنده های شبه کینازی در سه گیاه متفاوت: گوجه‌فرنگی، کلم بروکلی و ذرت

چکیده

گیرنده های شبه کینازی (RLKs) نقش مهمی در دفاع اولیه گیاهان در برابر پاتوژن‌ها دارند. مطالعه این ساختارهای ژنی می‌تواند درک ما را از عملکرد آنها افزایش دهد. هدف از این تحقیق شناسایی دمین‌های حفاظت‌شده در توالی گیرنده‌های RLKs در سه گیاه متفاوت گوجه‌فرنگی (*Solanum lycopersicum*)، بروکلی (*Brassica oleracea*) و ذرت (*Zea mays*) جهت انتخاب امیدوارکننده‌ترین توالی برای مقاومت به تنش‌های زیستی رایج می‌باشد. نتایج نشان داد که موتیف‌های ۱ و ۲ نسبت به سایر موتیف‌ها از قرابت بیشتری نسبت به یکدیگر برخوردار هستند، که نشان‌دهنده اهمیت آنها در توالی‌های گیرنده RLKs می‌باشد. علاوه بر این، سینتینی بین بلوک های ژنی که گیرنده‌های RLKs و همولوگ‌های آنها را کد می‌کنند، تراکم بالاتری از خطوط بین دو ژن *LTK1* و *LTK2* را نشان دادند که حاکی از شباهت بسیار بالای بین آنها می‌باشند. مهم‌ترین تفاوت در ژن‌های گیرنده *Brassica oleracea* و *Zea mays* به ترتیب به وجود لکترین‌های نوع *Bulb-Type Lectins (B lectin)* و توالی‌های تکراری غنی از لوسین (*LRR*) مربوط می‌شود. این دمین‌ها نقش حیاتی در ایمنی ذاتی دارند. در نهایت در برهمکنش بین دمین‌ها

مطالعات مهندسی کشاورزی زراعت و اصلاح نباتات

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در ژن *LePRK* مشخص شد که دمین *STIG1* دارای بالاترین امتیاز بوده و بیشترین نقش عملکردی را در رشد لوله کرده در این شبکه ایفا می‌کند.

کلمات کلیدی: آنالیز گسترده ژنومی، دمین‌های حفاظت شده، روابط بین بلوک‌های ژنی، گیرنده های شبه کینازی (*RLKs*).