



# A Synopsis of Different Plant LRR-RLKs Structures and Functionality

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## Plant Defense Mechanism

As sessile organism plants are exposed to multiple environmental threats. Unlike animals, they lack mobile immune cells. Hence, to safeguard themselves from a range of pathogens, plants come by a multi-tiered innate immune system [1,2]. The first line of defense mechanism is the recognition of the pathogen by detecting pathogen-associated molecular patterns (PAMPs) or microbial-associated molecular patterns (MAMPs) which are either extracellularly exposed or secreted extremely conserved pathogen-derived molecules [1,3]. This recognition is achieved by a cognate plant cell-surface pattern-recognition receptor (PRR). Once the invading pathogen's microbial signature 'PAMP' is recognized by the PRR, the plant cell initiates signaling cascades via the mitogen-activated protein kinase (MAPK). This first line of the plant defense mechanism is referred to as pattern-triggered immunity (PTI) [4-8].

## Pattern Recognition Receptors (PRRs)

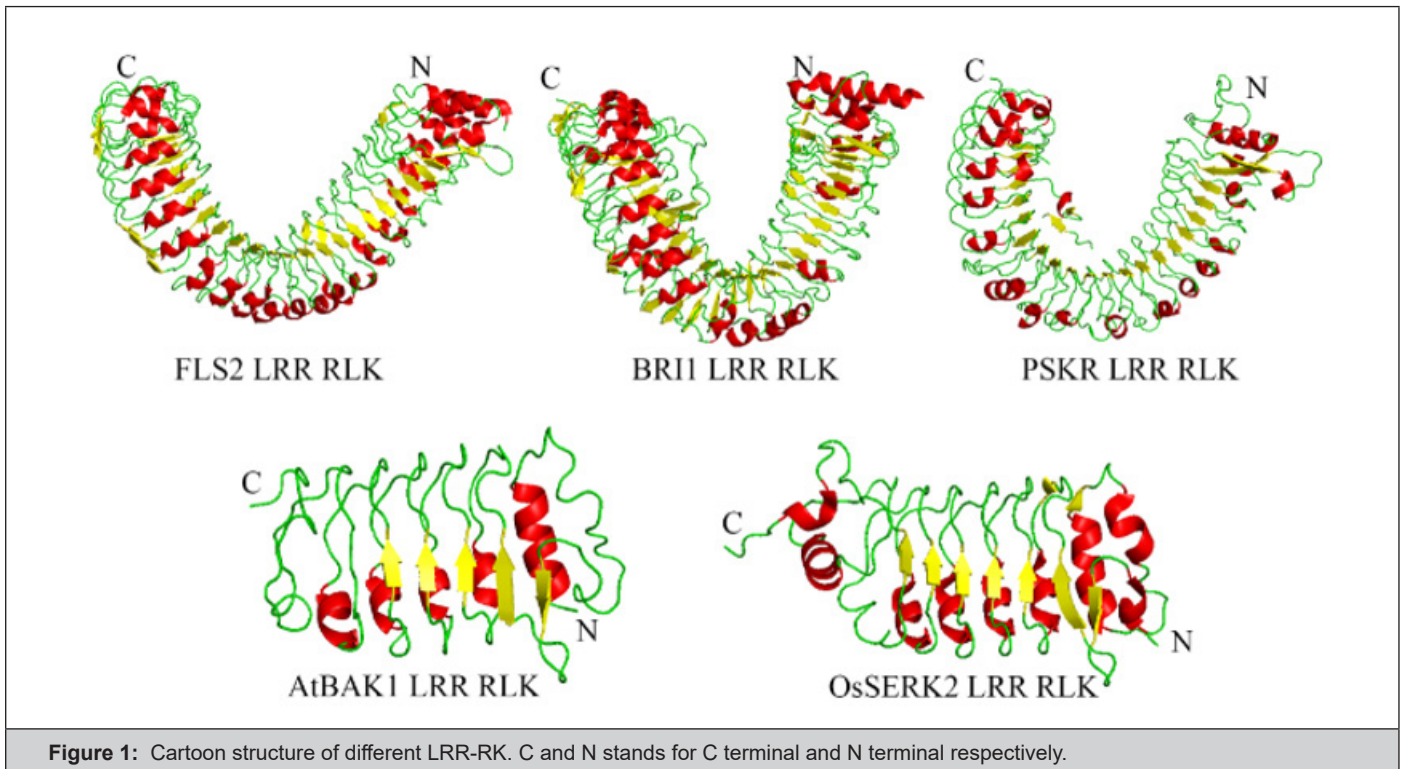
PRRs are grouped into receptor-like kinase (RLK) and receptor-like protein (RLP). RLKs contain an extracellular domain, transmembrane domain, and intracellular kinase domain while RLPs lack kinase domain [6,7,9-11]. The number of RLKs and RLPs are much higher in plants compared to animals [12]. In *Arabidopsis* plant, around 410 RLKs and 170 RLPs have found so far, which is around 640 and 90 for rice consecutively [12-14]. Again, the number of RLKs is much higher than the number of RLPs. In the success of terrestrial plants, these high number of presence of RLKs and RLPs might have played a crucial role [15].

Based on the extracellular domain (ECD), RLKs and RLPs are again categorized into several subfamilies which include epidermal growth factor-like (EGF) domains, lysine motif (LysM) and leucine-rich repeat (LRR) [16]. Among these subfamilies, leucine-rich

repeat like kinase (LRR-RLKs) is the largest family in plant [15]. With over 200 members of LRR-RLKs in *Arabidopsis*, they play a great role in plant development and defense processes which includes symbiosis, wounding response, hormone perception, stem cell maintenance and cell proliferation [17].

## Structure of Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK)

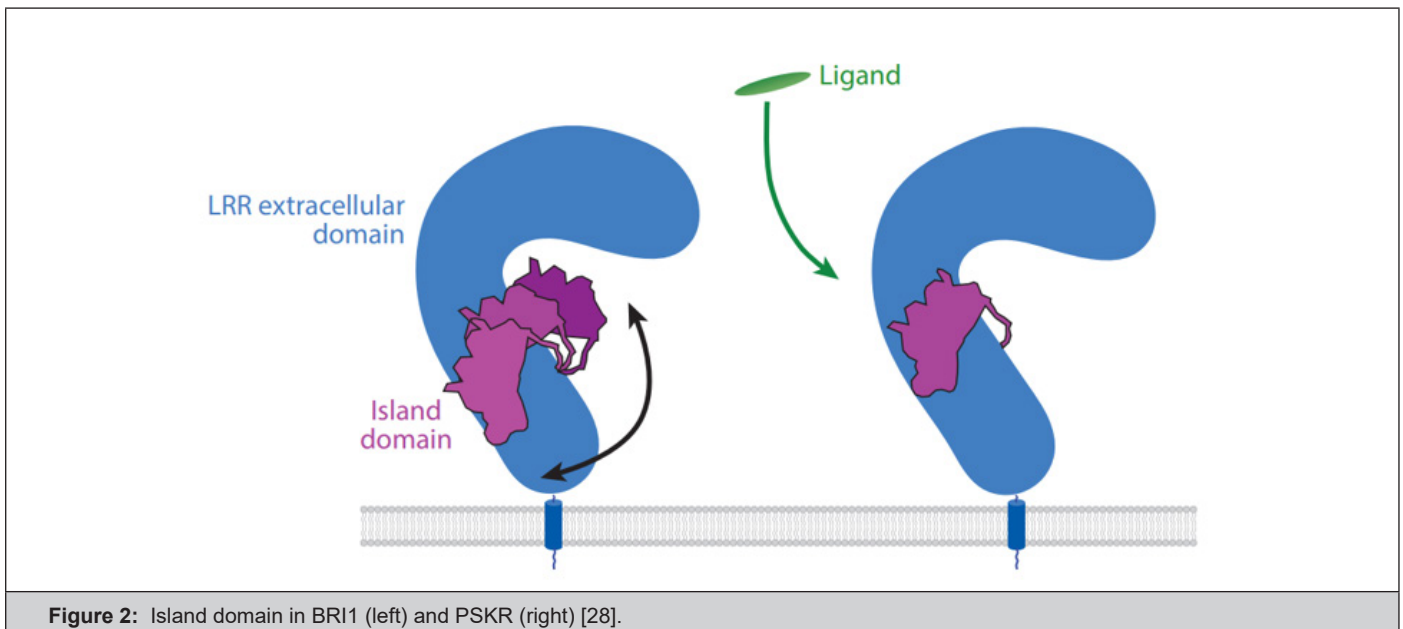
Plant LRR-RLKs are composed of a very specific consensus sequence LxxLxxLxLxxNxLSGxIPxxLGx, while x symbolizes non-conserved residues. This unique 24 amino acid sequence forms the beta sheet or beta turn which acts as protein-protein interaction surface. This unique motif forms a helical horse-shoe like structure in plant [18-21]. According to the recent studies, not all LRR-RLK domains composed of tandem arrays of multiple LRRs form horse-shoe like structure. Instead, some of them like plant brassinosteroid (BR) LRR form a right-handed superhelical structure which is different from solenoid conformation [19,22,23]. This unique GxIP sequence which form the helical structure is common in case of receptor-like protein kinase 2 (RPK2) [24], flagellin-insensitive 2 (FLS2) [25], BRI1-like receptor kinase 1 (BRL1) [26]. There is a notable difference in the size of LRR-RLK. Recent crystallographic structures reveal that this size varies from 21-19 LRRs. Recent studies showed that around 20-25 LRRs form this superhelical structure where inner surface and lateral side of the structure actively involves in binding with other proteins [25,27]. PGIP has 10 LRRs, SERK1 has 5 LRRs, HAESA has 21 LRRs, TDR/PXY has 22 LRRs, FLS2 has 29 LRRs, BRI1 has 25 LRRs, PSKR has 21 LRRs, RPK2 has 22 LRRs and TMK1 has 13 LRRs [28]. Small sized LRR-RLK is observed in AtBAK1 and OsSerk2 (Figure 1) which acts as a co-receptor for activation of PTI by PRR FLS2 and Xa21 respectively [25,29].



### Island domain in LRR-RLK

In LRRs, LRR-RLK stands between 1<sup>st</sup> to 322<sup>nd</sup> LRRs where there can be a spacer region at 4<sup>th</sup> to 5<sup>th</sup> LRR from the C terminal end of 30 to 70 amino acids known as island domain (ID) [9]. The ID is not likely for all the LRR-RLK and its sequence is not conserved

between species. These ID can interact with the PAMPs like BL with BRI1 [30] and PSK with PSKR [31,32] (Figure 2). Also, 2 ID were observed in the crystal structure of RPK2 which creates scaffold where the ligand binds [24]. This suggests the function of island domain as binding of LRR ectodomain with small ligands [28].



### Cys-pairs in LRR-RLK

Again, Cys-pairs which are placed between last LRR and transmembrane domain or near the start codon before LRR is another interesting extracellular domain in LRR-RLK [33]. Although

the function of the Cys-pair is not clear, the mutation of it showed a significant decrease in FLS2 activity while BRI1 and CLAVATA2 showed no effect [34]. Although Cys-Pairs in LRR-RLK is assumed to contribute towards trafficking, folding and binding, no strict decision can be drawn regarding the importance of it.

## Conclusion

The above discussion shows, in spite of the fact that most of the LRR-RLKs share a common shape, a significant difference is observed in the case of other factors such as diameter, LRR numbers, the presence of the island domain and cys-pairs. All this play a pivotal role in different binding mechanism in PTI complex at the early stage of the plant defense mechanism. It is needless to say, to obtain a precise idea about the detail function and interaction of different domains, further investigation needs to be done on LRR-RLK conserved protein structures, motif compositions, and gene structures.

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