

Genes of NBS-LRR superfamily in *Solanum phureja*



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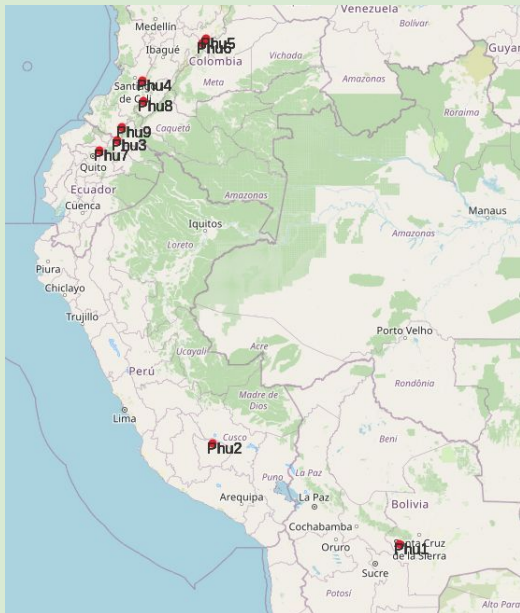
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NBS-LRR genes

Nucleotide-binding site (NBS) and leucine-rich repeat (LRR) genes is a huge superfamily of genes coding for the majority of resistance genes of plants. The most predominant disease resistance genes cloned to date are the NBS-LRR resistance genes. It is well known that their persistence strongly varies between different samples of one species. Thus their distribution within different samples and their polymorphism could be interesting for studying.



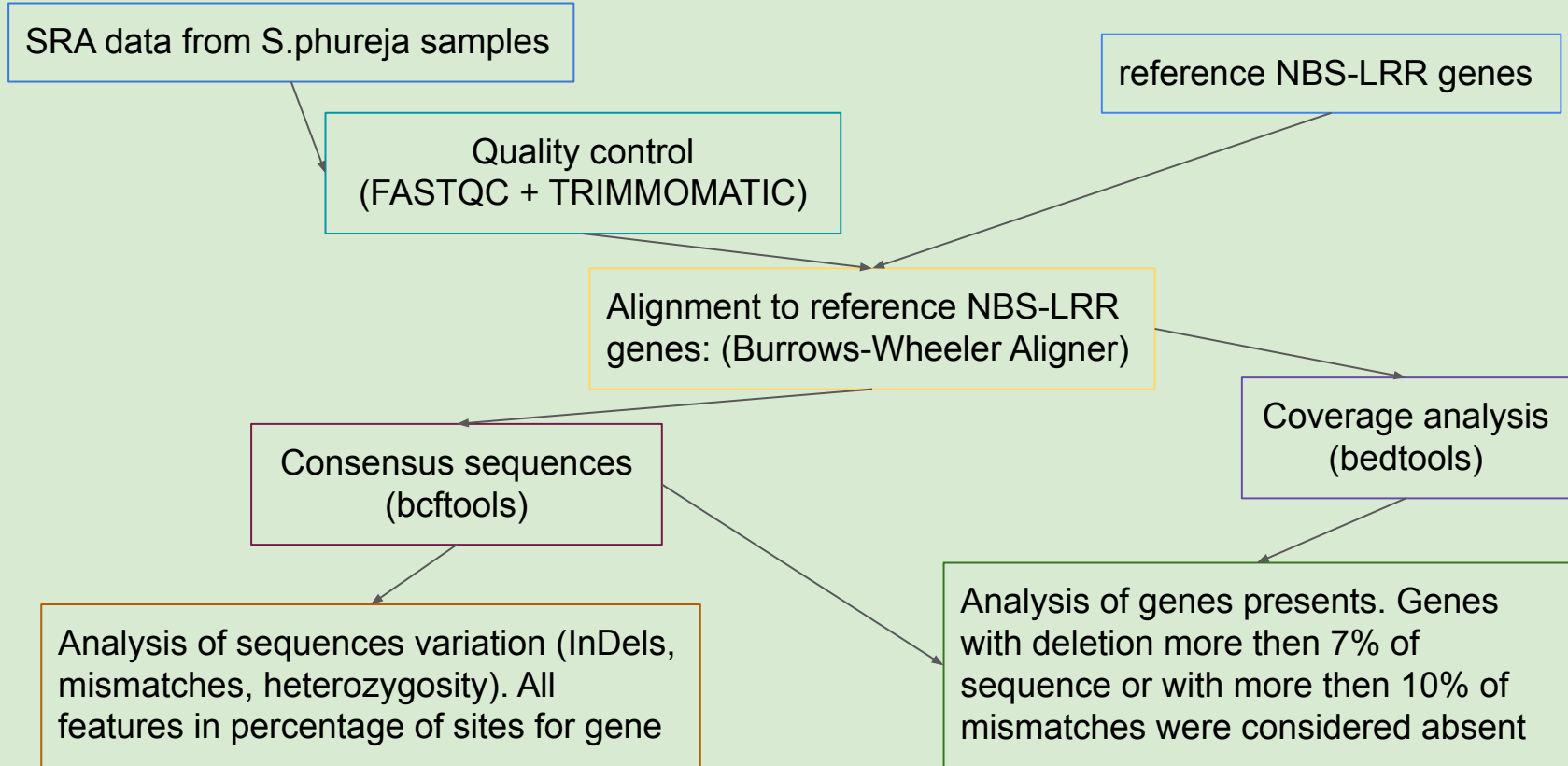
Materials

The material for this study was SRA data of 9 samples *S.phureja* (diploid primitive potatoes cultivars) from NCBI (PRJNA394943 project) (Pic.1)

As references genes we use 400 known NBS-LRR genes from potato reference genome (V3.4) and 30 NBS-LRR genes of other Solanaceae from NCBI

Pic.1: Location of samples collection points

Methods

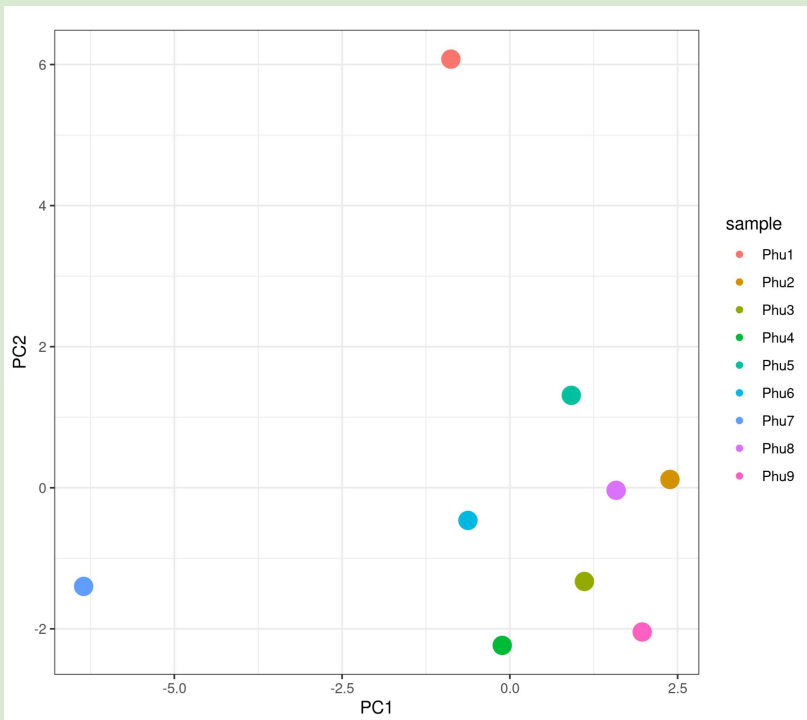


Distribution of different function NBS-LRR genes number by groups of presents

Estimated function of reference genes	Number of genes in group			
	Found in all samples	Found in part of samples (from 1 to 8)	Not found in samples	Total number of genes in group
Nematode resistance	5	2	1	8
Late blight resistance	26	39	5	70
Virus resistance	10	16	2	28
Bacterial spot resistance	5	10	1	16
Other resistance	96	80	16	192
Unknown function	43	34	9	86
Total genes	185	181	34	400

Analysis of variation of genes presents

Pic 2. Principal component analysis by NBS-LRR genes presents in different samples

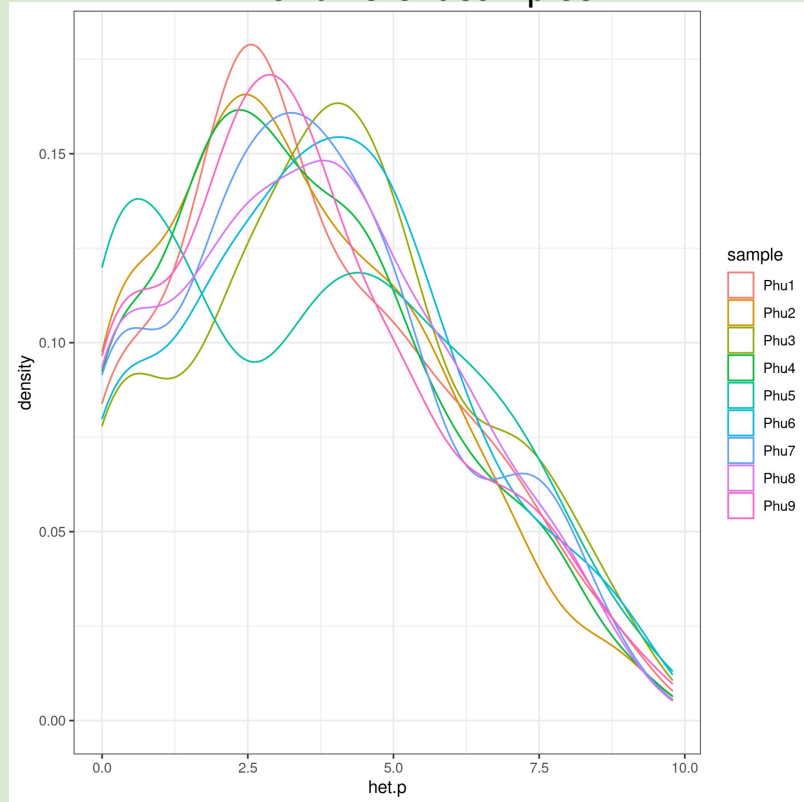


Overall in each sample presence almost the same number of NBS-LRR reference genes. In samples Phu1 and Phu7 total number of genes slightly reduced to 287 and 284 genes respectively. Phu1 sample has a reduced presence of category „other resistance“ genes, whereas Phu7 has significantly less number of late blight genes

Using data about genes presents, we make principal component analysis (Pic.2). We find that samples Phu1 and Phu7 strongly differ from other samples and from each other. At third principal component axis also Phu5 differ from other samples. We suppose that set of genes could be connected with conditionals of cultivation of samples.

Analysis of polymorphism of NBS-LRR genes

Pic.3. Density of percentage of heterozygous sites for different samples



Overall average values of percents of heterozygous, mismatches and InDels sites are not significantly differ between samples. Percentage of heterozygous sites is much higher than other variations. High level of heterozygosity previously noted many times as characteristic of primitive cultivated potatoes group, including *S.phureja*

Analyzing the distribution of heterozygosity (Pic.3), most of samples have the same character of distribution, whereas Phu5 has 2 peaks and one of them have much lower level of heterozygosity. We analyze distribution for different group of genes and found that mostly first peak provided by bacterial spot resistance genes.

Analyzing density distribution of heterozygosity of late blight resistance genes we find 2 peaks distribution in genes set of Phu8 sample, genes in peak with low level of polymorphism could be allelic variants effective for providing resistance, so these genes are worth paying attention to.

Conclusion

- ★ We investigate presence of set of NBS-LRR genes in 9 samples of *S.phureja*. Found common for all samples genes and varied genes.
- ★ We discovered differences between presents of different groups of resistance genes in samples
- ★ On average genes polymorphism is not significantly different between samples, but some for several groups of genes, level of polymorphism could differ both in smaller and larger directions
- ★ We find sample, which is presumably resistant to bacterial spot and further analysis of these sample and samples collected around it could be interesting for finding new source of resistance to bacterial spot disease
- ★ We also find some resistance genes to late blight, which could represent effective allelic variation, but it requires further investigations.

Thanks for your attention!



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