Target enrichment and next generation sequencing as tools to facilitate cloning of R genes from Solanum species

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Late blight caused by oomycete pathogen *P. infestans* is the most destructive disease in cultivated potato. Since *P. infestans* is known to quickly overcome resistance genes used in breeding programs, there is a constant necessity to identify and clone novel *R* genes (*Rpi*-resistance to *P. infestans*). Classical map-based cloning is a laborious and time-consuming effort, therefore we are developing a technique which combines target enrichment and next generation sequencing to accelerate cloning of new *R* gene families. This technique allows to avoid classical polymorphism discovery for fine-mapping of *R* genes. Ideally, our approach will allow to ‘map’ on the gene (cluster of genes) conferring resistance. Here we present the developed pipeline, discuss current troubleshooting and communicate potential of the approach. This newly developed technique should be applicable to facilitate cloning not only *R* but also other *R* genes from Solanaceae which are of NB-LRR type. A preliminary study using Agilent SureSelect with probes designed against 470 NB-LRR genes predicted from sequenced doubled monoploid potato genome (DM). Such enriched sample is sequenced using Illumina GA2 platform. Next, obtained data are analysed using various bioinformatic tools. Predicted SNP/InDels are confirmed by Sanger sequencing and fine-mapped using segregating populations.

**Summary:**
- Target enrichment against potato NB-LRRome is very efficient.
- Bioinformatic analysis of obtained data is still a challenge.
- Classical map-based cloning is a laborious and time-consuming effort.
- Our approach allows to avoid classical polymorphism discovery for fine-mapping of *R* genes.
- Ideally, our approach will allow to ‘map’ on the gene (cluster of genes) conferring resistance.

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