**Phytophthora infestans**, the causal agent of potato and tomato late blight disease, is a pathogen with high evolutionary potential. Rapid pathogen population shifts often undermine breeding efforts towards resistance and hinder effective control of this devastating disease. A new strategy in the fight against late blight is to identify universally expressed, essential pathogen effectors and tailor resistances towards recognition of these important pathogen molecules and all known alleles.

### Results:

The *P. infestans* genome contains more than 500 predicted RxLR containing effector candidates. Transient and stable silencing of 30 highly expressed effectors in *P. infestans* identified 20 that are functionally essential and include Avr3a and Avr2 [Figure 1]. A diversity study of Avr3a in 82 Mexican *P. infestans* isolates revealed that every isolate contains either the avirulent allele Avr3aK80I103, recognised by the cognate resistance protein R3a, and/or the virulent allele Avr3aE80M103 that evades recognition by R3a.

We are using a two-pronged approach to tailor more durable resistance based on recognition of both AVR3aK80I103 and AVR3aE80M103. Screening the Commonwealth Potato Collection (CPC) for very resistant potato accessions has yielded accessions such as *S. semidemissum* and *S. stoloniferum* that recognise both Avr3a alleles [Figure 2]. Furthermore, shuffling the leucine rich repeat (LRR)-encoding region of functional R3a has yielded multiple R3a variants with enhanced recognition specificity towards AVR3aK80I103 that have ‘gained’ recognition of AVR3aE80M103 [Figure 3]. A second round of shuffling will recombine advantageous mutations whilst discriminating against deleterious changes.

### Conclusions:

Unlike some pathogenic bacteria, *P. infestans* appears to contain functionally non-redundant and thus essential effectors. Wild potato accessions contain a mechanism to identify such effectors and known alleles and display, as predicted, good resistance towards the late blight pathogen. Furthermore, the recognition specificity of cloned R genes can be extended *in vitro* to yield variances that recognise previously avirulent and virulent effector alleles. Our effector recognition-driven approaches provide new and exciting opportunities to obtain more durable R genes that target indispensable pathogen molecules.