

# *Result of summarizing an opinion paper*

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### **1. First sentence**

Production of resistant cultivars is the main objective of Plant Breeding, which can be possible through gene stacking. Manipulating biochemical pathways involved in the pathogen response, is one of the ways to induce resistance. Multiple ways to effect a plants resistance by using NLR'S To make the R. Gene more durable by using Natural & Artificial methods. For R gene pyramids to be durable the associated R genes should be highly effective and not leaky. .Second, the R genes should be truly novel so that the corresponding pathogen population is completely naive, leaving the corresponding Avr mutants at the very low frequencies expected under mutation-drift equilibrium. Some pathogen effectors are not recognized by NLRs, but are able to suppress the host defence response or effector recognition by particular R genes. In a global collection including over 600 strains of the barley scald pathogen R. commune, more than 45% of strains had deleted the AvrRrs 1 gene NIPI. The virulence allele is already present in any strains in each field population and allele variants are no longer recognizable by R-gene. Prerequisite for durability is that the corresponding pathogen should only rarely recombine its genome. One consistent theme that emerges across all of these examples is need to keep the pathogen effective population size as low as possible in order to decrease the amount of standing genetic variation in the pathogen population and increase the effectiveness of the R gene pyramid. The development of R gene pyramids can take a considerable amount of time, especially if they are based on transgenic or cisgenic R gene cassettes that require government approval prior to field deployment. A better understanding of pathogen Avr diversity and how it evolves might allow us to engineer more complex R gene deployment strategies which more closely resemble those that evolved in wild plant populations that rarely experience epidemics. Although most agricultural fields are based on homogenous, high-density, it is easy to imagine how cleaning and gene editing techniques could be used to create R gene diversity within agricultural fields that the R gene diversity found in natural wild populations.

### **2. Most important sentence**

It is important to anticipate the success of R-gene pyramids in providing durable resistance against pathogen populations. Quantitative resistance genes

- large in number having additive effect /decreases population size
- single gene having large effect Eg Lr34 Ability of a pathogen to develop resistance through mutations.

At a particular point pathogen can't mutate R Gene Pyramids If the pathogen population had already been exposed to this R gene in its recent evolutionary history, the frequency of the virulent

mutant would be likely much higher as a result. Depending on the fitness costs associated with the mutation, when avr alleles that can avoid recognition are present at the low frequencies expected under mutation-drift equilibrium, pyramids may fail to deliver durable resistance if the effective population size is high. Even greater diversity has been shown recently for the AvrStb6 gene found in every test strain of the wheat pathogen. Standing genetic variation in the pathogen population is often sufficient to render qq R gene ineffective prior to its development into R gene pyramid. Series of independent de novo mutation would be needed to defeat the R-gene pyramid. A recombining pathogen population is expected to bring together independent virulence mutation much more rapid than an asexual pathogen. Adequate knowledge of the pathogen's population biology will enable a rough calculation of the likelihood that an R gene pyramid will be overcome. The maintenance of multiple alleles within the population is critical for the effectiveness of certain essential R genes. Experiments using cultivar mixtures composed of curly relevant cultivars carrying different R genes have shown that increasing diversity within agricultural fields provides an effective way to maintain disease resistance in crops. The effectiveness of R gene pyramids is likely to improve considerably when they are deployed in combination with OR or other management practices that reduce the pathogen effective population size. There are different methods to increase the durability of R-gene pyramids by reducing the population size of the pathogen, like QR and management practices. A high resistance gene diversity within an agricultural field can reduce pathogen ability to break the crop's resistance.

### **3. Summarize in a single sentence**

Resistance genes can either be present in large number & have an additive effect or can also be a single gene having a larger effect. One such type are NLR's that can sense pathogen-secreted virulence effectors & starts a signaling cascade causing autothysis of infected cell. The development of R gene pyramids require adequate knowledge to enable enough calculation and reduce the amount of time that will increase the effectiveness. Multiple cell-like variants for R genes are found in wild plants and result in an important role in effectiveness of R genes. Spores can be able to develop resistance to R genes under favorable conditions in the process of time. R-genes pyramids would be effective to healthy leaves but there are a few data of damaged ones so there can be virulent mutants in the field because of the pathogen's generation time. The R-genes should be new to pathogens to build up a long-run resistance. Low recombination rate of low gene flow Low pathogen genetic diversity of less beneficial recombination events The analyzed pathogen should contain low recombination rates and decreased level of gene flow between cultivated and wild-type populations, otherwise it could lead to increased genetic diversity which causes positive mutations for its survival. Resistance genes aren't able to defeat the disease because pathogen have already suppressed encountered that genes. Through the sexual recombination of pathogens, mutation can be brought much more rapidly than the asexual are. The development of R gene pyramids require adequate knowledge to enable enough calculation and reduce the amount of time that will increase the effectiveness. Multiple cell-like variants for R genes are found in wild plants and result in an important role in effectiveness of R genes.

### **4. With GPT-3: Summarize for second grade student**

A major goal of plant breeding is to create cultivars that are resistant against one or more pathogens. To achieve this, breeders have traditionally introgressed resistance from existing resistant varieties or from wild crop relatives. The resulting resistant cultivar is typically overcome by an evolved pathogen population within a few years. To make resistance more durable, one

proposed solution is to simultaneously 'stack' or 'pyramid' several resistance genes (R genes) into a single cultivar. The underlying principle supporting the development of R gene pyramids is that a pathogen is unlikely to simultaneously mutate the series of genes encoding the corresponding Avr effectors, with the probability of simultaneous mutations decreasing as the number of NLR genes in the pyramid increases. If a crop is going to be resistant to a pathogen, the pathogen should have a low rate of recombining its genome, and should have little gene flow between populations. This will help keep the pathogen population size low, and make it less likely that the crop's resistance will be defeated.

## **5. With GPT-3: Use TL;DR option**

R gene pyramids have been proposed as a solution to the problem of pathogen resistance breaking down in crops over time. Pyramids are created by introgressing several resistance genes (R genes) into a single cultivar to create more durable disease resistance. The underlying principle supporting the development of R gene pyramids is that a pathogen is unlikely to simultaneously mutate the series of genes encoding the corresponding Avr effectors, with the probability of simultaneous mutations decreasing as the number of NLR genes in the pyramid increases. However, for R gene pyramids to be durable, the associated R genes should be highly effective and not leaky, and the R genes should be truly novel so that the corresponding pathogen population is completely naive. R gene pyramids work by having multiple different genes that each recognize a different Avr effector. This way, if one gene becomes ineffective, the others will still work. However, if the pathogen recombines its genome, it can create a new strain that can defeat the entire pyramid. To prevent this, the pathogen's population size must be kept low so that new strains don't have a chance to evolve.