Euphytica 26 (1977) 5–21

THE INTEGRATED CONCEPT OF DISEASE RESISTANCE; A NEW VIEW INCLUDING HORIZONTAL AND VERTICAL RESISTANCE IN PLANTS

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Received 3 August 1976

INDEX WORDS

Differential resistance, gene-for-gene system, horizontal resistance, integrated concept, race-non-specific resistance, race-specific resistance, vertical resistance, uniform resistance, virulence.

SUMMARY

Horizontal, uniform, race-non-specific or stable resistance can be discerned according to Van der Plank, from vertical, differential, race-specific or unstable resistance by a test in which a number of host genotypes (cultivars or clones) are tested against a number of pathogen genotypes (races or isolates). If the total non-environmental variance in levels of resistance is due to main effects only (differences between cultivars and differences between isolates) the resistance and the pathogenicity (in the broad sense) are horizontal in nature. Vertical resistance and pathogenicity are characterized by the interaction between host and pathogen showing up as a variance component in this test due to interaction between cultivars and isolates.

A host and pathogen model was made in which resistance and pathogenicity are governed by five polygenic loci. Within the host the resistance genes show additivity. Two models were investigated; in model I resistance and pathogenicity genes operate in an additive way as envisaged by Van der Plank in his horizontal resistance. Model II is characterized by a gene-for-gene action between the polygenes of the host and those of the pathogen.

The cultivar/isolate test in model I showed only main effect variance. Surprisingly, the variance in model II was also largely due to main effects. The contribution of the interaction to the variance appeared so small, that it would be difficult to discern it from a normal error variance.

So-called horizontal resistance can therefore be explained by a polygenic resistance, where the individual genes are vertical and operating on a gene-for-gene basis with virulence genes in the pathogen. The data reported so far support the idea that model II rather than model I is the realistic one.

The two models also revealed that populations with a polygenic resistance based on the gene-for-gene action have an increased level of resistance compared with the addition model, while its stability, as far as mutability of the pathogen is concerned, is higher compared to those with an additive gene action. Mathematical studies of Mode too support the gene-for-gene concept.

The operation of all resistance and virulence genes in a natural population is therefore seen as one integrated system. All genes for true resistance in the host population, whether they are major or minor genes, are considered to interact in a gene-for-gene way with virulence genes, either major or minor, in the pathogen population.

The models revealed other important aspects. Populations with a polygenic resistance based on a gene-for-gene action have an increased level of resistance compared to populations following the addition model. The stability, as far as mutability of the pathogen is concerned, is higher in the interaction model than in the addition model.

The effect of a resistance gene on the level of resistance of the population consists of its effect

on a single plant times its gene frequency in the population. Due to the adaptive forces in both the host and the pathogen population and the gene-for-gene nature of the gene action an equilibrium develops that allows all resistance genes to remain effective although their corresponding virulence genes are present. The frequencies of the resistance and virulence genes are such that the effective frequencies of resistance genes tend to be negatively related to the magnitude of the gene effect. This explains why major genes often occur at low frequencies, while minor genes appear to be frequent. It is in this way that the host and the pathogen, both as extremely variable and vigorous populations, can co-exist.

Horizontal and vertical resistance as meant by Van der Plank therefore do not represent different kinds of resistances, they represent merely polygenic and oligogenic resistances resp. In both situations the individual host genes interact specifically with virulence genes in the pathogen. Van der Plank's test for horizontal resistance appears to be a simple and sound way to test for polygenic inheritance of resistance.

The practical considerations have been discussed. The agro-ecosystems should be made as diverse as possible. Multilines, polygenic resistance, tolerance, gene deployment and other measures should be employed, if possible in combination.

INTRODUCTION

In modern agriculture the dynamic nature of the host-pathogen relationship has become evident to us through the frequency by which the pathogen overcomes our introduced resistances. Loss of resistance has been observed as early as 1916 (KOMMEDAHL et al., 1970), but it took some forty years before the seriousness of the situation was realized in broader circles. Expecially VAN DER PLANK (1963, 1968, 1975) must be credited for his efforts to develop a general hypothesis explaining the problems generated by the dynamics of the host-pathogen relationship.

Before proceeding a few terms need clarification. Pathogenicity is used here in the broad sense, including virulence. Virulence is used only in a gene-for-gene context. The degree of resistance is usually assessed by extimating disease severity, where in the following disease severity is expressed as a percentage (for instance of affected tissue or affected plants). The dēgree of resistance is found by subtracting the value for disease severity from hundred. Only true resistance – resistance acting to hinder or prevent the establishment on or in and the coloniztion of the host by the pathogen – is considered. Resistances which hinder or prevent contact of the host with the pathogen could be called escape resistances and will not be discussed here.

THE CONCEPTS OF HORIZONTAL AND VERTICAL RESISTANCE

Van der Plank assumes that host-pathogen relationships will be either stable or unstable. The former case represents horizontal resistance (HR) and horizontal pathogenicity (HP), the latter vertical resistance (VR) and vertical pathogenicity (VP). The idea and the terminology have been elaborated upon by ROBINSON (1969, 1971, 1973). Whether one deals with HR, VR or both can be tested, according to Van der Plank, by evaluating the degree of resistance of a number of host-genotypes (clones, cultivars) for a number of pathogen-genotypes (isolates, races). When all non-environmental variation in the resulting disease severity can be explained by differences between cultivars and by differences between isolates (main effects) one deals with HR and HP, the effects being additive (Table 1A).

Table 1. Disease severities of four cultivars inoculated with four isolates in case the level of disease is caused by: A. Main effects only (cultivar and isolates); B. Interaction effects only (cultivars × isolates); C. Main effects and interaction effects together.

Cultivars	Isolates				
	1	2	3	4	mean
A. Main effects only					
I	10	20	30	40	25
II	20	30	40	50	35
III	30	40	50	60	45
IV	40	50	60	70	55
Mean	25	35	45	55	40
B. Interaction effects only					
I	10	30	50	70	40
II	30	50	70	10	40
III	50	70	10	30	40
IV	70	10	30	50	40
Mean	40	40	40	40	40
C. Main effects and interaction effects together					
I	10	30	40	20	25
II	40	20	30	70	40
III	30	30	50	50	40
IV	40	60	60	60	55
Mean	30	35	45	50	40

In case of VR and VP only, the non-environmental variation is caused solely by the interaction between cultivars and isolates. The main effects are zero (Table 1B). Table 1C exemplifies a situation where HR (main effects) and VR (interaction) both occur. This has been called two-dimensional resistance by ZADOKS (1972b). The consequence of VR is that the ranking of the cultivars according to disease severity may depend on the isolate used for testing. With HR the ranking of the cultivars is independent of the isolates.

Though the concepts of HR and VR were adopted by many scientists, at least in principle, other names became associated with these concepts. Uniform and race-non--specific resistance got a meaning equivalent to HR, while differential and race-specific resistance became to mean the same as VR.

CONFOUNDING OF MEANINGS

Van der Plank assumes that HR is controlled by polygenes, with a continuous variation in level of resistance (quantitative expression) as a consequence. Typical examples are the field resistance or partial resistance in potatoes against *Phytophthora infestans*, summarized by ULLRICH (1976); the partial or slow rusting resistance in maize to *Puccinia sorghi* (HOOKER, 1969) and that in barley to *Puccinia hordei* (CLIFFORD, 1972; PARLEVLIET & VAN OMMEREN, 1975). All three are reported to be polygenically inherited (BLACK, 1970; HOOKER, 1969; PARLEVLIET, 1976B). The reduced rate of

epidemic build-up is the combined result of several resistance components (ZADOKS, 1972a), namely a reduced infection frequency, a longer latent period, a reduced sporulation rate, and a reduced infectious period.

Vertical resistance is considered by Van der Plank to be monogenically or oligogenically controlled giving a discontinuous variation in level of resistance (qualitative expression). Many of such monogenically controlled, vertical resistances are of a hypersensitive nature.

The need to discern HR from VR, because of the assumed stability of the former, demanded an easy way to recognize HR. Van der Plank's cultivar/isolate test, when done exhaustively, is a very laborious one. It is understandable that other properties, like quantitative expression, slow rusting behaviour, etc. were used as indicators of HR. This however, reinforced the contention that stability, quantitative expression, polygenic inheritance, and race-non-specificity are properties of HR, instability, qualitative expression, monogenic inheritance, and race-specificity properties of VR. This confounding of meanings also led to the idea that there exist two kinds of resistances and two kinds of resistance genes. CLIFFORD (1975) worded this very clearly: 'In common with other workers, the author accepts the convenience of cataloguing resistance into two types. Nature, I am sure, never intended this division.' With this last sentence Clifford is quite right. In fact classifying resistance into two quite different types is a hindrance rather than a help in understanding how resistance genes operate in natural populations.

Only NELSON (1975) had a clearly different opinion. Although, like Van der Plank, he recognized race-specific or vertical and race-non-specific or horizontal effects, he assumed that each gene had a vertical and a horizontal component, and idea derived from this own work (NELSON et al., 1970). Vertical genes are considered to contribute someting in the way of resisting the pathogen at a point beyond hypersensitivity. The net result of a number of these genes within a single host genotype logically seems to be a collective resistance against colonization. Five genes able to react vertically to some races but not to others can collectively react in a horizontal way to the 'others' races (NELSON, 1975).

THE GENE-FOR-GENE SYSTEM

Through a series of genetic studies with the flax and flax rust *Melampsora lini*, FLOR (1955, 1956) has shown that host and parasite possess complementary genetic systems. Any resistance allele in the host acts if and only if there is on a corresponding locus in the pathogen an allele for avirulence. When the corresponding locus in the pathogen carries a virulence allele the resistance allele can not express itself. On the other hand a virulence allele can not come to expression if at the corresponding host locus no resistance allele is present. The present state of knowledge indicates the widespread existence of the gene-for-gene system in host-pathogen relationships (FLOR, 1971; DAY, 1974; SIDHU, 1975).

In fact vertical or race-specific resistances are most likely a reflection of gene-for-gene systems in operation, as ZADOKS (1966) recognized in 1966 by defining a race of a pathogen as a 'taxon' within the pathogen species characterized by a specific combination of virulence genes.

Although most resistance genes, shown or assumed to operate within a gene-for-gene system, are so called major genes (genes with large or easily identifyable effects), there is no reason why minor genes (genes with small effects) in the host could not operate in a gene-for-gene way with minor genes in the pathogen.

Where major genes are concerned, resistance operating on a gene-for-gene basis will give a vertical or race-specific pattern when host cultivars are tested against pathogen isolates. In case of minor genes, where the gene effects within the host are additive (polygenes), the pattern to be observed is unknown as no research has been reported of minor genes additively operating within the host and on a gene-for-gene basis with the pathogen. This, however, can be studied in a model.

POLYGENIC RESISTANCE AND PATHOGENICITY; A MODEL

To investigate the effects of genes with small effects a model has been designed. In this model resistance in the host population and pathogenicity in the pathogen population are assumed to be governed by five loci. The host is supposed to be diploid, the pathogen diploid or dikaryotic. Per locus two alleles, a + and a − one, are to be discerned. Each + allele in the host increases resistance by 10% (disease severity decreases with 10%), while each + allele in the pathogen decreases resistance with 10% (disease severity increases with 10%). To prevent arithmatical and statistical problems host-pathogen combinations, which, in the model, would lead to disease severities of over 100% or below 0% were avoided. Genes are assumed to exhibit neither dominance nor epistatic effects. Two situations are envisaged:

I. Within the host, within the pathogen, and between the host and the pathogen genotypes the + alleles act in an additive way. Each + allele in the host genotype increases resistance with 10%, each + allele in the pathogen genotype decreases the resistance with 10% irrespective of the locus on which the + allele is located. The genes of the host and the pathogen act in a gene-non-specific manner; there is no gene-for-gene action. Host and pathogen populations interact in a race-non-specific or uniform way. This is the true horizontal situation as envisaged by VAN DER PLANK (1975, p. 167). A mutation in the pathogen genotype from − to + on any locus will decrease the resistance with 10%. This is the *addition model.*

II. Within the host the resistance alleles act in an additive way as in model I. The genes on the five loci in the host, however, interact with the five loci in the pathogen in a gene-for-gene manner, i.e. in a race-specific or vertical way. A + allele in the pathogen increases disease severity only if at its corresponding host locus a + allele is present. A + allele on the host locus with a − allele on the corresponding pathogen locus increases resistance (decreases disease severity) with 10%. When that host locus, however, carries only − alleles, it will not express any resistance. Whether the corresponding locus of the pathogen carries − or + alleles makes no difference then, since full susceptibility is already expressed. Consequently a mutation from − to + in the pathogen is not always expressed. Such a mutation is effective by decreasing resistance with 10% only when on the corresponding host locus a + allele is present to be neutralized. This in the *interaction model.*

In Table 2 disease severity is expressed for several host-pathogen combinations according to model I and model II. In model I disease severity is not affected by the

Table 2. A simplified model involving five loci in both the host (H) and the pathogen (P). The host is supposed to be a self-fertilizing crop (wheat, barley) and therefore homozygous. The pathogen is assumed to be diploid or dikaryotic. The gene effects are additive within the host, within the pathogen and between the host and pathogen (the addition model) or they are only additive within the host, but interact with the pathogen in a gene-for-gene manner (the interaction model). Each + allele in the host decreases, each + allele in the pathogen increases the disease severity with 10%.

Genotype						Disease severity (%)	
	locus 1	locus 2	locus 3	locus 4	locus 5	addition	interaction
H	− −	− −	− −	− −	− −	100	100
P	− −	− −	− −	− −	− −		
H	+ +	+ +	+ +	+ +	+ +	0	0
P	− −	− −	− −	− −	− −		
H	+ +	+ +	− −	− −	+ +	40	40
P	− −	− −	− −	− −	− −		
H	+ +	+ +	− −	− −	+ +	70	40
P	− −	− −	+ +	+ −	− −		
H	+ +	+ +	− −	− −	+ +	70	50
P	+ −	− −	− −	+ +	− −		
H	+ +	+ +	− −	− −	+ +	70	70
P	− −	+ +	− −	− −	+ −		

identity of the loci on which the + pathogenicity alleles are located, as is shown by the last three combinations. In model II, the interaction or gene-for-gene model, the disease severity depends on the identity of the loci on which the + pathogenicity alleles occur, as indicated by the differences among the last three combinations.

Table 3 depicts a cultivar × isolate test as indicated by VAN DER PLANK (1968, 1975) to discern between HR and VR. When the gene action is according to the addition model a complete horizontal pattern is obtained. All variance (Table 4) is due to main effects (cultivars + isolates), the variance caused by cultivar-isolate interactions is zero. In case of vertical gene or gene-for-gene actions in the interaction model the total variance does not exist solely of interaction variance as in Table 1B, but of variance caused by both main effects and interaction effects. Surprisingly, the variance is predominantly due to the main effects and only for a minor part to the interaction effects. When mean squares are compared the ratio between main effects variance and interaction is 97.4% to 2.6%. With a trial error normally encountered in experiments of this type an interaction variance of this magnitude is not likely to be discerned as statistically significant.

In fact it means that Van der Plank's cultivar-isolate test to discern between HR and VR will not do so when the resistance genes have small, additive effects within the host. The test can only discern major vertical genes from genes with minor effects irrespective whether the latter are vertical or not. When horizontal effects are measured in both the host and the pathogen population it indicates polygenic inheritance of resistance as well as pathogenicity; it does, however, say nothing about the gene action.

Table 3. Disease severities as a percentage of plants of four cultivars times four isolates combinations when five loci are involved according to the addition and the interaction model as described in Table 2.

Genotype host					Locus	Genotype pathogen				
					1	−−	−−	++	+−	
					2	−−	−−	−−	−−	
					3	+−	++	+−	++	
					4	−−	−−	−−	+−	
					5	−−	−−	−−	−−	
Locus 1	2	3	4	5						
Disease levels in addition model										*Mean*
++	−−	−−	++	−−		70[1]	80	90	100	85
++	++	−−	−−	−−		70	80	90	100	85
++	++	++	++	−−		30	40	50	60	45
−−	++	++	++	++		30	40	50	60	45
mean						50	60	70	80	65
Disease levels in the interaction model										*Mean*
++	−−	−−	++	−−		60	60	80[2]	80	70
++	++	−−	−−	−−		60	60	80	70	67½
++	++	++	++	−−		30	40	50	60	45
−−	++	++	++	++		30	40	30	50	37½
mean						45	50	60	65	55

[1] The disease severity is obtained by starting at 100% disease for 10 − alleles in the host and subtracting 10% for each + host allele (4 × 10% here) and adding 10% for each + pathogen allele (1 × 10% here) irrespective of locus.

[2] As note 1, but + alleles in the pathogen are only effective when + alleles in the host occur at the corresponding locus. In this entry 80% results from 100% − 4 × 10% (+ host alleles) + 2 × 10% (two + pathogen alleles on locus 1, the + allele on locus 3 not being effective).

Comparing the addition and the interaction model with each other four interesting points emerge.

1. As already mentioned, in the addition model all mutations from − to + pathogenicity are effectively expressed, whereas in the interaction model only part of them are. This means, that the model based on race-specific minor genes is more stable than the model based on race-non-specific minor genes.
2. The variance in resistance level (Table 4) is considerably less in the interaction model than in the addition model. Part of the genetic variability remains concealed; only a proportion of the alleles for + pathogenicity can express themselves in the interaction situation, namely those which find a + resistance allele on the corresponding host locus. In the additive situation all variance is expressed since all + pathogenicity alleles are effective.
3. The average disease severity is lower in the interaction model than in the additive one for the same reason; not all + pathogenicity alleles are effective in the interaction model.
4. In the interaction model the disease severity of a cultivar is not solely depending on the numbers of + resistance genes and + pathogenicity genes, but also on the

Table 4. Analysis of variance[1] of the data of Table 3.

Object	Addtition model		Interaction model	
	SS	MS	SS	MS
Cultivars	6400	1600	3150	788
Isolates	2000	500	1000	250
Cultivars × isolates	0	0	450	28
Total	8400		4600	

[1] It is not possible to use degrees of freedom here as the data are not estimated but simulated. There is therefore no error and the mean square (MS) has been obtained by subdividing the sum of squares (SS) by the number of objects (4 cultivars, 4 isolates and 16 cultivars × isolate combinations).

identity of the loci carrying + genes. Table 3 shows this. Within the first and second pair of cultivars the number of + resistance alleles is the same (4 and 8, respectively), their average disease severities within each pair differ, however. In the additive situation this is not so.

From these four points a very important conclusion, to be discussed in more detail later on, can be drawn. For the host the interaction model is to be preferred above the addition model. Its stability is higher as far as mutability of the pathogen is concerned, whil the disease severity is lower (degree of resistance higher).

The two models discussed above have been kept very simple. Only a restricted number of loci, without dominance (intra-allelic interactions), or epistasis (inter-allelic interactions) have been introduced. A larger number of loci tends only to enhance the horizontal aspect of resistance by means of a cumulative action of minor genes operating on a gene-for-gene basis. The genetic effects, dominance and epistasis, may influence the ratio between main effect variance (MEV) to interaction variance (IAV) when there is significant interference with additivity in the host. Dominance does only affect the additivity within the locus and therefore it can only exert a minor influence on the ratio between MEV and IAV. When in the interacting model of table 3 the + pathogenicity alleles act in a recessive way the MEV to IAV ratio becomes 95.8% to 4.2%; when the + pathogenicity alleles act dominantly this ratio is 97.8% to 2.2%. Epistasis, affecting the additivity between loci, may increase the cultivar-isolate interaction variance. As long as the genetic variance due to additivity between loci is large compared with the genetic variance due to epistasis the effect of epistasis on the interaction component can be neglected. According to MATHER & JINKS (1971) the genetic variance in polygenic systems due to additive effects is generally large compared with the genetic variance caused by epistatic effects. EMARA (1972), too, found that the genetic variance for pathogenicity in the barley-*Ustilago hordei* system was mainly of the additive type with only a small contribution from dominance and epistasis.

OBSERVATIONS SUPPORTING THE INTERACTION MODEL

It is not easy to conclude from a cultivar-isolate test, whether the host and pathogen genes operate on an additive or on an interaction basis. In both cases the major part of the variance is caused by the main effects, cultivars and isolates. The difference between the additive and the interaction model is that in the former a truly horizontal or uniform pattern is expected, while in the latter minor cultivar-isolate interactions should be observed. In trials with a fairly large error such minor interactions are not discernable from the error variance. Only more detailed analyses may reveal such interactions.

Van der Plank himself realized that a truly uniform reaction in a cultivar-isolate test is not a realistic expectation. He preferred a ranking order test above the interaction test. In the former vertical resistance is considered to be involved when the order in which the cultivars are ranked differs with the isolate used (differential interaction, Table 5). In the interaction test vertical resistance is assumed to operate when a deviation of additivity occurs. The ranking test is more severe than the interaction test and tends to discern only vertical genes with somewhat larger effects. Not only Van der Plank, but also others clearly stated that a truly uniform or horizontal pattern is not to be expected; slight deviation from additivity are normal (NELSON, 1975; ULLRICH, 1976). ZADOKS (1972a) came to similar conclusions; reviewing his experiments in wheat with *Puccinia striiformis*, he wondered whether race-non-specific resistance was really race-non-specific. He observed a fluid transition between instances of near-horizontal resistances and instances of extreme vertical resistance.

In more specific investigations small cultivar-isolate interactions have been reported in host-pathogen relationships, which according to Van der Plank could be classified as typically horizontal. The partial resistance of potatoes to *Phytophthora infestans* and of barley to *Puccinia hordei* seem to be stable (VAN DER PLANK, 1971; PARLEVLIET, 1976a) and polygenically controlled (BLACK, 1970; PARLEVLIET, 1976b). Race-specific or vertical effects have been reported in both cases (CATEN, 1974; CLIFFORD & CLOTHIER, 1974; PARLEVLIET, 1976a, 1977; Table 5). Nevertheless the variance due to race-specific or vertical effects is small, though, compared with the horizontal ones, as predicted from the interaction model.

Table 5. Percentage leaf area affected of three barley cultivars by five isolates of leaf rust. *Puccinia hordei*, just prior to maturation. The barley-isolate-treatments were isolated from one another by autumn-sown rape (PARLEVLIET, 1977). The Julia-isolate 18 combination shows a differential interaction.

Cultivar	Isolate				
	1.2	11.1	18	22	24
Vada	0.6	0.8	0.5	0.2	0.1
Berac	3.1	8.1	6.7	5.0	0.9
Julia	1.8	4.5	12.1[1]	1.1	0.6

[1] Expected value if no interaction was present is 2.9%.

NELSON et al. (1970) presented the best observations supporting the interaction model. Studying the maize-*Trichometasphaeria turcica* system they found that the minor genes involved behaved in a race-specific way when they occurred individually in different maize genotypes, but in a horizontal way when working together in one genotype.

Unpublished data of Van Breukelen and Zadoks also suggest the operation of minor genes on an interaction basis. They followed the colonization process of two races of *Puccinia recondita* in seedling leaves of four wheat cultivars from appressorium formation to uredosorus formation. At different steps (substomatal vesicle formation, formation of penetration hyphe, pustule formation) the percentage successful infections were measured relative to the number successful at the preceding stage. The data indicate that minor cultivar-race interactions occurred at each step, and that these interactions were independent from one another.

The above mentioned observations indeed fit the interaction model very well. Theoretical studies of Mode, too, show that host-pathogen systems are likely to operate on a gene-for-gene basis. He concludes from a mathematical model, in which both the host and the pathogen population are variable and able to recombine their genes, that a gene-for-gene system is advantageous for both host and pathogen. Host-pathogen systems operating on a gene-for-gene basis will eventually (in nature) reach a stable equilibrium. This state of stable equilibrium is profitable to both host and pathogen. A stable pathogen population solves the host's problem of maintenance of resistance to a disease, while the pathogen is able to survive without eliminating its host (MODE, 1958). PERSON (1966) came to similar conclusion.

In the preceding sections it has been shown, that the interaction model offers advantages to both the host and the pathogen. For the host the lower rate of effective mutations in the pathogen population, the higher level of average resistance, and a stable equilibrium with the pathogen population are important advantages. For the pathogen it is important that it does not eliminate its host. In fact, a regular and abundant presence of the host is the best assurance for the pathogen to survive. Major as well as minor genes involved in the host-pathogen relationship therefore are likely to operate on a gene-for-gene basis. The scanty observations available at present support this view.

THE INTEGRATED CONCEPT

To understand the genetics of host-pathogen systems natural populations have to be considered first, since the co-evolution occurred in this phase. The most striking characteristic of natural host-pathogen systems is their remarkable variability so vivedly described by BROWNING (1974). He writes: 'Massive stands of robust and vigorous grains occur in Israel in very heterogeneous populations in dynamic equilibrium with pathogen populations, that are more diverse than outside their centre of origin.' And it is this equilibrium, which is so important for understanding the host-pathogen relationships. DAY (1974) stated that 'during evolution parasites have been kept in check by the requirement to conserve their hosts for further survival. Eliminations of a host population by a pathogen is a product of agriculture because all epidemics require a high degree of genetic uniformity among their host populations.'

As already discussed it is the operation of the genetic systems on a gene-for-gene basis, which makes a state of equilibrium possible (MODE, 1958). Resistance and virulence genes are therefore assumed to operate within one comprehensive system on a gene-for-gene basis. The adaptive forces in the pathogen population are proportional to the magnitude of the resistance in the host population, and vice versa. The resistance of the host population is derived from the cumulative effects of all resistance genes in the population. The effect of a single resistance gene on the total level of resistance in the population is the product of its effect on the individual plant times its gene frequency.

Major genes [1] occuring at low frequencies have a similar impact at the population level as minor genes[1] present at high gene frequencies. In both cases the pathogen population is reduced to some extent.

Within the scope of a dynamic equilibrium, onto which adaptive forces within the host and within the pathogen population operate, gene effects and gene frequencies should be both taken into consideration. It is not difficult to envisage that, in order to keep the effects of resistance genes at a population level about equal, the magnitude of gene effects and the gene frequencies tend to be negatively correlated; this also optimizes the co-existence of host and pathogen.

Resistance genes therefore may differ greatly in their effect on individual plant basis, the adaptive forces in the pathogen population are directed to the magnitude of the gene effect times the gene frequency. Minor genes then become as important as major genes because these adaptive forces allow a much higher frequency of the former than of the latter.

All these resistance genes are considered to operate together in one large system, their effects being additive; in the sense that each gene in its own way reduces the pathogen population in a slight measure. Some (major) genes, which occur relatively rare, keep some plants practically free from the pathogen, whereas other (minor) genes occurring with a high frequency cause most plants to be affected slightly less.

The additivity of these resistance genes with different effects, different frequencies and governing different resistance mechanisms, operates at the single plant level as well as at the population level. At the single plant level genes which seem to be completely different in all respects still have their effects added. Parlevliet (unpublished data), studying the resistance of the barley cultivars La Estanzuela and Cebada Capa, both of which carry the major hypersensitivity gene *Pa7* (PARLEVLIET, 1976c), observed that in the adult plant stage the low infection type of this gene became even lower by a series of minor genes conditioning a longer latent period which are also present in these cultivars.

Several authors (EMSWELLER & JONES, 1934; HOUGH et al, 1970; CALUB et al., 1973; HOOKER, 1973; DYCK & SAMBORSKI, 1974) reported modifying effects on the expression of major genes suggesting the additive effects of minor and major genes.

At the population level the additivity operates between individual plants. Each plant has a certain disease severity as a result of the interaction between its own re-

[1] Using the meanings 'major' and 'minor' genes might suggest the existence of two categories of genes. This, however, is certainly not what is meant. The magnitude of the effect of individual resistance genes can vary fully continuously from complete resistance (immunity or near-immunity) to a barely perceptible resistance.

sistance genes and the virulence genes of the pathogen individuals which reached this host plant. Disease severity accumulated over all host individuals is an expression of the resistance of the host population to the pathogen population.

Stability or longevity of resistance genes in terms of not easily 'broken' by the pathogen is not a factor of importance in this view on natural populations. In the integrated concept all resistance genes in the host population have already virulent counterparts in the pathogen population with which they occur in a dynamic equilibrium. The host population derives its degree of resistance from the diversity of resistance and virulence genes, diverse in their effect, frequency, and distribution over the individuals in the population. No single host genotype is fully susceptible nor fully resistant to all pathogen genotypes, neither is there a pathogen genotype fully virulent or fully avirulent to all host genotypes. In fact every resistance gene, although its corresponding virulence gene is present at a certain frequency, contributes to the average degree of resistance of the population, through its effect on the individual plant times its *effective* gene frequency in the population. This latter depends on the frequency of the resistance gene in the host population and the frequency of the corresponding virulence gene in the pathogen population.

In modern crops the host-pathogen relationship is quite different from the natural situation as described above. The dramatic change in the host population from genetically very heterogeneous to genetically extremely homogeneous disturbed the equilibrium between the natural host and the pathogen completely. The evolution of the host, slow in the natural state, was sped up under the guidance of man. The pathogen followed the evolution of the host closely as JOHNSON (1961) described so well as 'man-guided evolution of the pathogens'. The genetic specialization of the crop, to satisfy man's needs, made it possible for the pathogen to specialize too. Specific host genotypes were matched by specific pathogen genotypes, the race-specific resistance was selected, increased and applied over vast areas. The need arose for resistance genes to which the pathogen could not adapt and the problem of stability or longevity of resistance genes came forward.

In the modern crop situation we want insight into the problem of stability of resistance as undeniably large differences exist in the periods over which resistance genes remain effective.

STABILITY OF RESISTANCE IN CROP CULTIVARS

When no other factors, except mutation, contribute to the stability of polygenic systems the apparently paradoxal situation emerges that the addition model, with its true horizontal effects, is less stable than the interaction model, where the horizontal effects are derived from accumulated race-specific effects. However, the mutability or the *production* of the required virulence genes is only one aspect of the adaptation process of the pathogen population to an increased resistance level. Another aspect, possibly far more important, is the *exploitation* of the newly produced virulence genes. This exploitation phase comprises the increase in gene frequencies from very low to considerable, or said otherwise, the increase of genotypes with new virulence genes from virtually non-existing to common.

Differences in longevity of resistance can therefore be expected to result from the inability of the pathogen population to produce the required gene or genes, or from the inability to exploit the gene or genes that are present in low frequencies. The reproduction potential of most pathogens is so enormous that the production can hardly be a limiting factor. A cautious estimate of the number of uresdospores produced per ha by leaf rust in wheat, if 1% of the leaf area (at a leaf area index of 3.3) is occupied by sporulating uredospori producing 300 spores per mm^2 per day, is 10^{11} spores per day. At a spontaneous mutation frequency of 10^{-8} per locus this would mean a production of 1000 mutants per locus per day per ha. This agrees very well with LEYERSTAM's (1972) observations. He concluded that a hectare of wheat in Sweden affected in a normal way by powdery mildew, *Erysiphe graminis*, will produce 2000 mutants per locus per day.

The production of the required pathogenicity genes does in general not seem to be the limiting factor in adapting to increased levels of resistance. It is the phase of exploitation, that poses a serious problem. Such genes can only spread through the pathogen when they increase the fitness of the population. The pathogen population, though, must be assumed to have a maximal fitness. The components of the population, the genes arranged in a number of genotypes, are co-adapted (DOBZHANSKY, 1955). The gene combinations (genotypes) and their frequencies are not random entities, on the contrary, they occur in such a way to produce a maximum fitness under the prevailing conditions. Any change in this co-adapted system tends to decrease fitness and the population therefore will withstand changes. Resistance to genetic changes, *genetic homeostasis*, has been described in detail by LERNER (1954).

When a certain proportion of the commercial cultivars shows an increased level of resistance the fittness of the pathogen population may be reduced. Genes for increased virulence may now be tried out in the co-adapted system to increase the level of pathogenicity to the old level again, without losing fitness (of which pathogenicity is a part, often an important one). This adaptation to the new situation is expected to succeed much easier when only one major virulence gene has to be introduced into the co-adapted system, compared with the incorporation of several to many minor virulence genes. Even when only one virulence gene has to be fitted into the genetic system of the pathogen population many problems must apparently be solved. This can be concluded from the fact, that introduced monogenic resistance may hold a few to several years, although the number of mutants virulent to a monogenically resistant host and reaching it may be substantial, every season again. Among these many mutants apparently only a few are good enough to be of any use to the pathogen population. ZADOKS (1975) observed small abortive foci of yellow rust in resistant wheat cultivars, suggesting that new mutants were under trial, but were apparently not fit enough to become established.

In case of polygenic systems, the pathogen population must adapt on several to many loci. Here the genetic homeostasis may be expected to operate far stronger than in the monogenic situation.

The operation of genetic homeostasis, however, not only depends on the number of loci involved in the adaptation process. Recombination of the genes is an essential part of the adaptation process. The higher the recombination frequency, the easier new virulent genes can be incorporated in gene combinations with a high fitness

(less genetic homeostasis). Genetic homeostasis is therefore expected to operate stronger not only when more genes are involved in the adaptation process, but also when the possibilities to recombine genes become more restricted. Many pathogens do show a restricted recombination frequency as generative reproduction does not occur (fungi imperfecti, *Puccinia striiformis*, *Puccinia hordei* in most parts of the world) or is restricted to the overwintering or oversummering phase (*Melampsora lini*, *Puccinia hordei* in the Medirerranean area). Of course somatic recombination, the parasexual cycle, may occur, but its frequency is generally low.

It is concluded that the stability of resistance in a cultivar depends predominantly if not solely on the genetic homeostasis operating in the pathogen population. The main factors involved in this genetic homeostasis are considered to be the number of pathogenicity genes, which correspond with the introduced resistance genes, and the frequency of gene recombination occurring in the pathogen population. Stability of the resistance is assumed to be highest when many resistance genes and so pathogenicity genes are involved, and when recombination in the pathogen is strongly restricted.

PRACTICAL CONSIDERATION

To use the available sources of resistance genes in the best possible way a more diversified approach is needed. This was clearly recognized by BROWNING (1974), who said: 'Genes for specific resistance are a valuable natural resource that promise a permanent protection also for agro-ecosystems if, as in natural ecosystems, they are used in an ecologically sound way as part of a diverse population and, if possible, are backstopped by general resistance and/or tolerance.' What he meant with diversity can be seen from his statement that such diverse agro-ecosystems should have only four things in common: they must be planted at the same time, produce during the same growing season, be harvested together, and look more-or-less the same from a respectable distance. They can be diverse for other characteristics.

Although Browing too discerns two kinds of resistances, specific and general resistance, his conclusions are correct.

In agro-ecosystems the stability and so the effectiveness of resistance depends on the genetic homeostasis in the pathogen population. If this operates strongly the tendency to adapt to the introduced resistance is small. The genetic homeostasis in the pathogen population depends strongly on the diversity of the eocological niche in which the pathogen population operates; the more diverse it is the stronger the genetic homeostasis operates and the longer the resistance genes remain effective. In the natural populations, where both the host and pathogen are extremely diverse, genetic homeostasis operates so strongly, that virtually all resistance genes remain effective, although their corresponding virulence genes are present; they co-exist.

Our agro-ecosystems should be made as diverse as possible to exploit the genetic homeostasis to the utmost. This diversity can be seen at two levels; at the crop level and at the level of the agro-ecosystem. Diversity at the crop level means a crop, which meets man's needs as far as possible on a basis of heterogeneous resistance. Diversity at the level of the agro-system is a diversity obtained by using more different agronomic measures (larger diversity in crops, in crop rotation, in ways to control weeds, pests and diseases, etc.). It is not the aim of this paper to discuss the latter, but about the

former, diversity in resistances, some remarks can be made.

Resistance can be made diverse for the pathogen population by confronting the pathogen with several to many resistance genes. There are in principle two approaches to realize this objective.

1. The cultivar carries several to many resistance genes but the individual plants may differ in the resistance genes they carry. This is, in autogamous crops (wheat, barley, rice), the 'multiline' principle. In allogamous crops (rye, maize) this is often the normal situation.
2. All plants within the cultivar carry the same set of resistance genes, polygenes or duplicate genes. With the latter the situation is meant where each gene already gives full or nearly full resistance; it is in principle not different from the polygenic situation.

The multiline approach reviewed by BROWNING & FREY (1969) and summarized by BROWNING (1974) is, especially in the view of the integrated concept, a sound way to use resistance genes in agro-ecosystems. In this way someting like the dynamic equilibrium of the natural populations can be evoked. Within cultivars the resistance genes may vary in time by replacing lines, between cultivars the resistance genes may vary by using different genes in the component lines. This system together creates a dynamic diversity, which can be controlled by man.

The polygenic approach too is a sound one. Because the breeder cannot recognize the differen minor genes there is a large probability that the various cultivars produced contain sets of polygenes, which differ from one another. As cultivars tend to be replaced in time (for various agronomic reasons) the pathogen population is confronted with different sets of polygenes in time as well as in space, a dynamic diversity similar to that produced through the multiline approach.

The multiline and polygene approach are of course not the only strategies, which can be expected to work. If possible they should be backstopped by measures increasing the diversity even more as gene-deployment (FREY et al., 1973), use of tolerance (SCHAFER, 1971; BROWNING, 1974) and various disease control measures.

In case the polygenic approach is chosen, it is important to realize that it is a sound way to improve the resistance of crops provided that genes with relatively small effects are accumulated, genes if possible derived from quite different sources. Selection should start from a very heterogenous host population including both local and foreign material. This host population can be obtained by intercrossing cultivars or lines varying quantitatively in their degree of resistance and being of diverse origin, in a way similar to what SUNESON & WIEBE (1962) did in barley. To obtain the required cultivars or lines for intercrossing an inventory of available material should be made first. After crossing, partially resistant plants should be selected and if needed, intercrossed again. Several cycles of selection during recombination may be needed to obtain a reasonably high level of partial resistance together with the other agronomic characteristics required. Selection, based simply on the exclusion of major, so-called vertical genes, on the contention that polygenes tend to accumulate easily in their absence, is a far too optimistic view. A good screening method and thorough work on a broad genetic basis are the requirements of such a 'horizontal resistance' program.

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