The Effects of Phenotypic Plasticity on Genetic Correlations

Steve Stearns, Gerdien de Jong and Bob Newman

Recent theory suggests that genetic correlations should help to predict the simultaneous response to selection of two or more traits, and much recent research has been directed towards understanding the sources of variation in genetic correlations. Genetic correlations can change from sample to sample, from species to species, from population to population, during the course of development and – within a population, at a fixed stage of development – from one environment to another. These are changes not only in magnitude but also in sign. Theory suggests that genetic correlations should not change sign when the two traits are tightly integrated by physiology or development. Patterns of change of genetic correlations are caused by differences in development and physiology, an understanding of which appears to be necessary to predict the response to selection in natural, heterogeneous environments.

When two traits are genetically correlated, their response to selection, at least initially, differs from that expected if they were not. Recognition of this fact prompted the development of theories of multivariate phenotypic evolution[1] that, in their turn, stimulated the many recent measurements of genetic correlations[2,3] and their use in measuring natural selection on sets of traits[4–9].

It was recognized early on that genetic correlations change across environments, and Via and Lande[10] suggested one method to incorporate environmental variation into selection theory. Such approaches take the reaction of genetic correlations to environmental variation as something that can only be measured empirically. An alternative would be to try to understand how physiology and development produce predictable changes in the way that genetic variation is expressed in different environments.

Steve Stearns is at the Zoology Institute, University of Basel, Rheinsprung 9, CH-4051 Basel, Switzerland; Gerdien de Jong is at the Dept of Population and Evolutionary Biology, University of Utrecht, Padualaan 8, NL-3854 CH Utrecht, Netherlands; Bob Newman is at the Dept of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA.

Here we report on progress towards that goal and review an approach to the theory of genetic correlations in heterogeneous environments.

Sampling and changes in gene frequencies

Estimates of genetic correlations are very sensitive to sampling error. The sample size required to detect statistically significant differences between two genetic correlations is often out of practical reach (a fact that has not inhibited some interpretations). The sample sizes needed to demonstrate a significant difference between estimates of two genetic correlations of the same sign, both of which differ significantly from zero, are very large. For example, to use a half-sib design to detect a significant difference between a genetic correlation of 0.1 in a population where the heritabilities of the two traits were both 0.3, and a genetic correlation of 0.2 in a population where the heritabilities of the two traits were both 0.5, one would need to measure about 350 sibships with three sibs each in both populations.

Estimates of correlations vary among samples drawn from single populations measured under constant conditions. For example, Hughes and Clarke[11] extracted four sets of recombinant lines of *Drosophila*, and found that the genetic correlation between early fecundity and longevity ranged from +0.23 to −0.53. Because genetic correlations are sensitive to changes in gene frequencies and linkage disequilibrium, they also change during the course of selection and differ from population to population[12].

Taxonomic effects

Genetic correlations vary among and within taxa (Table 1). The taxonomic level at which genetic correlations differ varies with traits and groups. In the milkweed bugs and wood frogs, populations differ. In deer mice, genetic correlations of skull traits differ among species but not between two subspecies. The genetic correlations of pelvic traits differ between laboratory mice and rats, two genera in the same family.

Developmental effects

Genetic correlations between traits depend strongly on the age of the individuals measured. Roach[20] found that the genetic correlations of life history traits in *Geranium* changed from generally negative in the early juvenile stage to strongly positive in the adult. Atchley[21] and his co-workers[22,23] found significant

Table 1. Differences in genetic correlations among taxa

Taxonomic group	Traits examined	Differences found	Ref.
Deer mice (*Peromyscus*)	15 skull traits	Between two species; not between subspecies	13
Wood frogs (*Rana sylvatica*)	Development rate and size at metamorphosis	Between two populations	14
Chickens	Early growth rate and weight at maturity	Between two commercial races	15
Murid rodents	Eight pelvic traits	Between mice and rats	16
Milkweed bugs (*Oncopeltus*)	Age at maturity and eggs in first five clutches	Between two populations	17
	Wing length and life history traits	Between two populations, migratory and not	18
Fruitflies and the house fly	Morphological traits from same and different imaginal disks	Among species and imaginal disks	19

changes in the variances and genetic correlations of morphological characters of mice during ontogeny. Development is a major determinant of the genetic variance–covariance structure.

Developmental processes can effect a change in the covariance between two traits. Any initial variation in size of newborn mice will lead to differential growth and an increase in variation during the exponential growth phase. Targeted growth to a window of adult sizes will reduce variation after the window is reached. Such changes in genetic and environmental variation during targeted growth[23] will deeply influence the covariances between traits.

Different genes might be involved at different ages, one gene being expressed at an early age and another gene being expressed at a later age. The best-known example of genes for the same 'trait' that are 'on' and 'off' at different ages is the human haemoglobin genes. Presumably there is a quantitative difference in function here.

What we regard as 'traits' might also not be 'natural', but rather a composite of underlying traits not inherited as anything like a unit. The old discussion on scutellar bristles in *Drosophila melanogaster* – whether the character is bristle number or presence or absence of a bristle at a number of independent sites[24,25] – is relevant. If two 'traits' are not 'natural' units, their change in the developing organisms might lead to odd patterns in their covariance in the population over time.

The covariance structure can give an additional clue to the relation between traits in development. In adult *D. melanogaster*, traits from the same imaginal disk have higher genetic correlations than traits from different imaginal disks[19]. Here, genetic correlations can be used to generate hypotheses about the integration of development.

Environmental effects

Gebhardt and Stearns[26] measured changes in the broad-sense (full-sib) genetic correlation of age and size at eclosion in a fruitfly across a range of larval foods (Fig. 1). They found that it changed from positive under good nutritional conditions to negative under poor. Such changes occur within a single generation in flies exposed to different environments.

Newman[27–29] measured developmental rate and size at metamorphosis for five sibships of spadefoot toad (*Scaphiophus couchii*) tadpoles in ponds of short and long duration. His data imply a change from a strong negative full-sib genetic correlation in ponds of short duration to a strong positive one in ponds of long duration (Fig. 2). In ponds of short duration, the broad-sense genetic correlation of length at metamorphosis and developmental rate was -0.84 ($r^2 = 0.71$, $P = 0.07$); in ponds of long duration it was $+0.91$ ($r^2 = 0.83$, $P = 0.03$). In this case, broad-sense genetic correlation changed dramatically between two environments.

Sometimes, environmental effects induce changes in magnitude but not in sign. In *D. melanogaster*, the additive genetic correlation between early-life fecundity and starvation resistance changes from -0.91 ± 0.03 at 25°C on a rich medium in continuous light to -0.45 ± 0.18 at 15.5°C on a poorer medium in continuous dark[30]. Such changes in magnitude of genetic correlations across environments have also been found in mice, fruitflies, herbivorous insects and milkweed bugs[2,17,30–33]. Scheiner, Caplan and Lyman[34], on the other hand, document a case in which genetic correlations did *not* change significantly across environments. Clarke and Keith[35] measured 102 pairs of genetic correlations in two environments, and found that 95 were positive, one was negative, and only six showed a sign change. Of those six with sign changes, only two seem to differ significantly.

Thus, genetic correlations have complex behavior. They depend on stage of development, on the environment in which they are measured, and very much on the traits. All populations live in heterogeneous environments; their expression of genetic variation can be as heterogeneous as the environments they inhabit. Genetic correlations have both a transient component – dependent on gene frequencies and genotype-by-environment interactions – and a deep-rooted component that ex-

Box 1. Reaction norms

A reaction norm is the set of phenotypes expressed by a single genotype across a range of environmental variation. A reaction norm can also be considered to be the expression of a single genotype as a function of an environmental variable, such as temperature or food. While usually plotted for one trait as a function of one environmental variable (as in Fig. 3), it is often useful to plot the environmental reactions of two traits against one another (as in Figs 1 and 2). In such bivariate reaction norms the environment varies along the norm rather than along one of the two axes.

presses the effects of physiology, development, history and design[36]. Because genetic correlations can change from population to population, within populations as gene frequencies change, during the course of development and from environment to environment, responses to selection change in all the same ways.

A theory of evolutionary dynamics based on genetic correlations

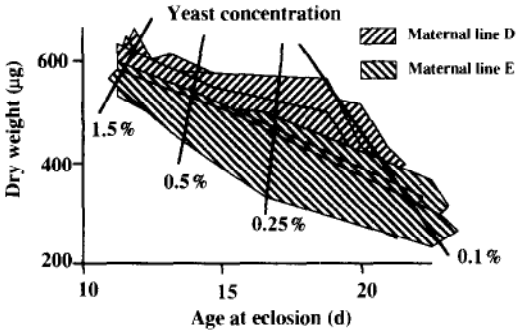


Fig. 1. Reaction norms (Box 1) for age and dry weight at eclosion of female *Drosophila mercatorum* from crosses of males from six isofemale lines from three field sites with females from two parthenogenetic maternal lines (D and E) held in the lab for years. Each hatched polygon depicts the 95% confidence envelope for the reaction norm from one cross. Not all crosses are depicted. The larvae were raised on yeast concentrations of 1.5%, 0.5%, 0.25% and 0.1% at 25°C. *Redrawn from Ref. 26.*

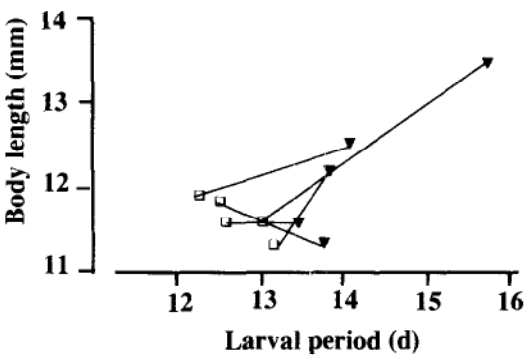


Fig. 2. Reaction norms for five sibships of spadefoot toads raised either in ponds of short duration (open squares) or in ponds of long duration (filled triangles). *Redrawn from single-variable graphs in Ref. 28.*

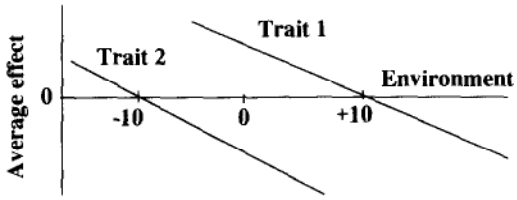


Fig. 3. One locus affecting two traits through linear reaction norms. Left of $x = -10$, its average effects on both traits are positive. Between -10 and $+10$, the average effects differ in sign. Above $x = +10$, both are negative. Because no particular environmental factor was chosen for purposes of illustration, the units on the environmental axis are arbitrary.

should make provisions for changes in the genetic correlations themselves. It would be even better to know when to expect regularities in such changes and how to interpret the cases in which changes of sign in genetic correlations did occur and those in which they did not. Analysis of genetic covariances is only a first step towards evaluating selection on suites of characters, and it may not be a necessary one. The greatest value of such studies is that they identify functionally integrated traits[19]. Studies of constraints on the response to selection will be most improved by looking at the underlying causes of the correlations. These are to be found in the functional integration of the traits.

A theoretical basis for sign changes in genetic correlations

Of several approaches to modelling genetic variation in phenotypic plasticity, that taken by Via and Lande[10] is perhaps the best known. Following Falconer[37], they describe genetic variation in phenotypic plasticity by treating one trait in two environments as if it were two traits, i.e. using the genetic correlation between the expressions of the trait in the two environments.

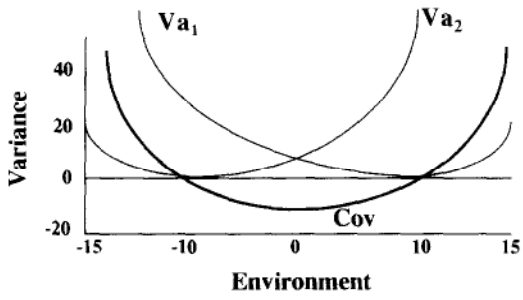


Fig. 4. The basic pattern in additive genetic variances (Va_1 and Va_2) for two traits and their additive genetic covariance (Cov) as determined by one locus acting on two traits. The linear allelic effects on reaction norms lead to quadratic environmental functions of genetic variances and covariances. The values given for variances, covariances and the environment were chosen to lie in the range where the effect depicted would appear. The units on the environmental axis are arbitrary.

For two environments as discrete as two different species of host plant[2], this approach is clear and appropriate. However, when the environment varies continuously, it is more natural to model phenotypic plasticity as a continuous function of a continuous environmental variable – as a reaction norm. Genetic variation in plasticity then involves variation in functions of the same environmental variable. In any one environment, genotype values are represented by the values of the function and genetic variances are calculable by classical means, as is the genetic correlation between two traits that are both expressed as reaction norms. Experimentally, such correlations might change sign between two environments (see Figs 1 and 2). Can we explain that sign change by developing a quantitative genetics of reaction norms?

Suppose that two traits are phenotypically plastic and that genetic variation is present for their plasticity. Assume that both traits are influenced by a single locus. In each environment, we can find the average effect of a gene substitution at that locus. However, because of phenotypic plasticity, the genotypic values for the two traits become functions of the environment, and the average effect of a gene substitution on each of the two traits will also be a function of the environment whenever the genotypic values are not parallel. By definition[10], genetic variation in phenotypic plasticity implies genotypic values that are not parallel functions of the environment. It follows directly that we are dealing with average effects of gene substitutions that are functions of the environment.

The average effect of a gene substitution might be a function of the environment that is always positive or always negative; it could also change sign once or more often (Fig. 3). For one locus, the additive genetic variance in trait 1 is $2pq\alpha_1^2(x)$, the additive genetic variance in trait 2 is $2pq\alpha_2^2(x)$, and the additive genetic covariance is $2pq\alpha_1(x)\alpha_2(x)$, where x represents the environment, α_i the average effect of a gene substitution for trait i, and p and q the allele frequencies at the locus. When we only consider a single locus, the genetic variance of one trait and the genetic covariance of that trait with any other both become zero when the average effect for that trait becomes zero. The genetic covariance is positive when the two average effects have the same sign and negative when they differ in sign. When one of the average effects changes sign and the other does not, the genetic covariance between the two traits changes sign (Fig. 4). The possibility of a sign change in the additive genetic covariance is therefore a direct consequence of genetic variation in phenotypic plasticity[38].

In the simplest model, the average effect of a gene substitution is a linear function of the environment[38–40]. Such a model is consistent with the work done on genotype-by-environment interactions by Gillespie and Turelli[41]. As in their model, genetic variation can be maintained by optimizing selection in a variable environment[39]. When two environments are involved, linear reaction norms and linear average effects can formally always be used, and the relation between linear reaction norms and the correlation between a trait in two environments[10,36] has been worked out[40]. The simple model of linear reaction norms fits straightforwardly with other quantitative genetic models.

In a single-locus model of linear reaction norms, nonparallel reaction norms represent genotype-by-environment interaction. There will be an environment, probably different for each trait, where the heritability of the trait is minimal. Between these two environments, the sign of the genetic covariance changes. If the average effects changed sign at exactly the same environmental value, however, the genetic covariance contributed by this single locus would not change sign. The locus does exert pleiotropic effects in both cases, but when the average effects change sign at the same environmental value, the effects of the locus on the two traits are more tightly related than when they do not; there is more structure to the pleiotropy, which is why de Jong[38] used the term *structured pleiotropy* to refer to this special case.

For polygenes and the model of linear average effects, the average effects at each locus might be drawn independently from a distribution that is different and independent between the two traits[38]. Under this assumption of complete independence, the additive genetic correlation always changes sign across environments. When structure is put into the pleiotropy by assuming that the average effects for the two traits are correlated, then the sign change does not appear if the correlation is large enough.

The single-locus model explains why a sign change in genetic correlations can occur in experiments, and the model of polygenic linear reaction norms predicts such a sign change under the hypothesis of independence. This prediction of a sign change in genetic covariance may fail experimentally under four conditions.

First, much depends on where the reaction norms cross on the environmental gradient. Mathematically, that point is arbitrary and the only important consideration is that it occur somewhere in the environmental range. Experimentally, there is no guarantee that the effect will occur within the range of conditions tested. Second, if pleiotropy is not weak but strong and structured, as should be the case in functionally integrated whole organisms, then these mechanisms will not lead to a sign change in genetic covariance. For example, we should expect that the genetic covariance of two traits affected only by the allocation of a single resource in limited supply would be constrained to be negative for all amounts of the resource (Box 2). Third, loci that contribute to the mean value of the trait but not to the genotype-by-environment interaction could obscure the sign change. Fourth, the average effects might be a function of the environment but never change sign, as would be the case for reaction norms that all decline to zero asymptotically without ever crossing.

Linearity of crossing reaction norms is one way to get a sign change in genetic covariance across environments, but it is not the critical feature of the model. The critical point is that the average effects of one locus on two traits must change sign at different points along the environmental axis for each of the two traits.

The analysis of these types of effect is just beginning. While there should be cases in which the sign of the genetic covariance does not change across an environmental gradient, under simple assumptions – nonparallel linear reaction norms, additive and independent effects of alleles and loci – the change is expected.

The special case of life history traits

Of special importance are covariances between life history traits, as they have been used as an indication of the life history strategies that the organism can follow. Phenotypic plasticity must be assigned a larger role here than it has had in the past.

Dingle *et al.*[42] found a difference in phenotypic plasticity in the milkweed bug *Oncopeltus fasciatus*: populations from Iowa (USA) and Puerto Rico differed in sensitivity of size to temperature. At the same time, the Iowa and Puerto Rico populations showed different genetic covariance patterns between life history characters. The difference in patterns between the island and continental populations was interpreted[43] in terms of a difference between a non-migratory and a migratory life history strategy. This interpretation, while cogently argued and clearly fitting the case, did not take into account any influence of phenotypic plasticity on the genetic covariance.

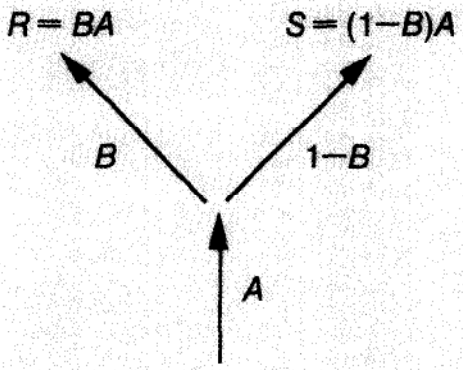
In such cases, attention to the consequences of genotype-by-environment interaction on the covariances between phenotypically plastic characters is necessary; it is possible to over-interpret data if the covariance changes with the environment. Some caution is called for before interpreting a change in sign of a genetic covariance between life history characters as a life history strategy.

Conclusion

Physiology and development play a key role in evolution by determining the environment-dependent expression of genetic variation and covariation. We suggest that genetic correlations, which appear to be genetic constraints, are not in themselves constraints but one of the possible expressions of genetic influence on physiology and development. For example, when there is genetic variation in two traits that are associated in a physiological trade-off within an *individual*, one expects a negative genetic correlation in the *population*. Physiology and development have a hand in the potential for a genetic response to natural selection, and one promising route to understanding the causes of constraints on the response to selection lies through them. The study of genetic correlations, while it may not help much

Box 2. Using physiology to infer properties of quantitative genetics

Environmentally induced changes in magnitude and sign of genetic covariances occur, but the genetic correlations of two plastic traits do not always change sign. What sorts of pairs of traits should show sign change, and what sorts should not? Functionally coupled traits, such as two traits drawing on the same resource pool within one individual, should have genetic correlations that do not change sign. Those that are not functionally coupled are not so constrained – their pleiotropy is not structured – and are more likely to show a sign change. Thus, the causes of stable genetic covariances that do not change sign are to be sought not in the genes but in physiology and development. Modifying the example developed by van Noordwijk and de Jong[44]:



There is a trade-off in energy used between reproduction (R) and survival (S). The total amount of energy acquired is set by A, where $A = R + S$. The fraction of energy allocated to reproduction by the ith genotype is determined by B_i so $R_i = B_iA$ and the fraction allocated to survival is what is left, i.e. $S_i = (1-B_i)A$, with B_i assumed to be genetic. For any fixed level of A, the covariance between R and S is negative, as the traits R and S are related by structured pleiotropy.

The message is not that genetics is unimportant, but that genetic correlations are only a superficial representation of genetic variation in developmental processes that could just as well be viewed as causing developmental constraints. An understanding of development is required to reveal both the causes of constraints and the causes of genetic correlations.

to predict the long-term response to selection, nevertheless remains of central interest in evolutionary biology because of the insight it gives into evolutionary constraints caused by the physiological and developmental integration of the organism. A quantitative genetic analysis helps to pinpoint traits that might be functionally related. Whether it is the most efficient way to pinpoint such traits remains an open question.

References

1 Lande, R. (1979) *Evolution* 33, 402–416
2 Via, S. (1984) *Evolution* 38, 896–905
3 Cheverud, J.M. (1988) *Evolution* 42, 958–968
4 Lynch, M.J. (1984) *Evolution* 38, 465–482
5 Arnold, S.J. and Wade, M.J. (1984) *Evolution* 38, 709–719
6 Arnold, S.J. and Wade, M.J. (1984) *Evolution* 38, 720–734
7 Price, T.D. and Grant, P.R. (1984) *Evolution* 38, 483–494
8 Grant, P.R. (1986) *Ecology and Evolution of Darwin's Finches*, Princeton University Press
9 Schluter, D. (1988) *Evolution* 42, 849–861
10 Via, S. and Lande, R. (1985) *Evolution* 39, 505–522
11 Hughes, D.M. and Clarke, A.G. (1988) *Evolution* 42, 1309–1320
12 Turelli, M. (1988) *Evolution* 42, 1342–1347
13 Lofsvold, D. (1986) *Evolution* 40, 559–573
14 Berven, K.A. (1987) *Evolution* 41, 1088–1097
15 Soller, M., Brody, T., Eitan, Y., Agursky, T. and Wexler, C. (1984) *Poult. Sci.* 63, 2103–2113
16 Kohn, L.A.P. and Atchley, W.R. (1988) *Evolution* 42, 467–482
17 Groeters, F.R. and Dingle, H. (1987) *Am. Nat.* 129, 332–346
18 Dingle, H., Evans, K.E. and Palmer, J.O. (1988) *Evolution* 42, 79–92
19 Cowley, D.E. and Atchley, W.R. (1990) *Am. Nat.* 135, 242–268
20 Roach, D.A. (1986) *Am. Nat.* 128, 47–57
21 Atchley, W.R. (1984) *Am. Nat.* 123, 519–540
22 Atchley, W.R., Plummer, A.P. and Riska, B. (1985) *Genetics* 111, 579–595
23 Riska, B., Atchley, W.R. and Rutledge, J.J. (1984) *Genetics* 107, 79–101
24 Robertson, A. (1965) *Am. Nat.* 99, 19–23
25 Rendel, J.M. (1965) *Am. Nat.* 99, 25–32
26 Gebhardt, M.D. and Stearns, S.C. (1988) *J. Evol. Biol.* 1, 335–354
27 Newman, R.A. (1988) *Evolution* 42, 763–773
28 Newman, R.A. (1988) *Evolution* 42, 774–783
29 Newman, R.A. (1989) *Ecology* 70, 1775–1787
30 Service, P.M. and Rose, M.R. (1985) *Evolution* 39, 943–945
31 Giesel, J.T. (1986) *Am. Nat.* 128, 593–603
32 Murphy, P.A., Giesel, J.T. and Manlove, M.N. (1983) *Evolution* 37, 1181–1192
33 Lynch, M.T., Spitze, K. and Crease, T. (1989) *Evolution* 43, 1734–1736
34 Scheiner, S.M., Caplan, R.L. and Lyman, R.F. (1991) *J. Evol. Biol.* 4, 51–68
35 Clarke, A.G. and Keith, L.E. (1988) *Genetics* 119, 595–607
36 Mitchell-Olds, T. and Rutledge, J.J. (1986) *Am. Nat.* 127, 379–402
37 Falconer, D. (1952) *Am. Nat.* 26, 293–298
38 de Jong, G. (1990) *J. Evol. Biol.* 3, 447–468
39 de Jong, G. (1989) *Evolutionary Biology of Transient Unstable Populations* (Fontdevila, A., ed.), pp. 3–18, Springer-Verlag
40 de Jong, G. (1990) *Genetica* 81, 171–177
41 Gillespie, J.H. and Turelli, M. (1989) *Genetics* 121, 129–138
42 Dingle, H., Blau, W.S., Brown, C.K. and Hegmann, J.P. (1982) in *Evolution and Genetics of Life Histories* (Dingle, H. and Hegmann, J.P., eds), pp. 209–229, Springer-Verlag
43 Dingle, H., Evans, K.E. and Palmer, J.O. (1988) *Evolution* 42, 79–92
44 van Noordwijk, A.J. and de Jong, G. (1986) *Am. Nat.* 128, 137–142

Resource Capture, Biomass Allocation and Growth in Herbaceous Plants

Eric Garnier

Plant species differ widely in their rate of biomass production, even when grown under optimal conditions. A key question concerns the extent to which these growth rates correlate with the uptake of carbon and nitrogen and with the biomass allocation between leaves and roots. Recent data show that the answer to this question differs for mono- and dicotyledons, and that more than biomass allocation, it is the ratio between the activities of leaves and roots that correlates with the growth rate of a plant.

Plant species may differ widely in their relative rate of biomass production, even when they are grown as isolated plants under productive conditions[1–3]. Since roughly 94% of the dry matter of a plant is composed of elements that enter the biomass through photosynthesis, it may be assumed that fast-growing plants will be those having a high carbon-gaining capacity at the whole-plant level. Thus, it might be expected that 'any allocation to any structures other than photosynthetic structures necessarily leads to a decrease in the maximal, resource-saturated growth rate of an individual plant'[4]. However, in experiments where species with different potential relative growth rates (RGR_{max}: see Box 1) were compared, the relationship between the proportional biomass allocation to leaves (or shoots) and the RGR_{max} of the plants has always been found to be very weak, and either positive[10–12], nonexistent[3,13,14] or negative[3,14,15].

A first possible reason for this result is that photosynthesis and respiration have to be considered as well as biomass allocation to the leaves to give a full account of the carbon balance of the plant. A second reason may be that roughly 6% of the dry matter of the plant biomass consists of elements – the mineral nutrients – that are not derived from photosynthesis. Any net CO_2 uptake should therefore be associated with a corresponding nutrient uptake to maintain this mineral concentration in the plant. This means that the activities of leaves and roots have to be balanced during growth, and this is usually expressed as[16,17]:

$$(\text{root mass} \times \text{rate of nutrient absorption}) \propto (\text{leaf mass} \times \text{rate of carbon uptake}) \quad (1)$$

After explaining how this expression has to be modified, this review examines recent research on the relationships between the components of this balance (and combinations thereof) and growth rate for herbaceous species.

A growth analysis approach

A central notion used throughout this review is that of relative growth rate (RGR), which is the dry mass increment per unit time and per unit biomass (Box 1). The highest RGR

Eric Garnier is at the Centre d'Ecologie Fonctionnelle et Evolutive (CNRS – Centre Louis Emberger), Route de Mende, BP 5051, 34033 Montpellier-Cedex, France.