

A Study of Breeding Scheme and Impact of Gene Flow on Gene Diversity within Populations

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Abstract

Expressions describing the increase of gene correlation within and amongst lineages and individuals of a population are derived. The model permits different migration rates by males and females and accounts for various breeding tactics within lineages. The resultant equations enable calculation of the probabilistic quantities for the fixation indices, rates of loss of genetic variation, accumulation of inbreeding, and coefficients of relationship for the population at any generation. All fixation indices were creating to attain asymptotic values rapidly despite the consistent loss of hereditary variation and accumulation of inbreeding within the population.

Keyword:- inbreeding, fixation, population

Introduction

Biological invasions have had profound effects on human society from the earliest times. The spread of the black death in the Middle Ages, the devastations of potato blight, the effects on indigenous species by grey squirrels, Dutch elm disease and flatworms have all been seen as detrimental to man or the environment. Others are seen as bringing benefits: most of our crops

evolved elsewhere in the world and many culinary and medicinal herbs were brought to Britain by the Romans. Perhaps the greatest invasion is the import of vast numbers of exotic plants to gardens and greenhouses. Ecological invasions are an intrinsic part of ecology and evolution and we only consider them bad if they impoverish our health, livelihood or living conditions.

Recent events brought awareness of a require to be knowledgeable and vigilant about where food comes from, how it is grown and what it might enclose. During the 1990s, agriculture and the food chain returned to be daily topics of conversation. In 1998, the concern was for genetically modified crops, and the term 'genetic pollution' came into common usage. There is no place in science for such emotive terms but openly funded science must answer, as far as it can, the public's fears with facts and sound reading.

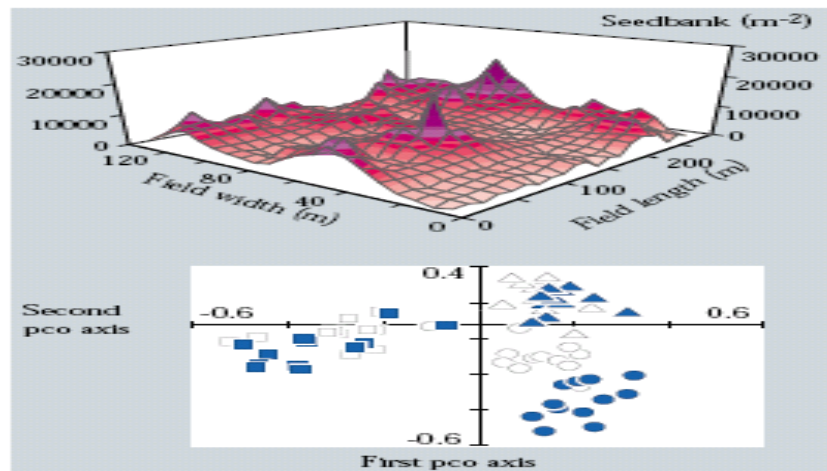
Gene flow in the environment

The difficulty lies in the option of interacting scales. enlargement or death, and exchange of genes, occurs through direct interactions between individuals. The individuals occur in patches or fragments and the fragments are scattered over the landscape. Single fragments evolve their own characteristics that fit them to the local atmosphere. The patches are not independent, but potentially

connected from side to side the migration of seed or transfer of pollen. The individuals in distant patches can therefore influence the interactions within any other patch. Clearly, the degree of connectivity will depend on whether the pollen or seed moves by wind or is carried by insects or other animals, and how sexually like-minded are the plants in the different patches. This system evolves therefore at scales of both the patch and landscape. This is what makes the study of gene flow and invasions so difficult and so challenging. Very advanced techniques are being developed and used to examine these exchanges.

New methodologies

Movement of seed or genes into a scrappy ecosystem usually begins slowly and proceeds gradually. Only when things are well on their way are they generally noticed. The crux is detecting



and interpret rare events and small numbers. Methods and techniques are needed to do three things: to show that an organism or gene has moved from one place to another; to determine its effect on the existing organisms at that place; and (because these two can only be done on a small number of the organisms) to build the greater picture from all the available data. The sciences of plant ecology, genetics, zoology, pathology, mathematics and statistics are all put to use in this work. Research not only has to break new ground in each subject but to find new ways of seaming them together.[3]

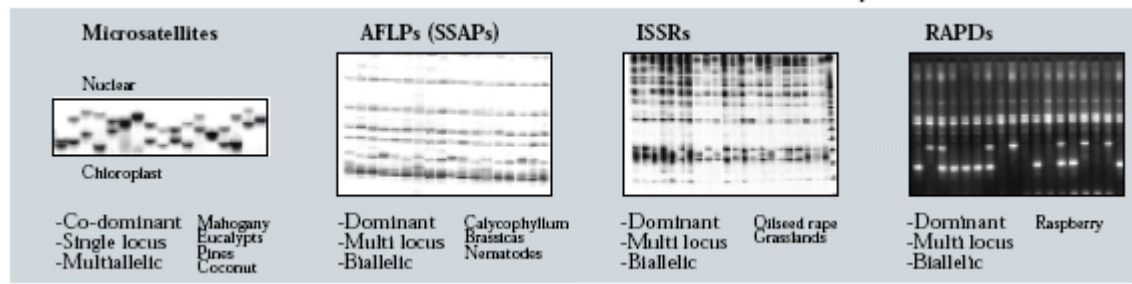
Genetic exchange and detection Advances in knowledge of the genetic code have led to robust techniques for genetically typing

individuals and for detecting the movement of genetic material from one plant to another.

Some of the technique now in use at the Institute are shown in Figure 1. Each is appropriate for a specific purpose. To confirm gene flow, it is essential to observe a transfer of genetic material from one individual or group to the progeny of another. Potential receptors and donors need to be genetically typed to search for distinguishing features in their DNA. Seed is collected from the potential receptor (mother) plants, germinated and the seedlings also genetically typed. The DNA of the mother plant and seedlings are then compared. Gene flow has occurred if a particular DNA sequence is found in a seedling but not in the mother plant. Further, if the number of

potential donors is reasonably small, then some of the techniques can trace the plant from which the pollen came. As Figure 1

shows, the approach is being used to detect and quantify gene flow in plants ranging from feral brassicas to tropical trees.



The implications for agricultural systems

The association of seed and pollen will have to be measured and managed much more in the future than it has been. This will be so whether GM crops are grown commercially or not. Crop products are becoming more specialized and there is an increasing general need for purity. Large sections of the public are insisting that agriculture protects and enhances the habitat and the wider environment.[11]

In principle, and as shown above, detection of gene flow from a GM or other specialised crop into a conventional crop is straightforward. The novel gene can be detected in seeds, or seedlings grown from them, by PCR-based methods. However,

when GM pollen from an extraneous source is competing with a much larger concentration of pollen from within the conventional crop itself, the proportion of seeds acquiring the novel gene may be very small. Thus, although PCR-based methods are extremely sensitive, there will be a lower limit below which gene flow will not be detected in practice.[5]

The detestability of gene flow has acquired considerable political importance in the context of food labeling, because consumers are demanding that food derived from GM crops be labelled as such, so that they can choose whether to buy it or not. In a crop such as sweet corn, gene flow from a nearby GM maize crop could result in a few kernels

on an otherwise non-GM cob being GM. A scientific question is: at what level is such “contamination” detectable? But there is also a political question: what level is acceptable? The Soil Association, representing organic farmers, wishes there to be a zero tolerance of GM gene flow into organic crops, but this is probably impracticable. A draft EC Regulation proposes a 1% tolerance level for the adventitious presence of GM-derived material in any food ingredient from a non-GM source, for labelling purposes. In a crop such as sugar beet, in which the yield is vegetative, the product will be unaffected by gene flow into the crop itself, but gene flow in the previous generation into the seed crop may be relevant. Moreover, with a product such as refined sugar, which contains neither nucleic acid nor protein from the source plant, there is no analytical way in which to determine whether it is derived from a GM crop, a non-GM crop, or whether gene flow has occurred in the crop. The consumer’s “right to know” may be satisfied only by an elaborate and costly system of traceability. An interesting sidelight on gene flow occurs when the companies that have developed GM crops try to enforce their prohibition on farmers saving seed from them. Companies

will have to counter the defense that the seed were saved from a conventional crop, which had acquired the novel gene by natural gene flow.

Managing gene flow

Such issues highlight the fact that gene flow will increasingly be a factor that has to be monitored and managed in daily agricultural practice. Isolation distances that cause detectable or acceptable gene exchange might need to be revised as our understanding of regional processes increases. Much greater co-ordination of planting between farms is likely, as happens already in certain parts of the UK¹⁸, both to reduce genetic exchanges and to manipulate seasonal habitat. New agronomy should result in greater diversity within and about the crop if cultivar mixtures are more widely grown and refuges more widely introduced for natural predators of insect pests. Whatever new technology comes in (GM or otherwise), its effects on the existing biodiversity have to be assessed, and land husbandry altered accordingly. In 1999, a new wave of research began at SCRI to tackle these issues. One thrust is through mathematical modelling which allows the

prediction of the risk of introducing a specified genetic type without necessarily deploying GM crops. Models to understand how to suppress herbicide-tolerant feral crop plants

Gene flow in the environment

Much 'firefighting' research is put in place in an try to provide the answers. The answer is a much sounder infrastructure for studying the flow of individuals, species and genetic information across the countryside.

and to prevent antifeedant genes harming non-target organisms are in this category. At some stage in the procedure of risk assessment, models and small trials are not enough. Given first appraisal of safety, farmscale trials are required to confirm or examine ecological processes or possible emergent properties. The farm-scale evaluation of the effect of GM herbicide tolerant crops on arable diversity is of this type. These government-funded trials, carried out by a consortium comprising ITE, IACR and SCRI, will lead to new definitions of arable ecosystems in the UK. They are, moreover, an example of 'open' research in a highly contentious area.

Fitting the cultivar to the system

There is ample scope also for the plant breeding industry to concentrate more on properties that discourage feral descendants from persist and spreading. For instance, the proportion of secondary dormancy (which encourages overwintering of feral populations) differs greatly between oilseed rape cultivars. This secondary dormancy occurs mainly when the imbibing seed is exposed to low temperature or water stress, so is less likely to occur when seed is sown as a crop than when it falls from feral plants. For crops such as oilseed rape, potato and sugar beet that leave ferals, breeding should consider the ecological as well as the agronomic properties of its new cultivars. The deployment of 'terminator' technology and engineered sterility, assuming they can be made to work reliably, is contentious and requires further ecological appraisal. Research is just beginning in some highly relevant topics, while greater effort is appropriate in some other areas.

New science The concerns over GM crops have brought to attention the need for science to understand agricultural systems, not only

the crop varieties or the specific genetic modification. Land has more than one purpose and science must help management optimise several functions rather than maximise one. Yet behind the intensity of the GM debate, two factors are repeatedly implicated. The first concerns the impartiality of the science and the scientists that are carrying out ecological risk assessment. While science must work with industry, it has to retain a degree of independence through public funding. Otherwise, people will not believe its findings on these issues. The second is that the information required to answer the most pressing questions of recent times is seldom immediately available.

Conclusion

In *C. mucedo* populations, both historical events and current population dynamics influence patterns of genetic diversity. In North America, a relatively large number of divergent mitochondrial genetic lineages have been maintained for the past 1.5 Myr, presumably within multiple glacial refugia throughout much of the Pleistocene. Slight genetic structuring in wild species can be ecologically important but often cannot be

detected by conventional methods. Identifying cases of subtle genetic differentiation in the face of gene flow is particularly crucial in species needing management or conservation plans (Waples 1998; Palumbi 2003). We have shown that SAShA is useful for detecting structure in species with relatively high migration rates and small sample sizes, complementing traditional approaches to population genetic analyses. The method is designed to account for diverse sampling schemes, can incorporate a variety of data types, and returns results that are easily interpreted in a geographically explicit context. Finally, analysis of individual alleles provides for a nuanced understanding of the processes underlying the trends observed in the data set.

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