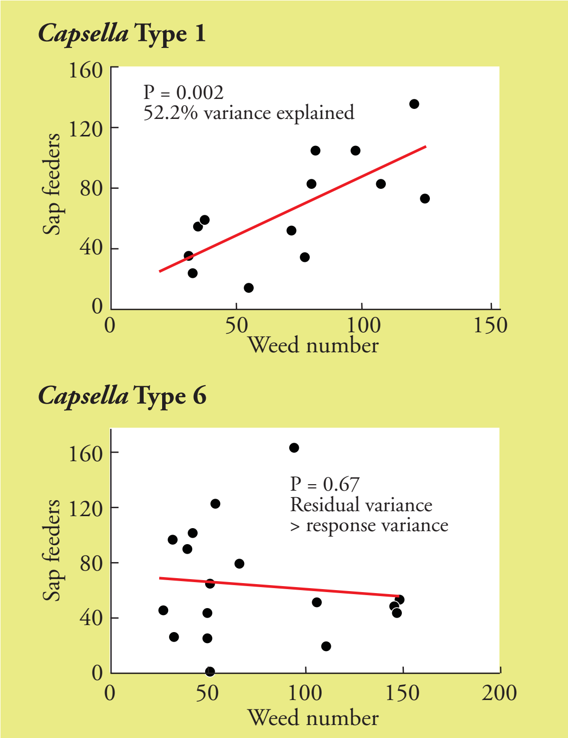
Management impacts on arable diversity and function

R.E. Wheatley, C. Hawes, T.J. Daniell & A.N.E. Birch

Loss of biodiversity has the potential to disrupt a range of agro-ecosystem functions such as nutrient cycling, population stability, system productivity and resilience. Examples include biocontrol of pests and diseases by natural enemies, pollination of crops and wild plant species and long term soil productivity. Such functions are essential for sustainable agriculture, and economists place an extremely high value on these ecological services globally; pollination of crops has an estimated worth of $117 billion, biocontrol around $400 billion and soil nutrient cycling is valued at over $3 trillion, per year[1]. Studies of the relationships between biodiversity and system functioning have indicated that as diversity increases so does resource use efficiency and system resilience to stress – both abiotic, e.g. shortages of water, nutrients, and energy, and biotic, e.g. pest epidemics and invasion by alien species. We have adopted a functional trait-based approach to quantify the link between diversity and function in arable systems, to determine the impact of management on this diversity.

In order to quantify the relation between diversity and function in arable systems we are developing a novel approach where organisms are characterised by functional traits that are important in energy and nutrient cycling. This approach is applied to whole field arable systems, from soil organisms and processes to whole plants and communities, and to invertebrate primary and secondary consumers. This is illustrated by two examples of recent research in the Environment Plant Interactions Programme.

Functional diversity in above-ground arable food webs Resilience and productivity in arable systems depends to a large extent on the characteristics of the system components with respect to a given process or function, and are thought to increase with functional diversity. We are quantifying the relation between functional diversity and system properties (energy flow and productivity), by classifying individual organisms according to functional traits that relate to resource acquisition and transfer. For arable weeds, functional



***Capsella* Type 1**

***Capsella* Type 6**

Figure 1 Within and between species variation in functional traits of plants and the impact on higher trophic groups was assessed at the patch scale. The positive relation between plant biomass and herbivore number in Ecotype 1 was not found for Ecotype 6 suggesting that there are differences between *Capsella* ecotypes in the quality of resource presented to insect herbivores.

traits include architecture (height and spread), determinacy, time from germination to flowering, annuality, development rate and nutritional characteristics that affect insect herbivores (host quality). At the field scale, we have shown that the abundance and functional diversity of arable weeds is affected by management practices and the type of crops sown. Changes in the amounts and quality of this weed resource have a significant impact on the abundance of the insect community. Work is in progress to explore the mechanisms behind this relation between plant and insect functional diversity and to determine the impact of functional diversity across all trophic levels on system properties (Fig. 1).

Spatial and temporal variation in soil microbial functioning Potential Nitrification Rates (PNR) estimated over the growing season of spring barley showed large spatial and temporal variability. Although there were large dynamic changes in PNR between sampling occasions certain areas within the field were always relatively high or low. Whole soil nucleic acid extracts were taken at such points, and PCR cloning in conjunction with a high-throughput sequencing approach targeting a fragment of the ammonium mono-oxidase A *(Amo-A)* subunit gene was performed. A neighbor-joining tree of all clones showing phylogenetic relationships between groups (Fig. 2) revealed that all detectable nitrifying bacteria at this site were of the *Nitrosospira* genus, not the classic nitrifying, closely related *Nitrosomonas* genus, and that the distribution of nitrifier types varied both with space and time.

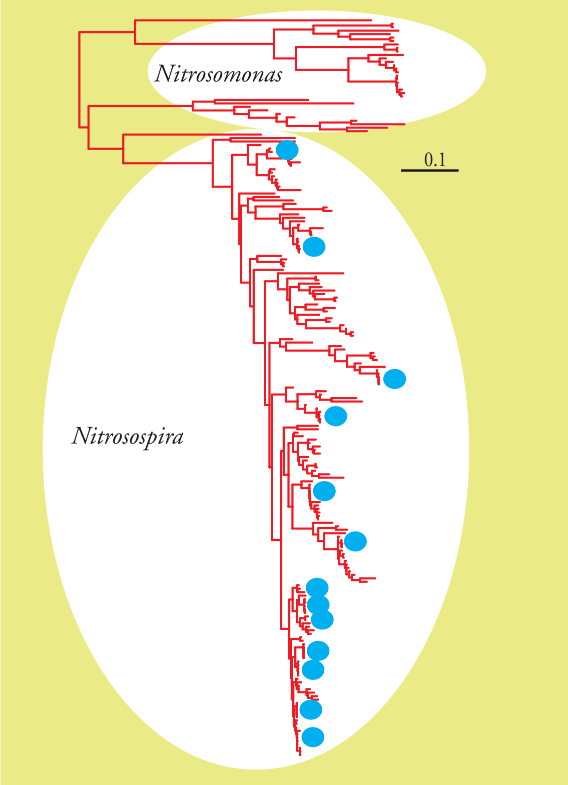


Figure 2 A neighbor-joining tree of all clones showing phylogenetic relationships between the nitrifiers, over time and space, in the field.

Experiments are in progress to investigate the drivers behind the observed diversity differences in both these examples. This will enable us to define the level of functional diversity necessary to maintain resilient, sustainable and productive agro-ecosystems.

References

[1] Constanza, R., d'Arge, R.R., De Groot, R., Farber, S., Grasso, M., Hannon, B., Naeem, S., Limburg, K., Paruelo, J., O'Neil, R., Raskin, R., Sutton, P. & Van den Belt, M. (1997). *Nature* **387**, 253-260.