Identifying novel natural product pathways in plants is extremely difficult because plant genomes are much larger and more complex than those of microbes. However, the recent discovery that genes for some types of plant natural product pathways are organised as physical clusters is now enabling systematic mining of plant genomes in the quest for new pathways and chemistries. The Osbourn lab has defined a large multi-gene cluster for the biosynthesis of antimicrobial triterpenes (avenacins) that protect oats against soil-borne pathogens such as take-all, and has now cloned and characterized all of the genes and enzymes of the pathway. Current projects include investigation of the origins of this gene cluster in oat, and metabolic engineering of triterpene biosynthesis into other plant species (e.g. Arabidopsis thaliana, rice, tobacco and wheat). In a collaborative project with Professor Bin Han (Shanghai Institute of Plant Physiology and Ecology) the genome sequence of our diploid oat reference species Avena strigosa (accession S75) has been determined de novo using whole genome shot-gun sequencing (>90% coverage; genome size 3.92 Gb) and will soon be frozen in preparation for assembly and annotation.