Options for conserving agrobiodiversity in a rapidly changing climate: adaptation or extinction?

Brian Ford-Lloyd

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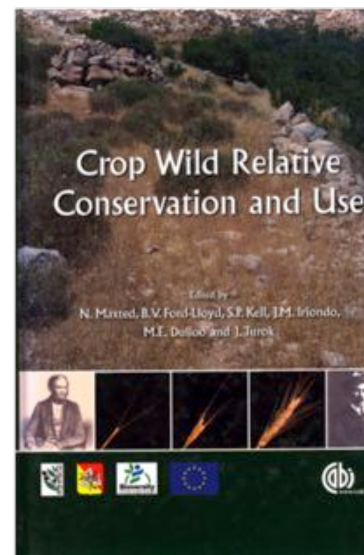
Plant Genetic Resources (Agrobiodiversity):
"the total genetic diversity of cultivated species and their wild relatives, much of which may be valuable to breeders"

Landraces,
Obsolete cultivars,
Breeding lines,
Genetic stocks

‘The extraordinary genetic diversity available in our rice genebanks captures the wisdom and experience not only of those who collected the material but also of the countless generations of farmers who saw, nurtured and carried forward novelty as they encountered it’ (Zeigler, 2013)

Related wild species – crop wild relatives (CWR)



Value of plant genetic resources

In 1990 the transfer from wild *Oryza longistaminata* of the *Xa21* gene for bacterial blight resistance really kick-started the systematic use of the wild rice gene pool: the release of the IR72 variety saw it out-yield all other varieties

More recently the SUB1 gene for transient submergence tolerance in rice cloned from a rice landrace – now transferred to several rice 'megavarieties'.

Crop wild relatives (CWR)

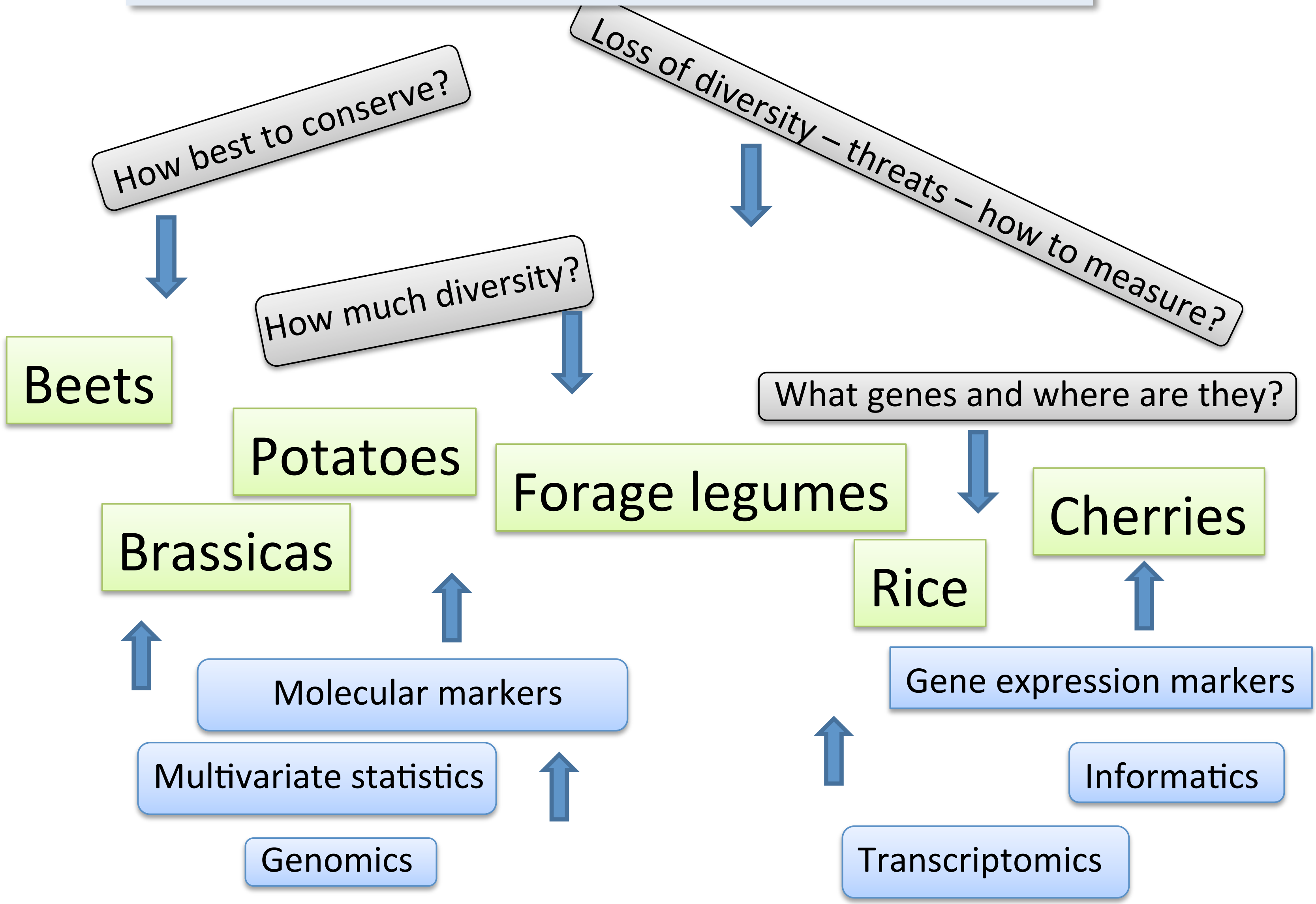
How many to conserve?

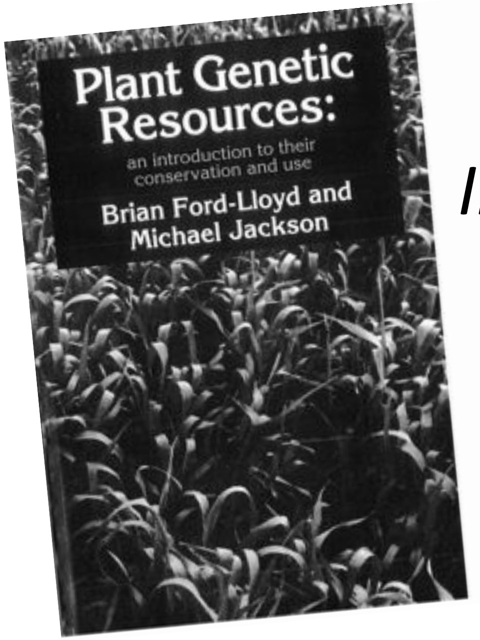
Globally: 91,800 (Maxted and Kell, 2008)

Europe and the Mediterranean: 25,687 (Kell *et al*., 2008)

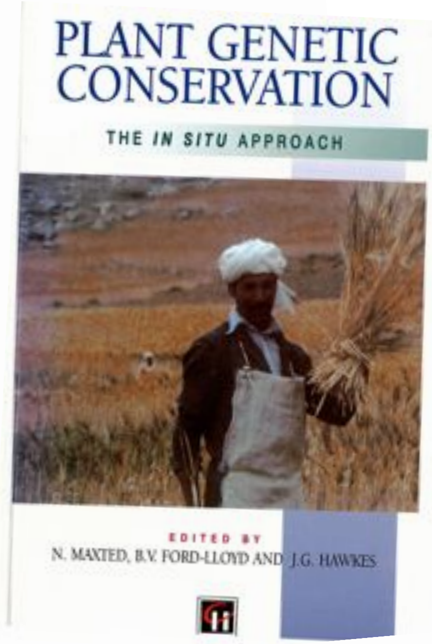
United Kingdom: 1,955 (native) (Scholten *et al*., 2008)

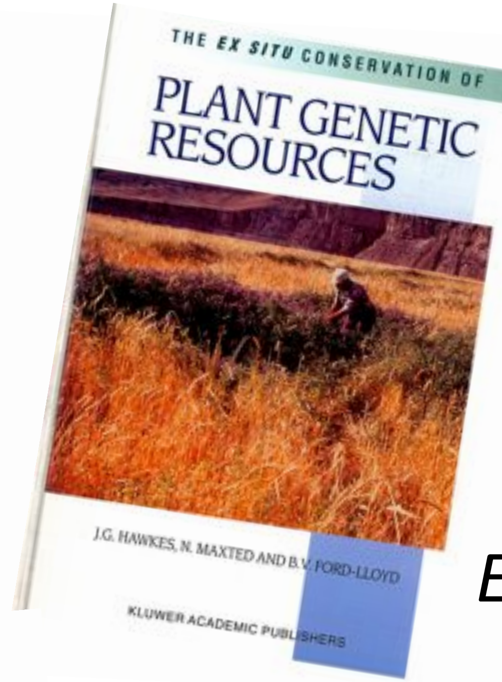
Where to start?





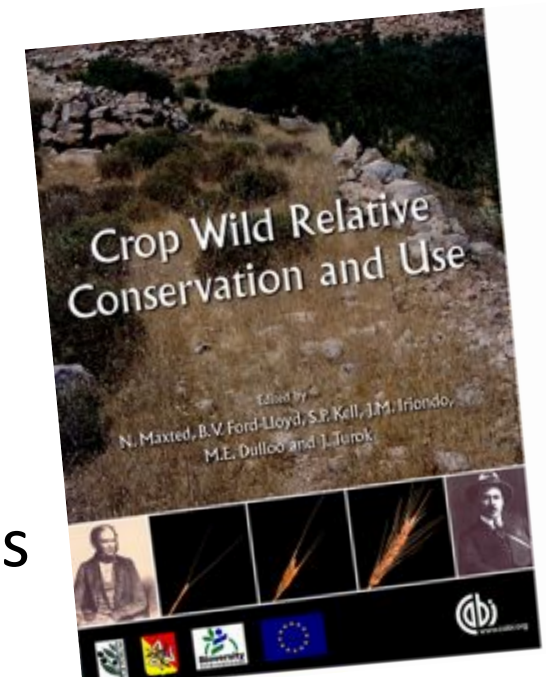
In situ

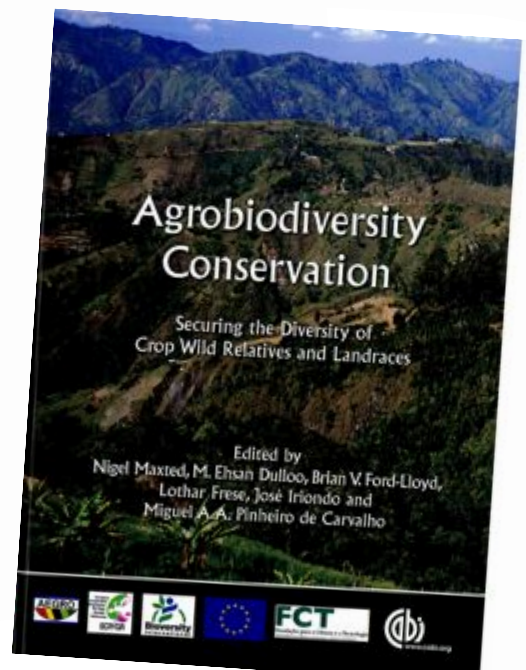




Ex situ

Wild species





Landraces

Firstly – beet (and the REF)

Feddes Repertorium	Band 87	Heft 5	Seite 289–292	Berlin, 5. 7. 1976

Patellaria: a new genus in the Chenopodiaceae

J. T. Williams[1], A. J. Scott[2] & B. V. Ford-Lloyd[3])

With 2 figures

Summary

Comparative taxonomic studies within the genus *Beta* have shown that the section *Patellares* is distinct and should be regarded as a new genus, *Patellaria*, with the type *Patellaria webbiana*. The transference of *Beta patellaris* to this genus requires a new specific name, *P. cordata*.

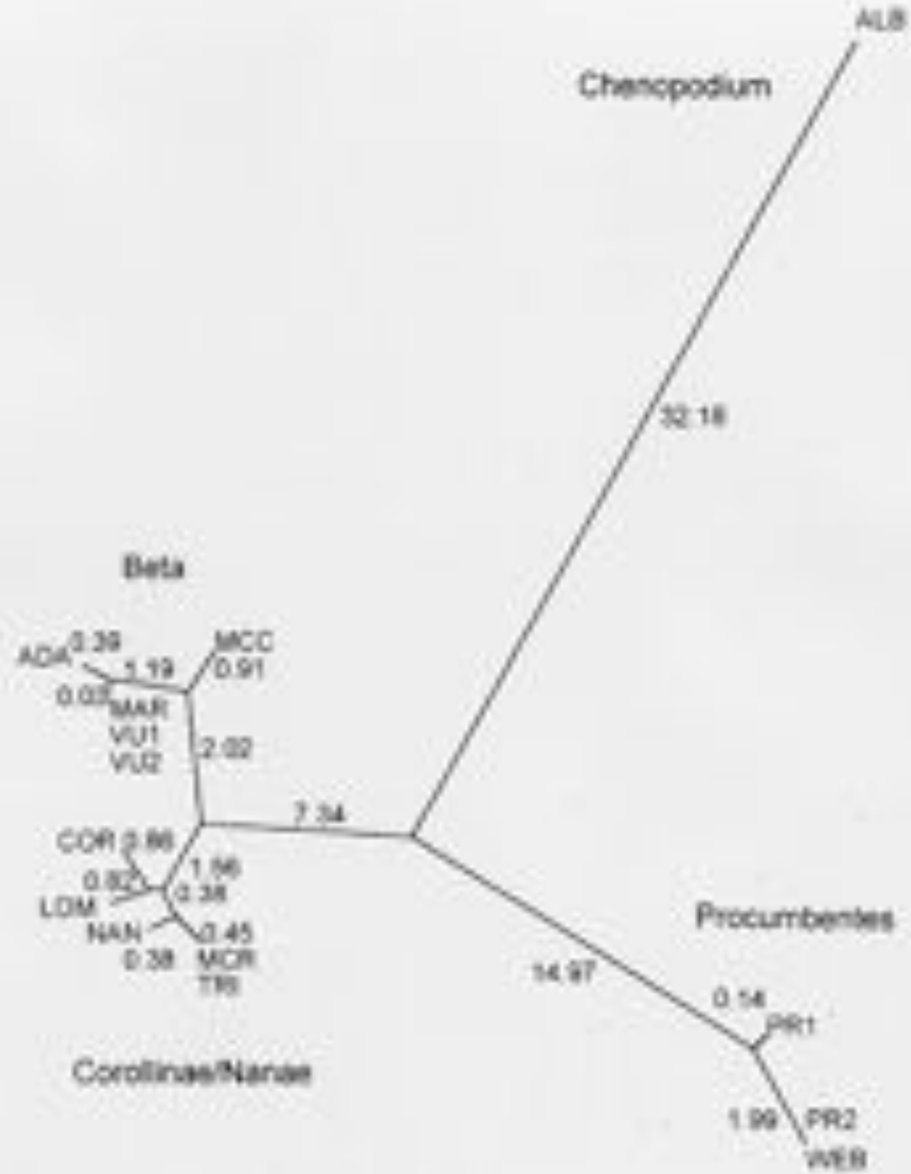


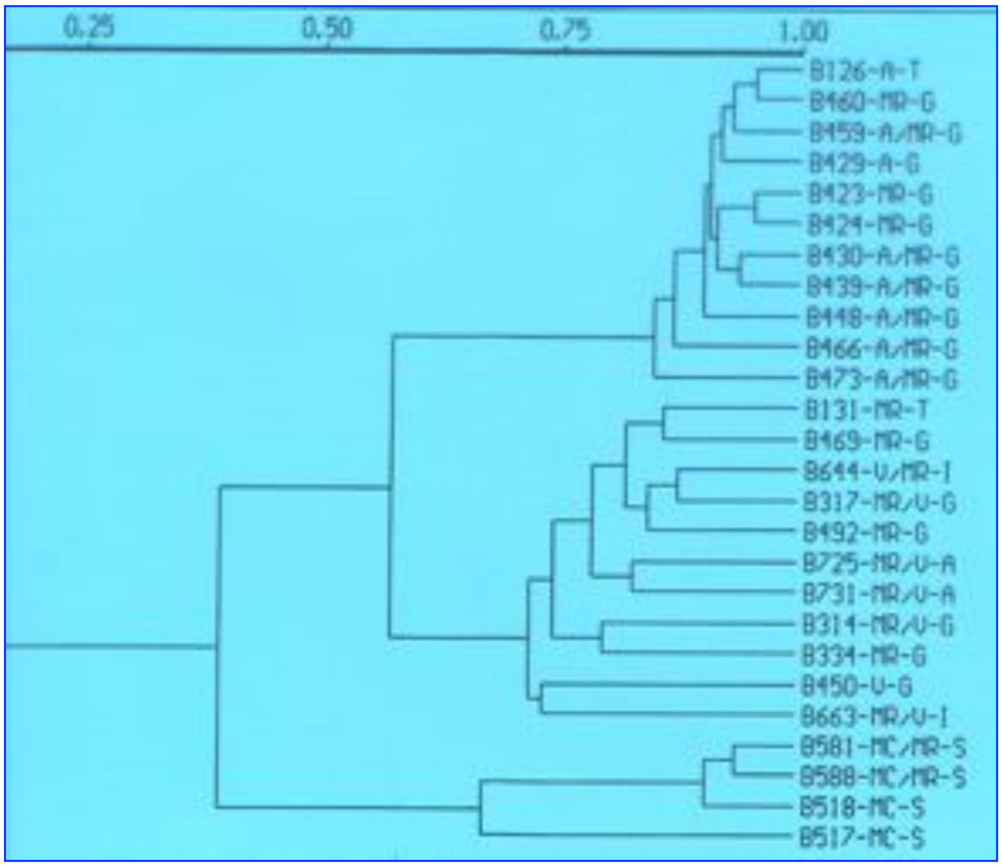
Fig. 3 Phylogenetic tree based upon data using the neighbour-joining method with the Kimura two-parameter distances displayed.

(Nagamine et al., 1989)

SUBSPECIES **Beta vulgaris subsp. adanensis**

UniProtKB (0) | Taxonomy help

Taxon identifier	444111
Scientific name	Beta vulgaris subsp. adanensis
Common name	-
Synonym	-
Other names	› Beta vulgaris subsp. adanensis (Pamukc. ex Aellen) Ford-Lloyd & J.T.Williams
Rank	SUBSPECIES



Wild forms of *Beta* section *Beta*

(Shen, Newbury and Ford-Lloyd, 1996)

Secondly potatoes: and Impact Case Studies

In vitro cultures of potato cv Record – somaclonal variation
(Juned, Jackson and Ford-Lloyd, 1991)

OLD PADDY'S A RIGHT WELLIE

His size nines are both the same foot

The most gorgeous girls are always in your No.1 Sun

Suzanne is a bite of alright

MINK ENDS IN THE DUSTCART

Crunch time for boffins

BOX OF TRICKS

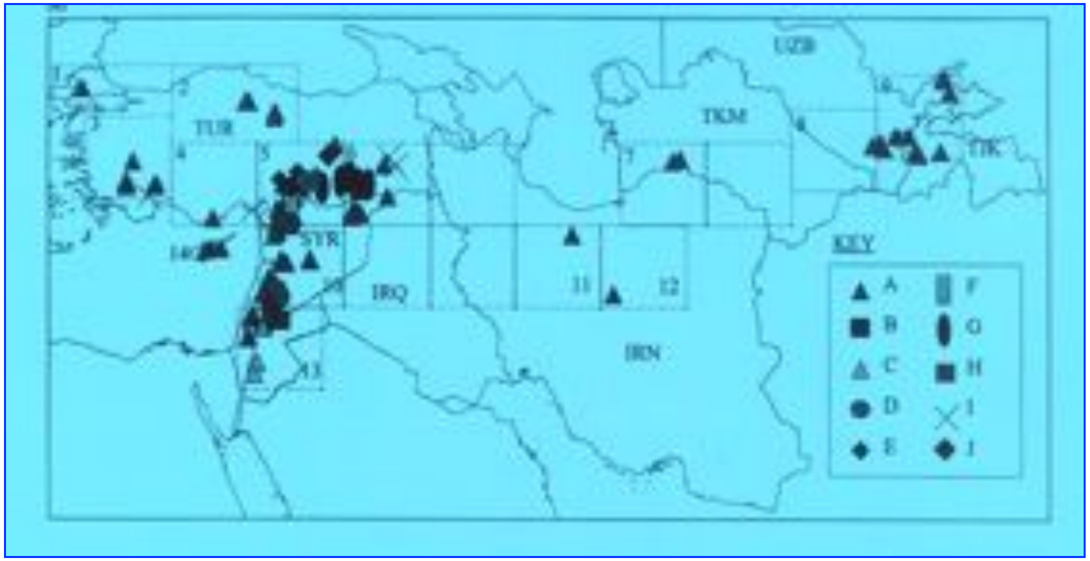
Crunch time for boffins

BOX O

Some examples: Improving the conservation and use of genetic diversity

Where do you find diversity: Mapping geographical variation in lentils to improve conservation (*Lens culinaris*)

(Ferguson et al., 1998)



Mapping members of clusters geographically

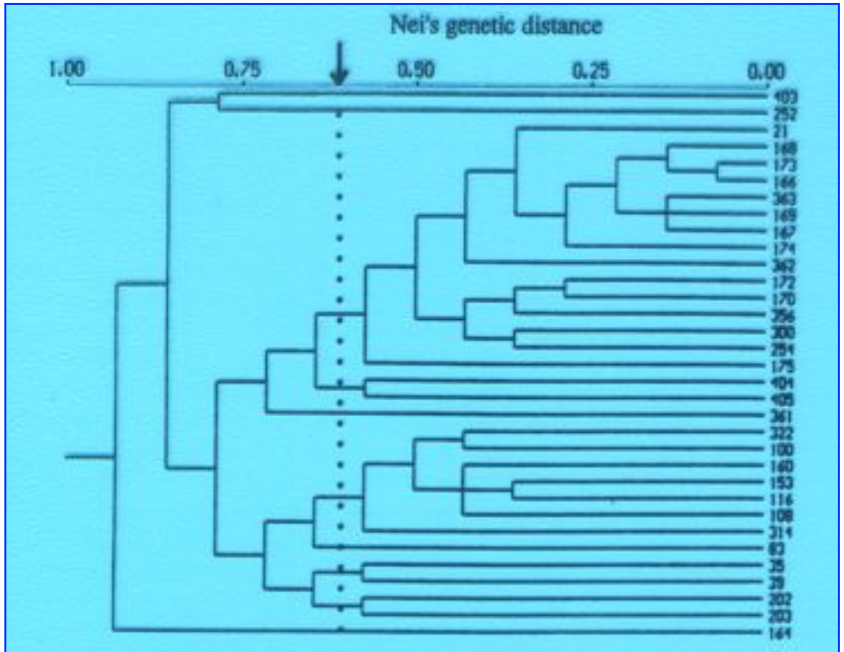
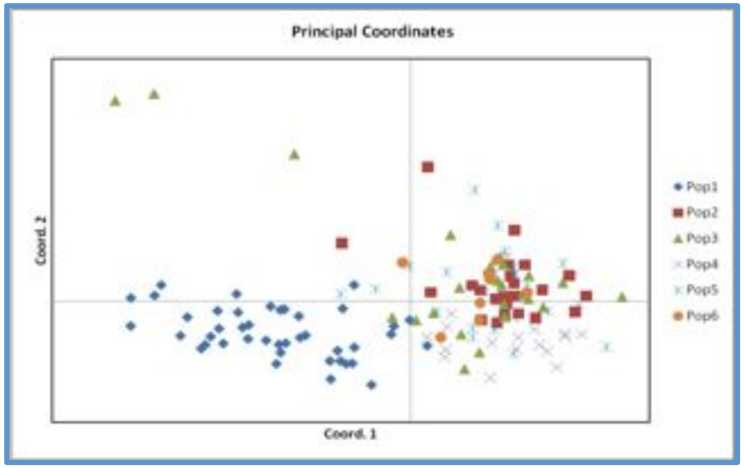


Fig. 1 Dendrogram showing how clusters of similar germplasm were defined in *Lens odemensis*.

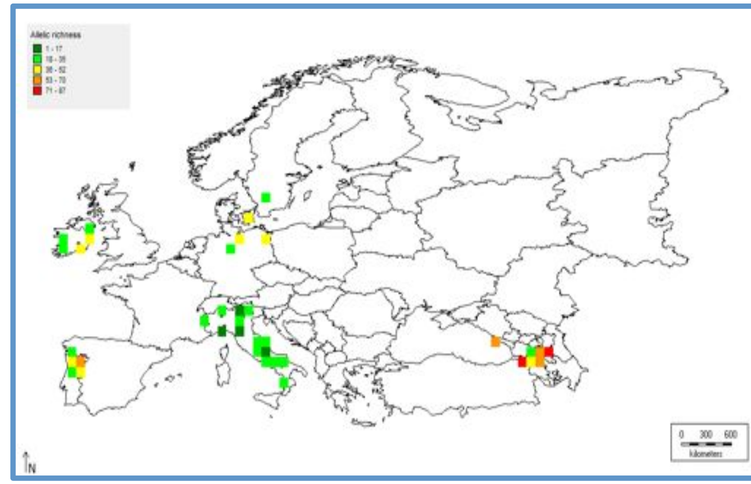
Identification of clusters of germplasm

Selection of *Prunus avium* (wild cherry) for *in situ* conservation in genetic reserves

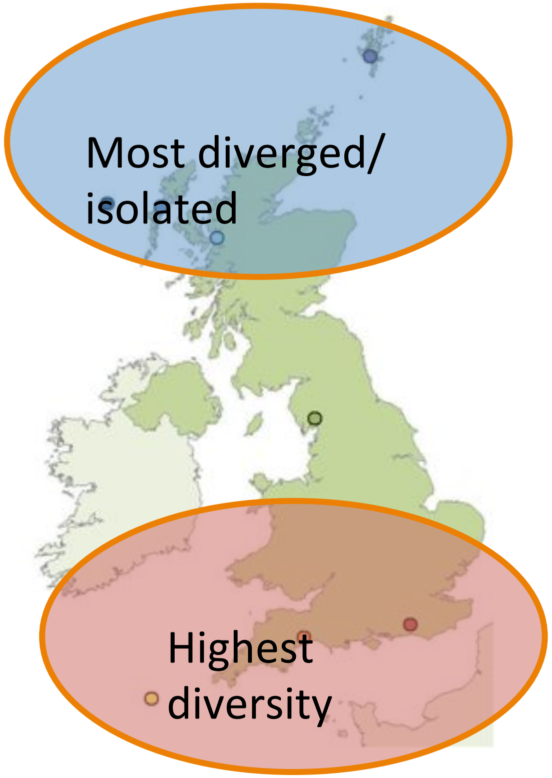
(Teeling et al., 2012)

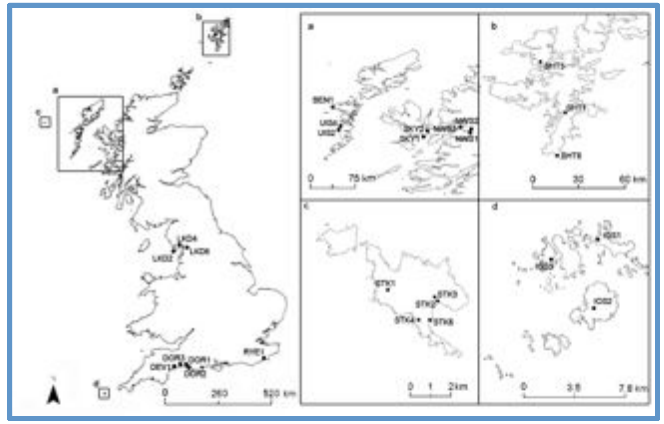


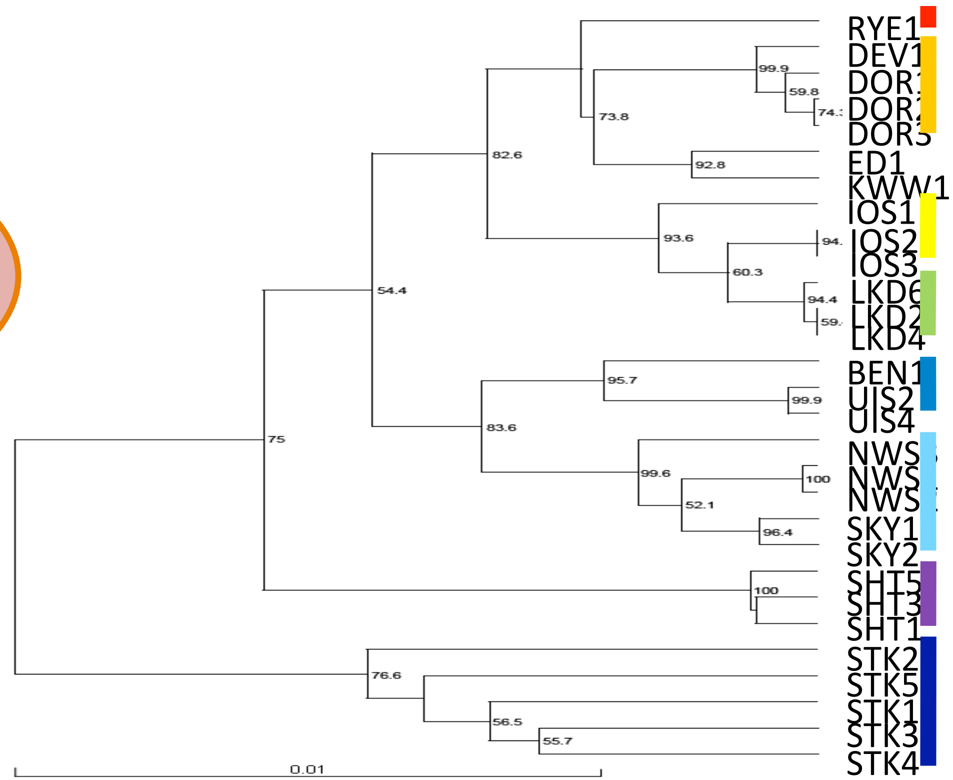
Measuring molecular genetic variation detects populations that overlap in their diversity and those that are distinct



Planning location of reserves based on molecular genetic and ecogeographic information



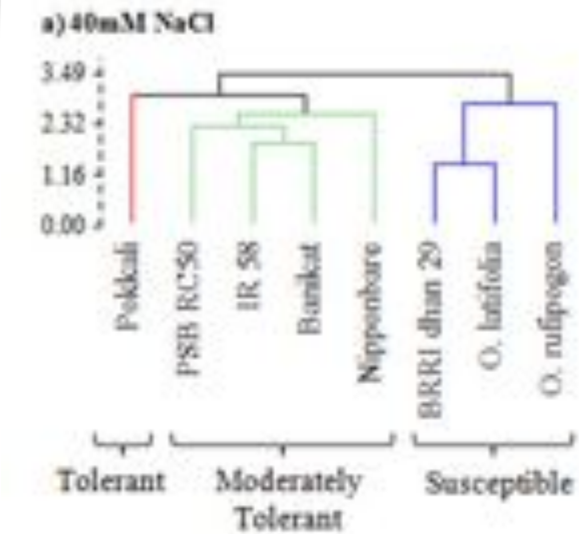




White clover conservation in the UK

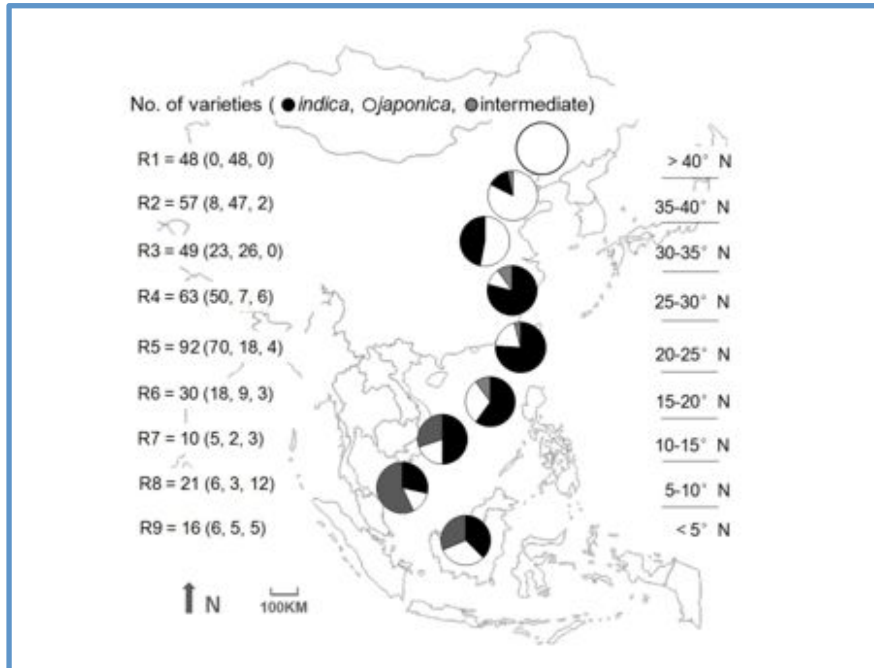
(Hargreaves et al., 2010)

Molecular genetic screening of germplasm: *Indica* and *Japonica* subspecies of rice



Precise phenotyping of germplasm identified that Nipponbare (*japonica*) show some degree of salt tolerance reducing the need to cross with *indica* rice

(Hossein *et al*., 2013)



Indica and *japonica* rice can only be precisely identified using Indel molecular markers and there are intermediate forms which can be more easily used in crosses for gene transfer

(Xiong *et al*., 2011)

Phenomics and transcriptomics (insect pest resistance)

- Choice of genetically diverse resistant and susceptible genetic resources
- Phenotypic screening to assess aphid feeding
- Whole genome gene expression analysis
- Development of a predictive model
- Used to predict whether unknown accessions are resistant or susceptible

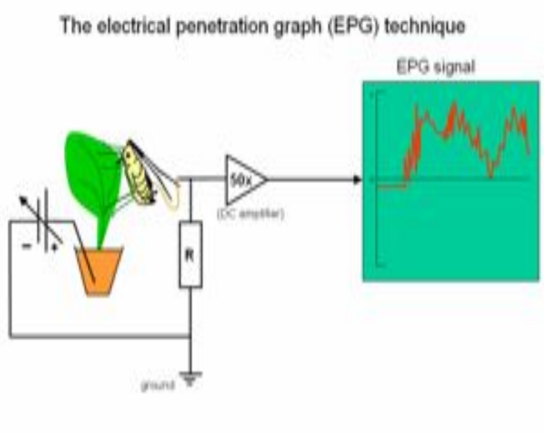
Predicting resistance to brown planthopper in rice using transcriptomics:

(Ghaffar et al., in prep)

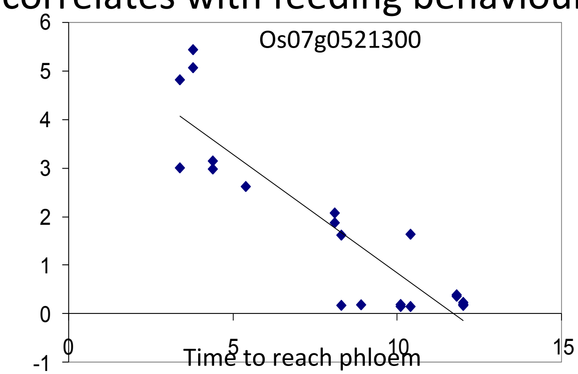
Around 1000 constitutive genes are differentially expressed between resistant and susceptible genotypes

Using around 200 genes: model that will predict whether a genotype is resistant or susceptible with 100% success

EPG/feeding behaviour confirms resistance/susceptibility class

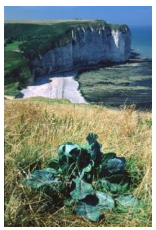


Candidate gene expression correlates with feeding behaviour



Resistance to aphids in brassicas using a similar transcriptomic approach (PGR Secure)

(Sharma et al.)



Wild species and landraces

Field trials ca. 200 accessions

Aphid feeding behaviour and EPG – high throughput phenotyping – 60 genotypes

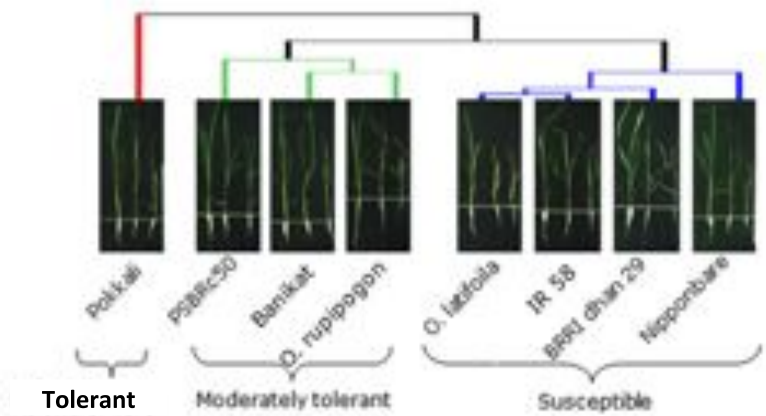
Affymetrix chip for transcriptomics – 60 genotypes

Modelling and prediction of resistance

Meeting the challenge of growing rice in saline areas through physiological & transcriptomic technologies

(Hossein, Ford-Lloyd, Pritchard)

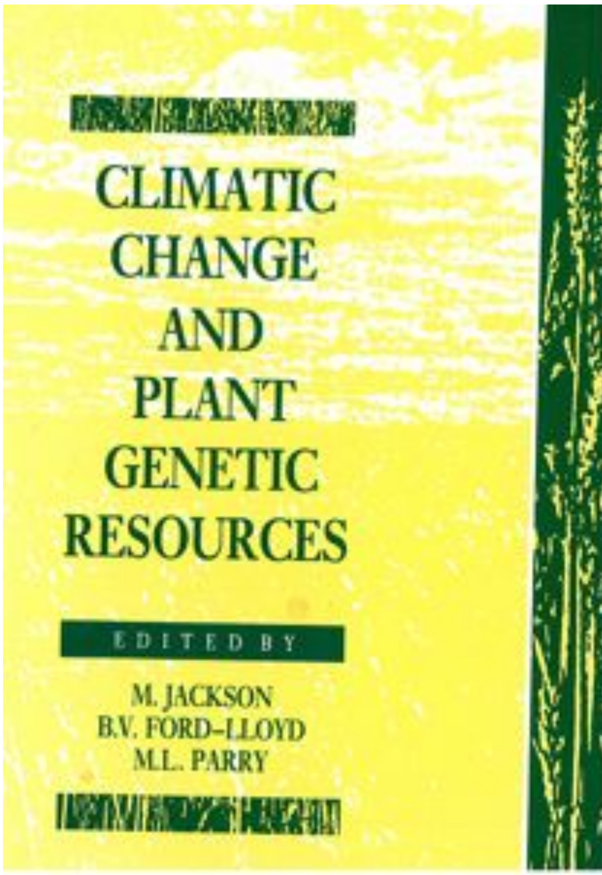
Screening for salt tolerance based on growth & physiological characterization

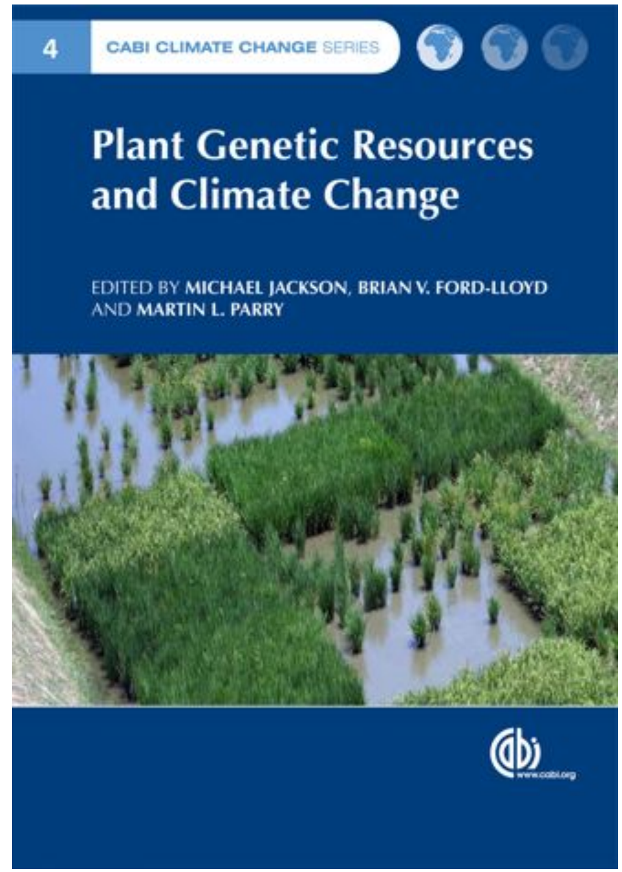


Gene expression profiling **to predict** salt tolerance in landraces and wild species

Probes up-regulated in pooled T but down-regulated in pooled S genotypes = 8	
Os06g0683700	Hypothetical protein.
Os07g0129300	Pathogenesis-related protein 1 precursor.
Os11g0702400	Zn-finger, C2H2 type domain containing protein.
Os01g0693300	Lipid phosphate phosphatase 2 (EC 3.1.3.-) (AtLPP2) (Phosphatidic acid phosphatase 2) (AtPAP2) (Prenyl diphosphate phosphatase).
Os11g0586800	Protein of unknown function DUF231 domain containing protein.
Os10g0450000	Plant protein of unknown function family protein.
Os11g0581900	Protein of unknown function UPF0005 family protein.
Os04g0565400	Cis-zeatin O-glucosyltransferase.

Options for conserving plant genetic resources under a rapidly changing climate





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The genetics of *in situ* versus *ex situ* conservation of landraces and CWR

- Erna Bennett in 1968 '....the difficulty is to find the borderline between adaptive change and genetic erosion'. She saw 'no advantage in the steady state – ....**but [a need]to conserve material so that it will continue to evolve'.**
- The dilemma: how to determine where the line is drawn between adaptive change and genetic erosion/extinction.

The key question: to what extent can genetic evolutionary adaptation occur over the short time scales predicted for climate change?

- There is now increasing evidence that it can and does occur (may be species and life history dependent)
- It also clear that crops can be made to adapt, whether it be to increased drought/salt, submergence or rapidly changing pests
- To see 'how' in more detail.....

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