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Improving Pearl Millet Drought Tolerance

RS Yadav¹*, FR Bidinger², CT Hash², GP Cavan¹, R Serraj² and CJ Howarth¹ (1. IGER, Aberystwyth, SY23 3EB, UK; 2. ICRISAT, Patancheru 502 324, Andhra Pradesh, India)

*Corresponding author: rattan.yadav@bbsrc.ac.uk

Quantitative trait loci (QTL) have been identified for drought tolerance of grain yield in pearl millet (Yadav et al. 1999 and 2002). Marker-assisted selection (MAS) is being used to develop improved parental lines by introgression of QTLs into a homozygous inbred line background for the subsequent production of improved hybrids (marker-assisted back crossing), and by transforming them into topcross pollinator populations that are more heterogeneous than inbred lines. Until - and unless - it is clearly demonstrated that the incorporation of these QTLs into elite breeding lines will significantly enhance the performance of cultivars based on those lines, the benefits of these QTLs are unlikely to ever reach farmers' fields.

Three topcross pollinator populations (TCPs) were developed by selecting and inter-mating individual genotypes from within the F_{2:4} mapping families of a pearl millet population used for mapping QTLs for drought tolerance (Fig. 1). The three TCPs produced were selected according to the following methods and criteria:

- Marker-assisted selection: genetic composition at the drought tolerance QTL (to constitute a MAS-based TCP);
- Phenotypic selection: field performance (best 16) in the drought trials used to identify QTLs (to constitute a phenotype-based TCP); and

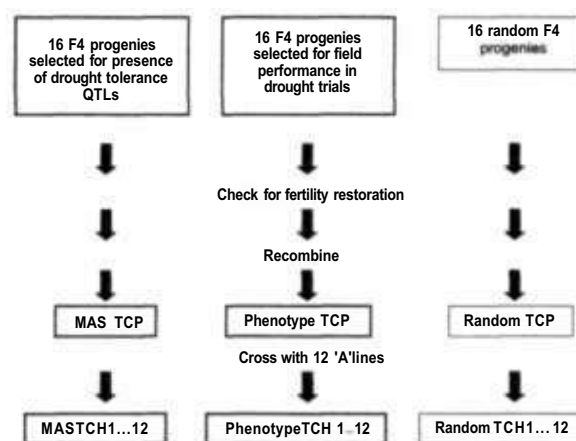


Figure 1. The scheme used to test marker-assisted selection for pearl millet QTLs controlling drought tolerance using topcross pollinators. Topcross pollinators based on phenotypic and random selections are controls for the pollinator based on marker-assisted selection.

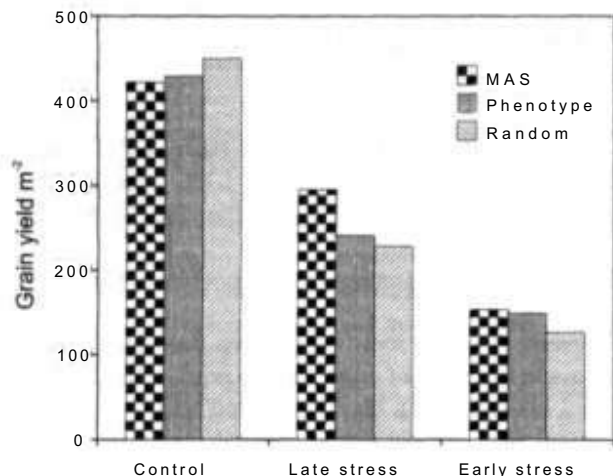


Figure 2. Grain yield performance of pearl millet hybrids made between three topcross pollinators and male-sterile line ICMA 92777 in a range of summer season drought nursery moisture environments, ICRISAT 2001.

- A random control: a random sample from within the mapping population (to constitute a random TCP).

The three TCPs were subsequently used as pollinators on 12 A-lines (male-sterile lines) to produce topcross hybrids, as shown in Figure 1. Compared to hybrids of the phenotype and random TCPs, the MAS TCP hybrids had better drought tolerance indices and grain yields (Fig. 2) in the drought-stress environments, although they had a lower yields in the irrigated control environment. Selecting simply on the basis of field performance under drought was ineffective, but MAS was able to produce improvement in this character, which is notoriously difficult to breed for using conventional methods.

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New Molecular Marker Technologies for Pearl Millet Improvement

MD Gale^{1*}, KM Devos¹, JH Zhu¹, S Allouis¹, MS Couchman¹, H Liu¹, TS Pittaway¹, XQ Qi¹, M Kolesnikova-Allen² and CT Hash² (1. John Innes Centre, Norwich, UK; 2. ICRISAT, Patancheru 502 324, Andhra Pradesh, India)

*Corresponding author: mike.gale@bbsrc.ac.uk

At a time when most of the world still viewed molecular technology as a luxury, for use only with major staple crops, a DFID-JIC-ICRISAT project anticipated as early as 1991 the application of molecular diagnostics in the breeding of orphan crops for developing countries.

The first molecular marker-based genetic linkage map of pearl millet [*Pennisetum glaucum* (L.) R. Br.] was built with restriction fragment-length polymorphisms (RFLPs), the marker system of choice in the early 1990s (Liu et al. 1994). This map has served as the base for subsequent pearl millet marker-based studies at JIC (Busso et al. 1996, 2000; Devos and Gale 2000; Devos et al. 2000; Liu et al. 1996, 1997). The RFLP framework in the consensus map now available (Fig. 1, see pages 18-19 of this issue) is based on 173 (out of 500 available) mapped *Pst*I genomic clones from inbred line Tift 23DB, which has now become the base genotype for pearl millet molecular genetics. The clones are available as DNA or, in some cases, as DNA sequences, and have been distributed freely worldwide.

ICRISAT was able to build one of the very early molecular marker facilities in the CGIAR system in the early 1990s, and has used this facility for pearl millet diversity assessment (Bhattacharjee et al. 2002), mapping population skeleton map construction (Azhaguvel 2001; Kolesnikova-Allen 2001), and marker-assisted backcrossing (Sharma 2001). The markers and maps have also been used at CAZS and IGER in the UK, Université d'Orsay in Paris, and Tifton in the USA, to map and tag genes controlling important traits in the pearl millet crop. These include downy mildew resistance (Jones et al. 1995 and 2002; Azhaguvel 2001; Kolesnikova-Allen 2001), foliar disease resistance (Morgan et al. 1998), drought tolerance (Yadav et al. 2002), plant height (Azhaguvel 2001), flowering time, and the multiple phenotypic changes that occurred when pearl millet was domesticated - the so-called 'domestication syndrome' (Poncet et al. 2000, 2002).

Molecular marker technologies have moved on, particularly with the development of the polymerase chain reaction (PCR) that allows the rapid and inexpensive amplification of small quantities of DNA precisely targeted to known regions. The amplification commences from small lengths of DNA of known sequence known as primers.