



Whole-Genome Profiling Service for Wheat and Barley

- ✿ High throughput
- ✿ Less than 1 / 10 the cost of other genotyping services
- ✿ Medium to high-density profiles
- ✿ Up to many thousand samples

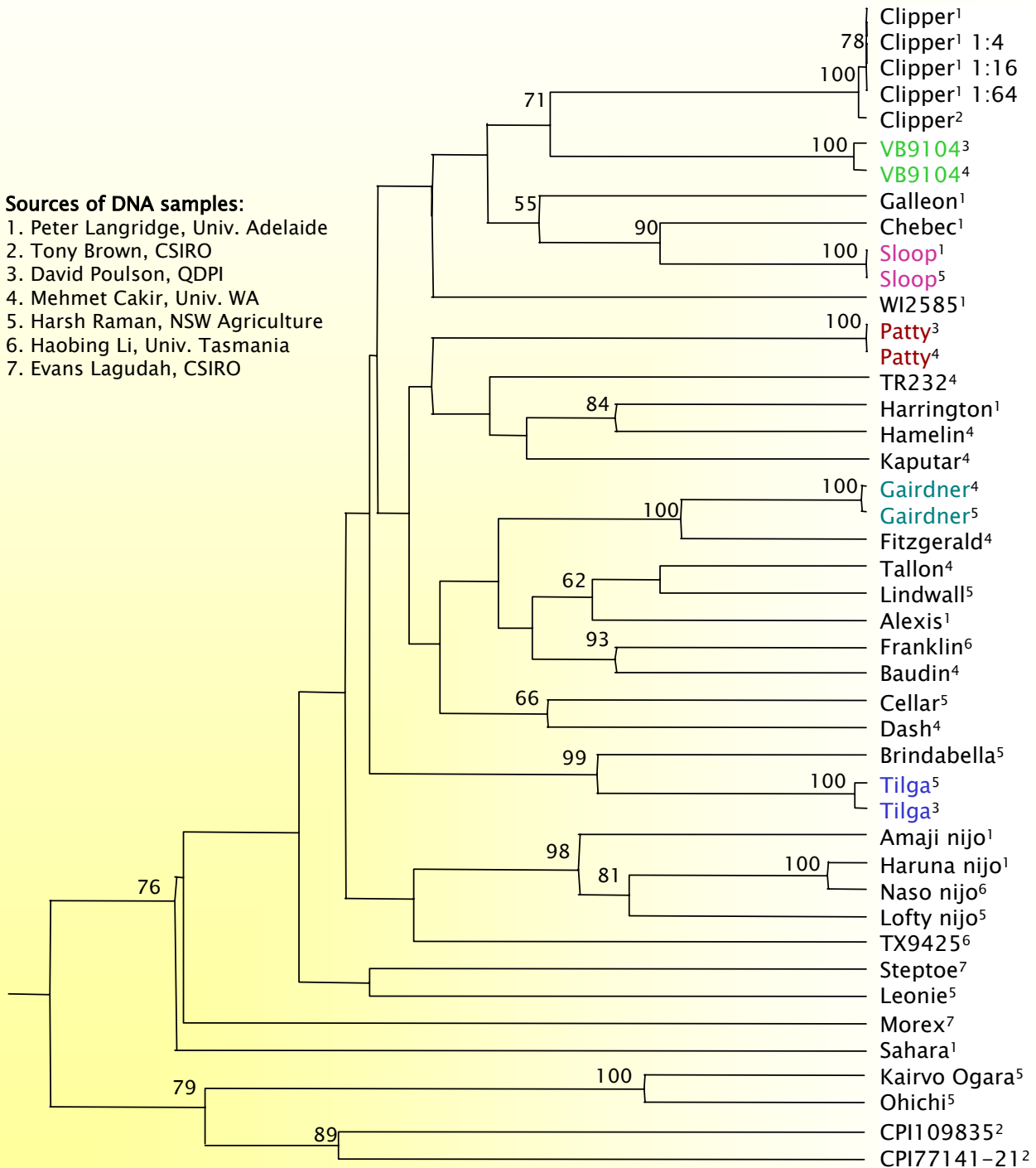
Barley Diversity Analysis



- Approximately 1,000 DArT™ markers in cultivated germplasm
- Average call rate: 98.0 %
- Scoring reproducibility: 99.8 %
- Identical results with 1.5–100 ng DNA

Sources of DNA samples:

1. Peter Langridge, Univ. Adelaide
2. Tony Brown, CSIRO
3. David Poulson, QDPI
4. Mehmet Cakir, Univ. WA
5. Harsh Raman, NSW Agriculture
6. Haobing Li, Univ. Tasmania
7. Evans Lagudah, CSIRO



UPGMA dendrogram displaying genetic relationships among barley cultivars. The dendrogram is based on 383 DArT™ markers. It groups related cultivars according to known genetic relationships. It also reveals genetic heterogeneity within certain cultivars. Several dilutions (up to 64-fold) of a single DNA sample of cv. Clipper were typed independently to demonstrate the reproducibility of the DArT™ assay.

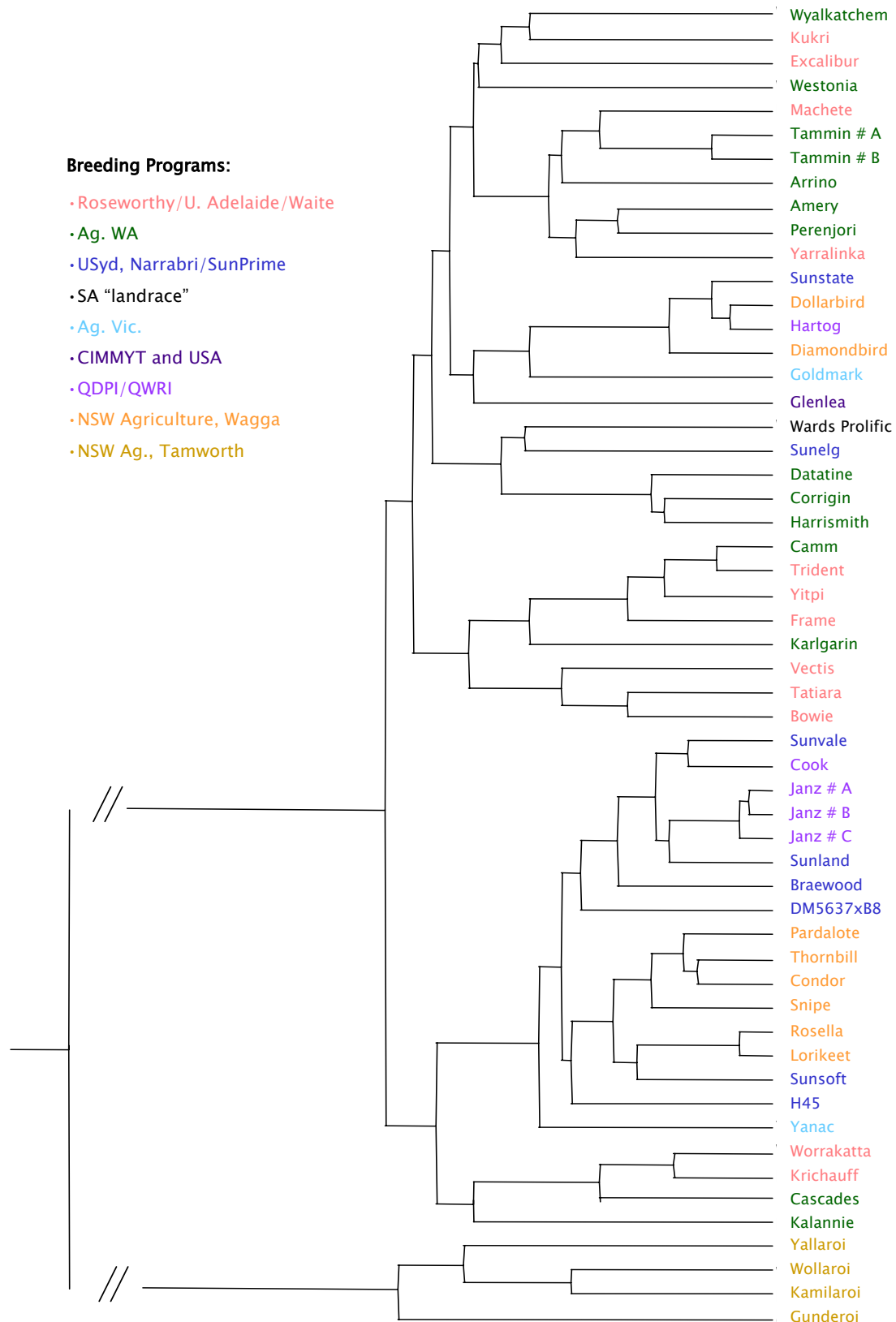
Wheat Diversity Analysis



- Approximately 1,000 DArT™ markers in cultivated germplasm
- High method quality, similar to barley

Breeding Programs:

- Roseworthy/U. Adelaide/Waite
- Ag. WA
- USyd, Narrabri/SunPrime
- SA "landrace"
- Ag. Vic.
- CIMMYT and USA
- QDPI/QWRI
- NSW Agriculture, Wagga
- NSW Ag., Tamworth



UPGMA dendrogram displaying genetic relationships among 48 Australian hexaploid and 4 durum wheat cultivars.

The dendrogram is based on 508 DArT™ markers. It groups related cultivars according to known pedigree information and clearly separates the durum group. The average number of polymorphisms between two wheat cultivars is close to 100, e.g., 150 polymorphisms were found between Kukri and Janz. For display purposes, the distance between the durum and the hexaploid groups has not been drawn to scale.

Triticarte™

Wheat and Barley

Whole-Genome Profiling

- ✿ Detects genetic relationships among cultivars and level of heterogeneity within cultivars
- ✿ Improved selection for traits with complex inheritance
- ✿ Accelerated backcrossing to maximise recovery of BC parental genome
- ✿ Aids introgression of wild relatives into adapted backgrounds and breaking of linkage blocks
- ✿ Low-cost, rapidly constructed genetic maps relevant to specific germplasm
- ✿ Improved and lower-cost gene discovery using bulked segregant analysis and association mapping
- ✿ Germplasm fingerprinting

Contact:

Dr Eric Huttner, Manager
Triticarte Pty Ltd,
GPO Box 3200, Canberra ACT 2601, Australia
Phone: +61 2 6246 4514 Fax +61 2 6246 4501
Email: ehuttner@triticarte.com.au

