## Symposium Program

### Day 1: August 15

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>9:00-22:00</td>
<td>Registration</td>
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### Day 2: August 16

<table>
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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8:30-9:10</td>
<td>Opening Ceremony</td>
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<tr>
<td>9:10-9:50</td>
<td>Symposium Photo and Coffee Break</td>
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| 9:50-10:50 | Opening keynote lecture: **Prof. German Spangenberg**, Agriculture Victoria, Australia
                      | Advances in systems biology and molecular breeding of forages |
| 10:50-11:20| Keynote speech: **Hitoshi Nakagawa**, National Institute of Agrobiological Sciences, Japan |
                      | Gamma-ray induced bloomless (bm) mutants and identification of the gene in sweet sorghum |
| 11:20-11:50| Keynote speech: **Gongshe Liu**, Chinese Academy of Sciences, China |
                      | Mechanism of gene alternative splicing and its impact on plant breeding |
| 11:50-12:20| Keynote speech: **Maofeng Chai**, The Samuel Roberts Noble Foundation, USA |
                      | Molecular mechanism of seed physical dormancy in *Medicago truncatula* |
| 12:20-14:30| **Lunch Break and Session I / II Posters Presentation** |
| 14:30-15:00| Keynote speech: **Luke Pembleton**, Agriculture Victoria, Australia |
                      | Enabling F1 hybrid breeding and rapid implementation of genomic selection in perennial ryegrass breeding |
| 15:00-15:15| **Jiangqi Wen**, The Samuel Roberts Noble Foundation, USA |
                      | Application of *Medicago* mutant resources in alfalfa breeding |
15:15-15:30  **Wengang Xie**, Lanzhou University, China
Transcriptomic analysis of Siberian wild rye (*Elymus sibiricus* L.) and identification of candidate genes essential for seed shattering

15:30-15:45  **Baldomero Alarcon-Zuniga**, Universidad Autonoma Chapingo, Mexico
Native tropical legumes as novel genetic resources to increase protein content in American tropical grassland

15:45-16:00  **Yanqi Wu**, Oklahoma State University, USA
Breeding hybrid cultivars assisted with molecular markers in switchgrass

16:00-16:20  **Coffee Break**

**Session II: Bioenergy and Biorenewables**

16:20-16:50  Keynote speech: **Toshihiko Yamada**, Hokkaido University, Japan
Molecular breeding of perennial biomass crops

16:50-17:20  Keynote speech: **Yiwei Jiang**, Purdue University, USA
Genetic control of flowering and biomass in switchgrass

17:20-17:50  Keynote speech: **Malay Saha**, The Samuel Roberts Noble Foundation, USA
Molecular breeding for sustainable switchgrass improvement

17:50-18:05  **Chunxiang Fu**, Chinese Academy of Science, China
A high throughput switchgrass genetic transformation system for gene function discovery and genetic improvement

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**Day 3: August 17**

**Session III: Abiotic and Biotic Stresses**

8:30-9:00  Keynote speech: **Suo-Min Wang**, Lanzhou University, China
The physiological adaptation and forage quality of T1 transgenic alfalfa co-expressing *ZxNHX* and *ZxVP1-1* from *Zygophyllum xanthoxylum* in response to stress conditions

9:00-9:30  Keynote speech: **Bingru Huang**, Rutgers University, USA
Molecular and metabolic regulatory mechanisms of stress-induced leaf senescence in grass species
9:30-10:00 Keynote speech: **Zhenfei Guo**, South China Agricultural University, China
Exploring cold tolerance in *Medicago sativa* spp. *falcata*

10:00-10:20 Coffee Break

10:20-10:35 **Zhulong Chan**, Chinese Academy of Sciences, China
Improved abiotic stress tolerance of bermudagrass by exogenous small molecules

10:35-10:50 **Aike Bao**, Lanzhou University, China
The mechanism and molecular basis underlying salt secretion in *Reaumuria soongorica*

10:50-11:05 **Longxi Yu**, Washington State University, USA
Genome-wide association studies on resistance to biotic and abiotic stresses in autotetraploid alfalfa (*Medicago sativa* L.) using genotyping by sequencing

11:05-11:20 **Hong Luo**, Clemson University, USA
MicroRNAs in plant development and stress response of perennial grasses

11:20-11:35 **Shyamal Talukder**, The Samuel Roberts Noble Foundation, USA
Deciphering summer dormancy for persistence of tall fescue in hot and dry conditions

**Session IV: Emerging Tools for Forage and Turf Research**

11:35-12:05 Keynote speech: **Paul Hooykaas**, Leiden University, The Netherlands
Agrobacterium mediated protein and T-DNA delivery: a toolbox for plants and fungi

12:05-12:20 **Shuizhang Fei**, Iowa State University, USA
High throughput RNAi for rapid gene discovery in brachypodium and creeping bentgrass

12:20-14:30 Lunch Break and Session III/IV/V Posters Presentation

14:30-15:00 Keynote speech: **Pieter Badenhorst**, Agriculture Victoria, Australia
The development of a field-based forage phenomics platform
Keynote speech: **Maria Monteros**, The Samuel Roberts Noble Foundation, USA
Alfalfa breeder’s toolbox and alfalfa genome sequencing

**Jianxiu Liu**, Chinese Academy of Sciences, China
The assessment, innovation and breeding of main warm season turfgrass conducted in NBG-CAS

**De Pater Sylvia**, Leiden University, The Netherlands
Nuclease-induced targeted mutagenesis and gene-targeting

Coffee Break

**Session V: Plant-Microbe Interactions**

Keynote speech: **Carolyn Young**, The Samuel Roberts Noble Foundation, USA
It's the little things that matter: microbes that impact forage production

Keynote speech: **Kevin Smith**, The University of Melbourne, Australia
Developing a co-existence framework for GM forages in grazing systems

**Jinlin Zhang**, Lanzhou University, China
Induced growth promotion and stress tolerance in ryegrass by *Haloxylon ammodendron* rhizobacteria

**Deborah Samac**, US Department of Agriculture-Agricultural Research Service, USA
Strategies for developing resistance to root rot diseases of alfalfa

**Muhammad Ibrahim**, COMSATS Institute of Information Technology, Pakistan
Computational analysis of NIMIN proteins interaction network during SA induced response in *Arabidopsis thaliana*

**Wei He**, Northwestern University, China
Characterization and comparison of fungal communities in rhizospheric and bulk soil of *Stellera chamaejasme* by amplicon sequencing
### Day 4: August 18

Interval conference trip to **Yuzhong Experimental Station for Grass and Forage Breeding of Lanzhou University** and **Tourism** in Lanzhou

### Day 5: August 19

**Session VI: Functional Genetics and Genomics and Genetic Mapping**

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<tr>
<th>Time</th>
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| 8:30-9:00     | Keynote speech: **Xinquan Zhang**, Sichuan Agricultural University, China  
Genomic selection in forage grasses |
| 9:00-9:30     | Keynote speech: **John Forster**, Agriculture Victoria, Australia  
Genetics and genomics of self-incompatibility in forage grasses |
| 9:30-10:00    | Keynote speech: **Zhuo Yu**, Inner Mongolia Agricultural University, China  
Construction of high-density molecular genetic maps and QTLs  
for main agronomic traits of tetraploid hybrid wheatgrass |
| 10:00-10:20   | **Coffee Break**                                                      |
| 10:20-10:50   | Keynote speech: **Noel Cogan**, Agriculture Victoria, Australia  
The structure of the perennial ryegrass genome |
| 10:50-11:05   | **Bushman Shaun**, US Department of Agriculture-Agricultural  
Research Service, USA  
Alleles of genes affecting flowering time in cocksfoot (*Dactylis glomerata*) |
| 11:05-11:20   | **Chuanen Zhou**, Shandong University, China  
Regulation of leaf development in *Medicago truncatula* and the forage quality improvement of Alfalfa |
| 11:20-11:35   | **Meiliang Zhou**, Chinese Academy of Sciences, China  
Functional analysis of phenylalanine metabolism related MYB factors in buckwheat |
| 11:35-11:50   | **Zhanmin Sun**, Chinese Academy of Science, China  
Function analysis of salt stress responsive AP2/ERF  
transcription factor *LeSRA1* from *Lotus corniculatus* L. |
11:50-12:05  **Zhipeng Liu**, Lanzhou University, China  
Development and cross-species transferability of EST-SSR markers in *Elymus sibiricus*

12:05-12:20  **Yongzhen Pang**, Chinese Academy of Science, China  
Genome-wide identification of UDP-glycosyltransferases involved in flavonol glycoside biosynthesis in *Lotus japonicus*

12:20-14:30 **Lunch Break and Session VI  Posters Presentation**

14:30-14:45  **Jiyu Zhang**, Lanzhou University, China  
Analysis of phylogenetic relationships and genetic diversity in the genus *Melilotus*

14:45-15:00  **Quanwen Dou**, Chinese Academy of Science, China  
Comparative cytogenetic analysis in *Medicago sativa* complex: sativa-coerulea-falcata

15:00-15:15  **Zhaoqing Chu**, Chinese Academy of Sciences, China  
Cool season turf molecular breeding benefits from genomic and genetic analyses on *Brachypodium distachyon*

15:15-15:30  **Hans Daetwyler**, Agriculture Victoria, Australia  
Genomic selection in forage grasses

15:30-15:45  **Mingxiang Liang**, Nanjing Agricultural University, China  
Cloning and functional characterization of *Helianthus tuberosus* fructan 1-exohydrolases (1-FEHs)

15:45-16:00  **Wanjun Zhang**, China Agriculture University, China  
Using an Arabidopsis orphan gene, *QQS*, improved forage quality of perennial ryegrass and alfalfa

16:00-16:20  **Coffee Break**

16:20-16:35  **Bin Xu**, Nanjing Agricultural University, China  
Improving forage quality by controlled regulation of senescence-associated genes in perennial ryegrass

16:35-17:35  Closing keynote lecture: **Prof. Zeng-Yu Wang**, The Samuel Roberts Noble Foundation, USA  
Future perspectives of forage improvement