INTERNATIONAL COTTON
ADVISORY COMMITTEE

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Dr John Zhihong Yu

Dr John Yu has been working with the USDA-ARS since 1995. He earned his PhD in plant genomics and molecular genetics at Cornell University. He demonstrated outstanding dedication, with 36 years of professional experience, and received significant recognition as an international authority in cotton genomics for developing genetic resources that are currently being used by scientists worldwide. He made major contributions on cotton genomics and germplasm, including:

- Genome mapping and sequencing,
- Characterisation of gene pools, and
- Identification of QTLs for molecular breeding.

Dr Yu developed the world's first integrated genetic, physical and transcript maps of cultivated tetraploid cotton chromosomes with large insert DNA clones, molecular markers, and EST genes; and high-density cotton genetic maps of portable SSR and SNP markers. He has freely filled numerous requests from the global cotton research community for genomic resources and information. Dr Yu has received several national and international awards and published more than 100 peer-reviewed papers, which have 8,945 citations. Dr Yu has also delivered more than 60 talks/seminars to the global scientific community.

Dr Yu demonstrated dynamic, outstanding organisational capacity in a leadership role to benefit the global cotton community. This includes his election in 2005 — and re-election in 2015 — by the global cotton community as Chairman of the International Cotton Genome Initiative (ICGI), the first international organisation to facilitate global collaborative research work on cotton genomics and genetics.

Dr Yu led international efforts to develop and release genome sequences for *G. arboreum*, *G. raimondii*, and *G. hirsutum,* among other cotton species. The research opens a new paradigm in cotton genomics that revolutionises genetic improvement of cotton plants through better exploitation of genetic variation otherwise buried in *Gossypium* germplasm. His discovery of gene-rich islands and sub-genomic roles in upland cotton provides critical information for genetic applications. His development of new concepts and methodologies for standardising characterisation of *Gossypium* germplasm makes it possible for cotton researchers worldwide to collaborate, relate and utilise genetic diversity data among cotton germplasm collections.