Plant and Agricultural Research Panels

DAICEL arbor biosciences by 2BScientific

Plant and Agricultural related	**Types of Panels**	**Panel description**	**What it works for?**	**What challenges the panels helps with?**	**How Daicel Arbor helps?**	**Research Application purpose**
myBaits Kit – Angiosperms-353	myBaits Expert Angiosperms 353 v1	Captures panel targeting **353 single-copy loci** conserved across highly **diverse flowering plants.** **Compatible with fresh, herbarium, and museum samples and non-model plants** Works with degraded DNA Standardised analysis via HybPiper Data available at Kew Tree of Life Explorer	**Reconstructing phylogenetic trees across angiosperm lineages** mainly • **Studying plant diversification, speciation, and biogeography** Resolving taxonomic relationships in complex or poorly understood groups Generating reference datasets for comparative genomics Plant "Tree of Life" research	Degraded DNA from herbarium or field-collected samples. Limited starting materials Need for universal markers across diverse plant taxa Working with non-model species lacking genomic resources Desire for cost-effective, scalable solutions for large sample sets	Proven performance with low-quality and degraded DNA. Universal probe set applicable across angiosperms or other broad plant taxonomic groups. Validated protocols and available bioinformatics support services. Scalable workflows for large phylogenomic projects.	Phylogenetic research; Ecology and Evolutionary research for plant species

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myBaits Kit – Compositae-1061 (formerly CompCOS)	Compositae-1061 Catalog Kit	Capture panel for phylogenetic research across **Compositae (Asteraceae)** and **Calyceraceae**. Probes designed from **1061 loci**, each with 2–3 representative sequences to maximize taxonomic breadth **Targets >1000 nuclear genes** Works with degraded DNA (including herbarium specimens) Universal probe set for daisy family and relatives	Reconstructing phylogenetic trees across angiosperm lineages Studying plant diversification, speciation, and biogeography Resolving taxonomic relationships in complex or poorly understood groups Working with museum/herbarium specimens and non-model plants Generating reference datasets for comparative genomics	Poor-quality DNA from old samples Need for broader phylogenetic markers; high-throughput sequencing for large database (MORE GENE SEQUENCED IN ONE GO) Clarifying evolutionary relationships in a diverse group	Enables high-throughput target capture (Hyb-Seq) Improves resolution of evolutionary relationships Works across diverse samples ancient, degraded and complex Supports insight on genetic diversity and evolutionary history Validated and scalable protocols and bioinformatics	Phylogenetic research population genetics systematic studies climate change impact studies

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Wheat Exosome Panels	myBaits Expert Wheat Exome v1 Kit	Developed with IWGSC using Chinese Spring RefSeq v1.0 assembly and v1.1 annotation Tiles **2 million baits** across >200 Mbp of target space in hexaploid wheat. Optimised for specificity and sensitivity through trials on multiple wheat varieties.	Identifying genetic variants linked to important agronomic traits (e.g., yield, disease resistance, drought tolerance), to better understand the complex wheat species Conducting genome-wide association studies (GWAS) Performing marker-assisted selection and genomic selection Studying genetic diversity and evolutionary history of wheat Working with wild relatives and landraces to introduce novel traits	Large, complex polyploid wheat genome High-resolution genotyping & variant discovery Resolving QTLs for trait mapping Cost-effective for large breeding populations Working with low-quality DNA	Targeted capture of exonic regions Optimised for hexaploid and other ploid wheat High coverage of coding regions Compatible with wild relatives Validated protocols & bioinformatics support and full NGS service available from QC, Library prep to data analysis using myReads services	Cost-effective for wheat's very large and complex genome, discover variants and traits Breeding information, functional genomic and mutation analysis Insight on wheats adaptive landscape, crop improvement research

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Wheat Regulome / "promoters" community panel	**"Wheat Promoters" Community Pane**	Community-designed panel targeting ~168 Mb of **promoter and regulatory regions** in wheat, based on IWGSC RefSeq v1.0. Focuses on non-coding regions controlling gene expression for trait studies like flowering time or grain yield	Detecting regulatory variants (SNPs/indels/structural changes) within promoters and other control elements that influence traits Linking promoter haplotypes to gene expression differences and phenotypes Integrating capture data with eQTL, ATAC-seq/DNase-seq, and GWAS to pinpoint causal non-coding variants Characterising wild relatives and landraces	Large polyploid genome Variants in non-coding regions missed by exome panels Need scalable assays for breeding population Work with low quality DNA Reduce data volume while enriching regulatory signals	Targeted capture of promoter/regulatory regions across the wheat genome Optimised for hexaploid and other ploid wheat and compatible with wild relatives High coverage of regulatory regions for functional genomics and variant discovery Validated protocols and bioinformatics support Cost-effective solution for large-scale breeding and diversity studies, versus WGS or other methods Offers Full NGS service options with myReads	Functional regulomics Discovery of regulatory variants, Trait studies, Breeding programs Wheats adaptive landscape