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## REFERENCES

- [1] X. Zhang *et al.*, "Combining QTL-seq and linkage mapping to fine map a wild soybean allele characteristic of greater plant height," *BMC Genomics*, vol. 19, no. 1, p. 226, Mar. 2018.
- [2] M. P. M. Thoen *et al.*, "Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping," *New Phytol.*, vol. 213, no. 3, pp. 1346–1362, Feb. 2017.
- [3] M. Schreiber, N. Stein, and M. Mascher, "Genomic approaches for studying crop evolution," *Genome Biology*, vol. 19, no. 1. BioMed Central Ltd., pp. 1–15, 21-Sep-2018.
- [4] B. M. Sharif *et al.*, "Genome-wide genotyping elucidates the geographical diversification and dispersal of the polyploid and clonally propagated yam (*Dioscorea alata*)," *Ann. Bot.*, vol. 126, no. 6, pp. 1029–1038, Nov. 2020.
- [5] S. Dreisigacker *et al.*, "Tracking the adoption of bread wheat varieties in Afghanistan using DNA fingerprinting," *BMC Genomics*, vol. 20, no. 1, pp. 1–13, Aug. 2019.
- [6] M. A. Nadeem *et al.*, "DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing," *Biotechnol. Biotechnol. Equip.*, vol. 32, no. 2, pp. 261–285, Mar. 2018.
- [7] N. Qureshi *et al.*, "Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes Yr47 and Lr52 in wheat," *Theor. Appl. Genet.*, vol. 130, no. 3, pp. 495–504, 2017.
- [8] A. Rasheed *et al.*, "Crop Breeding Chips and Genotyping Platforms: Progress, Challenges, and Perspectives," *Molecular Plant*, vol. 10, no. 8. Cell Press, pp. 1047–1064, 07-Aug-2017.
- [9] H. Ayalew *et al.*, "Comparison of TaqMan, KASP and rhAmp SNP genotyping platforms in hexaploid wheat," *PLoS One*, vol. 14, no. 5, p. e0217222, May 2019.
- [10] L. Mansueto *et al.*, "Rice SNP-seek database update: New SNPs, indels, and queries," *Nucleic Acids Res.*, vol. 45, no. D1, pp. D1075–D1081, Jan. 2017.
- [11] Z. Li *et al.*, "The 3,000 rice genomes project," *Gigascience*, vol. 3, no. 1, p. 7, Dec. 2014.
- [12] H. Peng *et al.*, "MBKbase for rice: An integrated omics knowledgebase for molecular breeding in rice," *Nucleic Acids Res.*, vol. 48, no. D1, pp. D1085–D1092, 2020.
- [13] K. Y. Morales *et al.*, "An improved 7K SNP array, the C7AIR, provides a wealth of validated SNP markers for rice breeding and genetics studies," *PLoS One*, vol. 15, no. 5, p. e0232479, May 2020.
- [14] M. Yunus *et al.*, "Mapping of Resistance Genes to Brown Planthopper in Untup Rajab, an Indonesian Local Rice Variety," *J. AgroBiogen*, vol. 14, no. 2, p. 75, Dec. 2018.
- [15] S. Dellaporta, J. Wood, and J. Hicks, "A plant {DNA} mini-preparation: version {III}..," *Plant Mol. Biol. Report.*, vol. 41, no. 4, pp. 19–21, 1983.
- [16] "7k Infinium SNP genotyping - Genotyping Services Laboratory." [Online]. Available: [https://sites.google.com/a/irri.org/snp-genotyping-mmml/genotyping/infinium-7k?override\\_mobile=true](https://sites.google.com/a/irri.org/snp-genotyping-mmml/genotyping/infinium-7k?override_mobile=true). [Accessed: 04-Jun-2020].
- [17] "Rice SNP-Seek Database." [Online]. Available: <https://snp-seek.irri.org/>. [Accessed: 04-Jun-2020].
- [18] S. Purcell *et al.*, "PLINK: A tool set for whole-genome association and population-based linkage analyses," *Am. J. Hum. Genet.*, vol. 81, no. 3, pp. 559–575, Sep. 2007.
- [19] Perrier X. and J.-C. J.P., "DARwin - Dissimilarity Analysis and Representation for Windows," 2006. [Online]. Available: <https://darwin.cirad.fr/>. [Accessed: 04-Jun-2020].
- [20] I. Letunic and P. Bork, "Interactive Tree of Life (iTOL) v4: recent updates and new developments," *Nucleic Acids Res.*, vol. 47, no. W1, pp. W256–W259, Apr. 2019.
- [21] A. R. Quinlan, "BEDTools: The Swiss-Army tool for genome feature analysis," *Curr. Protoc. Bioinforma.*, vol. 2014, no. 1, pp. 11.12.1-11.12.34, Sep. 2014.
- [22] "KASP genotyping chemistry | LGC Biosearch Technologies." [Online]. Available: <https://www.biosearchtech.com/products/per-kits-and-reagents/genotyping-assays/kasp-genotyping-chemistry>. [Accessed: 04-Jun-2020].
- [23] R. Van Berloo, "GGT 2.0: Versatile Software for Visualization and Analysis of Genetic Data," *J. Hered.*, no. 2, pp. 232–236, 2008.
- [24] "Random number." [Online]. Available: <https://www.google.com/search?q=random+number>.
- [25] S. Sandmann *et al.*, "Evaluating Variant Calling Tools for Non-Matched Next-Generation Sequencing Data," *Sci. Rep.*, vol. 7, no. 43169, pp. 1–12, 2017.
- [26] F. Pfeiffer *et al.*, "Systematic evaluation of error rates and causes in short samples in next-generation sequencing," *Sci. Rep.*, vol. 8, no. 10950, pp. 1–14, 2018.
- [27] X. Tang *et al.*, "A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice," *Genome Biol.*, vol. 19, no. 1, p. 84, Jul. 2018.
- [28] T. R. Hargrove, W. R. Coffman, and V. L. Cabanilla, "Genetic interrelationships of improved rice varieties in Asia," *IRRI Res. Pap. Ser.*, vol. 23, p. 34p, 1978.
- [29] M. Exposito-Alonso *et al.*, "The rate and potential relevance of new mutations in a colonizing plant lineage," *PLoS Genet.*, vol. 14, no. 2, p. e1007155, Feb. 2018.
- [30] M. J. Thomson *et al.*, "Large-scale deployment of a rice 6 K SNP array for genetics and breeding applications," *Rice*, vol. 10, no. 1, p. 40, Dec. 2017.
- [31] C. He, J. Holme, and J. Anthony, "SNP genotyping: The KASP assay," *Methods Mol. Biol.*, vol. 1145, pp. 75–86, 2014.
- [32] S. Yang *et al.*, "An extended KASP-SNP resource for molecular breeding in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*)," *PLoS One*, vol. 15, no. 10, p. e0240042, Oct. 2020.
- [33] S. Bustin and J. Huggett, "qPCR primer design revisited," *Biomolecular Detection and Quantification*, vol. 14. Elsevier GmbH, pp. 19–28, 01-Dec-2017.
- [34] F. C. Silva, G. T. Torrezan, R. C. Brianese, R. Stabellini, and D. M. Carraro, "Pitfalls in genetic testing: a case of a SNP in primer-annealing region leading to allele dropout in *BRCA1*," *Mol. Genet. Genomic Med.*, vol. 5, no. 4, pp. 443–447, Jul. 2017.
- [35] P. Stothard, "Sequence Manipulation Suite: PCR Primer Stats." [Online]. Available: [https://www.bioinformatics.org/sms2/pcr\\_primer\\_stats.html](https://www.bioinformatics.org/sms2/pcr_primer_stats.html). [Accessed: 30-Mar-2020].
- [36] B. C. Colburn, S. A. Mehlenbacher, and V. R. Sathuvalli, "Development and mapping of microsatellite markers from transcriptome sequences of European hazelnut (*Corylus avellana* L.) and use for germplasm characterization," *Mol. Breed.*, vol. 37, no. 2, pp. 1–14, Feb. 2017.
- [37] P. Gramazio, J. Prohens, D. Borràs, M. Plazas, F. J. Herraiz, and S. Vilanova, "Comparison of transcriptome-derived simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers for genetic fingerprinting, diversity evaluation, and establishment of relationships in eggplants," *Euphytica*, vol. 213, no. 12, pp. 1–18, Dec. 2017.
- [38] S. A. Kaiser, S. A. Taylor, N. Chen, T. S. Sillett, E. R. Bondra, and M. S. Webster, "A comparative assessment of SNP and microsatellite markers for assigning parentage in a socially monogamous bird," *Mol. Ecol. Resour.*, vol. 17, no. 2, pp. 183–193, Mar. 2017.
- [39] R. Kamboj, B. Singh, T. K. Mondal, and D. S. Bisht, "Current status of genomic resources on wild relatives of rice," *Breed. Sci.*, vol. 70, no. 2, pp. 135–144, 2020.
- [40] J. A. Labate, J. C. Glaubitz, and M. J. Havey, "Genotyping by sequencing for SNP marker development in onion," *Genome*, vol. 63, no. 12, pp. 607–613, 2020.
- [41] J. Ha *et al.*, "Soybean-VCF2Genomes: A database to identify the closest accession in soybean germplasm collection," *BMC Bioinformatics*, vol. 20, no. S13, p. 384, Jul. 2019.
- [42] L. Li *et al.*, "An accurate and efficient method for large-scale SSR genotyping and applications," *Nucleic Acids Res.*, vol. 45, no. 10, p. e88, 2017.
- [43] D. Iamartino *et al.*, "Design and validation of a 90K SNP genotyping assay for the water buffalo (*Bubalus bubalis*)," *PLoS One*, vol. 12, no. 10, p. e0185220, 2017.
- [44] Q. You, X. Yang, Z. Peng, L. Xu, and J. Wang, "Development and applications of a high throughput genotyping tool for polyploid crops: Single nucleotide polymorphism (SNP) array," *Frontiers in Plant Science*, vol. 9. Frontiers Media S.A., p. 104, 06-Feb-2018.