












	Title	Citation	Species		Goal of the study
1	Random PCR-based genotyping by sequencing technology GRAS-Di (genotyping by random amplicon sequencing, direct) reveals genetic structure of mangrove fishes	Mol Ecol Resour. 19:1153-1163. (2019)		F. amboinensis L. fulvus Z. dunckeri	GRAS-Di method is applied to ecological studies where a large number of SNPs is required, such as population structure analysis of marine fish, while high quality DNA samples are not always available
2	Genetic Diversity and Genetic Structure of the Wild Tsushima Leopard Cat from Genome-Wide Analysis	Animals (Basel). 10:1375. (2020)		Wild Tsushima Leopard Cat	The identification of individuals in the Tsushima leopard population is difficult using microsatellite marker analysis due to the population's low genetic diversity, so more DNA markers must be developed to design an appropriate conservation program  To identify SNPs using genome-wide analysis with the GRAS-Di approach that would clarify the genetic diversity and structure of the wild Tsushima leopard cat.
3	East Asian origin of the widespread alpine snow-bed herb, <i>Primula cuneifolia</i> (Primulaceae), in the northern Pacific region	J Biogeogr. 00: 1– 13. (2020)		East Asian origin of the widespread alpine snow-bed herb, <i>Primula cuneifolia</i> (Primulaceae) ( <i>P. cuneifolia</i> and its sister species)	To explore the molecular evidence for the recent northward migration of alpine snow-bed species in the northern Pacific region.
4	Divergence and introgression in small apes, the genus <i>Hylobates</i> , revealed by reduced representation sequencing	bioRxiv 2020.05.31.126078. (2020)		Gibbons in the genus <i>Hylobates</i>	To uncover the divergence history and the contributions of hybridisation and introgression to the evolution of <i>Hylobates</i>
5	GRAS-Di system facilitates high-density genetic map construction and QTL identification in recombinant inbred lines of the wheat progenitor <i>Aegilops tauschii</i>	Nature Scientific Reports (2020)10:21455		Recombinant inbred lines of the wheat progenitor <i>Aegilops tauschii</i>	Developed a high-density linkage map and identify quantitative trait loci (QTLs) for recombinant inbred lines of <i>Aegilops tauschii</i> , a D-genome donor of bread wheat, using the recently developed genotyping by Random Amplicon Sequencing-Direct (GRAS-Di) system, which facilitates skimming of the large and complicated genome and generates a large number of genetic markers. The deduced linkage groups based on the GRAS-Di genetic markers corresponded to the chromosome number of <i>Ae. tauschii</i> .
6	Genetic Dissection of a Precocious Phenotype in Male Tiger Pufferfish ( <i>Takifugu rubripes</i> ) using Genotyping by Random Amplicon Sequencing, Direct (GRAS-Di)	Marine Biotechnology. doi: 10.1007/s10126-020-10013-4		Male Tiger Pufferfish ( <i>Takifugu rubripes</i> )	In this study, we tested the utility of GRAS-Di for genetic analysis in a cultured population of the tiger pufferfish <i>Takifugu rubripes</i> . The genetic analyses included family structure analysis, genetic map construction, and quantitative trait locus (QTL) analysis for the male precocious phenotype using a population consisting of four full-sib families derived from a genetically precocious line.

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7	A Major and Stable Quantitative Trait Locus qSS2 for Seed Size and Shape Traits in a Soybean RIL Population	Front. Genet., 16 April 2021   doi.org/10.3389/fgene.2021.646102		Recombinant inbred line (RIL) population developed from K099 (small seed size) × Fendou 16 (large seed size)	Seed size and shape traits are important determinants of seed yield and appearance quality in soybean [ <i>Glycine max</i> (L.) Merr.]. Understanding the genetic architecture of these traits is important to enable their genetic improvement through efficient and targeted selection in soybean breeding, and for the identification of underlying causal genes.
8	QTL analysis of crown gall disease resistance in apple: first plant R gene candidates effective against <i>Rhizobium rhizogenes</i> (Ti)	Tree Genetics & Genomes volume 17, Article number: 25 (2021)		Full-sib F1 population derived from a 'JM7' (susceptible) × Sanashi 63 (resistant)	In this study, we used a full-sib F1 population derived from a 'JM7' (susceptible) × Sanashi 63 (resistant) cross to identify quantitative trait loci (QTLs) that control resistance to tumour-inducing <i>Rhizobium</i> isolates found in apple production areas in Japan.
9	Biological and molecular characterization of linalool-mediated field resistance against <i>Xanthomonas citri</i> subsp. <i>citri</i> in citrus trees.	Tree Physiol. tpab063 (2021)		F1 population of the resistant Ponkan mandarin and susceptible 'Harehime' ('E-647' × 'Miyagawa-wase') cultivar	Quantitative trait locus (QTL) analysis revealed that linalool accumulation and Xcc (citrus canker disease, caused by the bacterial pathogen <i>Xanthomonas citri</i> subsp. <i>Citri</i> ) susceptibility QTLs overlapped.
10	Analysis of the possible cytogenetic mechanism for overcoming hybrid lethality in an interspecific cross between <i>Nicotiana suaveolens</i> and <i>Nicotiana tabacum</i> .	Sci Rep. 11:7812 (2021)		The seedlings of hybrid parents ( <i>N. suaveolens</i> and <i>N. tabacum</i> ), two lethal hybrid seedlings, and one hybrid seedling that overcame lethality.	Finding hybrids that overcome lethality, either spontaneously or by artificial culture, lack the distal part of the Q chromosome, a region that includes the gene responsible for lethality.
11	Detection of a major QTL related to smut disease resistance inherited from a Japanese wild sugarcane using GRAS-Di technology.	Breeding Science. doi:10.1270/jsbbs.20137 (2021)		Japanese wild sugarcane	Detection of an identical QTL for indices of smut disease incidence with a markedly high LOD score at the end of linkage group 8 of 'Yaenoushie'. This QTL could be used for marker-assisted selection (MAS) to significantly improve smut disease resistance without negative effects on other agronomic traits.

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