1	Title:	Exploring the areas of applicability of whole-genome prediction methods for Asian rice (Oryza sativa L.)
	Author:	Akio Onogi, Osamu Ideta, Yuto Inoshita, Kaworu Ebana, Takuma Yoshioka, Masanori Yamasaki, Hiroyoshi Iwata
	Journal:	Theoretical and Applied Genetics, January 2015, Volume 128, Issue 1, pp 41-53
	Abstract:	Key message Our simulation results clarify the areas of applicability of nine prediction methods and suggest the factors that affect their accuracy at predicting empirical traits. Whole-genome prediction is used to predict genetic value from genome-wide markers. The choice of method is important for successful prediction. We compared nine methods using empirical data for eight phenological and morphological traits of Asian rice cultivars (Oryza sativa L.) and data simulated from real marker genotype data. The methods were genomic BLUP (GBLUP), reproducing kernel Hilbert spaces regression (RKHS), Lasso, elastic net, random forest (RForest), Bayesian lasso (Blasso), extended Bayesian lasso (EBlasso), weighted Bayesian shrinkage regression (wBSR), and the average of all methods (Ave). The objectives were to evaluate the predictive ability of these methods in a cultivar population, to characterize them by exploring the area of applicability of each method using simulation, and to investigate the causes of their different accuracies for empirical traits. GBLUP was the most accurate for one trait, RKHS and Ave for two, and RForest for three traits. In the simulation, Blasso, EBlasso, and Ave showed stable performance across the simulated scenarios, whereas the other methods, except wBSR, had specific areas of applicability; wBSR performed poorly in most scenarios. For each method, the accuracy ranking for the empirical traits was largely consistent with that in one of the simulated scenarios, suggesting that the simulation conditions reflected the factors that affected the method accuracy for the empirical results. This study will be useful for genomic prediction not only in Asian rice, but also in populations from other crops with relatively small training sets and strong linkage disequilibrium structures.
	Database:	SpringerLink

2	Title:	Advances in Setaria genomics for genetic improvement of cereals and bioenergy grasses
	Author:	Mehanathan Muthamilarasan, Manoj Prasad
	Journal:	Theoretical and Applied Genetics, January 2015, Volume 128, Issue 1, pp 1-14

Abstract:	Key message
	Recent advances in Setaria genomics appear promising for genetic improvement of cereals and biofuel crops towards providing multiple securities to the steadily increasing global population. The prominent attributes of foxtail millet (Setaria italica, cultivated) and green foxtail (S. viridis, wild) including small genome size, short life-cycle, in-breeding nature, genetic close-relatedness to several cereals, millets and bioenergy grasses, and potential abiotic stress tolerance have accentuated these two Setaria species as novel model system for studying C4 photosynthesis, stress biology and biofuel traits. Considering this, studies have been performed on structural and functional genomics of these plants to develop genetic and genomic resources, and to delineate the physiology and molecular biology of stress tolerance, for the improvement of millets, cereals and bioenergy grasses. The release of foxtail millet genome sequence has provided a new dimension to Setaria genomics, resulting in large-scale development of genetic and genomic tools, construction of informative databases, and genome-wide association and functional genomic studies. In this context, this review discusses the advancements made in Setaria genomics, which have generated a considerable knowledge that could be used for the improvement of millets, cereals and biofuel crops. Further, this review also shows the nutritional potential of foxtail millet in providing health benefits to global population and provides a preliminary information on introgressing the nutritional properties in graminaceous species through molecular breeding and transgene-based approaches.

Database:	SpringerLink

3

Title:	Training set optimization under population structure in genomic selection
Author:	Julio Isidro, Jean-Luc Jannink, Deniz Akdemir, Jesse Poland, Nicolas Heslot, Mark E. Sorrells
Journal:	Theoretical and Applied Genetics, January 2015, Volume 128, Issue 1, pp 145-158

Abstract:	Key message
	Population structure must be evaluated before optimization of the training set population. Maximizing the phenotypic variance captured by the training set is important for optimal performance.
	The optimization of the training set (TRS) in genomic selection has received much interest in both animal and plant breeding, because it is critical to the accuracy of the prediction models. In this study, five different TRS sampling algorithms, stratified sampling, mean of the coefficient of determination (CDmean), mean of predictor error variance (PEVmean), stratified CDmean (StratCDmean) and random sampling, were evaluated for prediction accuracy in the presence of different levels of population structure. In the presence of population structure, the most phenotypic variation captured by a sampling method in the TRS is desirable. The wheat dataset showed mild population structure, and CDmean and stratified CDmean methods showed the highest accuracies for all the traits except for test weight and heading date. The rice dataset had strong population structure and the approach based on stratified sampling showed the highest accuracies for all traits. In general, CDmean

minimized the relationship between genotypes in the TRS, maximizing the relationship between TRS and the test set. This makes it suitable as an optimization criterion for long-term selection. Our results indicated that the best selection criterion used to optimize the TRS seems to depend on the interaction of trait architecture and population structure.

| Database: | SpringerLink |

4

Title:	Imaging of oxygen transmission in the oak wood of wine barrels using optical sensors and a colour camera
Author:	I. Nevares, R. Crespo, C. Gonzalez and M. del Alamo-Sanza
Journal:	Australian Journal of Grape and Wine Research, Volume 20, Issue 3, pages 353–360, October 2014

Abstract:	Background and Aims

Background and Aims

Wine ageing in oak barrels is characterised by a series of physical and chemical processes, in many of which oxygen plays an important role. Therefore, to control better this phase of winemaking, it is not enough to know that oxygen penetrates into the barrel through the oak wood; it is also important to know how oxygen moves through the wood into the barrel, in what quantity and which factors are involved.

Methods and Results

We attempted to answer these questions with a high-resolution colour camera, ratiometric calibration and a planar optode with which the two-dimensional distribution and dynamics of oxygen within an oak barrel stave were studied. It was possible to make two-dimensional measurements when combined with microscopic optics and an appropriate camera, which permitted the measure of the transmission of oxygen into the barrel through the oak stave and the study of the mechanism of transmission. The trial was applied to both dry and wet oak wood, which revealed how the moisture content of the wood influenced oxygen transmission. The measurements were made in an airtight chamber under controlled temperature and pressure, which accurately reproduced the conditions of a stave in an oak wood barrel filled with liquid.

Conclusion

We were able to visualise the diffusion of oxygen in both dry and in wet French oak wood under conditions similar to those operating in a barrel. The moisture content of the wood influenced the oxygen transmission rate (OTR) through the wood.

Significance of the Study

For the first time, the dissolved oxygen dynamics and two-dimensional distribution of oxygen within the thickness of a barrel stave have been demonstrated. Wood water saturation is a key factor in the diffusion of oxygen through wood with barrel OTR decreasing during the ageing period.

| Database: | Wiley Online Library |

5	Title:	[Automated estimation of leaf area index from grapevine canopies using cover photography, video and computational analysis methods](#)
	Author:	S. Fuentes, C. Poblete-Echeverría, S. Ortega-Farias, S. Tyerman and R. De Bei
	Journal:	Australian Journal of Grape and Wine Research, Volume 20, Issue 3, pages 465–473, October 2014
	Abstract:	Background and Aims Monitoring of canopy vigour is an important tool in vineyard management to obtain balanced vines (vegetative vs reproductive organs). Leaf area index is the main parameter representing canopy vigour. Our aim was to test an automated computational method to obtain leaf area index and canopy vigour parameters from grapevines with digital photography and video analysis using MATLAB programming techniques for rapid data uptake and gap size analysis. Methods and Results The proposed method was tested against allometry at a Chilean experimental site planted with cv. Merlot. A temporal and spatial assessment of the method was also tested in a drought and drought/recovery experiment with cv. Chardonnay in the Riverland, South Australia. These data were geo-referenced and compared to the normalised difference vegetation index extracted from the WorldView-2 satellite images at a 2 m2 per pixel resolution. Conclusions The maximum leaf area index data obtained with cover digital photography and video analysis are an accurate, cost-effective and easy-to-use method to estimate spatial and temporal canopy LAI and structure when compared to standard measurements (allometry and plant canopy analyser). Significance of the Study This study has demonstrated that the method proposed is an accurate and inexpensive tool for application in experiments and by the industry to monitor spatio-temporal distribution of vigour.
	Database:	Wiley Online Library

6	Title:	[Winemaking practice affects the extraction of smoke-borne phenols from grapes into wines](#)
	Author:	D. Kelly, A. Zerihun, Y. Hayasaka and M. Gibberd
	Journal:	Australian Journal of Grape and Wine Research, Volume 20, Issue 3, pages 386–393, October 2014
	Abstract:	Background and Aims Exposure to smoke and uptake of taint imparting phenols in grapes and wines is a significant problem in bushfire-prone regions of Australia and other countries. The effects of smoke exposure on taint occurrence in wines, however, can be variable. This study assessed the influence of cultivar on uptake and accumulation of smoke-borne phenols in grapes and of subsequent processing and winemaking methods on extraction of phenols into wines.

	Methods and Results
	Smoke-exposure experiments were conducted in commercial vineyards of Chardonnay, Merlot and Sauvignon Blanc 14 days after the onset of veraison. At maturity, grapes were harvested for winemaking, which included malolactic fermentation (MLF) for Merlot. Volatile and glycoconjugated phenols were determined in grapes and the resultant wines. All cultivars had a similar concentration of smoke-derived total phenols in their grapes. The apparent extraction of total phenols from grapes into wines, however, differed markedly among the three traditional winemaking methods. Red winemaking (Merlot) with skin contact extracted 88% of total grape phenols, whereas white winemaking either by crushing before pressing (Sauvignon Blanc) or by whole-bunch pressing without crushing (Chardonnay), respectively, released 39 and 18% of total phenols. For Merlot wines, MLF did not affect the extraction of total smoke-derived phenols. Conclusions Under standardised exposure conditions (duration, intensity and phenology), the three cultivars studied accumulated a similar concentration of total phenols in grapes. The grape-processing and winemaking methods, however, can bring about a fourfold difference in the concentration of total phenols of wines. The smoke-derived phenols extracted from grapes into wine and the distribution of these phenols between the volatile and conjugated pools were not affected by MLF. Significance of the Study The key findings reported here have the potential to improve decision-making by grapegrowers and winemakers on the effect of cultivar and winemaking practice on potential smoke taint in wine.
Database:	Wiley Online Library

7

Title:	Preservation of mango quality by using functional chitosan-lactoperoxidase systems coatings
Author:	Mohamed Cissé, Jessica Polidori, Didier Montet, Gérard Loiseau, Marie Noëlle Ducamp-Collin
Journal:	Postharvest Biology and Technology, Volume 101, March 2015, Pages 10–14
Abstract:	Influence of chitosan coating with or without the active antimicrobial lactoperoxidase system was studied on postharvest mangoes. Mangoes were treated with three concentrations of chitosan (0.5; 1; 1.5%) containing or not lactoperoxidase with or without iodine as a second electron donor. Coatings containing 1 and 1.5% chitosan incorporated with lactoperoxidase system efficiently inhibited fungal proliferation and delayed mango ripening. Iodine did not influence antifungal activity. Ripening parameters (firmness, respiration, weight loss and color) were not influenced by the lactoperoxidase system, but were more influenced by chitosan concentration. Chitosan coating alone reduced weight loss, and delayed the decline in firmness and respiration rate. It exhibited a beneficial effect on the contents of total soluble solids (TSS), ascorbic acid, total acidity (TA) and pH.
Database:	ScienceDirect

8	Title:	**Transcriptional profiling of apple fruit in response to heat treatment: Involvement of a defense response during Penicillium expansum infection**
	Author:	A. Spadoni, M. Guidarelli, J. Phillips, M. Mari, M. Wisniewski
	Journal:	Postharvest Biology and Technology, Volume 101, March 2015, Pages 37–48
	Abstract:	Heat treatment of harvested fruit has been demonstrated to be an effective and a safe approach for managing postharvest decay. In the present study, the effect of a hot water treatment (HT) (45 °C for 10 min) on the response of apple to blue mold infection was investigated. HT was applied to 'Ultima Gala' apples using 2 different methods. Wounded apples were: (1) inoculated with a Penicillium expansum spore suspension and then heat-treated after 1, 4 and 24 h (Inoc-HT); or (2) first heat-treated and then inoculated with a P. expansum spore suspension after 1, 4 and 24 h (HT-Inoc). All treated/inoculated apples were stored at 20 °C for 6 days. Significant reductions in fruit rot incidence, up to 100%, were observed using the Inoc-HT protocol at 4 and 24 h while a 30% reduction in blue mold incidence was found at 1 and 4 h using the HT-Inoc method. In vitro experiments showed no evident lethal effect of HT at 45 °C for 10 min on the germination of P. expansum conidia, indicating that this pathogen has a high heat tolerance. In order to investigate the molecular mechanisms involved in fruit response to heat treatment, an apple microarray was used to conduct a global transcriptional analysis of gene expression in apple at 0, 15, 30 min, 1, 4, 8 and 24 h after the heat treatment. The results provided evidence that at 1 and 4 h after heating, the HT apples had the highest number of differentially expressed genes. A significant upregulation of heat shock proteins, heat shock cognate protein, and heat shock transcription factor genes, involved in thermotolerance were observed. This indicates that the apple fruit respond to the heat treatment in a programmed manner and suggests that the genes responsible for thermotolerance may also be involved in the induced resistance response.
	Database:	ScienceDirect

9	Title:	**Genetic and physical mapping of Co, a gene controlling the columnar trait of apple**
	Author:	Takuya Morimoto, Kiyoshi Banno
	Journal:	Tree Genetics & Genomes, Volume 11, Issue 1, February 2015, 11:807
	Abstract:	The columnar trait in apple (Malus × domestica Borkh.) is characterized by short internodes, reduced branching, and increased spurs, which are labor-saving features useful for high-density planting. In this study, we used six segregating populations of a descendant of the columnar-type cultivar 'Maypole' and constructed a genetic linkage map for the columnar gene (Co). Based on the linkage map of the Co gene, contig sequences of the Co region between simple sequence repeat (SSR) markers CH03d11 and Hi01a03 of the apple genome were screened for SSR motifs. Amplification of 14 out of 26 newly designed SSR markers yielded fragments specifically linked to the Co gene.

Genotyping of recombinants with the 14-marker set and five additional Co-linked markers delimited the Co region to a 530-kb region of the apple genome that overlap those found in previous studies in spite of the different genetic materials and backgrounds. Eight markers showed co-segregation with the Co locus. Genotypes of columnar cultivars/selections and normal-type cultivars were determined for four closely linked markers. For three markers, Co-linked fragments were generated not only from columnar-type cultivars but also from the 'McIntosh' and its normal-type offspring. In contrast, the Co-specific marker 29f1-JWl1r corresponded completely with the columnar trait in all cultivars and recombinants, indicating that this marker would be valuable for marker-assisted selection during columnar apple breeding.

| Database: | SpringerLink |

10

Title:	Genome-wide analysis of HD-Zip genes in grape (Vitis vinifera)
Author:	Haiyang Jiang, Jing Jin, Huan Liu, Qing Dong, Hanwei Yan, Defang Gan, Wei Zhang, Suwen Zhu
Journal:	Tree Genetics & Genomes, Volume 11, Issue 1, February 2015, 11:827
Abstract:	Grape (Vitis vinifera) is one of the most important fruit trees worldwide, and genomics research has played an important role in grape breeding and culture. According to numerous studies in higher plants, homeodomain-leucine zipper (HD-Zip) proteins are a specific class of transcription factors that play an important role in plant development. In this study, bioinformatics methods were used to carry out genome-wide analysis of a complete set of candidate genes encoding HD-Zip proteins in grape, including analysis of the number, physical locations, and encoded amino acid sequences of grape HD-Zip genes, as well as phylogenetic analysis. We identified 31 HD-Zip genes (Vvhdz1–31) in the grape genome, which were categorized into four classes (HD-Zip I–IV). These HD-Zip proteins contain 20 conserved motifs; their amino acids sequences were deduced. Chromosomal location analysis revealed that these genes are distributed unevenly across all 18 chromosomes. The digital EST expression analyses provided a first glimpse of the expression patterns of HD-Zip genes in grape. The results of this study provide an important theoretical reference for more thorough investigations of HD-Zip genes in grape, as well as studies examining the growth, development, and breeding of grape.
Database:	SpringerLink