

only as biofuel. Algae oil, copaiba, honge oil, jatropha oil, jojoba oil, milk bush, petroleum nut oil. Drying oils that dry to a hard finish at normal temperatures which are used as the basis of oil paints, and in other paint and wood finishing applications like dammar oil, poppy seed oil, stillingia oil, tung oil, vernonia oil which can be used to make epoxies for manufacturing adhesives, varnishes and paints, and industrial coatings. A few other oils which are not used as edible oils are amur cork tree fruit oil, balanos oil, bladderpod oil, brucea javanica oil, burdock oil (bur oil) candlenut oil (kukui nut oil), carrot seed oil (pressed), chaulmoogra oil, crambe oil, cuphea oil jojoba oil, lemon oil, mango oil, mowrah butter, neem oil, orange oil, palm kernel oil, rosehip seed oil, sea buckthorn oil, shea butter, snowball seed oil (viburnum oil), tall oil, tamanu oil and tonka bean oil (cumaru oil).

CONCLUSION

Due to the high economic value of worldwide trade of fresh horticultural produce, a considerable number of investigations are done on these crops with special emphasis on oils produced from them. The research and study on the oils produced by horticultural crops is in its grass root level as most of us are aware of only a few oils, further research on the oils extracted from horticultural crops is most important and farmers must be encouraged to grow these crops stressing the importance of the oils extracted from them to commercialize the horticultural crops for oil extraction.

Storability, longevity and rancidity: A genomic perspective on evolutionary constraints in major oilseeds

RAMYA PARAKKUNNEL^{*1}, BHOJARAJA NAIK K¹, GIRIMALLA VANISHREE¹, KT RAMYA³, ANJITHA GEORGE¹, KV SRIPATHY¹, CS SHANTHARAJA¹, S ARAVINDAN¹, K UDAYA BHASKAR¹, A ANANDAN¹, AND SANJAY KUMAR².

¹ICAR- Indian Institute of Seed Science, Regional Station, GKVK Campus, Bengaluru, India- 560065.

²ICAR- Indian Institute of Seed Science, Mau, Uttar Pradesh, India-275103.

³ICAR- Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad 500030.

*Corresponding author: ramyakurian@gmail.com

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ABSTRACT

Limited longevity and accelerated chemical decomposition during storage are major problems found in oilseeds. In the present study the genomic composition of rancidity prone soybean and sunflower are compared with oil seeds with fairly good storability like sesame and olive. The chromosomal location, gene duplications, syntenic relationships, cis-element architecture and protein-protein interactions were studied with respect to 250 genes affecting lipid decomposition like lipases, lipoxygenases and oleosins. The expansion of lipoxygenases and phospholipaseD genes in soybean and sunflower indicate the importance of gene duplication in functional divergence. Moreover the effect of strong purifying selection in lipid decomposition genes was evident in shaping the genomic diversity.

Keywords: Lipase, Lipoxygenase, Oilseeds, Oleosin, Rancidity

Plant-based edible oils are rich in triacylglycerols (TAGs) and constitute a major share of human dietary consumption. However, the lipid rich seeds have limited longevity and are prone to chemical decomposition leading to loss of germination and viability during storage. Lipid oxidation during storage leads to loss of essential fatty acids meanwhile producing free radicals and peroxides, ultimately resulting in irreversible damage to membranes, proteins, DNA and cell repair mechanisms. Moreover, rancidity development as a consequence of this the most important factor contributing to reduction in oil quality and quantity during storage. The major players involved in this cascade are lipases like phospholipaseD and triacylglycerol lipase (TGAL); lipoxygenases (LOXs) and oleosins which are the major surface proteins modulating the size and stability of oil bodies (OB)

containing TAGs. The mobilization of lipid reserves stored in OBs during germination by lipases and lipoxygenases make them a boon for germination while becoming a bane for lipid stability. In this context we investigated the genomic architecture of lipases, lipoxygenases and oleosins in major oilseed crops like soybean, sunflower, sesame and olive with wide differences in long term storability and rancidity development.

MATERIALS AND METHODS

The gene sequences for the study were obtained from Soybase (<https://www.soybase.org/>), Phytozome (<https://phytozome-next.jgi.doe.gov/>) and sesame pan-genome (Yu et al. 2019). The protein sequences were

aligned using CLUSTAL X ver 2.1 and were subjected to Bayesian phylogenetic inference using MCMC by BEAST ver 2.6.6 (Bouckaert et al. 2019). The syntenic relationships between all four genomes and the non-synonymous/synonymous (Ka/Ks) mutation ratio were probed with MCScanX using TB tools. Protein-protein interaction network was visualized with the help of STRING ver 11.5 (<https://string-db.org/>). The cis-element identification was done by subjecting upstream 2000bp sequences from all the genomes to PLANT CARE (<https://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) and comparing with the reported Arabidopsis cis-elements.

RESULTS AND DISCUSSION

Gene copy numbers for all the categories were much lesser in sesame and olive when compared to more rapidly deteriorating soybean and sunflower. There was an expansion of multi-intronic lipoxygenase and phospholipase D genes in soybean and sunflower compared to sesame and olive. This expansion was confirmed phylogenetically and involved eight and seven intron genes in LOX and nine intron genes in phospholipase D resulting in unique homologs with wide variation in protein parameters. Although the number of genes detected in soybean was much higher than sesame, the exon number per gene was similar; 8.76 and 8.64 respectively. Maximum number of introns noticed for single gene was 23 in olive phospholipase D gene *Oeu031987.1*. The oleosin genes were more conserved within species with most of them being intron less and having molecular weight of 73-258kDa. All of the studied TGAL genes had 3 introns although difference in molecular weight was prominent. Sequence conservation was evident within the order Lamiales involving sesame and olive even though more duplicates were accounted for soybean and sunflower.

The collinearity percentage between sunflower and soybean was 17.34% compared to 23.77% between sesame and olive. In sunflower 78% of the studied genes were dispersed duplicates whereas 43% of soybean genes

were single copy genes. Majority of the lipases, lipoxygenases and oleosins were under purifying selection in olive and sunflower while none of the studied loci in soybean exhibited significant selection effects. However, all of the oleosin genes in sesame were under positive selection. The age for LOX genes was calculated as 5-150 MYA while the oleosin genes under positive selection evolved 40-70MYA. ABRE elements had important roles to play in the functioning of LOX and TGAL genes while STRE elements were crucial for phospholipase D and oleosin genes. MYB and MYC elements were common in all the four categories. The protein-protein interaction studies indicated that in soybean which is more prone to rapid deterioration under storage, the fatty acid metabolism was combined with oxidative stress response leading to senescence under Jasmonic Acid (JA) mediated signaling (Mir *et al.* 2018; Ruan *et al.* 2019). Sesame which is less prone to rancidity had different interaction scenario where the role of oleosins were limited. Here the same category genes were involved with stress response and starch synthesis as well as release of fatty acids from germinating seedlings in addition to JA mediated signaling. The study of key genes involved in lipid oxidation, stress response and germination indicate the role of accelerated evolution through gene duplication leading to functional differentiation and enhanced adaptation.

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Impact assessment of front line demonstration of safflower on farmers' fields

S A SHINDE, D P WASKAR, S B GHUGE AND C V AMBADAKAR

AICRP on Safflower, Vasantrao Naik Marathwada Krishi Vidyapeeth Parbhani-413 512, Maharashtra, India.
Email: santoshashinde338@gmail.com

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ABSTRACT

AICRP on Safflower, VNMKV, Parbhani conducted 160 demonstrations on safflowers during Five consecutive years from 2017–18 to 2021–22. The critical inputs were identified in existing production technology through meetings and discussions with farmers. Uncontrolled weeds, ignorance about fertilizers and lack of plant protection measures, were the predominant identified causes of low productivity of safflower. The average results of Five years study revealed that the Seed yield under demonstration plots was 1290 Kg/ha as compared to 994 kg /ha in traditional farmer practices plots. The results clearly indicate the positive effects of FLDs over the existing practices. Percentage increase Seed yield over farmer practice was found 30%.

Keywords: Frontline demonstrations, Safflower