

## Erratum

In Article “Contribution of the IAM Pathway to IAA Pool in Developing Rice Grains ”, with the number of DOI: <http://dx.doi.org/10.1590/1678-4324-2016150677>, published in journal Brazilian Archives of Biology and Technology, vol. 59, the 01 page. that read:

*“Twenty four fungal species were screened for their ability to produce alkaline L-methioninase on methionine-glucose liquid medium. Aspergillus ustus AUMC 10151 displayed the highest yield of enzyme (10.8 U/mg protein), followed by A. ochraceus and Fusarium proliferatum. Upon optimization of the submerged fermentation (SmF) conditions, the maximum enzyme yield (18.23 U/mg protein) was obtained on a medium containing L-methionine (0.5%), sucrose (0.95%), KH<sub>2</sub>PO<sub>4</sub> (0.1%) and 175 rpm. Seven agro-industrial by-products were screened as substrates for L-methioninase production under solid-state fermentation (SSF). Wheat bran resulted 38.1 U/mg protein, followed by rice bran (27.6 U/mg protein) and soya bean meal (26.6 U/mg protein). Maximum alkaline L-methioninase (99.56U/mg protein) was achieved at initial moisture content of 71.5%, inoculum size of 2.0 mL of spore suspension, initial pH 8.5, incubation period eight days at 30°C and supplementation of the salt basal medium with pyridoxine(100 µg/mL) and beet molasses (20% v/v). The productivity of L-methioninase by A. ustus under SSF was higher than that of SmF about 5.45 fold under optimum conditions.*

**Key words:** L-methioninase, *Aspergillus ustus*, Submerged fermentation, Solid state fermentation, Wheat bran.”

Read:

*“A possible role for the indole-3-acetamide (IAM) pathway in the indole-3-acetic acid (IAA) production was investigated in developing rice grains. IAM-hydrolase proposed to convert IAM to IAA primarily through the identification of IAM and IAM-hydrolase activity in some plant species. Expression profiles of the two putative rice IAM-hydrolase genes, OsAM11&2, were compared to the previously quantified IAA level. The abrupt increase in IAA level between 4 and 7 days after anthesis (DAF) was not found to correlate with changes in the expression of OsAM11 or OsAM12 suggesting that the IAM pathway may not contribute significantly to IAA pool in rice grains. Production of a biological compound other than IAA may explain the high activity of OsAM11&2 in developing rice grains. OsAM11 that reported to be conserved across the plant kingdom showed higher expression level in most analyzed reproductive rice tissues whereas OsAM12 showed more fluctuation in expression comparing to OsAM11. Role of the IAM pathway in IAA production was also discussed in other plant systems and Arabidopsis seed was recommended as an ideal tissue to identify enzyme(s) convert(s) tryptophan to IAM as well as physiological effects of IAA produced via this pathway.*

**Keywords:** indole-3-acetamide, IAM-hydrolase, Auxin, Indole-3-acetic acid, Tryptophan”