Table 1. Investigations of herbivore dung as sources of enzymes

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| Source of dung | Aim of the study | Preliminary investigation | References |
| Giraffe, zebra and impala | To evaluate the faeces of wild herbivores in South Africa as a potential source of hydrolytically active microbes | Dung from three indigenous herbivores in Pietermaritzburg, South Africa were sampled. Soil and faecal droppings was measured by triphenyltetrazolium chloride and fluorescein diacetate for hydrolase and dehydrogenase activity respectively. Cellulose, amylase and protease producers were determined by viable plate count on solid agar media containing cellulose, skim milk, starch and Tween 80. Zebra dung displayed the highest hydrolytic activity confirming potential target for new hydrolytic enzyme. | [1] |
| Cow dung from India | A review on cow dung as a cheap available bioresource. | Cow dung contains high diversity of microbial population. Due to this characteristic, it’s feasible to obtain microbial enzymes with potential biocatalytic application that can be harnessed to produce enzymes from its high microbial diversity. *Bacillus* sp from cow is capable of producing cellulose, carboxymethy cellulose and cellulose. | [2] |
| Cow dung used as substrate | To produce a protease from dung for enzyme bioprocess | In the study, a halo-tolerant-alkaline protease from *Halomonas* sp. PVI was produced under solid-state fermentation. Cow dung serves as a good substrate for enzyme production of detergent-stable dehairing protease by alkaphilic *B subtilis.* Dehairing process was important as it eliminated use of hazardous sodium sulphide. | [3, 4] |
| Cow dung | Statistical optimization of fibrinolytic enzyme | Considering its cheap and readily available cow dung was used as substrate for production of fibrinolytic enzyme from *Pseudoalteromonas* sp. under solid-state culture. The newly protease producing *Pseudoalteromonas* sp. has been reported by various researchers as a potential producer of thrombolytic enzyme. Hence, in the reported study it was worthwhile to screen *Pseudoalteromonas* sp. for fibrinolytic enzyme secretion and statistical model of central composite design employed for enzyme production | [5] |
| Koala faeces | Screening dung from koala species for enzymes production | Thirty-seven (37) fungal strains isolated from koala faeces were identified by molecular tools of 18S rDNA whereby, they were amplified and sequenced. The enzymes extracted from the fungi were screened for various enzyme production such as xylanase, protease, ligninase and endoglucanase. Using plate agar technique one third of the fungi displayed a halo indicating presence of amylase and tannase activity. Some isolates degraded crystalline cellulose while others displayed lipase activity. It was concluded that koala dung could be harbouring wide array of biocatalytic enzymes capable of breaking down recalcitrant substrates. | [6] |
| Cow dung | Investigate potential of enzyme production from herbivore dung | A potent bacteria *Bacillus* sp. Identified by 16S rDNA was isolated from cow dung. On preliminary screening, the strain showed potential to produce a thermotolerant endoglucanase (CMCase). The strain was purified 8.5-fold with recovery of 39.5 % and characterized for different parameters including temperature, effect of metal ions, chemicals and pH stability. The enzyme in this strain could be applied for bioconversion of lignocellulosic biomass into fermentable sugars. | [7] |

Table 2. The table below details microbial and plant sources of IOS and FOS synthesizing enzymes

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| Fungal source | References | Plant source | References | Bacterial source | References |
| *Aureobasidium pullulans*  *Aureobasidium sp.*  *Aspergillus oryzae*  *Aspergillus japonicas*  *Aspergillus niger*  *Aspergillus phoenics*  *Aspergillus phoenics*  *Aspergillus foetidus*  *Aspergillus sydowi*  *Calviceps purpurea*  *Fusarium oxysporum*  *Penicillium frequentans*  *Penicillium spinulosum*  *Phytophthora parasitica*  *Penicillium citrinum*  *Scopulariopsis brevicaulis*  *Saccharomyces cerevisiae* | [8]  [9]  [10]  [11]  [12]  [13]  [14]  [15]  [16]  [17]  [18]  [19]  [20]  [21]  [21] | *Agave vera cruze*  *Agave americana*  *Asparagas officinalis* (asparagus roots)  *Cichorium intybus* (Chicory)  *Allium cepa*  *Crinum longifolium* (Sugar beet)  *Helianthus tuberosus* (Jerusalem artichoke)  *Lactuca sativa*  *Lycoris radiate*  *Taraxacum officinale* | [22]  [23]  [11]  [24]  [12]  [24]  [13]  [25]  [26] | *Lactobacillus reuti*  *Arthrobacter sp*  *Bacillus macerans*  *Zymomonas mobilis*  *Pseudomonas* sp. | [27]  [28]  [29]  [17]  [30] |

Table 3. A synopsis of studies of microbes used for FOS production produced

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| --- | --- | --- | --- | --- | --- |
| Source of microbe | Enzyme | Optimal condition | Substrate (g/L sucrose) | Yield (%) | Reference |
| *Aspergillus niger* AS 0023 | β-fructofuranosidase  (EC2.1.4.9) free enzymes  Extracellular ftase  Intracellular ftase | 40 – 60 °C, pH 6.0 -8.5  Sucrose 40 - 70 % | 500 | 54 | [9] |
| *Aspergillus japonicus* | β-fructofuranosidase  (EC 3.2.1.26) free enzymes.  Intra and extracellular ftase  Extracellular ftase  Extracellular ftase | 55 °C, pH 5.5,  Sucrose 65 % | 400 | 55.8 | [31] |
| *Aspergillus oryzae* CFR 202 | Fructosyltransferase  (EC 2.1.4.9) free enzymes  Extracellular ftase | 55 °C, pH 5.5, 24 h  Sucrose 55% | 600 | 58 | [12]  [32] |
| *Penicillium citrum* | Neo-fructosyltransferase  free mycelia | 50 °C, 40 h - 100 rpm  Sucrose 70 % | 700 | 55 | [33, 34] |
| *Rhodotorula* sp | Extraxelluar β-fructofuranosidase and fructosyltransferase | 72 °C – 75 °C, pH 4.0, 65 °C – 70 °C, 48 h | 500 | 48 | [35] |
| *Zymomonas mobilis* | Levansucrase | 24 h | 500 - 600 | 24 - 32 | [36] |
| *Aspergillus* sp N74 | Fructosyltransferase  (EC 2.1.4.9) | pH 5.5 temp 60 ºC at 350 rpm sucrose con 70% w/v | 700 | 57 | [37, 38] |
| *Bacillus macerans* EG-6  *B. macerans* EG-6 | Fructosyltransferase  (EC 2.4.1.9) free enzymes  fructosyltransferase | 50 °C, pH 5.0 - 7.0, 100 h  37 °C, pH 6.0, 40 h | 500  500 | 33  GF4 (42.3) | [39]  [40] |
| *Aureobasidium pullulans* CFR 77 | Fructosyltransferase  (EC 2.1.4.9) free enzymes  Extracellular ftase | 55 °C, pH5.5, 9 - 24 h  Sucrose 80 % | 200 | 59 | [41, 42]  [43] |
| *Aureobasidium pullulans* CCY-27-1-1194 | Extracellular and intracellular fructosyltransferase | 55 °C, pH 5.5, 48 - 72 h | 350 | 52 - 56 | [44] |
| *Penicillium purpurugenum* | Extracellular and intracellular fructosyltransferase | 30 °C, pH 5.5, 720 h | 10 | 58 | [45] |
| *Aspergillus japonicus* | β-fructofuranosidase | 28 °C, pH 5.5, rpm 200, 72 h | 150 - 180 | 55.2 | [46] |
| *Aspergillus aculeatus* | Ftase from commercial enzyme: Pectinex Ultra SP-L | 60 °C, pH 5.0 – 7.0, 24 h  60 °C, pH 6.0, 16 h | 600  600 | 60.7  88 | [47]  [48]  [49] |
| *Penicillium expansum* | β-fructofuranosidase | 60 °C, pH 5.0 – 6.5, | 200 | GF2 80 %, GF3 19 %, GF4 1% | [50] |
| *Aspergillus foetidus* NRRL 337 | Extracellular fructosyltransferase  (EC 2.4.1.9) | 40 °C – 45 °C, pH 5.0, 120 h | 260 - 470 | 26% - 47 % | [51] |
| *Penicillium citrium* FERM P-15944 | Β-fructofuranosidase | 30 °C, pH 4.0, 100 rpm, 72 h | 100 | 57 | [52] |