## SUPPLEMENTARY DATA:



**Suppl. Fig. 1:** Graphical representation of the different classes of metabolites extracted and identified using LC-MS from tender fruit endosperm of *Borasssus flabellifer* using methanol as solvent

**S. Table 1:** List of proteins detected from pulp part of green *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein   | Score | Accession   | Function   | Reference  |
|------|---|-------|-------------|--|--|
| 1    | Chaperone protein<br>ClpB3, chloroplastic             | 50    | CLPB3_ARATH | *Molecular chaperone essential for chloroplast development and<br>seedling viability.<br>*Mediates internal thylakoid membrane formation and confers<br>thermo tolerance to chloroplasts during heat stress. | https://www.uniprot.org/uni<br>protkb/Q9LF37/entry |
| 2    | protein translocase<br>subunit SecA,<br>chloroplastic | 48    | SECA_OSTLU  | *Has a central role in coupling the hydrolysis of ATP to the transfer of proteins across the thylakoid membrane.   | https://www.uniprot.org/uni<br>protkb/A4RW83/entry |
| 3    | Signal recognition<br>particle 54 kDa protein 2       | 47    | SR542_ARATH | *Binds to the signal sequence of presecretory protein when<br>they emerge from the ribosomes and transfers them to TRAM<br>(translocating chain-associating membrane) protein                                | https://www.uniprot.org/uni<br>protkb/P49966/entry |
| 4    | Germacrene A oxidase                                  | 46    | GAO_LACSA   | Involved in the biosynthesis of germacrene-derived sesquiterpene lactones.   | https://www.uniprot.org/uni<br>protkb/D5J9U8/entry |
| 5    | Flotillin-like protein 2                              | 46    | FLOT2_MEDTR | *May act as a scaffolding protein within caveolar membranes,<br>functionally participating in formation of caveolae or caveolae-   | https://www.uniprot.org/uni<br>protkb/D2XNQ9/entry |

|    |   |    |             | like vesicles (By similarity).<br>*Required for early symbiotic events and nodules formation  |  |
|----|---|----|-------------|---|--|
| 6  | G2/mitotic-specific<br>cyclin-1 (Fragment)                      | 45 | CCNB1_MEDSA | Essential for the control of the cell cycle at the G2/M (mitosis) transition  | https://www.uniprot.org/uni<br>protkb/P30286/entry |
| 7  | NAC domain-containing<br>protein 74                             | 44 | NAC74_ORYSJ | *Transcription activator involved in heat and endoplasmic<br>reticulum (ER) stress responses<br>*Regulates the expression of genes involved in ER protein folding<br>and heat stress-responsive genes<br>*Binds directly to the promoter of BZIP74 and regulates its<br>expression in response to heat stress | https://www.uniprot.org/uni<br>protkb/Q7GCL7/entry |
| 8  | Probable linoleate 9S-<br>lipoxygenase 4                        | 44 | LOX4_ORYSJ  | <ul> <li>* may be involved in a number of diverse aspects of plant<br/>physiology including growth and development, pest resistance,<br/>and senescence or responses to wounding.</li> <li>*Catalyzes the hydroperoxidation of lipids containing a cis,cis-<br/>1,4-pentadiene structure</li> </ul>           | https://www.uniprot.org/uni<br>protkb/Q53RB0/entry |
| 9  | Cinnamoyl-CoA<br>reductase 1                                    | 44 | CCR1_ARATH  | Catalyzes one of the last steps of monolignol biosynthesis, the conversion of cinnamoyl-CoAs into their corresponding cinnamaldehydes.  | https://www.uniprot.org/uni<br>protkb/Q9S9N9/entry |
| 10 | DEAD-box ATP-<br>dependent RNA helicase<br>47                   | 44 | RH47_ARATH  | *Essential protein required during embryogenesis. Required for<br>mitochondrial metabolism.<br>*Necessary for normal plasmodesmata (PD) development and<br>aperture regulation.   | https://www.uniprot.org/uni<br>protkb/Q8W4E1/entry |
| 11 | Catalase isozyme 2  | 44 | CATA2_SOLLC | Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide.   | https://www.uniprot.org/uni<br>protkb/Q9XHH3/entry |
| 12 | Chalcone synthase 2   | 44 | CHS2_MEDSA  | The primary product of this enzyme is 4,2',4',6'-<br>tetrahydroxychalcone (also termed naringenin-chalcone or<br>chalcone) which can under specific conditions spontaneously<br>isomerize into naringenin.  | https://www.uniprot.org/uni<br>protkb/P30074/entry |
| 13 | Myb-related protein Hv1   | 43 | MYB1_HORVU  | *Possible transcription activator in response to an external signal.<br>*May be involved in the regulation of flavonoid biosynthesis  | https://www.uniprot.org/uni<br>protkb/P20026/entry |
| 14 | Probable mannan<br>synthase 10                                  | 43 | CSLAA_ARATH | Probable mannan synthase which consists of a 4-beta-<br>mannosyltransferase activity on mannan using GDP-mannose.   | https://www.uniprot.org/uni<br>protkb/Q9LR87/entry |
| 15 | Alpha,alpha-trehalose-<br>phosphate synthase<br>[UDP-forming] 5 | 43 | TPS5_ARATH  | 2-deoxyglucose, but not phenformin, enhances the phosphorylation of TPS5.   | https://www.uniprot.org/uni<br>protkb/O23617/entry |
| 16 | Putative pumilio<br>homolog 10                                  | 42 | PUM10_ARATH | Sequence-specific RNA-binding protein that regulates translation and mRNA stability by binding the 3'-UTR of target mRNAs.  | https://www.uniprot.org/uni<br>protkb/Q9LP21/entry |
| 17 | Oxygen-evolving<br>enhancer protein 2-1,                        | 42 | PSBP1_ARATH | May be involved in the regulation of photosystem II.  | https://www.uniprot.org/uni                        |

|    | chloroplastic  |    |                 |   | protkb/Q42029/en try                               |
|----|--|----|-----------------|---|--|
| 18 | Protein disulfide<br>isomerase-like 1-3                                  | 42 | PID13_ORYSJ     | Acts as a protein-folding catalyst that interacts with nascent<br>polypeptides to catalyze the formation, isomerization, and reduction<br>or oxidation of disulfide bonds. May play a role in storage protein<br>biogenesis | https://www.uniprot.org/uni<br>protkb/Q69ST6/entry |
| 19 | FACT complex subunit<br>SSRP1  | 41 | SSRP1_VICFA     | The FACT complex is involved in multiple processes that require<br>DNA as a template such as mRNA elongation, DNA replication<br>and DNA repair.  | https://www.uniprot.org/uni<br>protkb/O04235/entry |
| 20 | Glycine-rich protein<br>GWK  | 40 | GRP1_CUCM E     | Possesses antifungal activity against a number of phytopathogenic fungi, including <i>H. sativum</i> and <i>F.culmorum</i>  | https://www.uniprot.org/uni<br>protkb/P84064/entry |
| 21 | ATPase 8, plasma<br>membrane-type  | 40 | PMA8_ARATH      | The plasma membrane H+ ATPase of plants and fungi generates a proton gradient that drives the active transport of nutrients by H+-symport.  | https://www.uniprot.org/uni<br>protkb/Q9M2A0/entry |
| 22 | Membrin-11   | 40 | MEM11_ARAT<br>H | Involved in transport of proteins from the cis/medial-Golgi to the trans-Golgi network.   | https://www.uniprot.org/uni<br>protkb/Q9SJL6/entry |
| 23 | Mitochondrial import<br>inner membrane<br>translocase subunit<br>TIM23-3 | 40 | TI233_ARATH     | *Essential component of the TIM17:23 complex, a complex that<br>mediates the translocation of transit peptide-containing proteins<br>across the mitochondrial inner membrane.<br>*Links the inner and outer membranes       | https://www.uniprot.org/uni<br>protkb/Q9S837/entry |
| 24 | BTB/POZ domain-<br>containing protein<br>At3g50840                       | 47 | Y3084_ARATH     | May act as a substrate-specific adapter of an E3 ubiquitin-protein<br>ligase complex (CUL3-RBX1- BTB) which mediates the<br>ubiquitination and subsequent proteasomal degradation of target<br>proteins.                    | https://www.uniprot.org/uni<br>protkb/Q8LPQ3/entry |
| 25 | Probable pectate lyase 19  | 46 | PLY19_ARATH     | Eliminative cleavage of (1->4)-alpha-D -galacturonan to give<br>oligosaccharides with 4-deoxy-alpha- D-galact-4-enuronosyl<br>groups at their non-reducing ends.  | https://www.uniprot.org/uni<br>protkb/Q9LFP5/entry |
| 26 | Retinoblastoma-related<br>protein 3                                      | 46 | RBR3_MAIZE      | May play a role in the entry into mitosis, negatively regulating the cell proliferation.  | https://www.uniprot.org/uni<br>protkb/Q3LXA7/entry |
| 27 | Antiviral protein MAP  | 45 | RIPP_MIRJA      | Inhibits viral infection of plants, and protein synthesis in vitro.   | https://www.uniprot.org/uni<br>protkb/P21326/entry |
| 28 | Serine carboxypeptid<br>ase II-2 (Fragment)                              | 45 | CBP22_HORVU     | Preferential release of a C-terminal arginine or lysine residue.  | https://www.uniprot.org/uni<br>protkb/P55748/entry |
| 29 | Probable carboxylestera<br>se 9  | 44 | CXE9_ARATH      | Carboxylesterase acting on esters with varying acyl chain length.   | https://www.uniprot.org/uni<br>protkb/O64641/entry |
| 30 | 30S ribosomal protein<br>S8, chloroplastic                               | 44 | RR8_NEPOL       | One of the primary rRNA binding proteins, it binds directly to 16S rRNA central domain where it helps coordinate assembly of the platform of the 30S subunit.   | https://www.uniprot.org/uni<br>protkb/Q9TL24/entry |

| 31 | Hexokinase-3   | 44 | HXK3_ORYSJ  | Fructose and glucose phosphorylating enzyme.   | https://www.uniprot.org/uni<br>protkb/Q2KNB4/entry |
|----|--|----|-------------|--|--|
| 32 | Phenylalanine ammonia-<br>lyase  | 44 | PALY_WHEAT  | Key enzyme of plant metabolism catalyzing the first reaction in<br>the biosynthesis from L-phenylalanine of a wide variety of natural<br>products based on the phenylpropane skeleton  | https://www.uniprot.org/uni<br>protkb/Q43210/entry |
| 33 | Putative geranylgeranyl<br>pyrophosphate synthase<br>8, chloroplastic      | 44 | GGPP8_ARATH | Catalyzes the trans-addition of the three molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate   | https://www.uniprot.org/uni<br>protkb/Q9LRR0/entry |
| 34 | 6-phosphogluc onate<br>dehydrogenas e,<br>decarboxylatin g                 | 44 | 6PGD1_ORYSJ | Catalyzes the oxidative decarboxylation of 6-phosphogluconate<br>to ribulose 5-phosphate and CO2, with concomitant reduction of<br>NADP to NADPH   | https://www.uniprot.org/uni<br>protkb/Q9L100/entry |
| 35 | Putative cellulose<br>synthase A catalytic<br>subunit 11 [UDP-<br>forming] | 44 | CESAB_ORYSJ | Catalytic subunit of cellulose synthase terminal complexes<br>('rosettes'), required for beta-1,4-glucan microfibril<br>crystallization, a major mechanism of the cell wall formation.   | https://www.uniprot.org/uni<br>protkb/Q69XK5/entry |
| 36 | ABC transporter G family member 32   | 42 | AB32G_ARATH | *May be a general defense protein (By similarity).<br>*Required for the formation of the cuticle layer of the cell wall  | https://www.uniprot.org/uni<br>protkb/O81016/entry |
| 37 | DEMETER-like protein<br>2  | 41 | DML2_ARATH  | Potential transcriptional activator that may act by nicking the target promoter.   | https://www.uniprot.org/uni<br>protkb/Q9SR66/entry |
| 38 | Serpin-Z2B   | 41 | SPZ2B_ORYSJ | Probable serine protease inhibitor   | https://www.uniprot.org/uni<br>protkb/Q53KS9/entry |
| 39 | Protein TIFY 8   | 41 | TIF8_ARATH  | Repressor of jasmonate responses.  | https://www.uniprot.org/uni<br>protkb/Q84MB2/entry |
| 40 | Cytochrome P450 78A5   | 41 | C78A5_ARATH | <ul> <li>*Plays a role in regulating directional growth at the meristem/organ boundary.</li> <li>* Functions probably in association with CYP78A7 in regulating relative growth of the shoot apical meristem and plant organs. Is required locally in developing ovules to stimulates cell proliferation and promote seed growth.</li> </ul> | https://www.uniprot.org/uni<br>protkb/Q9LMX7/entry |
| 41 | Copalyl diphosphate<br>synthase 2  | 41 | TPS10_SELML | Monofunctional diterpene synthase converting geranylgeranyl diphosphate to copalyl diphosphate.  | https://www.uniprot.org/uni<br>protkb/J9R388/entry |
| 42 | Ribulose bisphosphate<br>carboxylase large chain                           | 41 | RBL_NEPOL   | *RuBisCO catalyzes two reactions: the carboxylation of D-<br>ribulose 1,5-bisphosphate, the primary event in carbon dioxide<br>fixation, as well as the oxidative fragmentation of the pentose<br>substrate in the photorespiration process.<br>*Both reactions occur simultaneously and in competition at the<br>same active site.          | https://www.uniprot.org/uni<br>protkb/Q9T4F2/entry |
| 43 | Indole-3-acetate O-<br>methyltransferase 1                                 | 41 | IAMT1_ARATH | *Catalyzes the methylation of the free carboxyl end of the plant<br>hormone indole-3-acetic acid (IAA).  | https://www.uniprot.org/uni<br>protkb/Q9FLN8/entry |

|    |  |    |             | *Regulates IAA activities by IAA methylation.   |  |
|----|--|----|-------------|---|--|
| 44 | Long-chain-fatt y-acid<br>[acyl-carrier-protein]<br>ligase AEE15,<br>chloroplastic | 41 | AAE15_ARATH | Probably involved in the activation of fatty acids to acyl-carrier-<br>protein prior to fatty acid elongation in plastids.      | https://www.uniprot.org/uni<br>protkb/Q8W471/entry |
| 45 | Nuclear-pore anchor  | 40 | NUA_ARATH   | Plays a role in meristematic cell division by interacting with spindle assembly checkpoint protein                              | https://www.uniprot.org/uni<br>protkb/A4GSN8/entry |
| 46 | Serine/threonine-protein<br>kinase SRK2I   | 40 | SRK2I_ARATH | In response to ABA, phosphorylate s the ESCRT-I complex component FREE1, which is required for ABA-induced FREE1 nuclear import | https://www.uniprot.org/uni<br>protkb/Q39193/entry |
| 47 | Ubiquinol oxidase 2,<br>mitochondrial  | 40 | AOX2_ARATH  | May increase respiration when the cytochrome respiratory pathway is restricted, or in response to low temperatures              | https://www.uniprot.org/uni<br>protkb/O22049/entry |

**S. Table 2:** List of proteins detected from pulp part of black *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein  | Score | Accession   | Function   | Reference  |
|------|--|-------|-------------|--|--|
| 1    | Aluminum-activated<br>malate transporter 1                                       | 56    | ALMT1_ARATH | Malate transporter critical for aluminum tolerance. The STOP1 transcription factor is required for ALMT1 expression.   | https://www.uniprot.org/uni<br>protkb/Q9SJE9/entry |
| 2    | Protein MADS<br>AFFECTING<br>FLOWERING 5   | 49    | MAF5_ARATH  | *Transcription factor involved in the negative regulation of<br>flowering time in short days, probably through the photoperiodic<br>and vernalization pathways.  | https://www.uniprot.org/uni<br>protkb/Q683D7/entry |
| 3    | Electron transfer<br>flavoprotein-ubiquinone<br>oxidoreductase,<br>mitochondrial | 48    | ETFQO_ORYSJ | Accepts electrons from ETF and reduces ubiquinone.   | https://www.uniprot.org/uni<br>protkb/Q337B8/entry |
| 4    | Oleosin GRP-17   | 47    | GRP17_ARATH | Lipid-binding oleosin pollen coat protein required to mediate pollen recognition by stigma cells and subsequent pollen hydration   | https://www.uniprot.org/uni<br>protkb/Q9LY09/entry |
| 5    | Uncharacterized<br>mitochondrial protein<br>AtMg01230                            | 47    | M1230_ARATH | A stretch of 270 kb of the mitochondrial genome is duplicated within the centromere of chromosome 2 resulting in the duplication of the gene. The expression of the duplicated gene (At2g07697) is not demonstrated. | https://www.uniprot.org/uni<br>protkb/P92553/entry |
| 6    | Leghemoglobin-1  | 46    | LGB1_VICFA  | Provides oxygen to the bacteroids. This role is essential for symbiotic nitrogen fixation.   | https://www.uniprot.org/uni<br>protkb/P02232/entry |

| 7  | ATP-dependent zinc<br>metalloprotease FTSH<br>10, mitochondrial | 45 | FTSHA_ARATH | Probable ATP-dependent zinc metallopeptidase. Involved in the assembly and/or stability of the complexes I and V of the mitochondrial oxidative phosphorylation system.  | https://www.uniprot.org/uni<br>protkb/Q8VZ18/entry |
|----|---|----|-------------|--|--|
| 8  | CBL-interacting protein<br>kinase 30                            | 44 | CIPKU_ORYSJ | CIPK serine-threonine protein kinases interact with CBL proteins.<br>Binding of a CBL protein to the regulatory NAF domain of CIPK<br>protein lead to the activation of the kinase in a calcium-dependent<br>manner                      | https://www.uniprot.org/uni<br>protkb/Q5JLQ9/entry |
| 9  | Nitrate reductase<br>[NADH], clone<br>PBNBR1405                 | 43 | NIA1_BRANA  | Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.  | https://www.uniprot.org/uni<br>protkb/P39867/entry |
| 10 | Expansin-A3   | 43 | EXPA3_ARATH | Causes loosening and extension of plant cell walls by disrupting<br>non-covalent bonding between cellulose microfibrils and matrix<br>glucans. No enzymatic activity has been found  | https://www.uniprot.org/uni<br>protkb/O80932/entry |
| 11 | CMP-sialic acid<br>transporter 3                                | 43 | CSTR3_ARATH | Sugar transporter involved in the transport of CMP-sialic acid fromthe cytoplasm into the Golgi.   | https://www.unprot.org/uni<br>protkb/Q9C5H6/entry  |
| 12 | Ribonuclease 3-like<br>protein 3                                | 42 | RTL3_ARATH  | Ribonuclease that cleaves double-stranded RNA (dsRNA).   | https://www.uniprot.org/uni<br>protkb/Q9FKF0/entry |
| 13 | ATP synthase subunit<br>beta, chloroplastic                     | 42 | ATPB_DIOEL  | Produces ATP from ADP in the presence of a proton gradient across<br>the membrane. The catalytic sites are hosted primarily by the beta<br>subunits.   | https://www.uniprot.org/uni<br>protkb/A6MML4/entry |
| 14 | CSC1-like protein<br>At1g32090                                  | 42 | CSCL1_ARATH | Acts as an osmosensitive calcium-permeable cation channel.   | https://www.uniprot.org/uni<br>protkb/Q9FVQ5/entry |
| 15 | Protein-tyrosine-<br>phosphatase MKP1                           | 42 | MKP1_ARATH  | *May be involved in salt and genotoxic stress responses.<br>*Involved in UV-B stress tolerance.  | https://www.uniprot.org/uni<br>protkb/Q9C5S1/entry |
| 16 | Nudix hydrolase 21,<br>chloroplastic                            | 41 | NUD21_ARATH | Probably mediates the hydrolysis of some nucleoside diphosphate derivatives.   | https://www.uniprot.org/uni<br>protkb/Q8VY81/entry |
| 17 | PHD finger protein<br>ALFIN-LIKE 2                              | 41 | ALFL2_ARATH | Histone-binding component that specifically recognizes H3 tails trimethylated on 'Lys-4' (H3K4me3), which mark transcription start sites of virtually all active genes.  | https://www.uniprot.org/uni<br>protkb/Q9SRM4/entry |
| 18 | Polygalacturonate-4-<br>alpha-<br>galacturonosyltransferase     | 41 | GAUT1_ARATH | *Involved in pectin biosynthesis. Catalyzes the transfer of galacturonic acid from uridine<br>*5'-diphosphogalacturonic acid onto the pectic polysaccharide homogalacturonan.  | https://www.uniprot.org/uni<br>protkb/Q9LE59/entry |
| 19 | EPIDERMAL<br>PATTERNING<br>FACTOR-like protein 8                | 41 | EPFL8_ARATH | Controls stomatal patterning.  | https://www.uniprot.org/uni<br>protkb/Q1G3V9/entry |
| 20 | Ethylene-responsive<br>transcription factor<br>WIN1             | 40 | WIN1_ARATH  | *Promotes cuticle formation by inducing the expression of<br>enzymes involved in wax biosynthesis<br>*May be involved in the regulation of gene expression by stress<br>factors and by components of stress signal transduction pathways | https://www.uniprot.org/uni<br>protkb/Q9XI33/entry |

| 21 | ABC transporter G<br>family member 40                        | 40 | AB40G_ARATH | *May be a general defense protein<br>*Functions as a pump to exclude Pb <sup>2+</sup> ions and/or Pb <sup>2+</sup> -containing<br>toxic compounds from the cytoplasm. Contributes to Pb <sup>2+</sup> ions<br>resistance.                         | https://www.uniprot.org/uni<br>protkb/Q9M9E1/entry  |
|----|--|----|-------------|---|---|
| 22 | Protein argonaute 13   | 40 | AGO13_ORYSJ | Probably involved in the RNA silencing pathway. May bind to short<br>RNAs such as microRNAs (miRNAs) or short interfering RNAs<br>(siRNAs), and represses the translation of mRNAs which are<br>complementary to them                             | https://www.uniprot.org/uni<br>protkb/Q852N2/entry  |
| 23 | ADP-ribosylation factor<br>GTPase-activating<br>protein AGD3 | 47 | AGD3_ARATH  | *Involved in the spatial control of provascular differentiation.<br>Required for the formation of the normal pattern of continuous<br>secondary veins.<br>*Involved in auxin signaling but not in polar auxin transport or in<br>auxin responses. | https://www.uniprot.org/uni<br>protkb/Q5W7F2/entry  |
| 24 | Nitrate reductase<br>[NAD(P)H]                               | 47 | NIA7_HORVU  | Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.   | https://www.uniprot.org/uni<br>protkb/P27968/entry  |
| 25 | Metal-nicotianamine<br>transporter YSL1                      | 46 | YSL1_ARATH  | Involved in iron loading of the seeds. Acts probably as a transporter of iron- a metal-nicotianamine chelates.  | https://www.uniprot.org/uni<br>protkb/Q6R3L0/entry  |
| 26 | Serine protease inhibitor<br>2                               | 45 | SPI2_SOLTU  | Protects the plant by inhibiting proteases of invading organisms, decreasing both hyphal growth and zoospores germination of <i>Phytophthora infestans</i> .  | https://www.uniprot.org/uni<br>protkb/P58515/entry  |
| 27 | Twinkle homolog<br>protein, chloroplastic/<br>mitochondrial  | 45 | TWIH_ARATH  | *Has both DNA primase and DNA helicase activities and may be<br>involved in organelle DNA replication.<br>*Capable of producing RNA primers of 9 to 18 bases from a single-<br>stranded DNA template.   | https://www.uniprot.org/uni<br>protkb/B5X582/entry  |
| 28 | Glutaredoxin-C 8   | 44 | GRXC8_ARATH | Has a glutathione-disulfide oxidoreductase activity in the presence<br>of NADPH and glutathione reductase. Reduces low molecular<br>weight disulfides and proteins  | https://www.uniprot.org/uni<br>protkb/Q8LF89/entry  |
| 29 | DEAD-box ATP-<br>dependent RNA helicase<br>30                | 43 | RH30_ARATH  | ATP-dependent RNA helicase involved nonsense-mediated mRNA decay and ribosome biogenesis through rRNA processing.   | https://www.uniprot.org/uni<br>protkb/Q8W4R3/entry  |
| 30 | Transcription factor<br>HBI1                                 | 43 | HBI1_ARATH  | Transcriptional activity is inhibited when binding to the bHLH transcription factor IBH1.   | https://www.uniprot.org/uni<br>protkb/Q9ZPW3/entry  |
| 31 | Chaperone protein<br>ClpB3, mitochondrial                    | 43 | CLPB3_ORYSJ | Molecular chaperone that may not be involved in heat stress response or tolerance.  | https://www.uniprot.org/uni<br>protkb/Q0E3C8/entry  |
| 32 | Serine hydroxymethylt<br>ransferase 1,<br>mitochondrial      | 42 | GLYM1_ARATH | Functions in the photorespiratory pathway in catalyzing the<br>interconversion of serine and glycine. Involved in controlling cell<br>damage caused by abiotic stress,  | https://www.uniprot.org/uni<br>protkb/Q9SZJ5/en try |
| 33 | DNA-directed RNA<br>polymerase subunit beta                  | 42 | RPOC1_CHAVU | DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.   | https://www.uniprot.org/uni<br>protkb/Q1ACN5/entry  |
| 34 | Anoctamin-like protein                                       | 41 | CACLC_ORYSJ | May act as a calcium-activated chloride channel.  | https://www.uniprot.org/uni                         |

|    | Os01g0706700   |    |                 |   | protkb/Q0JJZ6/entry                                |
|----|--|----|-----------------|---|--|
| 35 | Auxin response factor<br>16                                    | 41 | ARFP_ORYSI      | Auxin response factors (ARFs) are transcriptional factors that bind specifically to the DNA sequence 5'-TGTCTC-3'found in the auxin-responsive promoter elements (AuxREs).  | https://www.uniprot.org/uni<br>protkb/A2YAA5/entry |
| 36 | Auxin response factor<br>11                                    | 41 | ARFK_ARATH      | *Auxin response factors (ARFs) are transcriptional factors that<br>bind specifically to the DNA sequence 5'-TGTCTC-3' found in<br>the auxin-responsive promoter elements (AuxREs).<br>*Could act as transcriptional activator or repressor.                   | https://www.uniprot.org/uni<br>protkb/Q9ZPY6/entry |
| 37 | Calnexin homolog   | 40 | CALX_SOYBN      | *Calcium-binding protein that interacts with newly synthesized<br>monoglucosylated glycoproteins in the endoplasmic reticulum.<br>*It may act in assisting protein assembly and/or in the retention<br>within the ER of unassembled protein subunits.         | https://www.uniprot.org/uni<br>protkb/Q39817/entry |
| 38 | Succinate-semialdehyde<br>dehydrogenase,<br>mitochondrial      | 40 | SSDH_ORYSJ      | Oxidizes specifically succinate semialdehyde. Involved in plant<br>response to environmental stress by preventing the accumulation<br>of reactive oxygen species  | https://www.uniprot.org/uni<br>protkb/B9F3B6/entry |
| 39 | 9-cis-epoxycarotenoid<br>dioxygenase NCED3,<br>chloroplastic   | 40 | NCED3_ARATH     | Catalyzes the first step of abscisic-acid biosynthesis from carotenoids, in response to water stress.   | https://www.uniprot.org/uni<br>protkb/Q9LRR7/entry |
| 40 | LRR receptor-like<br>serine/threonine-protein<br>kinase ERECTA | 40 | ERECT_ARATH     | *Forms a functional ligand-receptor pair with EPF2 (ACQ8LC53)<br>*Modulates plant transpiration efficiency by controlling stomatal<br>density, leaf photosynthetic capacity, epidermal cell expansion,<br>mesophyll cell proliferation and cell-cell contact. | https://www.uniprot.org/uni<br>protkb/Q42371/entry |
| 41 | MLO-like protein 1   | 40 | MLO1_ARATH      | May be involved in modulation of pathogen defense and leaf cell<br>death. Activity seems to be regulated by Ca2+-depende nt<br>calmodulin binding and seems not to require heterotrimeric G<br>proteins   | https://www.uniprot.org/uni<br>protkb/O49621/entry |
| 42 | Small RNA degrading<br>nuclease 1                              | 40 | SDN1_ARATH      | 3'-5' exonuclease degrading single-stranded small RNAs  | https://www.uniprot.org/uni<br>protkb/A3KPE8/entry |
| 43 | Oleosin GRP-17   | 40 | GRP17_ARAT<br>H | *Lipid-binding oleosin pollen coat protein required to mediate<br>pollen recognition by stigma cells and subsequent pollen<br>hydration<br>*Also implicated in the formation of pollen coat   | https://www.uniprot.org/uni<br>protkb/Q9LY09/entry |
| 44 | Pentatricopeptide repeat-<br>containing protein<br>At5g15300   | 40 | GRP17_ARAT<br>H | *Lipid-binding oleosin pollen coat protein required to mediate<br>pollen recognition by stigma cells and subsequent pollen hydration<br>*Also implicated in the formation of pollen coat  | https://www.uniprot.org/uni<br>protkb/Q9LY09/entry |
| 45 | Chaperonin 60 subunit<br>beta 3, chloroplastic                 | 40 | CPNB3_ARAT<br>H | Involved in protein assisted folding.   | https://www.uniprot.org/uni<br>protkb/C0Z361/entry |

**S. Table 3:** List of proteins detected from shell part of green *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein  | Score | Accession       | Function  | Reference  |
|------|--|-------|-----------------|---|--|
| 1    | Superoxide dismutase<br>[Mn] 3.1,<br>mitochondrial         | 54    | SODM1_MAIZE     | Destroys superoxide anion radicals which are normally produced within the cells and which are toxic to biological systems.  | https://www.uniprot.org/uni<br>protkb/P09233/entry |
| 2    | Glutamate receptor 3.4                                     | 52    | GLR34_ARATH     | *Acts as negative regulator of lateral root initiation and<br>development *May restrict primordia numbers and position along<br>the root axis by a signaling process originating in the phloem  | https://www.uniprot.org/uni<br>protkb/Q8GXJ4/entry |
| 3    | Cation/calcium<br>exchanger 3                              | 48    | CCX3_ARATH      | Endomembrane-localized H+-dependent K+ and Na+ transporter.<br>May have a function associated with the pollen vacuole during<br>tube elongation and polarized top growth.   | https://www.uniprot.org/uni<br>protkb/Q9LJI2/entry |
| 4    | Copper-transporting<br>ATPase RAN1                         | 48    | HMA7_ARATH      | Involved in copper import into the cell. Essential for ethylene signaling, which requires copper. Acts by delivering copper to create functional hormone receptors.   | https://www.uniprot.org/uni<br>protkb/Q9S7J8/entry |
| 5    | Prohibitin-5,<br>mitochondrial                             | 46    | PHB5_ARATH      | Prohibitin probably acts as a holdase/unfold ase for the stabilization of newly synthesized mitochondrial proteins.   | https://www.uniprot.org/uni<br>protkb/Q9LY99/entry |
| 6    | Chromatin structure-<br>remo deling complex<br>protein BSH | 45    | BSH_ARATH       | It changes chromatin structure by altering DNA-histone contacts<br>within a nucleosome, leading eventually to a change in<br>nucleosome position, thus facilitating or repressing binding of<br>gene-specific transcription factors.                      | https://www.uniprot.org/uni<br>protkb/P93045/entry |
| 7    | Dynamin-related<br>protein 5A                              | 44    | DRP5A_ARAT<br>H | Probable microtubule-associated force-producing protein that is<br>targeted to the forming cell plate during cytokinesis. May play a<br>role in cell division   | https://www.uniprot.org/uni<br>protkb/F4HPR5/entry |
| 8    | Protein phosphatase<br>2C 32                               | 44    | P2C32_ARATH     | Involved in the regulation of pedicel length and of CLAVATA<br>pathways controlling stem cell identity at shoot and flower<br>meristems.  | https://www.uniprot.org/uni<br>protkb/Q8RWN7/entry |
| 9    | 1-phosphatidyli<br>nositol-3-phos phate<br>5-kinase FAB1B  | 44    | FAB1B_ARATH     | *Plays an important role in maintenance of endomembrane<br>homeostasis including endocytosis, vacuole formation, and<br>vacuolar acidification processes.<br>*Required for development of viable pollen. Might mediate<br>recycling of auxin transporters | https://www.uniprot.org/uni<br>protkb/Q9LUM0/entry |
| 10   | UDP-glycosyltr<br>ansferase 89A2                           | 43    | U89A2_ARATH     | Glucosyltransferase that glucosylates benzoates and benzoate derivatives in vitro.  | https://www.uniprot.org/uni<br>protkb/Q9LZD8/entry |
| 11   | Photosystem II<br>reaction center protein<br>K             | 43    | PSBK_STAPU      | Converts photonic excitation into a charge separation.  | https://www.uniprot.org/uni<br>protkb/Q32RW6/entry |
| 12   | Ninja-family protein<br>Os03g0214200                       | 43    | NNJA1_ORYSJ     | Mediates deactivation and degradation of BZIP46, a positive<br>regulator of ABA signaling and drought stress tolerance.<br>Promotes BZIP46 degradation via interaction with the U-box type<br>ubiquitin E3 ligase PUB70.                                  | https://www.uniprot.org/uni<br>protkb/Q10Q07/entry |

| 13 | Protein RALF-like 10                                   | 41 | RLF10_ARATH  | Cell signaling peptide that may regulate plant stress, growth, and development.  | https://www.uniprot.org/uni<br>protkb/O65919/en try |
|----|--|----|--------------|--|---|
| 14 | Probable metal-<br>nicotian amine<br>transporter YSL16 | 41 | YSL16_ORYS J | May be involved in the transport of nicotianamine- chelated metals.  | https://www.uniprot.org/uni<br>protkb/Q7XN54/entry  |
| 15 | Glutamatecysteine<br>ligase, chloroplastic             | 40 | GSH1_ARATH   | Participates in the detoxification process, the antioxidant response and is essential for embryo development and proper seed maturation. | https://www.uniprot.org/uni<br>protkb/P46309/entry  |

**S. Table 4:** List of proteins detected from shell (mesocarp) part of black *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein  | Score | Accession   | Function   | Reference   |
|------|--|-------|-------------|--|---|
| 1    | CBL-interacting protein kinase 2                                     | 54    | CIPK2_ORYSJ | CIPK serine-threonin e protein kinases interact with CBL<br>proteins. Binding of a CBL protein to the regulatory NAF<br>domain of CIPK protein lead to the activation of the kinase in<br>a calcium-depen dent manner                          | https://www.uniprot.org/u<br>nipro tkb/Q7X996/en try    |
| 2    | Polycomb group<br>protein FIE1                                       | 52    | FIE1_MAIZE  | They probably act via the methylation of histones,<br>rendering chromatin heritably changed in its expressibility  | https://www.uni<br>prot.org/unipro<br>tkb/Q8VZY7/e ntry |
| 3    | Cold shock<br>domain-<br>containing protein<br>4                     | 48    | CSP4_ARATH  | Regulates the flowering transition and flower and seed<br>development, particularly at late stages of embryo<br>development, through regulation of gene expression<br>(including MEA, FIS2, AP1, CAL, AG and SHP2                              | https://www.uni<br>prot.org/unipro<br>tkb/Q38896/en try |
| 4    | ATP synthase 28<br>kDa subunit,<br>mitochondrial<br>(Fragment)       | 48    | ATP7_SPIOL  | During catalysis, ATP synthesis in the catalytic domain of F1 is coupled via a rotary mechanism of the central stalk subunits to proton translocation. Part of the complex F0 domain.  | https://www.uni<br>prot.org/unipro<br>tkb/P80088/ent ry |
| 5    | Probable sucrose-<br>phosphatase 3                                   | 46    | SPP3_ORYSJ  | Catalyzes the final step of sucrose synthesis  | https://www.uniprot.org/u<br>nipro tkb/A3AZW5/e<br>ntry |
| 6    | NADP-dependent<br>D-sorbitol-6-<br>phosphate<br>dehydrogenase        | 45    | S6PD_MALDO  | Synthesizes sorbitol-6-phosphate, a key intermediate in the<br>synthesis of sorbitol which is a<br>major photosynthetic product in many members of the Rosaceae<br>family.   | https://www.uniprot.org/uni<br>protkb/P28475/entry      |
| 7    | Ribulose<br>bisphosphate<br>carboxylase large<br>chain<br>(Fragment) | 44    | RBL_ANTLU   | RuBisCO catalyzes two reactions: the carboxylation of D-<br>ribulose 1,5-bisphosphate, the<br>primary event in carbon dioxide fixation, as well as the oxidative<br>fragmentation of the pentose<br>substrate in the photorespiration process. | https://www.uniprot.org/uni<br>protkb/Q31672/entry      |

| 8  | MLO protein<br>homolog 1   | 44 | MLOH1_HORVU   | May be involved in modulation of pathogen defense and leaf cell death.   | https://www.uniprot.org/uni<br>protkb/O49873/entry      |
|----|--|----|---|--|---|
| 9  | ATPase 7, plasma<br>membrane-typ e<br>OS   | 44 | PMA7_ARATH  | The resulting external acidification and/or internal alkinization may mediate growth responses   | https://www.uni<br>prot.org/unipro<br>tkb/Q9LY32/en try |
| 10 | NAC domain-<br>containing protein<br>12  | 43 | NAC12_ARATH   | May also regulate the secondary cell wall lignification of<br>other tissues. Binds to and activates the promoter of<br>MYB46.                                  | https://www.uni<br>prot.org/unipro<br>tkb/Q9LP17/ent ry |
| 11 | Guanine nucleotide-<br>binding protein<br>subunit beta   | 43 | GBB_NICPL   | Guanine nucleotide-binding protein (G proteins) are involved as<br>a modulator or transducer in<br>various transmembrane signaling systems.                    | https://www.uniprot.org/uni<br>protkb/P93339/entry      |
| 12 | Non-specific lipid-<br>transfer protein 10       43       NLTPA_ARATH       *Plant non-specific lipid-transfer proteins transfer<br>phospholipids as well as galactolipids across mem<br>*May play a role in wax or cutin deposition in the<br>of expanding epidermal cells and certain secretor |    | *Plant non-specific lipid-transfer proteins transfer<br>phospholipids as well as galactolipids across membranes.<br>*May play a role in wax or cutin deposition in the cell walls<br>of expanding epidermal cells and certain secretory tissues | https://www.uniprot.org/uni<br>protkb/Q9LZV9/entry   |   |
| 13 | Dynamin-related<br>protein 5A  | 41 | DRP5A_ARATH   | Probable microtubule-associated force-producing protein that is<br>targeted to the forming cell plate during cytokinesis. May play a<br>role in cell division. | https://www.uniprot.org/uni<br>protkb/F4HPR5/entry      |

## **S. Table 5:** List of proteins detected from liquid (free nuclear endosperm) part of black *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein   | Score | Accession   | Function   | Reference  |
|------|---|-------|-------------|--|--|
| 1    | ATP-dependent zinc<br>metalloprotease<br>FTSH 6,<br>chloroplastic         | 45    | FTSH6_ORYSJ | Probable ATP-dependent zinc metallopeptidase   | https://www.uniprot.org/uni<br>protkb/Q67WJ2/entry |
| 2    | Serine protease<br>inhibitor 7  | 44    | SPI7_SOLTU  | Inhibitor of trypsin (serine protease). May protect the plant by inhibiting proteases of invading organisms  | https://www.uniprot.org/uni<br>protkb/P30941/entry |
| 3    | Homeobox-leucine<br>zipper protein<br>PROTODERMAL<br>FACTOR 2             | 43    | PDF2_ARATH  | Involved, together with HDG proteins, in the regulation of flower<br>organs development by promoting the expression of APETALA 3<br>(AP3) in the epidermis and internal cell layers of developing<br>flowers | https://www.uniprot.org/uni<br>protkb/Q93V99/entry |
| 4    | Phosphatidylinositol<br>/phosphatidylcholine<br>transfer protein<br>SFH10 | 42    | SFH10_ARATH | Required for transport of secretory proteins from the Golgi<br>complex. Catalyzes the transfer of phosphatidylinositol and<br>phosphatidylcholine between membranes in vitro                                 | https://www.uniprot.org/uni<br>protkb/Q9SI13/entry |
| 5    | Probable L-type<br>lectin-domain<br>containing receptor<br>kinase I.2     | 42    | LRK12_ARATH | Involved in resistance response to the pathogenic fungus<br>Alternaria brassicicola  | https://www.uniprot.org/uni<br>protkb/Q7FK82/entry |
| 6    | Probable anion<br>transporter 2,<br>chloroplastic                         | 41    | PHT42_ORYSJ | Probable anion transporter   | https://www.uniprot.org/uni<br>protkb/Q53WP9/entry |

| 7  | Chaperone protein<br>ClpB4,<br>mitochondrial                                  | 41 | CLPB4_ARATH | Molecular chaperone that does not seem to be involved in heat stress response or tolerance   | https://www.uniprot.org/uni<br>protkb/Q8VYJ7/entry |
|----|---|----|-------------|--|--|
| 8  | Eukaryotic<br>translation initiation<br>factor 4G                             | 40 | IF4G_ARATH  | Component of the protein complex eIF4F, which is involved in<br>the recognition of the mRNA cap, ATP-dependent unwinding of<br>5'-terminal secondary structure and recruitment of mRNA to the<br>ribosome. | https://www.uniprot.org/uni<br>protkb/Q76E23/entry |
| 9  | Protein HUA2-LIKE<br>2  | 40 | HUAL2_ARATH | Plays diverse and essential roles in the control of plant development, physiology and flowering time   | https://www.uniprot.org/uni<br>protkb/F4IN78/entry |
| 10 | 50S ribosomal<br>protein L1,<br>chloroplastic                                 | 40 | RK1_PEA     | This protein binds directly to 23S ribosomal RNA   | https://www.uniprot.org/uni<br>protkb/P49208/entry |
| 11 | Pentatricopeptide<br>repeat-containing<br>protein At3g49170,<br>chloroplastic | 40 | PP272_ARATH | May play a role in embryogenesis   | https://www.uniprot.org/uni<br>protkb/Q5G1T1/entry |
| 12 | Golgin candidate 6  | 39 | GOGC6_ARATH | Golgi matrix protein playing a role in tethering of vesicles to<br>Golgi membranes and in maintaining the overall structure of the<br>Golgi apparatus  | https://www.uniprot.org/uni<br>protkb/B0F9L4/entry |
| 13 | NAP1-related<br>protein 2   | 39 | NRP2_ORYSJ  | Acts as histone H2A/H2B chaperone in nucleosome assembly   | https://www.uniprot.org/uni<br>protkb/Q69JW2/entry |
| 14 | Elongator complex<br>protein 4  | 39 | ELP4_ARATH  | Involved in the repression of the abscisic acid (ABA) signaling<br>pathway during seed germination and seedling growth. Required<br>for auxin distribution or signaling.                                   | https://www.uniprot.org/uni<br>protkb/Q9C778/entry |
| 15 | Glycine-rich cell<br>wall structural<br>protein                               | 39 | GRP1_ARATH  | Responsible for plasticity of the cell wall.   | https://www.uniprot.org/uni<br>protkb/P27483/entry |
| 16 | Protein-L-<br>isoaspartate O-<br>methyltransferase                            | 39 | PIMT_WHEAT  | It plays a role in the repair and/or degradation of damaged proteins.  | https://www.uniprot.org/uni<br>protkb/Q43209/entry |
| 17 | Cytokinin<br>dehydrogenase 7  | 39 | CKX7_ORYSJ  | Catalyzes the oxidation of cytokinins  | https://www.uniprot.org/uni<br>protkb/Q6YW50/entry |

**S. Table 6:** List of proteins detected from liquid (free nuclear endosperm) part of green *B. flabellifer* analyzed by LC-MS/MS using 100 mM of phosphate buffer, pH 7.6 and trypsin digested.

| S.No | Protein                               | Score | Accession   | Function   | Reference  |
|------|---------------------------------------|-------|-------------|--|--|
| 1    | Beta-glucosidase 45                   | 40    | BGL45_ARATH | Hydrolyzes p-nitrophenyl beta-D-glucoside and natural glucosides<br>such as syringin, coniferin and p-coumaryl alcohol glucoside.<br>May be involved in lignification by hydrolyzing monolignol<br>glucosides. | https://www.uniprot.org/uni<br>protkb/O80689/entry |
| 2    | IAA-amino acid<br>hydrolase ILR1-like | 40    | ILL8_ORYSJ  | Hydrolyzes certain amino acid conjugates of the plant growth regulator indole-3-acetic acid (IAA)  | https://www.uniprot.org/uni<br>protkb/Q8H3C8/entry |

|    | 8   |    |              |   |  |
|----|---|----|--------------|---|--|
| 3  | ATP synthase<br>subunit a   | 40 | ATP6_TRITI   | It may play a direct role in the translocation of protons across the membrane.  | https://www.uniprot.org/uni<br>protkb/P68526/entry         |
| 4  | Phosphatidylinositol/<br>phosphatidylcholine<br>transfer protein<br>SFH2              | 40 | SFH2_ARATH   | Catalyzes the transfer of phosphatidylin ositol and<br>phosphatidylch oline between membranes in vitro  | https://www.uniprot.org/uni<br>protkb/F4JVA9/entry         |
| 5  | 30S ribosomal<br>protein S4,<br>chloroplastic   | 40 | RR4_ANGEV    | One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit.   | https://www.uniprot.org/uni<br>protkb/A2T335/entry         |
| 6  | CBL-interacting<br>serine/threonine-<br>protein kinase 23                             | 40 | CIPKN_ARAT H | *Confers tolerance to low potassium conditions.<br>*Involved in drought sensitivity and leaf transpiration.   | https://www.uniprot.org/uni<br>protkb/Q93VD3/entry         |
| 7  | Plasma membrane<br>ATPase 1   | 40 | PMA1_SOLLC   | *The proton gradient it generates drives the active transport of nutrients by H+-symport.   | https://www.uniprot.org/uni<br>protkb/P22180/entry         |
| 8  | Structural<br>maintenance of<br>chromosomes<br>protein 3                              | 40 | SMC3_ARATH   | Structural maintenance of chromosomes protein 3   | https://www.uniprot.org/uni<br>protkb?query=SMC3_ARA<br>TH |
| 9  | Exocyst complex<br>component SEC15A   | 39 | SC15A_ARATH  | Involved in polarized cell growth and organ morphogenesis.<br>During cytokinesis, involved in cell plate initiation, cell plate<br>maturation and formation of new primary cell wall. | https://www.uniprot.org/uni<br>protkb/Q9LXX6/entry         |
| 10 | ATP synthase<br>subunit b,<br>chloroplastic   | 39 | ATPF_SPIOL   | F1F0 ATP synthase produces ATP from ADP in the presence of a proton or sodium gradient  | https://www.uniprot.org/uni<br>protkb/P06453/entry         |
| 11 | Probable disease<br>resistance protein<br>At5g45510                                   | 38 | DRL36_ARATH  | Probable disease resistance protein   | https://www.uniprot.org/uni<br>protkb/Q8VZC7/entry         |
| 12 | Probable cytokinin<br>riboside 5'-<br>monophosphate<br>phosphoribohydrolas<br>e LOGL5 | 38 | LOGL5_ORYSJ  | Phosphoribohydrolase that converts inactive cytokinin nucleotides<br>to the biologically active free-base forms   | https://www.uniprot.org/uni<br>protkb/Q84M85/entry         |
| 13 | Transportin-1   | 38 | TNPO1_ARATH  | Functions in nuclear protein import as nuclear transport receptor.  | https://www.uniprot.org/uni<br>protkb/Q8H0U4/entry         |
| 14 | Protein trichome<br>birefringence-like 11   | 38 | TBL11_ARATH  | May act as a bridging protein that binds pectin and other cell wall polysaccharides.  | https://www.uniprot.org/uni<br>protkb/Q5BPJ0/entry         |
| 15 | Glycoprotein 3-<br>alpha-L-<br>fucosyltransferase A                                   | 38 | FUT11_ARATH  | Involved in cell wall synthesis   | https://www.uniprot.org/uni<br>protkb/Q9LJK1/entry         |

**S. Table 7:** List of identified mineral oxides from lyophilized and powdered tender fruit endosperm of *B. flabellifer* by X- ray diffraction (Scan range-  $5^{\circ}$  to  $90^{\circ}$ )

| Name of the<br>sample | 2θ values (in degrees) for the major<br>peaks  | Match found in reference database  | Crystallography Open<br>Database- Entry no.  |
|-----------------------|--|--|--|
| Black variety         | 25.27, 25.61, 25.74, 26.17, 26.28, 26.70,<br>27.18, 27.44, 27.58, 27.44, 27.58, 27.76,<br>27.97, 28.08, 28.32, 28.64, 28.86, 30.16,<br>30.35, 30.61, 32.07 | Lead oxide bromide/chloride $(Br_{1.25} ClO_{2.75} Pb_{3.88})$<br>Calcium zirconium tantalum oxide $(Ca_7 O_{36} Ta_6 Zr_7)$<br>$O_{118} Sc_{12.14} Zr_{49.86}$<br>$Cs_{48} O_{21} Sn_{20}$<br>Bismuth strontium copper oxide $(Bi_4 Cu_5 O_{20.5} Sr_8)$<br>Arsenpolybasite $(Ag_{29.786} As_{3.762} Cu_{2.214} S_{22} Sb_{0.238})$ | Entry no.: 96-433-2260<br>Entry no.: 96-200-3174<br>Entry no.: 96-153-2825<br>Entry no.: 96-153-7111<br>Entry no.: 96-100-6013<br>Entry no.: 96-901-0622 |
| Green variety         | 24.48, 24.96, 25.36, 26.46, 27.03, 27.97,<br>28.79, 29.24, 29.70, 30.21, 30.44, 30.80,<br>31.03, 31.34, 31.66, 31.92, 32.52                                | Vurroite $(As_{4.71} Bi_{6.97} Cl_3 Pb_{9.6} S_{27} Sn_{0.72})$<br>$B_{10} Cu_{15} O_{30}$<br>$Cs_{48} O_{21} Sn_{20}$<br>$Bi_{46} O_{89} V_8$<br>Barium fluoroniobate $(Ba_4 F_{12} Nb_2 O_3)$<br>$Ce_2 Fe O_2 Se_2$  | Entry no.: 96-901-0439<br>Entry no.: 96-210-5419<br>Entry no.: 96-153-7111<br>Entry no.: 96-153-6257<br>Entry no.: 96-100-0325<br>Entry no.: 96-710-5871 |