

(19) **DANMARK**



Patent- og
Varemærkestyrelsen

(10) **DK/EP 3536800 T3**

(12) Oversættelse af
europæisk patentskrift

-
- (51) Int.Cl.: **C 12 P 7/64 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2021-11-01**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2021-08-04**
- (86) Europæisk ansøgning nr.: **18161079.1**
- (86) Europæisk indleveringsdag: **2018-03-09**
- (87) Den europæiske ansøgnings publiceringsdag: **2019-09-11**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
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- (54) Benævnelse: **EKSTRAHERING AF FORNYELIGE TRIGLYCERIDER FRA OLIEHOLDIGE MIKROORGANISMER**
- (56) Fremdragne publikationer:
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DESCRIPTION

[0001] The present invention refers to a method for extracting a triglyceride, a sugar and/or an amino acid from an oleaginous microorganism. Further, it is directed to the use of an enzyme system comprising an enzyme having hydrolase activity in such method.

Technical background

[0002] In the past decade, the global demand for plant- and animal-based lipids as platform for pharmaceutical, food, biofuel and oleochemical industry increased by 65%. To meet the increase of market demand with taking into consideration the environmental aspects as to mitigate the CO₂ emissions motivate industry to develop novel sustainable bioprocesses.

[0003] With an ability to accumulate up to 70% lipids of their dry weight, oleaginous microorganisms are poised to be the next generation for host lipid production. The conversion of microorganism's lipids into bio-kerosene, bio-diesel and bio-lubricants as well pharmaceutical and food applications has been well documented.

[0004] For example *Trichosporon oleaginosus* (*T. oleaginosus*; ATCC 20509), first isolated in 2011, shows a high ability to uptake varied monomeric carbon sources of pentoses and hexoses as well as complex waste material feedstocks. Under stress conditions, such as nitrogen, phosphate or sulfate limitation, *T. oleaginosus* converts these C-sources into triacylglycerol lipids, which are subsequently stored in sub-cellular droplets. In addition, commonly used oleaginous microorganisms exhibit fast growth rates and the fatty acid profile is close to that of the vegetable oils.

[0005] Biofuel, as yet, is occupied the main focusing of the single cell oil (SCO) production. Conversely, creating biopharmaceutical-based applications, so called red biotechnology of SCO has not well established so far. A very recent report, has expressed that SCO can be a valuable source of food-additive PUFAs. Görner *et al.* presented the engineering of *T. oleaginosus* for enhanced production of long-chain unsaturated fatty acids, such as eicosatrienoic, eicosadienoic and α -linolenic acid (Görner, C., et al., Genetic engineering and production of modified fatty acids by the non-conventional oleaginous yeast *Trichosporon oleaginosus* ATCC 20509. *Green Chemistry*, 2016, 18(7): p. 2037-2046). Moreover, Devyani *et al.* confirm that *Lipomyces starkey* can produce a PUFAs through submerged fermentation (Salunke, D., et al., Production of polyunsaturated fatty acids in recombinant *Lipomyces starkeyi* through submerged fermentation. *Bioprocess and biosystems engineering*, 2015, 38(7): p. 1407-1414).

[0006] Under stress conditions, oleaginous microorganisms generate lipid (triglyceride) droplets (LD) as storage compartments for triacylglycerols. The ultrastructure of lipid droplets consists of a phospholipid monolayer that contains bound proteins, which enables attachments

to other cell compartments that represents a stable emulsifier system. Furthermore, a rigid cell-wall renders the cells resistant to many solvents, which complicates downstream lipid extraction procedures.

[0007] Conventional triglyceride extraction procedures require two discrete consecutive steps: The initial step comprises cell-wall lysis either via temperature shocks, chemical treatment or high pressure homogenization. In the second step triglycerides are extracted with organic solvent such as petroleum ether, methanol, or chloroform. None of these methods are easily scaled to industrial level due to cost issues and lack of environmental sustainability. Moreover, the latter application of organic solvents negatively impacts the quality of the finished product. Hence, the complexity of solvent removal is considered as extra cost and energy squandering.

[0008] Enzymatic approaches have previously been applied to enhance the cell rupture of oleaginous yeasts. To that end enzyme-assisted lipid release and subsequent ethyl acetate lipid extraction has recently been reported for *Rhodospiridium toruloides*. In analogy, a process termed enzyme-assisted aqueous extraction processing (EAEP) was applied to lipid extraction in the microalgae *Chlorella vulgaris*, *Scenedesmus dimorphus*, and *Nannochloropsis* sp. In the EAEP, a pretreatment of ultrasonic irradiation and posttreatment of heating at 95 °C was required. These pre-/post-treatments considered as a high-energy consuming process thus it is inapplicable at industrial scale. In 2011, a mix of different enzymes papain, pectinase, snailase, neutrase, alcalase and cellulase were optimized on the filamentous fungus *Mortierella alpina* for arachidonic acid extraction. To support the hydrolysis procedure, an addition of hexane was still required. Overall published processes, various pretreatments have been applied prior to the enzymatic cell lysis. Moreover, the lipids still have to be extracted with an organic solvent to recover the triglycerides.

[0009] It is of great interest to gain triglycerides of high purity and high rate of yield from microorganisms also due to problematic agricultural gaining of oil such as palm oil. It is divisive because palm oil was initially touted as a "green" crop and literally a fuel in making products less harmful to the atmosphere. The oil is a key component in biodiesel, considered a potential replacement for fossil fuel-based gasoline as an energy source for automobiles.

[0010] WO 2010/138620 discloses methods for the extraction of triglycerides from microbial biomass using an organic solvent and/or surfactants. WO 2002/10423 describes the extraction of microbial oil by cell lysis using enzymatic, physical or mechanical methods and separation of the oil, preferably polyunsaturated fatty acids (PUFA), via centrifugation. WO 2003/092628 refers to methods for the extraction of PUFAs from a plant or microorganism using surfactants Zheng et al. (Algal Research 2016, vol. 14, p. 100-108) discloses the use of amine co-polymers for increasing enzymatic cell wall disruption.

[0011] Hence, there is a need for an efficient, environmentally compatible, low-energy consuming method for gaining a triglyceride which method is suitable for small scale as well as industrial applications.

[0012] For the first time the present invention provides a single step pretreatment recovery process for single microorganism oils based on enzymatic lysis of an oleaginous microorganism followed by a simple demulsification. The process is scalable from lab to technical scale without causing any major investments.

Summary

[0013] The present invention is as defined in the claims. It refers to a method for extracting a triglyceride from an oleaginous microorganism comprising the steps:

1. a) adding an enzyme system to the oleaginous microorganism, wherein the enzyme system comprises hydrolase activity to hydrolyze the cell wall of the microorganism,
2. b) optionally adding a protease, which is for example a serine protease or a group thereof, to the hydrolyzed oleaginous microorganism, and
3. c) adding a short-chain polymer, which is for example linear, branched or cross-linked, to the hydrolyzed oleaginous microorganism of step a) and/or b) for demulsification, wherein three separate layers are formed, one comprising the triglyceride, a second comprising cell debris and a third comprising sugar and/or amino acids, and
4. d) optionally isolating the triglyceride layer, which comprises for example short-chain, medium-chain or long-chain triglycerides or a combination thereof

[0014] The oleaginous microorganism is for example a fungi, yeast, bacteria or algae such as microalgae for example selected from the group consisting of *Trichosporon oleaginosus*, *Trichosporon capitatu*, *Trichosporon asahii*, *Lipomyces starkeyi*, *Rhodospiridium toruloides*, *Yarrowia lipolytica*, *Rhodotorula graminis*, *Rhodotorula glutinis*, *Cutaneotrichosporon oleaginosus*, *Apiotrichum curvarum*, *Cryptococcus curvatus*, *Candida sp*, *Rhodotorula gracilis*, *Chlorella sp.*, *Pseudochlorococcum sp.*, *Nannochloris sp*, *Nannochloropsis sp.*, *Isochrysis sp*, *Tribonema minus*, *Dunaliella sp.*, *Ankistrodesmus sp.*, *Botryococcus braunii*, *Pavlova sp.*, *Scenedesmus sp.*, *Skeletonema sp.*, *Nitzschia sp.*, *Rhodococcus opacus*, *Acinetobacter calcoaceticus* and *Bacillus alcalophilus*.

[0015] The hydrolase activity of the enzyme system used in the method of the present invention is selected from the group consisting of cellulase, hemicellulase, mannase, laminarinase, glucanase, galacturonase, polygalacturonase, pectinase, glucosidase and a combination thereof.

[0016] The pH of step a) is for example in the range of 3 to 7, in the range of 4 to 6 or in the range of 4 to 5, and the temperature T is for example in the range of 30 °C to 70°C, in the range of 40 °C to 55 °C or in the range of 40 °C to 45 °C for any of the pH ranges.

[0017] The pH of step b) is for example in the range of 6 to 10, in the range of 7 to 9 or 8, and

the temperature T is for example in the range of 25 °C to 45°C, in the range of 30 °C to 40 °C or in the range of 35 °C to 37 °C for any of the pH ranges.

[0018] The short-chain polymer used according to the present invention is selected from the group consisting of polyglycol, polyadduct of polyglycol and alkenyl succinic acid anhydride, polyester of polyglycol, alkenyl succinic anhydride polyester, block copolymer of propylenoxide and ethylenoxide, polyglycerol, polyester of poly- α -olefine and a combination thereof.

[0019] The triglycerides isolated by the method of the present invention comprise for example palmitic acid (C_{16:0}), stearic acid (C_{18:0}), oleic acid (C_{18:1}), linoleic acid (C_{18:2}), α -linolenic acid (C_{18:3}), arachidic acid (C_{20:0}), arachidonic acid (C_{20:4}), eicosapentaenoic acid (C_{20:5}), behenic acid (C_{22:0}), lignoceric acid (C_{24:0}) or a combination thereof.

[0020] In addition to or alternatively to isolating the triglyceride layer, the sugar layer is isolated, wherein the sugar is for example selected from the group consisting of glucuronic acid, rhamnose, fucose, mannitol, xylose, mannose, glucose and a combination thereof, optionally comprising an amino acid which is further isolated.

[0021] The present invention further refers to the use of an enzyme system comprising an enzyme having hydrolase activity as defined in claim 1, in a method of the present invention.

[0022] All documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, may be employed in the practice of the invention.

Description of figures

[0023] The following figures show the invention in more detail, however, the invention is not limited to these figures.

Figures 1A and 1C depict the biomass composition of *Trichosporon oleaginosus*, cultivated for 5 days at 28 °C. **Figures 1B and 1D** show sugar compositions of *Trichosporon oleaginosus* via chemical hydrolysis at 2.0, 3.0, 10.0 [% v/v] H₂SO₄, for 60 min at 121 °C. The media used are YPD media in **Figures 1A and 1B** and minimal Nitrogen Media in **Figures 1C and 1D**.

Figure 2 shows a residual biomass of treated *T. oleaginosus* with mix 15 (comprising mannanase, Cellic Ctec2, Cellic Htec and beta-glucosidase) and mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase). Cells were incubated for 12 hours (white) and 18 hours (black) at pH 5.0 (Acetate buffer, 50.0 mM), 55.0 °C with 250 rpm. Starting (striped): the amount of biomass at the starting of reaction, Control 2 (dotted) biomass was incubated at same condition without any enzyme additions.

Figure 3 depicts a released triglyceride of treated *T. oleaginosus* with mix 15 (comprising mannanase, Cellic Ctec2, Cellic Htec and beta-glucosidase) and mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase). Cells were incubated for 12 hours (white) and 18 hours (black) at pH 5.0 (Acetate buffer, 50.0 mM), 55.0 °C with 250 rpm. Used controls: Chemical (striped) the extracted triglyceride after high-pressure homogenizer followed by solvent extraction. Control (dotted) biomass was incubated at same condition without any enzyme additions.

Figure 4 depicts a residual biomass of treated *T. oleaginosus* at different pH conditions which were pH 4.0, 4.5, 5.0, 5.5 and 6.0 (Acetate buffer, 50.0 mM). Cells were incubated with mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 12 (white) and 18 (black) hours at 55 °C and 250 rpm. Used controls: Starting (striped): the amount of biomass at the starting of reaction, Control 2 (dotted) biomass was incubated at same condition without any enzyme additions.

Figure 5 shows released lipid of treated *T. oleaginosus* at different pH conditions which were 4.0, 4.5, 5.0, 5.5 and 6.0 (Acetate buffer, 50.0 mM). Cells were incubated with mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 12 (white) and 18 (black) hours at 55 °C and 250 rpm. Used controls: Chemical (striped) the extracted triglyceride after high-pressure homogenizer followed by solvent extraction, Control (dotted) biomass was incubated at same condition without any enzymes additions.

Figures 6A - 6C show the density blot and cell count of treated *T. oleaginosus* (logarithmic scaling of x- and y-axis is identical). **Figure 6A** refers to untreated samples (Control), **Figure 6B** to samples treated at pH 4.5 and **Figure 6C** to samples treated at pH 5.0 (Acetate buffer, 50.0 mM). Samples were incubated with mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 18 hours at 55 °C and 250 rpm.

Figure 7 depicts residual biomass of treated *T. oleaginosus* under different temperatures: 40, 45, 50 and 55°C. Cells were incubated with mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 12 (white) and 18 (black) hours, at pH 4.0 (Acetate buffer, 50.0 mM) with 250 rpm. Used controls: Starting (striped): the amount of biomass at the starting of the reaction, Control 2 (dotted) biomass was incubated at same condition without any enzyme additions.

Figure 8 depicts released triglyceride of treated *T. oleaginosus* under different temperatures: 40, 45, 50 and 55°C. Cells were incubated with mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 12 (white) and 18 (black) hours, at pH 4.0 (Acetate buffer, 50.0 mM) with 250 rpm. Used controls: Chemical (striped) the extracted triglyceride after high-pressure homogenizer followed by solvent extraction, Control (dotted) biomass was incubated at same condition without any enzyme additions.

Figure 9 shows the relative cell count of treated *T. oleaginosus* at different incubation periods (0, 3, 7 and 18 h) with Mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) at 0.55 [% w/w]. Cells were incubated at pH 4.5 and a temperature of

45.0 °C, the control refers to treatment with 3 times high-pressure homogenizer.

Figure 10 depicts the relative cell count of treated *T. oleaginosus* at different incubation periods (0, 5.5, 8, 13 and 18 h) with Mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) at 0.8 [% w/w]. Cells were incubated at pH 4.5 and a temperature of 5.0 °C. Control 1 is an untreated sample, Control 2 refers to treatment with 3 times high-pressure homogenizer.

Figures 11A - 11F show the density blot of treated *T. oleaginosus* at different incubation time periods (0, 3, 7 and 18 h) with Mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) at 0.55 [% w/w]. Cells were incubated at pH 4.5 and a temperature of 45.0 °C. The control refers to treatment with 3 times high-pressure homogenizer. **Figures 11G - 11K** depict the corresponding fluorescence microscope observation at a microscope magnification of 100x and exposure time of 39 m sec. Logarithmic scaling of x- and y-axis in **Fig. 11A-11C, 11E and 11F** is identical.

Figure 12 shows the relative cell count of treated *T. oleaginosus* at different concentrations (0, 0.55, 0.8 and 1.1 [% w_{protein} / dw_{biomass}]) of Mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 5.5 h. Cells were incubated at pH 4.5 and a temperature of 45.0 °C. Control 1 refers to an untreated sample, Control 2 to the treatment with 3 times high-pressure homogenizer.

Figure 13 depicts the relative cell count of treated *T. oleaginosus* at different concentrations (0, 0.25, 0.8 and 1.3 [% w_{protein} / dw_{biomass}]) of Mix 21 (comprising Liquebeet, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase) for 13 h. Cells were incubated at pH 4.5 and a temperature of 45.0 °C. Control 1 refers to an untreated sample, Control 2 to the treatment with 3 times high-pressure homogenizer.

Figures 14A - 14F depict the density blot of treated *T. oleaginosus* at different concentrations of Mix 21 (comprising Liquebeet, i.e., a glycoside hydrolase, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase): **Fig. 14A:** 0.0 [% w/w], **Fig. 14B:** 0.55 [% w/w], **Fig. 14C:** 0.8 [% w/w], **Fig. 14D:** 1.1 [% w/w], **Fig. 14E:** 1.3 [% w/w], and **Fig. 14F:** 3x Avestin (Control). Cells were incubated for 13 hours at pH 4.5, 45 °C and 250 rpm.

Figures 15A - 15D show released triglyceride of *T. oleaginosus* treated with glycoside hydrolase and Mix 21 (comprising Liquebeet, i.e., a glycoside hydrolase, CLA, mannanase, 1,3-beta-glucanase and beta-glucosidase), respectively, at different times (0, 10.5 and 15.5 h) and protease concentrations (0, 0.73 and 1.7 [% w_{protein} / dw_{biomass}]), transverse striped column is without protease addition. Cells were incubated at pH 4.5 and a temperature of 45.0 °C for cell-lysis. Protease treatment was conducted at pH 8.0 and a temperature of 37.0. Control 1 (checked) refers to the extracted lipid after high-pressure homogenizer followed by solvent extraction, Control 2 (longitudinally striped) to the untreated biomass.

Figures 16A - 16D show released lipid (**Fig. 16A**), residual biomass (**Fig. 16B**), density blot and cell counts (**Fig. 16C**) and corresponding fluorescence microscope observation of treated *T. oleaginosus* at different time points (13 and 15.5 h for cell-lysis and 5.5, 8.0 and 10.5 h for

protease treatment) and enzymes concentrations (1.1 and 1.3 [% w/w] for cell-lysis and 0.73, 1.2 and 1.7 [% w/w] for protease treatment; **Fig. 16D**). Cells were incubated at pH 4.5 and a temperature of 45.0 °C for cell-lysis. Protease treatment was conducted at pH 8.0 and a temperature of 37.0. Control 1 (in green) refers to the extracted triglyceride after high-pressure homogenizer followed by solvent extraction, Control 2 (in orange) refers to untreated biomass. Microscope magnification of 100x at exposure time 39 m sec.

Figures 17A - 17D show electron microscope scatter for untreated cell (**Fig. 17A**), TO after treatment with 3x Avestin (**Fig. 17B**), *T. oleaginosus* after cell lysis step (**Fig. 17C**) and after protease treatment (**Fig. 17D**). Magnification of 1500 x, 5.0 KV with SEM detector.

Figures 18A - 18D depict electron microscope photos for untreated cells (**Fig. 18A**), *T. oleaginosus* after treatment with 3x Avestin (**Fig. 18B**), *T. oleaginosus* after cell lysis step (**Fig. 18C**) and after protease treatment (**Fig. 18D**). Magnification of 10000 x, 5.0 KV with SEM detector.

Figure 19 shows released triglyceride after addition of different short-chain polymers (dissolvan). Cells were incubated at pH 4.5 and a temperature of 45.0 °C with Mix 21 for cell-lysis. Protease treatment was conducted at pH 8.0 and a temperature of 37.0 °C. Used short-chain polymers: **1.** Polymer of mixed alkoxylat-ethyl-glycerol, **2.** Propoxylated EO/PO block polymer-bis glycidyl ether with excess of EO, **3.** Propoxylated EO/PO block polymer-bis glycidyl ether (low, < 50 % PO), **4.** Polypropylenglycol of high MW with excess of EO (> 30 %), **5.** Cross-linked PEG, **6.** Poly- α olefin-polyester (active ingredient > 80%), **7.** Poly- α olefin-polyester (active ingredient > 98%) and **8.** Propoxylated EO/PO block polymer-bis glycidyl ether (high, > 50 % PO).

Figure 20 depicts the fatty acid profiles of extracted triglycerides via (blue) chemical method and (red) enzymatic method. The fatty acid profile was quantified using GC-FID after methylation under acid and base conditions. C19 TAG was used as internal standard for methylation efficiency.

Figure 21 shows the sugar profile of hydrolysis of the cell-wall polysaccharides of *T. oleaginosus*.

Figures 22A - 22C depict the releasing of triglyceride layer on the top of the reaction tube (**Fig. 22A**). The separation was obtained via centrifugation at 9000 g for 20 min. The density blot, "Y" axis is fluorescence at 588±24 nm and "X" axis is forward scatter (**Fig. 22B**) and the density blot, "Y" axis is side scatter and "X" axis is forward scatter (**Fig. 22C**).

Detailed description

[0024] The present invention is directed to a novel downstream process for triglyceride recovery from oleaginous microorganisms such as bacteria, fungi, yeast and algae, e.g.

microalgae, with low energy consumption and a recovery rate of up to 99.9 % for example 90, 91, 92, 93, 94, 95 96, 97, 98, 99 or 99.9 % of the total accumulated lipid in the microorganism with a method completely free of the use of a solvent. Cell lysis is based on enzymatic treatment using an enzyme system comprising for example a combination of enzymes having a synergistic lysis effect. In addition, the method of the present invention comprises the addition of a short-chain polymer as defined in claim 1, to the hydrolyzed oleaginous microorganism resulting in the formation of a triglyceride layer and a cell debris layer and a sugar layer optionally comprising an amino acid.

[0025] In the following, the elements of the present invention will be described in more detail. These elements are listed with specific embodiments, however, it should be understood that they may be combined in any manner and in any number to create additional embodiments falling within the scope of the claims. The variously described examples and embodiments should not be construed to limit the present invention to only the explicitly described embodiments. This description should be understood to support and encompass embodiments which combine the explicitly described embodiments with any number of the disclosed elements. Furthermore, any permutations and combinations of all described elements in this application should be considered disclosed by the description of the present application unless the context indicates otherwise and as long as they fall within the scope as defined in the claims.

[0026] Throughout this specification and the claims, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated member, integer or step or group of members, integers or steps but not the exclusion of any other member, integer or step or group of members, integers or steps. The terms "a" and "an" and "the" and similar reference used in the context of describing the invention (especially in the context of the claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by the context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as", "for example"), provided herein is intended merely to better illustrate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[0027] The present invention refers to a solvent free, e.g., *in-situ* method for direct release of lipids from oleaginous microorganisms. The method is characterized by moderate conditions regarding temperature with low energy consumption based on enzymatic hydrolysis of the cell-wall followed by a demulsification step comprising breaking the emulsifier system of the cell via protease treatment and treatment with a short-chain polymer of the residual biomass to recover pure lipids after mild centrifugation or separation, e.g., using a milk-separator or milk-

separator like device. In a side aspect, the method of the present invention creates operating costs in total about ten times less than operating costs of classical methods.

[0028] One of the key challenges for the scalability of single cell lipid production is the need to implement an industrial-applicable downstream process for lipid recovery with low energy consumption and an additional criteria for food and pharmaceutical application is the recovery of a triglyceride and optionally other end-products such as sugar and/or amino acids free from any traces of organic solvent.

[0029] The method of the present invention relates to extracting a triglyceride from an oleaginous microorganism which is a bacteria, fungi, yeast or algae such as a microalgae. A bacteria is for example *Rhodococcus opacus*, *Acinetobacter calcoaceticus* or *Bacillus alcalophilus*, a fungi is for example *Mucor circinelloides* and *Mortierella alpine*, *Aspergillus oryzae* or *Humicola lanuginosa*, a yeast is for example *Lipomyces starkeyi*, *Rhodospiridium toruloides*, *Yarrowia lipolytica*, *Rhodotorula graminis*, *Rhodotorula glutinis*, *Cutaneotrichosporon oleaginosu*, *Apiotrichum curvarum*, *Cryptococcus curvatus*, *Candida sp*, *Rhodotorula gracilis*, *Trichosporon capitatum* or *Trichosporon asahii* and an algae such as a microalgae is for example *Chlorella sp.*, *Pseudochlorococcum sp.*, *Nannochloris sp*, *Nannochloropsis sp.*, *Isochrysis sp*, *Tribonema minus*, *Dunaliella sp.*, *Ankistrodesmus sp.*, *Botryococcus braunii*, *Pavlova sp.*, *Scenedesmus sp.*, *Skeletonema sp.*, or *Nitzschia sp.*. The oleaginous microorganism used in the present invention is for example only one single type of oleaginous microorganism, a mixture of different oleaginous fungi, yeast, bacteria or algae such as microalgae, or a mixture of different oleaginous fungi, yeast, bacteria and algae such as microalgae.

[0030] The method of the present invention, as defined in claim 1, comprises or consists of the steps:

1. a) adding an enzyme system to the oleaginous microorganism, wherein the enzyme system comprises an enzyme having hydrolase activity to hydrolyze the cell wall of the microorganism,
2. b) adding a protease to the hydrolyzed oleaginous microorganism, and
3. c) adding a short-chain polymer to the hydrolyzed oleaginous microorganism of step b) for demulsification, wherein three separate layers are formed, one comprising the triglyceride, a second comprising cell debris and a third comprising sugar and/or amino acids. The steps a) to c) are performed separately one after the other, or all compounds added in steps a) to c), steps a) and b), steps b) and c) or steps a) and c) are added to the oleaginous microorganism at once. In case of separate steps a) to c) the time between the steps takes seconds, minutes, hours or days, and the time between the steps is identical or differs.

[0031] In step c) one or more short-chain polymer(s) are added, i.e., the short-chain polymer is one type of short-chain polymer or a mixture of different short-chain polymers in different

ratios.

[0032] In step c) different layers are formed: one comprising or consisting of triglyceride, one comprising or consisting of sugar and/or amino acid and one comprising or consisting of cell debris. The layers are separate and comprise or consist of the triglyceride, sugar and/or amino acid or cell debris from about 50 % to 100 %, 60 % to 99 %, 70 % to 98 %, 80 % to 97 %, 90 % to 96 %, or 95 %, 96 %, 97 %, 98 %, 99 %, 99.9 % or 100 % (purity). The layers are formed for example by centrifugation, e.g., using a milk-separator or a milk-separator-like device. In an optional step d) the triglyceride layer, the sugar layer and/or amino acid layer and/or the layer of cell debris are isolated, e.g., by detracting via a syringe. The isolated triglyceride, sugar, amino acid and/or cell debris may be further purified or treated or directly used in food or fuel production.

[0033] The enzyme system used in the method of the present invention comprises or consists of any enzyme having one or more hydrolase activity/ies, wherein the enzymes of the enzyme system have a synergistic hydrolase activity effect. Enzymes of the enzyme system are a cellulase, a hemicellulase, a mannanase, a laminarinase, a glucanase, a galacturonase, a polygalacturonase, a pectinase, a glucosidase or combinations thereof. Concentrations of the enzyme system used in the method of the present invention are for example 0.1 to 5, 0.2 to 4.5, 0.3 to 4.0, 0.4 to 3.5, 0.5 to 3.0, 0.6 to 2.5 or 0.5 to 2.7 [% $w_{\text{protein}}/dw_{\text{biomass}}$], which is percent weight of the protein bzw. enzyme / dry weight of the biomass.

[0034] The design of a specific enzyme system is essential for cell lysis and oil recovery. The enzyme system is for example optimized on a biomass such as an artificial biomass in order to carry out a complete cell lysis into monosaccharaides. In the first stage of optimization for example, the biochemical components of a partially purified cell-wall of a well-established oleaginous microorganism such as *T. oleaginosus* is analyzed. Data resulting from biomass analysis are for example used for the selection of required enzyme activates for selective cell lysis of the well-established oleaginous microorganism. Subsequently, the optimized enzyme system is tested for example directly on harvested culture of living cells without any pretreatment. Process conditions of pH, incubation temperature, enzyme concentration and space-time conversion yields are for example evaluated in order to minimize the process cost and duration. For the demulsification of the cell lysate, a protease activity is for example added to the enzyme system to accomplish a direct release of single cellular lipid. FACS cell counting in combination with fluoresce-/ electron- microscope and gravimetric analysis are used for example to evaluate the efficiency of the newly established process. Finally, for example triglyceride extraction at scale of 2 liters is performed to verify the scalability of the suggested downstream process.

[0035] In the method of the present invention the pH is controlled in the different method steps. In step a) the pH is for example in the range of 3 to 7, in the range of 4 to 6 or in the range of 4 to 5, or the pH is 2, 3, 4, 5, 6, 7 or 8. In step b) the pH is for example in the range of 6 to 10, in the range of 7 to 9 or the pH is 5, 6, 7, 8 or 9. The pH is increased or decreased with any type of acidic or basic compound.

[0036] Optionally, the temperature is controlled in the different method steps independent of the pH. In step a) the temperature T is for example in the range of 30 °C to 70°C, in the range of 40 °C to 55 °C or in the range of 40 °C to 45 °C, or 30, 35, 40, 45, 50, 55, 60, 65 or 70 °C. In step b) the temperature T is for example in the range of 25 °C to 45°C, in the range of 30 °C to 40 °C or in the range of 35 °C to 37 °C, or 25, 30, 31, 32, 33, 34, 35, 36 37, 38, 39, 40 or 45 °C.

[0037] The method of the present invention comprises a demulsification, wherein a protease is added to the hydrolyzed oleaginous microorganism. The protease is one type of protease, a group of the same type of protease or a combination of different types of proteases. The different types of proteases are serine protease, cysteine protease, threonine protease, aspartic protease, glutamic protease, metalloprotease and asparagine peptide lyase, respectively.

[0038] The demulsification further comprises the addition of a short-chain polymer, i.e., a low molecular weight polymer (e.g., MW about 10.000 g/mol to about 20.000 g/mol such as < 20.000 g/mol, <15.000 or < 10.000 g/mol), in particular a polycondensate. The polymer used in a method of the present invention breaks for example a water-in-oil-emulsion or an oil-in-water-emulsion. The polymer is for example linear, branched or cross-linked. Said polymers are polyglycol, polyadduct of polyglycol and alkenyl succinic acid anhydride, polyester of polyglycol, alkenyl succinic anhydride polyester, block copolymer of propylenoxide and ethylenoxide, polyglycerol, polyester of poly- α -olefine or shown in the following **Table 1** or a combination thereof:

Polymer	Active ingredient
Propoxylated EO*/PO** block polymer - bis glycidyl ether (high, > 50 % PO), e.g., 1 conc.	e.g., > 97 %
Propoxylated EO/PO- block polymer bis-glycidyl ether (low, < 50 % PO), e.g., 1 conc.	e.g., 100
Polypropylenglycol of high MW with excess of EO (> 30 %), e.g., 1 conc.	e.g., 100
Propoxylated EO/PO block polymer - bis glycidyl ether (high, > 50 % PO) with an excess of EO, e.g., 1 conc.	e.g., 100
Cross-linked PEG, e.g., 1 conc.	e.g., > 79 %
Polymer of mixed alkoxylat-ethyl-glycerol, e.g., 1 conc.	e.g., 100
Poly- α olefin- polyester	e.g., 80 or 98 %
*EO - ethylenoxide **PO - propylenoxide	

[0039] The polymer may be dissolved in a solvent such as S. Naphtha or 2- Ethylhexanol.

[0040] After the demulsification the oleaginous microorganism treated according to the method

of the present invention is allowed to stand for separation of the different layers comprising or consisting of a triglyceride, a sugar and/or an amino acid, and/or cell debris, or it is subjected to a, e.g., mechanical, separation step using a centrifuge or a separator such as a milk-separator or milk-separator-like device.

[0041] The triglyceride extracted and isolated, respectively, by a method of the present invention comprises or consists of for example a short-chain, a medium-chain or a long-chain triglyceride or a combination thereof. The triglyceride comprises any saturated and/or unsaturated fatty acid for example palmitic acid (C_{16:0}), stearic acid (C_{18:0}), oleic acid (C_{18:1}), linoleic acid (C_{18:2}), α -linolenic acid (C_{18:3}), arachidic acid (C_{20:0}), arachidonic acid (C_{20:4}), eicosapentaenoic acid (C_{20:5}), behenic acid (C_{22:0}) and/or lignoceric acid (C_{24:0}). The sugar extracted and isolated, respectively, by a method of the present invention comprises or consists of any sugar for example selected from the group consisting of glucuronic acid, rhamnose, fucose, mannitol, xylose, mannose, glucose and a combination thereof.

[0042] The amino acid extracted and isolated, respectively, by a method of the present invention comprises or consists of any amino acid depending on the protease(s) used for the demulsification. The amino acid is in a separate layer in a purity of 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 % or in mixture with the sugar for example in an aqueous phase. In the latter case, the amino acid may be separated from the sugar in one or more additional purification steps.

[0043] The method of the present invention optionally comprises an additional step f) for recycling the compounds used in the method of the present invention for example the enzyme system, the protease and/or the polymer.

[0044] The present invention further refers to the use of an enzyme system comprising an enzyme having hydrolase activity as defined in claim 1, in a method of the present invention.

[0045] The description further discloses a kit comprising an enzyme system and optionally a carrier or support system and/or a device such as a reaction tube for example to perform a method of the present invention for extraction of a triglyceride.

Examples

[0046] The following examples illustrate different embodiments of the present invention, but the invention is not limited to these examples.

Example 1: Biomass analysis

[0047] Glucuronoxylomannan (GXM) has been reported to be the expressed in the cell walls of

some *Trichosporon* spp., i.e. *Trichosporon beigelii*, *Trichosporon asahii* and *Trichosporon cutaneum*. GXM is a 1,3-linked mannan backbone attached to short side chains of 1,4-linked mannose and 1,2-linked xylose residues. Depending on the strain type, the ratio of this polysaccharide to the protein is varied in the cell membrane. **Fig. 1A** shows the overall biomass analysis of the *T. oleaginosus*. The cell wall displays a high amount of protein content about 50 % and relatively low lipid content of 15 %, while the total carbohydrates was nearly 27 %. However, no ash was detectable after incineration at 1000 °C.

[0048] The compositional sugars consist mainly of glucose, mannose, xylose, rhamnose and mannitol (**Fig. 1B**). The cell-wall composition is altered when the *T. oleaginosus* is cultivated in Minimal-N media. **Fig. 1C** shows a decrease in the protein content to be 5.3 %. Contrariwise, sugar, ash and lipid were increased up to 42.3, 1.5 and 51.3 % respectively. However, the sugar profile was almost identical.

Example 2: Investigation of enzyme system

[0049] An enzyme system was tested that is able to hydrolyze the cell-wall of the *T. oleaginosus* without the need to any pretreatment. Additionally, the more monomeric sugars are produced via the enzyme system, the better the process since the sugars are considered as an advantageous side product which can be utilized in further applications. Data obtained of the biomass analysis (**Fig. 1A - 1D**) define the necessary enzyme activities like cellulases, hemicellulases, mannanases, laminarases and a β -glucosidase.

[0050] In the optimization phase, two criteria were used for the differentiation between 48 various enzyme mixtures at varied concentrations. These criteria are the increase of sugar concentration and decrease of residual biomass weight. Two exemplary mixtures (Mix 15 and Mix 21) showed good activity within an acceptable time frame and adequate concentration. Mix 15 contains Novozymes enzyme products Mannanase, Cellic Ctec2, Cellic Htec and β -glucosidase, while Mix 21 contains Clariant enzymes Liquebeet, CLA, Mannanase, 1,3- β -glucanase and β -glucosidase. Both enzyme mixes showed almost the same activity with less than 30 [% w/w] residual biomass and about 15 g/l glucose after 3 days. The used enzyme mixture concentration was 1.4 [% $w_{\text{enzyme}}/dw_{\text{biomass}}$].

[0051] The *T. oleaginosus* was cultivated in minimal nitrogen media for 5 days. Afterwards, the biomass was harvested then divided into 15-ml falcon tubes. Each falcon tube was treated under different conditions of pH, temperature, concentration, and time. After incubation, the analysis was done as described in the materials and methods.

Example 3: Optimization of Enzyme Mix

[0052] As first step, the best two mixtures were tested on harvested culture. The conditions

mentioned in proof of concept were used in this experiment. However, the analysis was done at two time intervals which were 12 and 18 h.

[0053] **Fig. 2** and **Fig. 3** show the residual biomass and released lipid, respectively. 50 [% w/w] of the lipid was moved out to the upper layer in the falcon tube. At the same ratio of lipid release, the biomass was decreased also about [50 % w/w]. Both mixes showed almost the same activity. Hence, in the further studies the Mixture 21 was used.

a) pH optimization

[0054] Sometimes the increase of released triglyceride showed a symmetric result with the decrease of the biomass. Alternatingly, the pH of the reaction from 4.0 to 6.0 (at 55 °C) showed no significant effect on the decrease of the biomass (**Fig. 4**). Conversely, pH 4.5 and 5.0 showed the best triglyceride release results. **Fig. 6** shows the intact cell after treatment at pH 4.5 and 5.0 corresponding to 29.2 and 48.1 % of starting cell count respectively. Therefore, pH 4.5 is considered advantageous for this process.

b) Temperature optimization

[0055] Increasing temperature from 40.0 to 55.0 °C (pH 4.0, 50.0 mM) showed a remarkable effect on the residual biomass rather than its impact on lipid release. Treatment at 40 °C resulted in more lipid within a shorter time period (**Fig. 8**). By increasing the time, 50 °C showed slight preponderance. In different way, lowest value of residual biomass was recorded at 45 °C (**Fig. 7**). Thus, temperatures of 40- 45 °C showed better results for the cell lysis step.

c) Optimization of the enzyme concentration

[0056] The duration of the cell lysis and the enzyme load have a serious effect on the cost and the process efficiency. Generally, the more enzyme is used, the less time is required and *vice versa*. Thus, a range of 0.25 - 1.4 [% w_{protein}/dw_{biomass}] within a time period of 3 -18 h (at pH 5.0 and 55.0 °C) was selected. The best blend was evaluated by cell count associated with fluorescence microscopy.

[0057] **Fig. 9** and **Fig. 10** show the decrease of total cell count by increasing the treatment time at two enzyme concentrations: Low enzyme concentration of 0.55 [% w/w] intact-cell count dwindle down to about 40 % and 30 % after 7 and 8 hours, respectively. If the concentration is increased to 0.8 [% w/w], about 80 % of total cell count were degraded within 8 hours.

[0058] **Fig. 11** shows the cell density destruction gotten by FACS vs. obtained photos of the same treatment time. Staining with Nile Red confirmed the increase of cell aggregation by

increasing treatment time. However, a big red spot of released lipid (stained with Nile Red) appeared after 18 h compared to homogenized mass when the samples is treated with Avestin for 3 times (**Fig. 11K**). Moreover, it can be seen from the microscope scatter, that those which appear at intact-cell region of the cell density diagrams are actually aggregated together (**Figure 11H, 11I and 11J**) which is an indication that cells are effect by the cell lysis treatment.

[0059] Furthermore, **Fig. 12** and **Fig. 13** show the impact of the enzyme concentration on the degree of the cell lysis. After short treatment time (**Fig. 12**, 5.5 h) 50% of the cells are destructed if a 1.1 [% $w_{\text{enzyme}}/dw_{\text{biomass}}$] is loaded. Nevertheless, a rate of 80 and 90% destructive cell can be obtained if the treatment continue to 13 h at concentration of 0.8 and 1.3 [% $w_{\text{enzyme}}/dw_{\text{biomass}}$] respectively. Figure 14 shows the fading of the cell density in the area of intact cells.

Example 4: Investigating Demulsification Step

[0060] Demulsification treatment consists of two phases: the first phase is addition of protease while the second refers to the addition of a short-chain polymer.

[0061] Previous work showed that the optimal pH and temperature for the selected protease is 8.0 and 37 °C, respectively (Data not shown). The optimization of these parameters cannot be separated from the cell-lysis step which has a significant impact on the demulsification step.

[0062] Hence, varied concentrations of short-chain polymers and different time intervals for incubation were studied. The samples were also treated at varied conditions of cell lysis to evaluate the impact of cell lysis step on the protease effectively.

[0063] **Fig. 15** shows the released lipid after different protease treatment for time intervals of 10.5 and 15.5 h at concentrations of 0.73 and 1.7 [% $w_{\text{protein}}/dw_{\text{biomass}}$]. Those samples were treated at different cell lysis conditions of time intervals (10.5 and 15.5 h) and concentrations (0.55 and 1.1 3 [% $w_{\text{protein}}/dw_{\text{biomass}}$]). The comparison of the diagrams shows a proportional increase of effectiveness of protease by increase of the intensity of cell wall lysis.

[0064] **Fig. 16** shows the best results for the cell lysis and protease treatment. The total time was in the range 20-25 h, while the total concentration was about 1.9-2.8 [%w/w]. The treatment was able to release up to 97 % to the total lipid comparing to the chemical method (**Fig. 16A**). These results are confirmed by the residual biomass measurements (**Fig. 16B**), insured FACS cell counting and fluorescence microscope observation (**Fig. 16C and 16D**). **Fig. 17 and 18** show a comparison between Avestin and enzymatic cell lysis.

[0065] Additional experiments were performed with enzyme mix 21 to evaluate eight different types of short-chain polymers (1. Polymer of mixed alkoxylat-ethyl-glycerol, 2. Propoxylated EO/PO block polymer-bis-glycidyl ether with excess of EO, 3. Propoxylated EO/PO block

polymer-bis-glycidyl ether (low, < 50 % PO) 4. Polypropylenglycol of high MW with excess of EO (> 30 %), 5. cross-linked PEG, 6. Poly- α olefin-polyester (active ingredient > 80 %), 7. Poly- α olefin-polyester (active ingredient > 98 %) and 8. Propoxylated EO/PO block polymer-bis-glycidyl ether (high, > 50 % PO). In this test, the biomass treated under different conditions of cell wall lysis and protease was collected, mixed and then divided equally into 8 tubes. Hence, 4 μ l of each short-chain polymer was added into tubes, separately. After centrifugation, Poly- α olefin-polyester (active ingredient > 98 %) again provided the best result (**Fig. 19**).

[0066] The final product was subjected to GC FID to compare its lipid profile vs. the lipid profile extracted by the classical chemical procedure. **Fig. 20** displays the fatty acids consisting mainly of C_{16:0}, C_{18:0}, C_{18:1} in addition to traces of other fatty acids. No significant variations were detected between the two profiles.

Example 5: Hydrolysate analysis

[0067] HPLC (Agilent 1100 series) was used for the analysis of monomeric sugars. The HPLC was associated with Refractive Index [Shodex, RI101] and Ultraviolet Index [Sedere-France, Sedex75] as detectors. For best isolation of the monomeric sugars, two different methods were used: firstly, a Rezex ROA-Organic Acid (Aminex HPX 87H) column was used with H₂SO₄ (5.0 mM) as mobile phase at a flow rate of 0.5 ml/min. The column was heated at 70 °C, and the detector was set at 40 °C. Secondly, an Aminex HPX-87P column. An isocratic mobile phase of ddH₂O was pumped at a rate of 0.6 mL/min. Temperature was at 70 °C with the detector set at 50 °C.

[0068] The cell lysis via enzymatic-based approach has additional advantage. Hydrolysis of the polysaccharides of the cell wall lead to produce a fermentable sugars. **Fig. 21** shows the sugar analysis of the hydrolysate which contain mainly glucose, and galacturonic acid.

Example 6: Cell lysis optimization

[0069] After harvesting the biomass, 1.0 or 0.5 g of lipid-accumulated biomass was distributed into 15 ml falcon tube. Later, 8-4 ml of acetate buffer (50.0mM) at different pH range 4.0 - 6.0. The reaction started by addition of enzyme solutions at different concentration 0.5-2.0 [% $w_{\text{enzyme}}/w_{\text{biomass}}$]. The reaction were incubated at different temperature 40.0-60.0 °C For varied incubation time 1-18 h.

[0070] To evaluate the effectively of the enzymes system on cell lysing and lipid releasing, three controls were used in parallel to the reactions: Control 1: A sample was treated with standard method of lipid extraction. The extracted amount of lipid was considered as 100% yield and it was used as reference to released lipids. Control 2: A sample contain the biomass and buffer. This sample incubated at the same conditions of temperature, pH, time and rotation

without any addition of enzyme. Control 3: Point zero; sample was taken directly after addition of enzymes. Treatment time is 0 h.

[0071] Cell-lysis was followed by four assay methods. Samples were treated under different conditions were divided into two parts. The first part (1 ml) was used cell counting and microscope observation. The second part (the rest of samples) was centrifugation at 10,000 rpm for 20 min. after centrifugation three layers were formed (**Fig. 22A**). The lower layer, the water phase, was used for sugar analysis.

[0072] The upper layer was the released lipid. This layer was pipetted out into a known-weight 15 ml falcon tube for weight measurement.

[0073] The middle layer between the lipid and the water phases, was the sold residual biomass. This layer was subjected into known-weight 15 ml falcon tube for weight measurement after lyophilization under 0.0045 mbar at -80 °C for 2 days.

[0074] Cell Counting was performed using the FACS with laser beam of 488 nm and 100 mW. The counting was conducted using 100 µl of sample after 100 times dilution. **Fig. 22B** shows the cell density diagram "Y" axis is fluorescence at 588 ± 24 nm and "X" axis is Forward scatter. **Fig. 22C** depicts the cell density diagram, "Y" axis is Side scatter and "X" axis is Forward scatter.

[0075] The Visual Observation was performed by florescence microscope after staining the samples with Nile red using 100x objector.

Example 7: Lipid Extraction and Lipid Profile analysis

[0076] The standard method of lipid extraction is based on Bligh-Dyer's method (Bligh, E.G. and W.J. Dyer, A rapid method of total lipid extraction and purification. Canadian journal of biochemistry and physiology, 1959, 37(8): p. 911-917) as following: the biomass was treated with High-pressure homogenizer (Avestin emulsiflex C3) in order to disrupt the cell wall. Afterword, Folch Solution was used 3time to extract the lipids. Lipids amount were determinate gravimetrically.

[0077] The methylation of fatty acids (Dumay et al. 2006) (Griffiths et al. 2010) was performed in order to obtain the methyl ester derivatives for analysis by gas chromatography. 50.0 µl of lipid extract were diluted in 450 µl toluene. 50.0 µl (2mg/ml) Trinonadecnoin (C_{19:0}-TAG) were added prior to the reaction as an internal standard. Subsequently, 100 µl of 2,2-dimethoxypropane and 1.00 mL of sodium methoxide were added and the samples mixed briefly by vortexing before being placed in an incubator at 80 °C shaking at 900 rpm for 20 min. Samples were cooled for 5 min to room temperature and 1.00 mL HCl/methanol was added before repeating the incubation. After cooling for 5 min to room temperature, 400 µl be-distilled water and 360 µl n-hexane were added and the tubes mixed by vortexing. The samples were

centrifuged at 4,000 rpm for 2 min and the upper hexane layer containing the FAME extract was transferred to vials for GC. Following lipid extracts were converted to FAMES.

REFERENCES CITED IN THE DESCRIPTION

Cited references

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- **BLIGH, E.G.W.J. DYER** A rapid method of total lipid extraction and purification *Canadian journal of biochemistry and physiology*, 1959, vol. 37, 8911-917 [\[0076\]](#)

PATENTKRAV

1. Fremgangsmåde til ekstrahering af en triglycerid fra en olieholdig mikroorganisme, der omfatter trinnene:

a) at tilføje et enzymesystem til den olieholdige mikroorganisme, hvor enzymesystemet omfatter et enzym, der har hydrolaseaktivitet med henblik på at hydrolysere mikroorganismens cellevæg, og hvor hydrolaseaktiviteten er udvalgt fra gruppen bestående af cellulase, hemicellulase, mannase, laminarinase, glucanase, galacturonase, polygalacturonase, pectinase, glucosidase og en kombination deraf.

b) eventuelt at tilføje en protease til den hydrolyserede olieholdige mikroorganisme, og

c) at tilføje en eller flere kortkædede polymerer til den hydrolyserede olieholdige mikroorganisme i trin a) og/eller b) med henblik på demulgering, hvor tre separate lag dannes, hvoraf et omfatter triglyceriden, et andet omfatter cellerester, og et tredje omfatter sukker og/eller aminosyrer, og hvor den kortkædede polymer er udvalgt fra gruppen bestående af polyglycol, polyadditionsprodukt af polyglycol og alkenylsuccinsyreanhydrid, polyester af polyglycol, alkenylsuccinanhydrid-polyester, block-copolymer af propylenoxid og ethylenoxid, polyglycerol, polyester af poly- α -olefin og en kombination deraf

d) eventuelt at isolere triglyceridlaget.

2. Fremgangsmåde ifølge krav 1, hvor den olieholdige mikroorganisme er udvalgt fra gruppen bestående af *Trichosporon oleaginosus*, *Trichosporon capitatu*, *Trichosporon asahii*, *Lipomyces starkeyi*, *Rhodosporidium toruloides*, *Yarrowia lipolytica*, *Rhodotorula graminis*, *Rhodotorula glutinis*, *Cutaneotrichosporon oleaginous*, *Apiotrichum curvarum*, *Cryptococcus curvatus*, *Candida sp.*, *Rhodotorula gracilis*, *Chlorella sp.*, *Pseudochlorococcum sp.*, *Nannochloris sp.*, *Nannochloropsis sp.*, *Isochrysis sp.*, *Tribonema minus*, *Dunaliella sp.*, *Ankistrodesmus sp.*, *Botryococcus braunii*, *Pavlova sp.*, *Scenedesmus sp.*, *Skeletonema sp.*, *Nitzschia sp.*, *Rhodococcus opacus*, *Acinetobacter calcoaceticus* og *Bacillus alcalophilus*.

3. Fremgangsmåde ifølge et hvilket som helst af krav 1 eller 2, hvor pH-værdien i trin a) ligger i intervallet 3 til 7, i intervallet 4 til 6 eller i intervallet 4 til 5.

4. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 3, hvor temperaturen T i trin a) ligger i intervallet 30 °C til 70 °C, i intervallet 40 °C til 55 °C eller i intervallet 40 °C til 45 °C.
5. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 4, hvor pH-værdien i trin b) ligger i intervallet 6 til 10, i intervallet 7 til 9 eller 8.
6. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 5, hvor temperaturen T i trin b) ligger i intervallet 25 °C til 45 °C, i intervallet 30 °C til 40 °C eller i intervallet 35 °C til 37 °C.
7. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 6, hvor den kortkædede polymer er lineær, forgrenet eller tværforbundet.
8. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 7, hvor triglyceridlaget omfatter kortkædede, mellemkædede eller langkædede triglycerider eller en kombination deraf.
9. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 8, hvor triglyceriderne omfatter palmitinsyre (C_{16:0}), stearinsyre (C_{18:0}), oliesyre (C_{18:1}), linolsyre (C_{18:2}), α-linolsyre (C_{18:3}), arachinsyre (C_{20:0}), arachionsyre (C_{20:4}), eicosapentaensyre (C_{20:5}), behensyre (C_{22:0}), lignocerinsyre (C_{24:0}) eller en kombination deraf.
10. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 9, der desuden omfatter trin e) til isolering af sukkerlaget.
11. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 10, hvor sukkeret udvælges fra gruppen bestående af glucuronsyre, rhamnose, fucose, mannitol, xylose, mannose, glucose og en kombination deraf.
12. Fremgangsmåde ifølge et hvilket som helst af krav 1 til 11, hvor proteasen er en serinprotease, en cysteinprotease, en threoninprotease, en asparaginprotease, en glutaminprotease, en metalloprotease og en asparaginpeptidlyase eller en kombination deraf.

13. Anvendelse af et enzymsystem, der omfatter et system, der har hydrolaseaktivitet som defineret i krav 1, i en fremgangsmåde ifølge et hvilket som helst af krav 1 til 12.

DRAWINGS

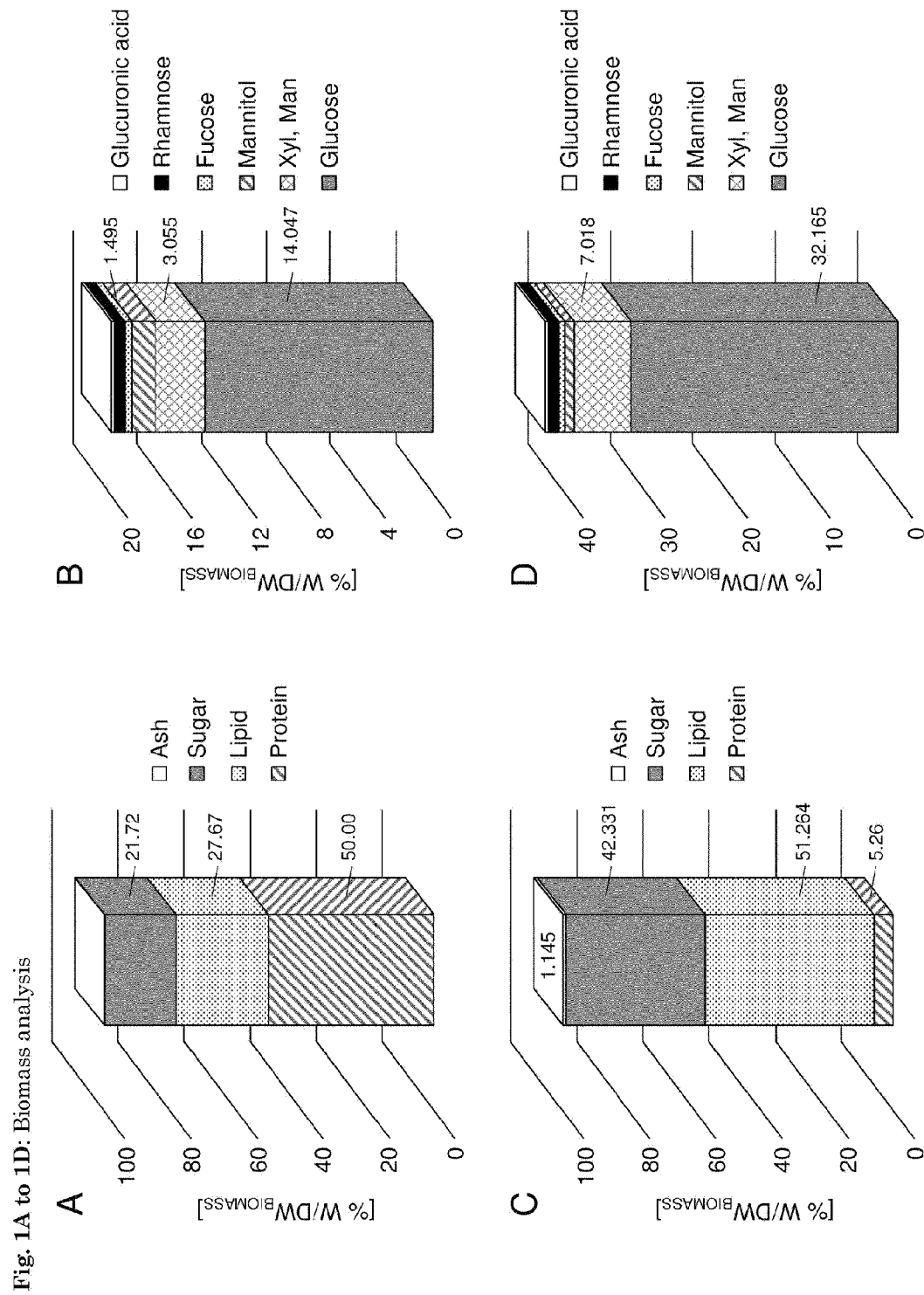


Fig. 2: Testing enzyme system on residual biomass

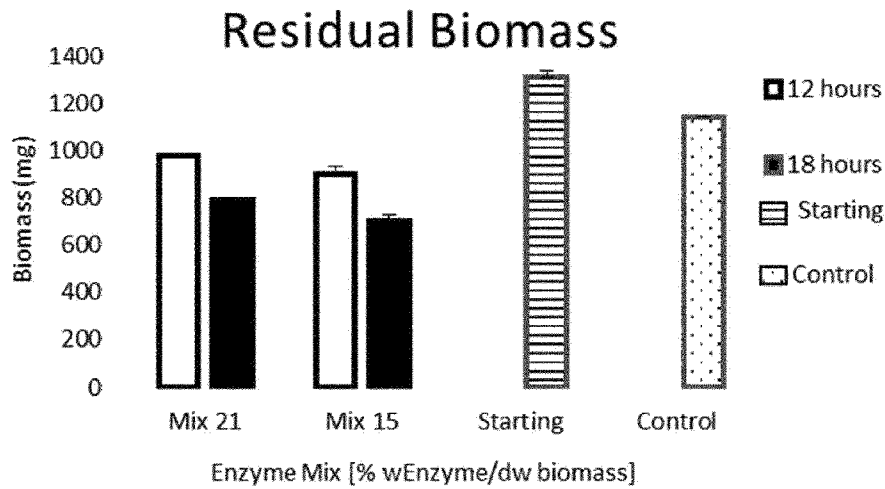


Fig. 3: Testing enzyme system on released triglyceride

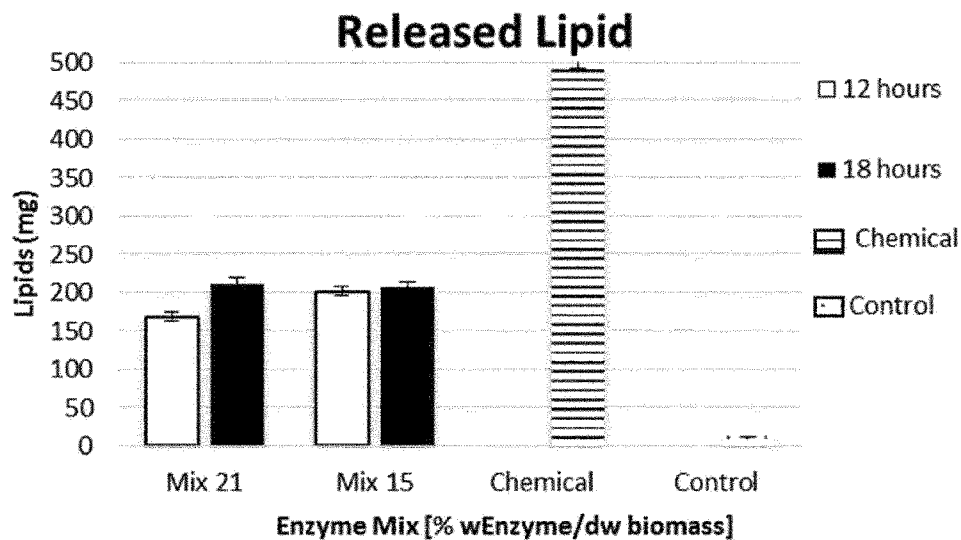


Fig. 4: Testing pH conditions on residual biomass

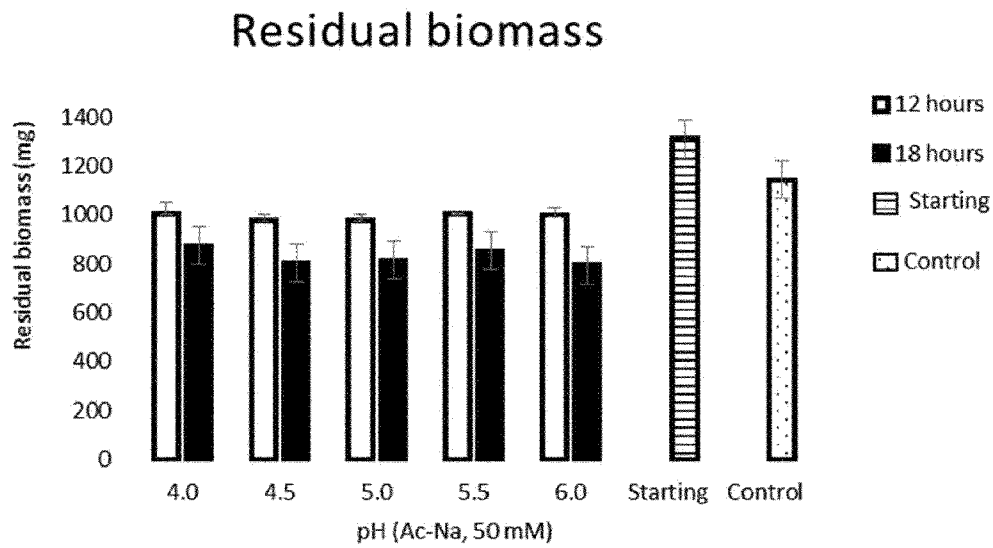


Fig. 5: Testing pH conditions on released triglyceride

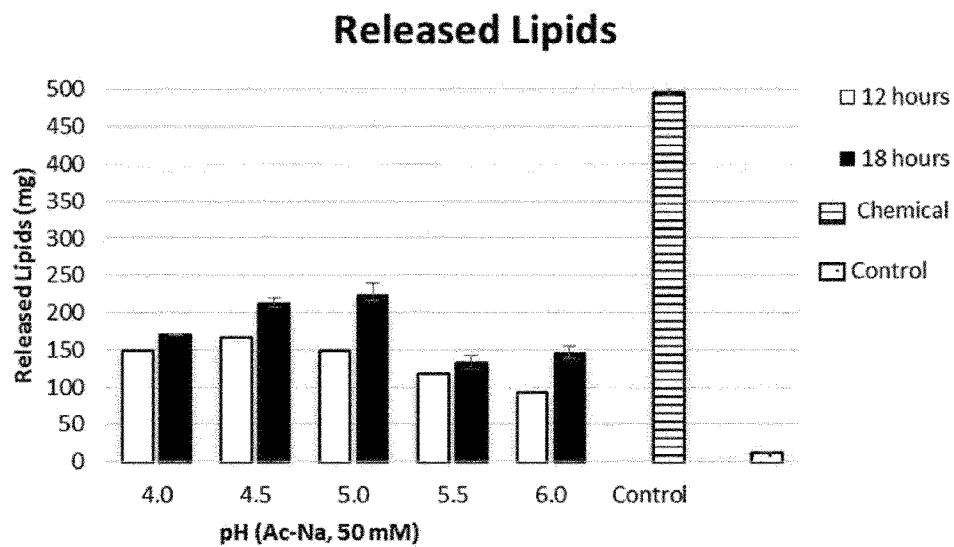


Fig. 6A to 6C: Density blot

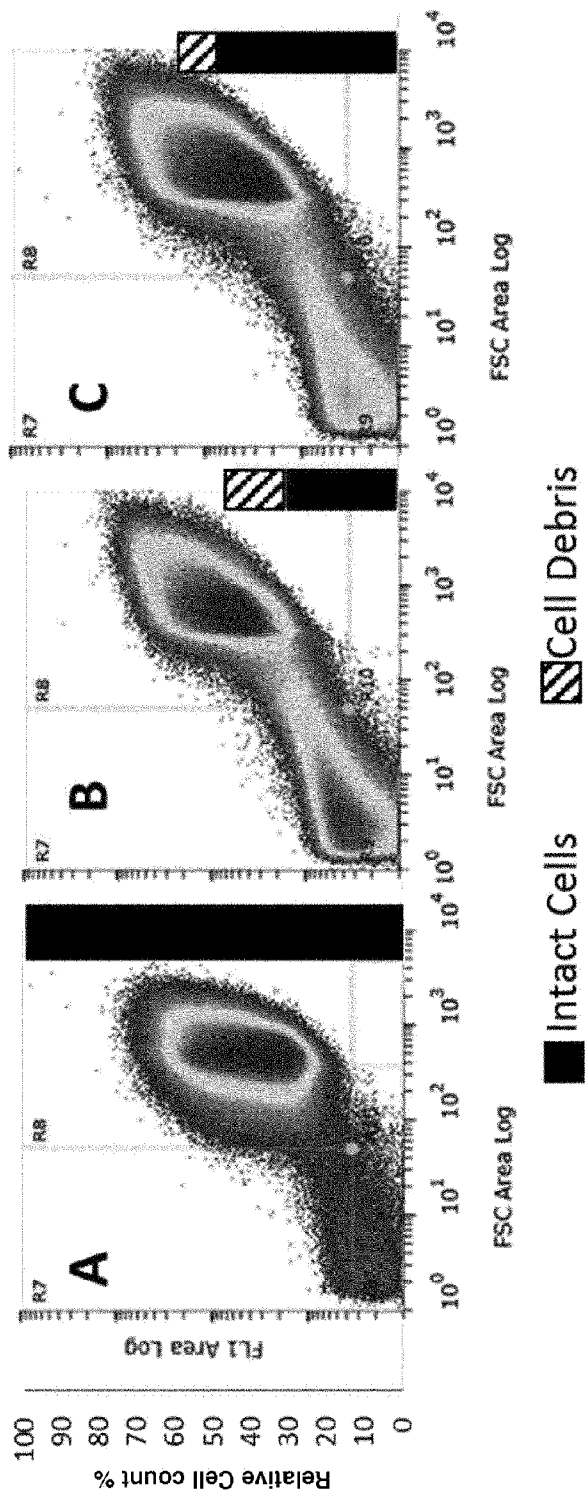


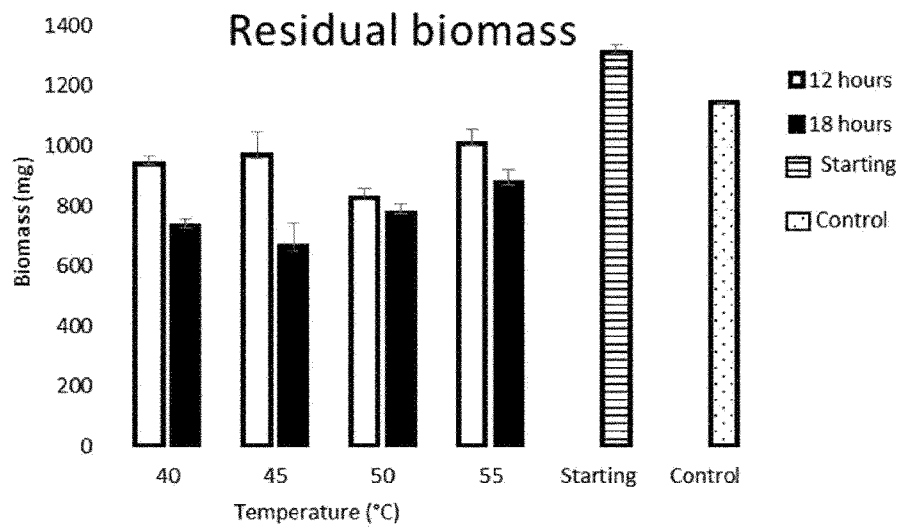
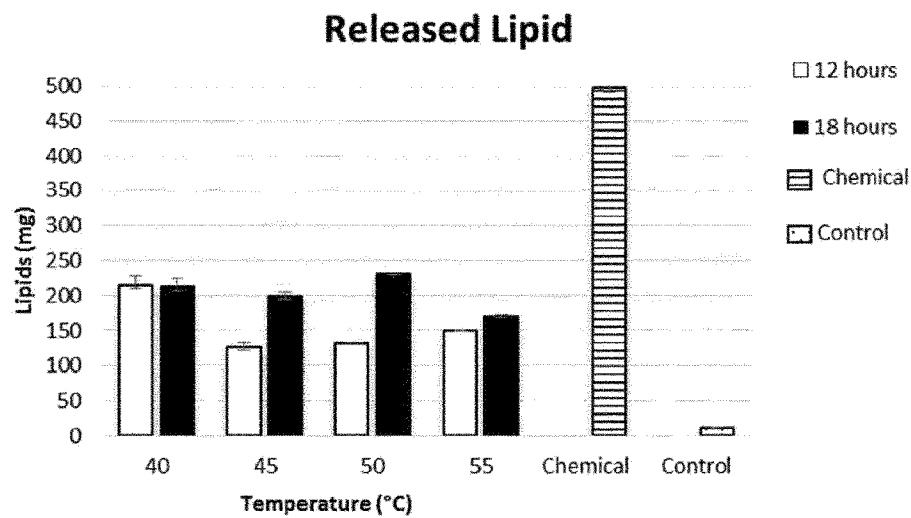
Fig. 7: Testing temperature conditions on residual biomass**Fig. 8:** Testing temperature conditions on released triglyceride

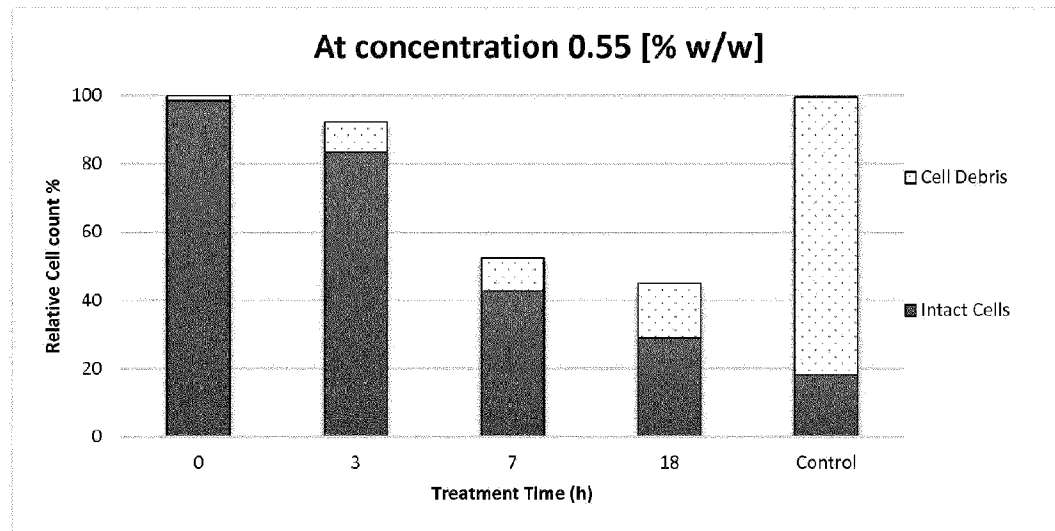
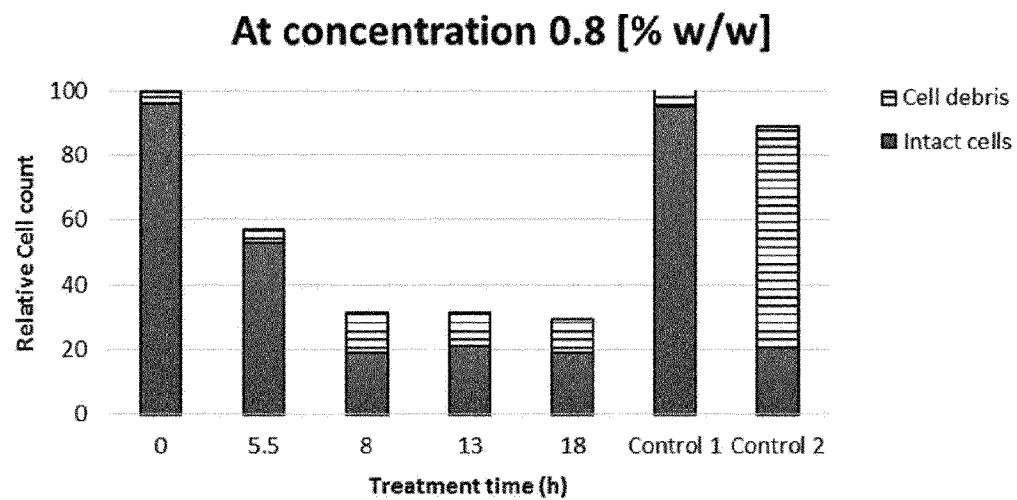
Fig. 9: Testing treatment time with 0.55 [% w/w]**Fig. 10:** Testing treatment time with 0.58 [% w/w]

Fig. 11A-C and G-I: Density blot

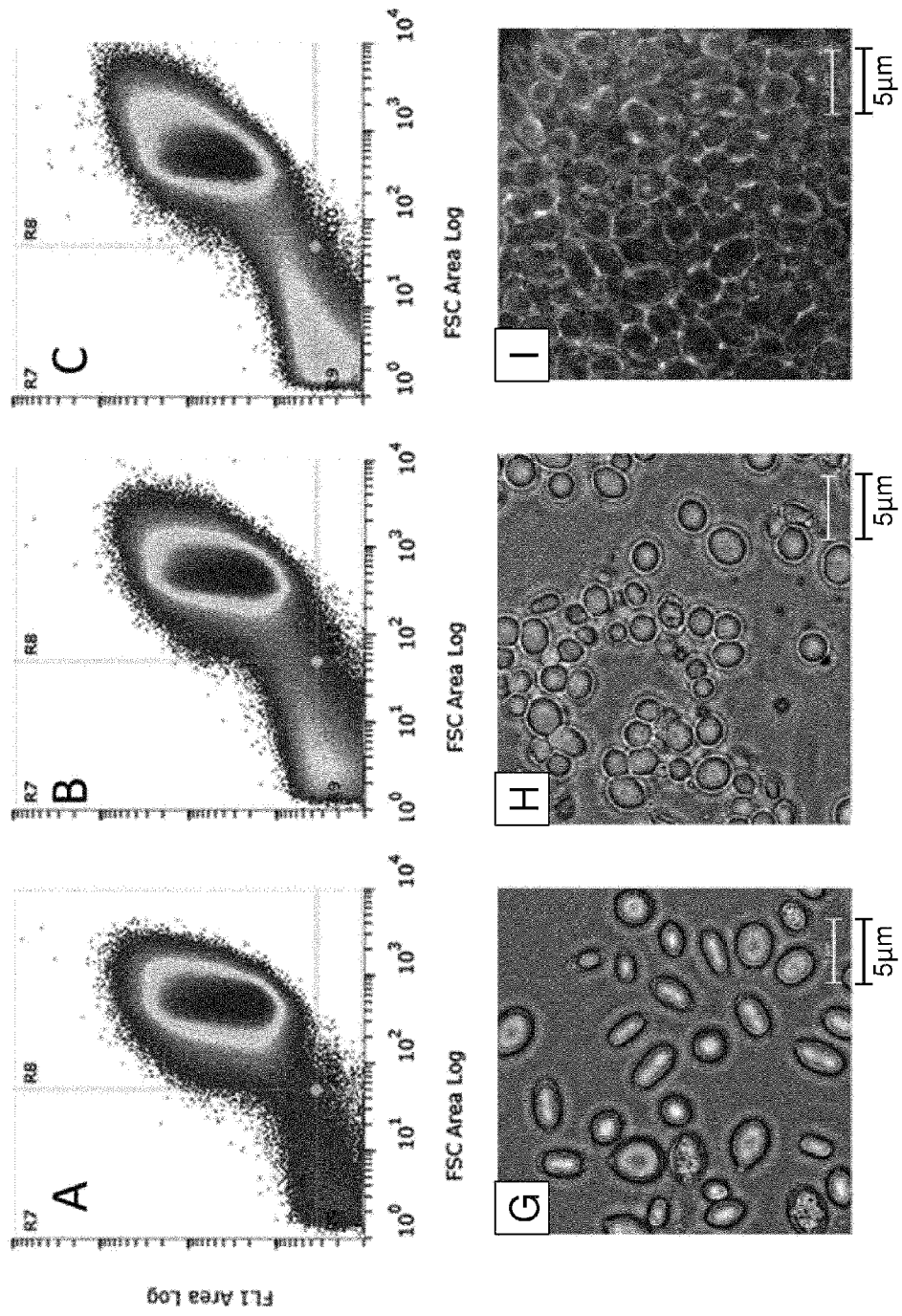


Fig. 11E-F and J-K: Density blot

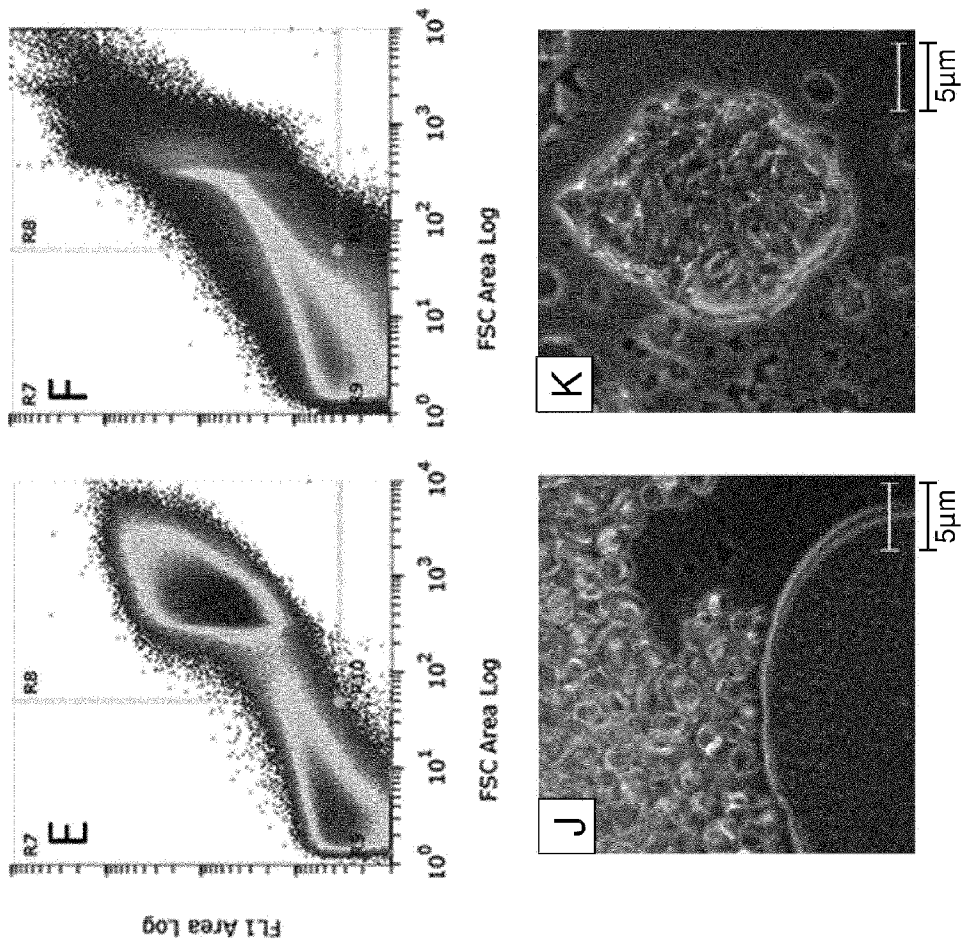


Fig. 12: Testing treatment time – 5.5 h

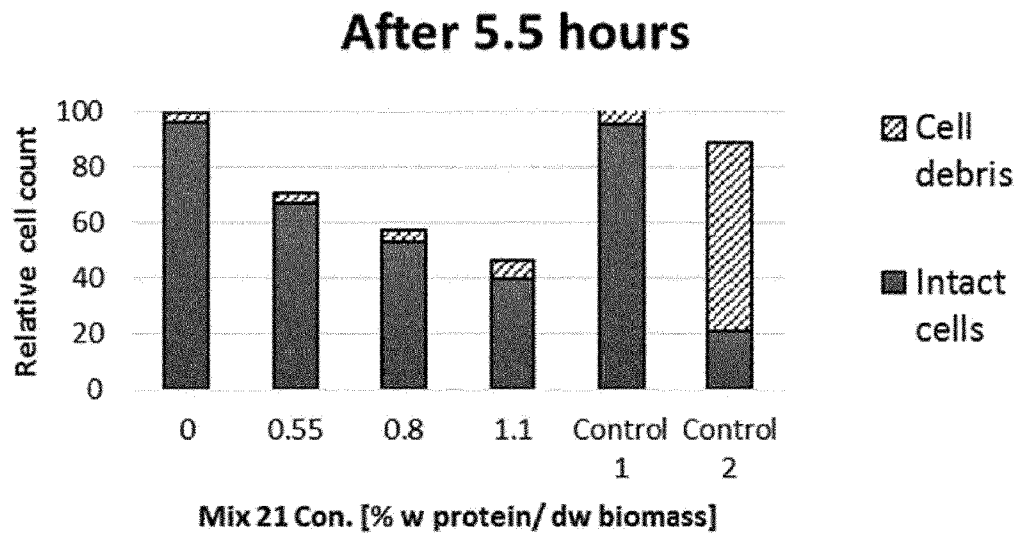


Fig. 13: Testing treatment time – 13 h

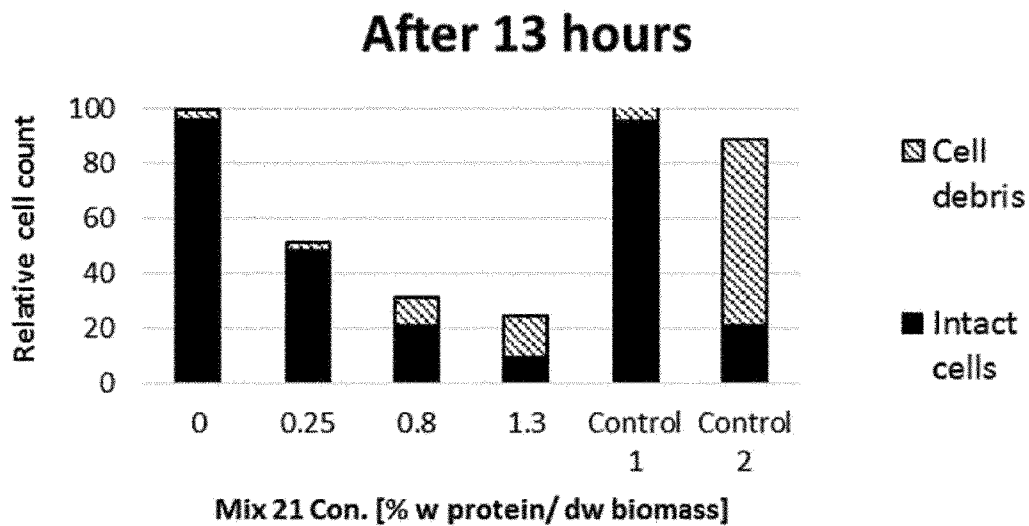


Fig. 14A to 14F: Density blot

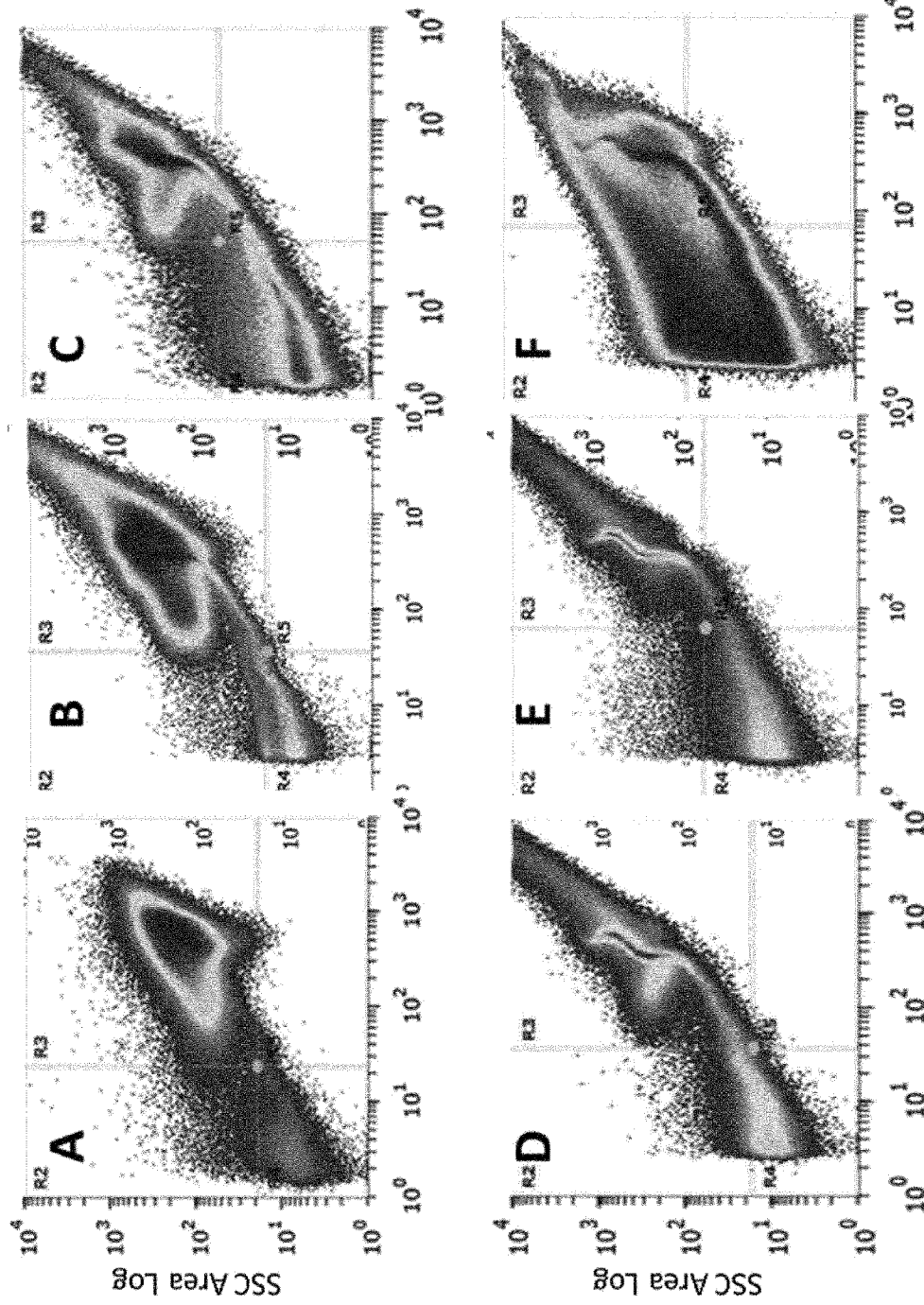


Fig. 15A to 15D: Testing incubation time and protease concentration on triglyceride release

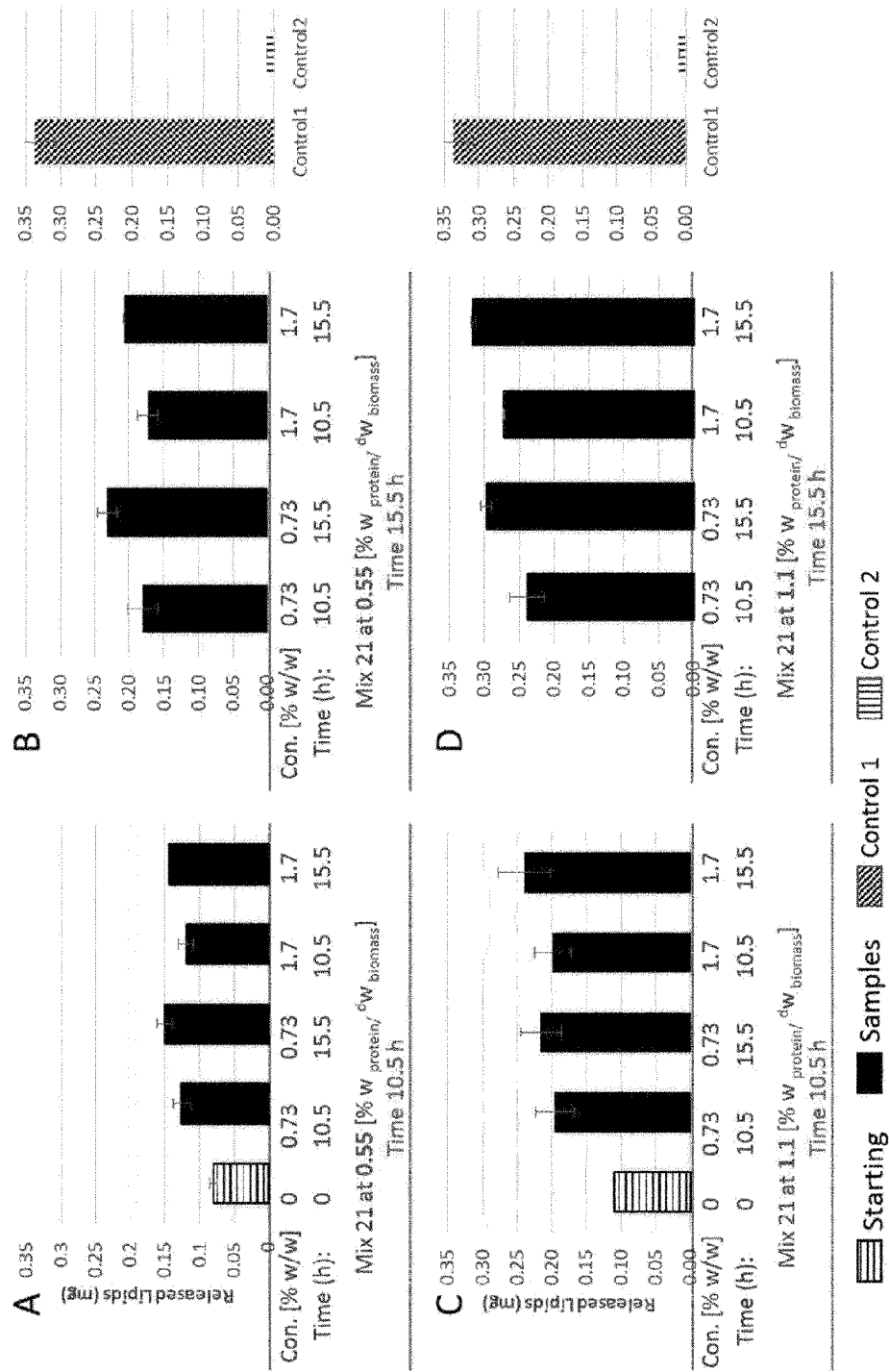


Fig. 16A to 16B: Results protease treatment

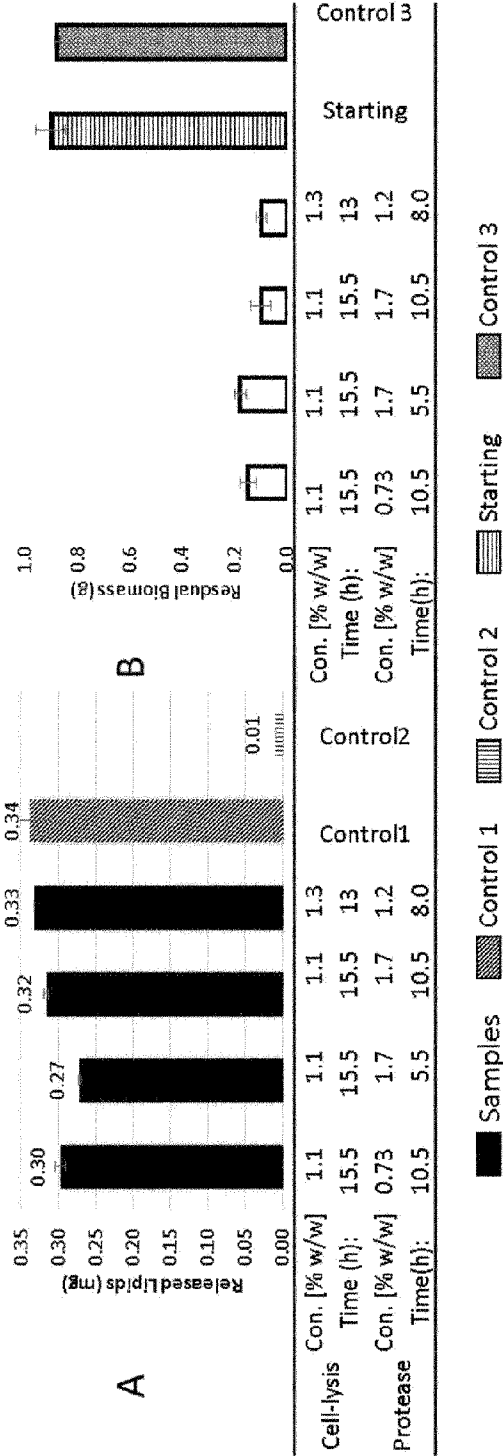


Fig. 16C to 16D (1-3, 7-9): Results protease treatment

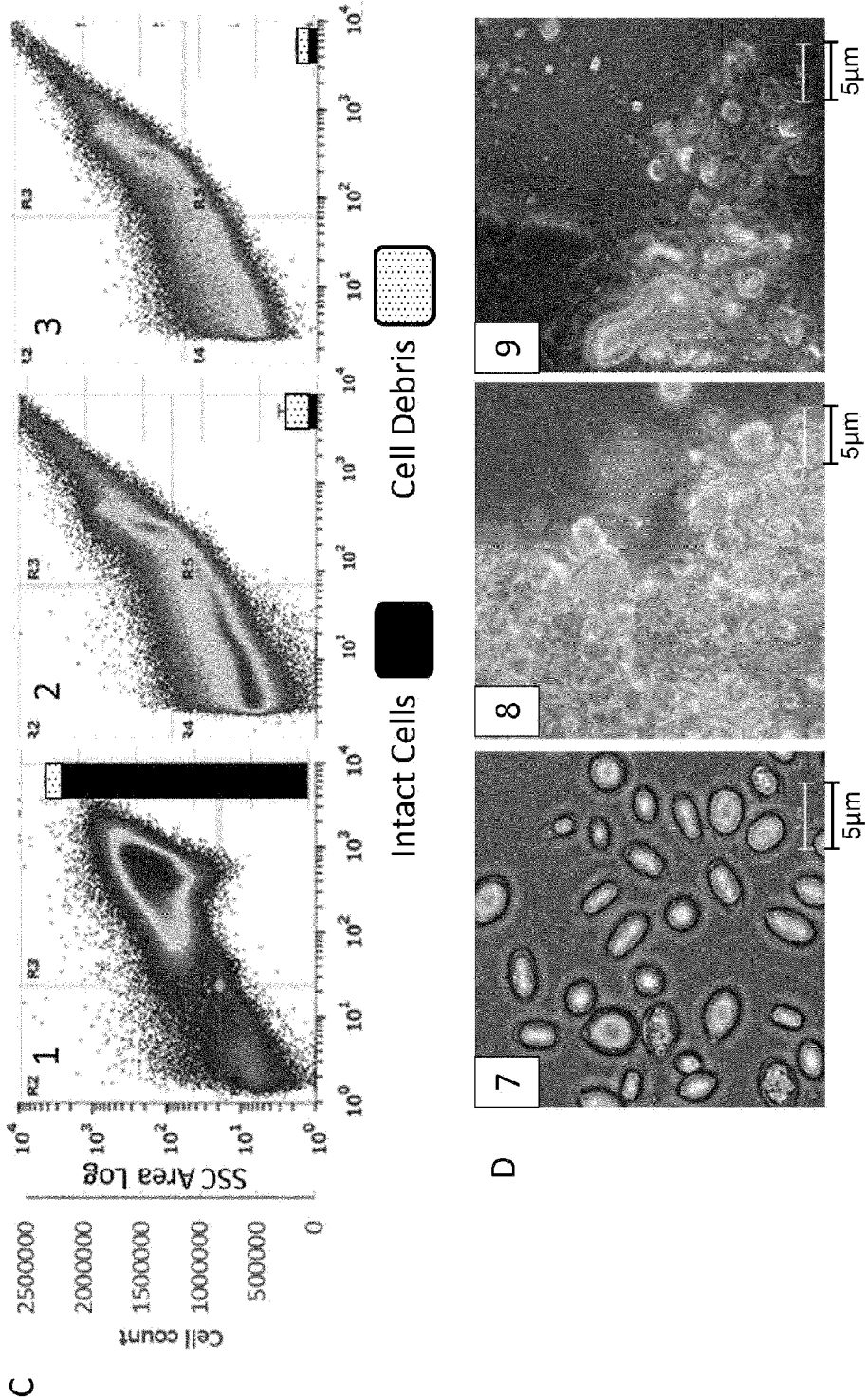


Fig. 16C to 16D (4-6, 10-12): Results protease treatment

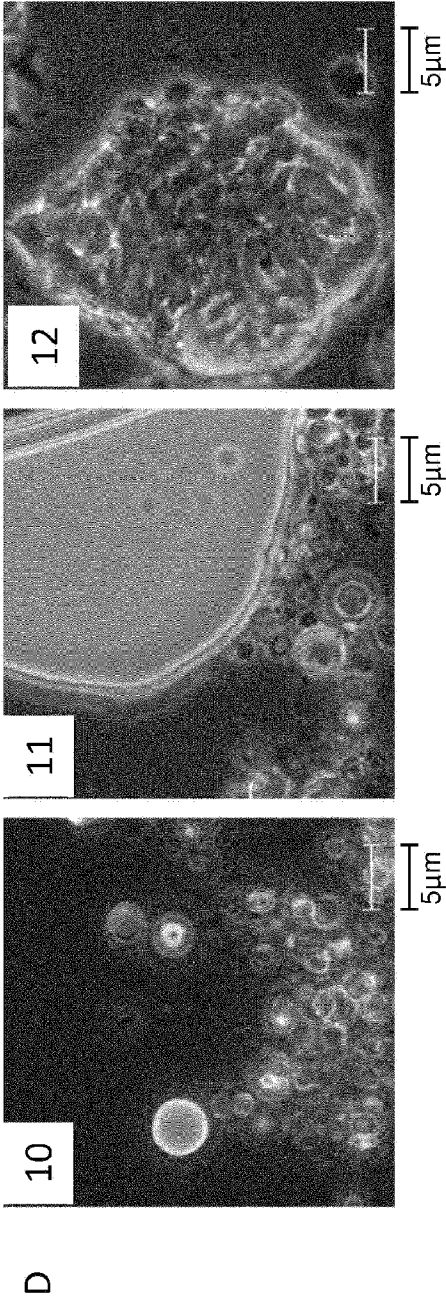
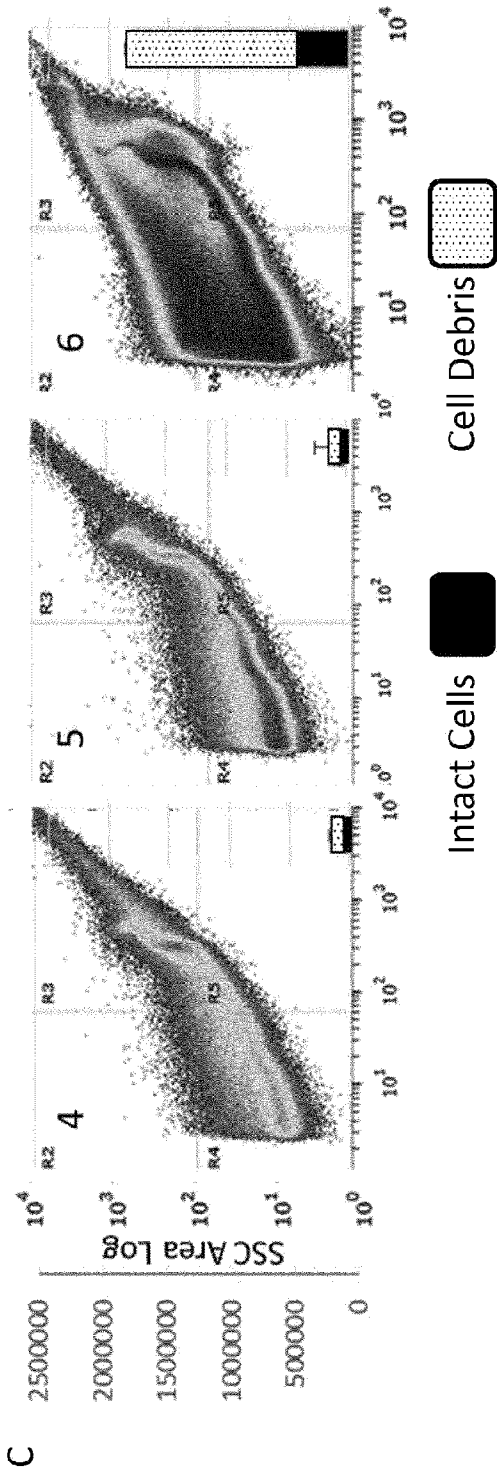
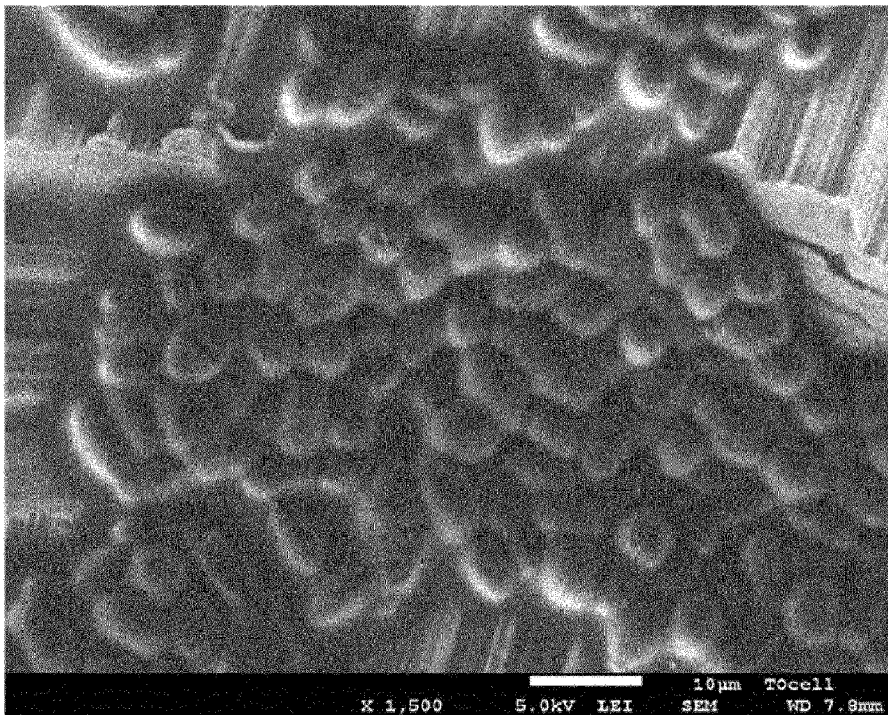


Fig. 17A to 17D: Results protease treatment

A



B

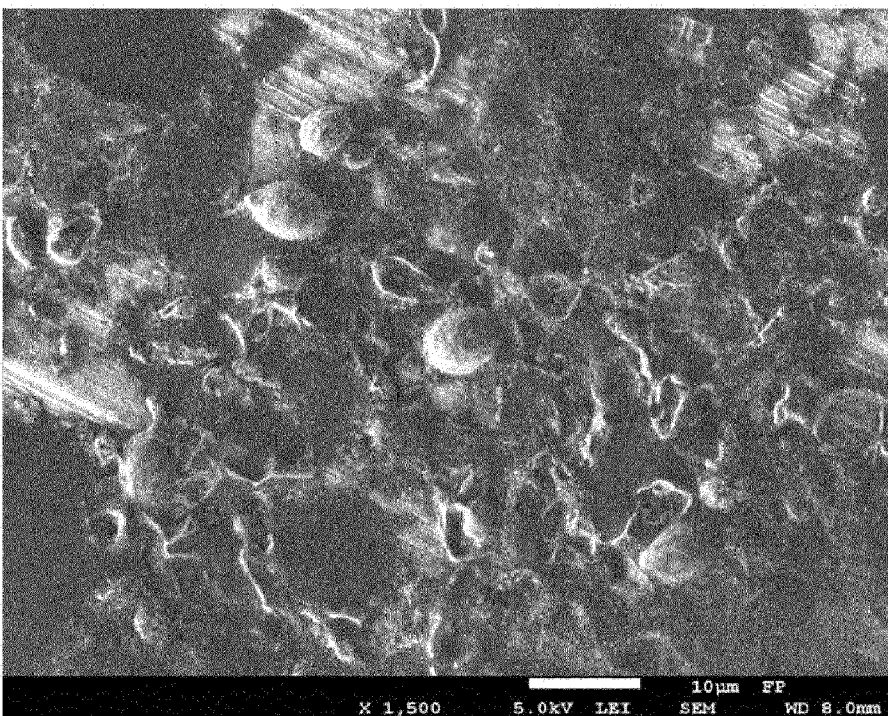
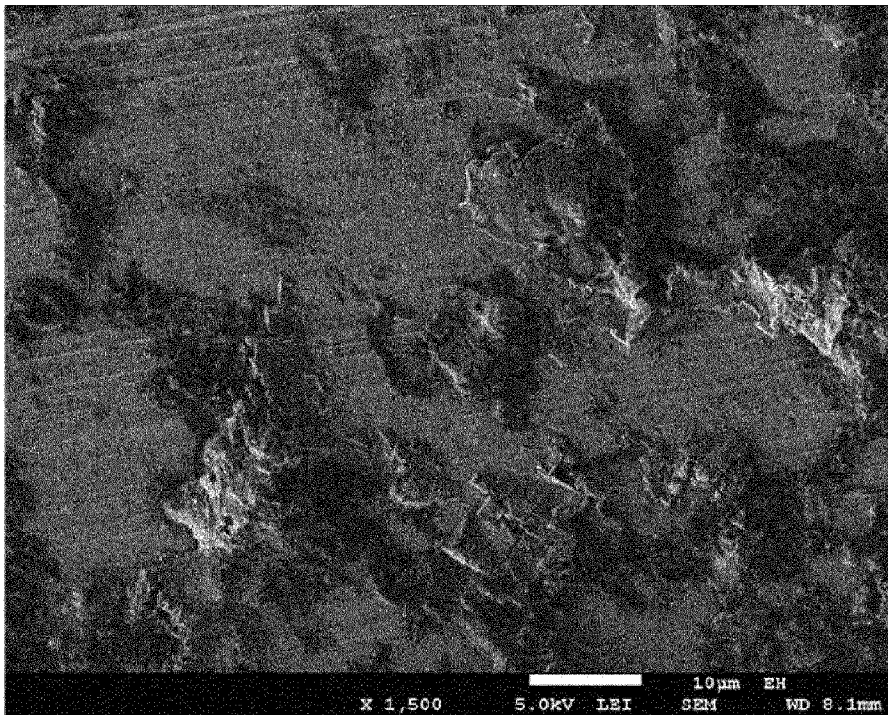


Fig. 17A to 17D: Results protease treatment

C



D

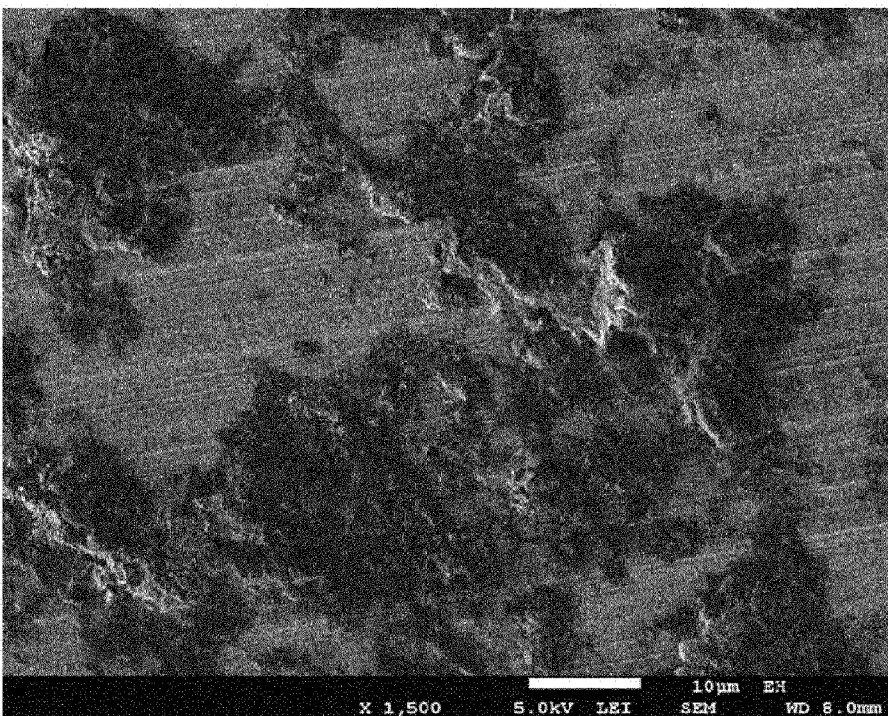


Fig. 18A to 18D: Results protease treatment

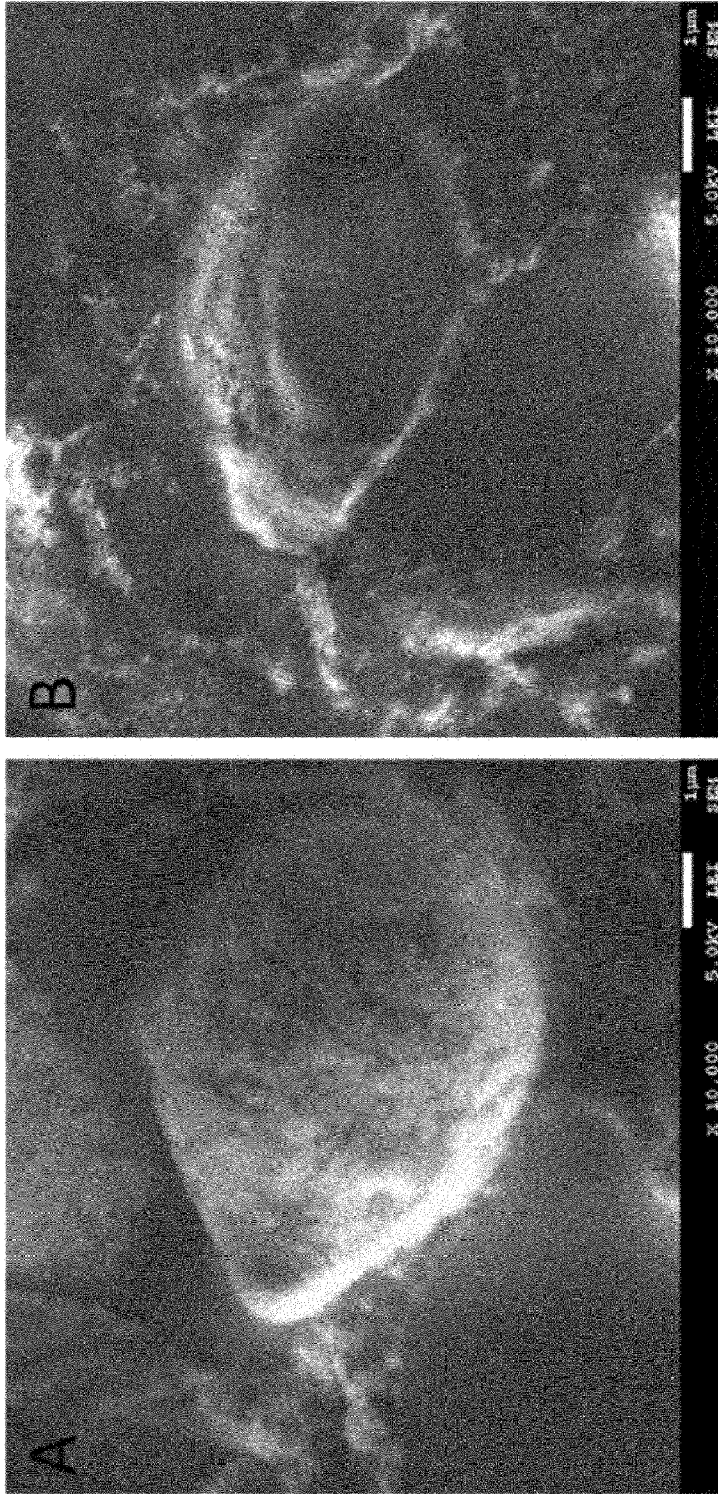


Fig. 18A to 18D: Results protease treatment

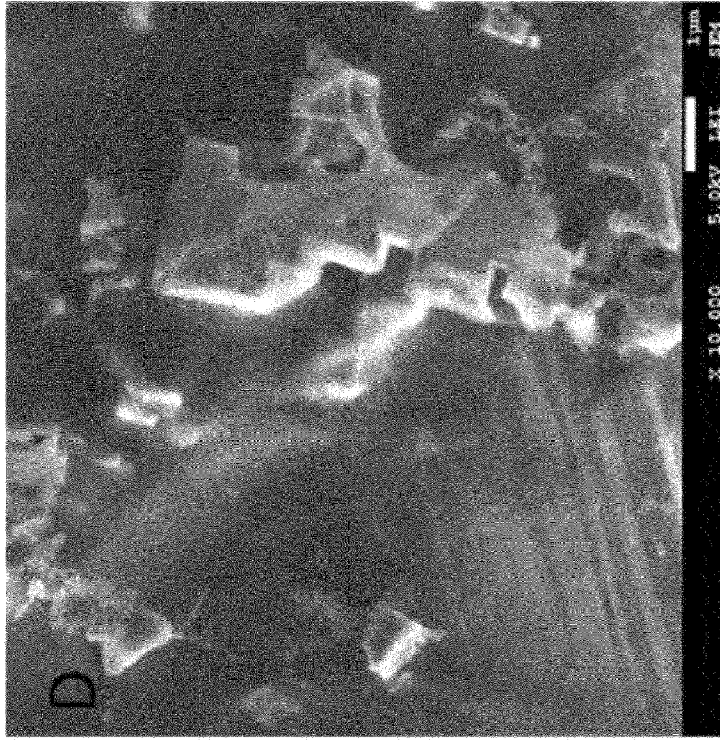
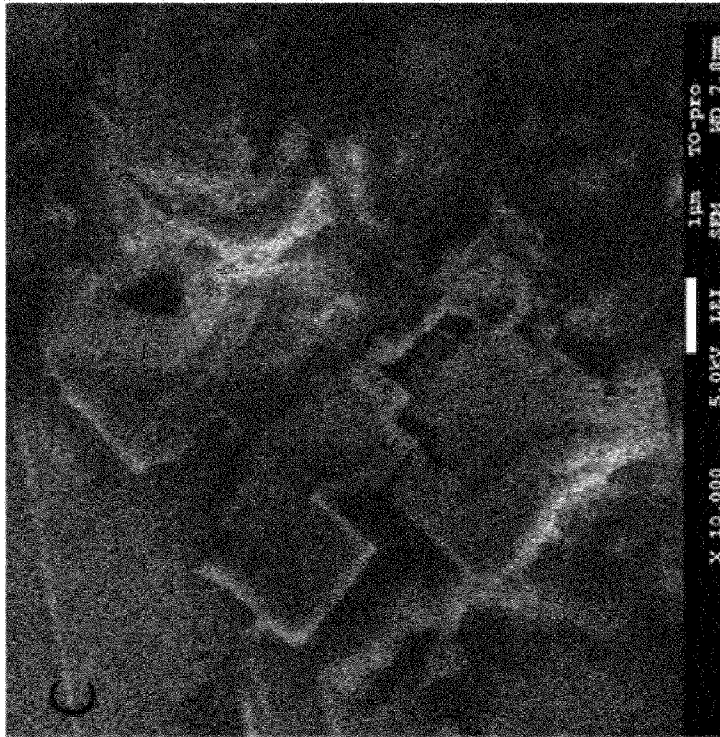


Fig. 19: Results polymer treatment

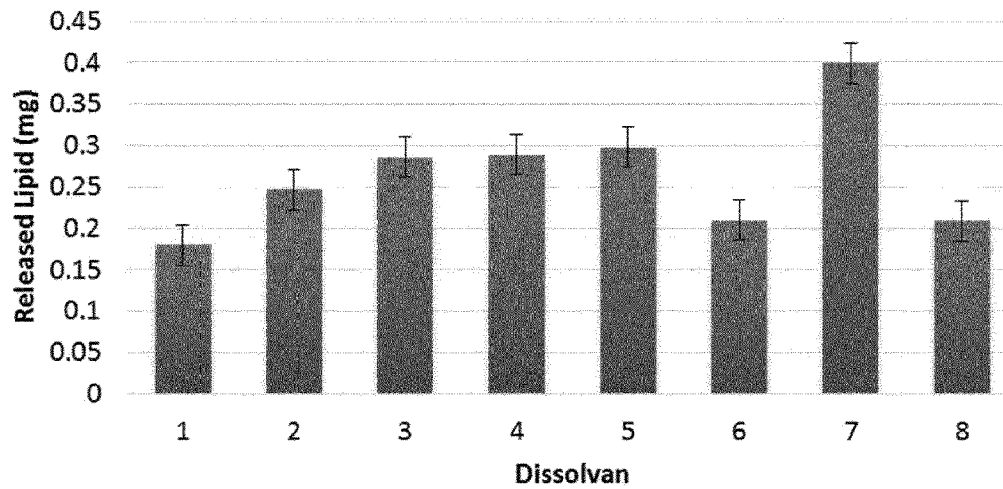


Fig. 20: Lipid profile analysis

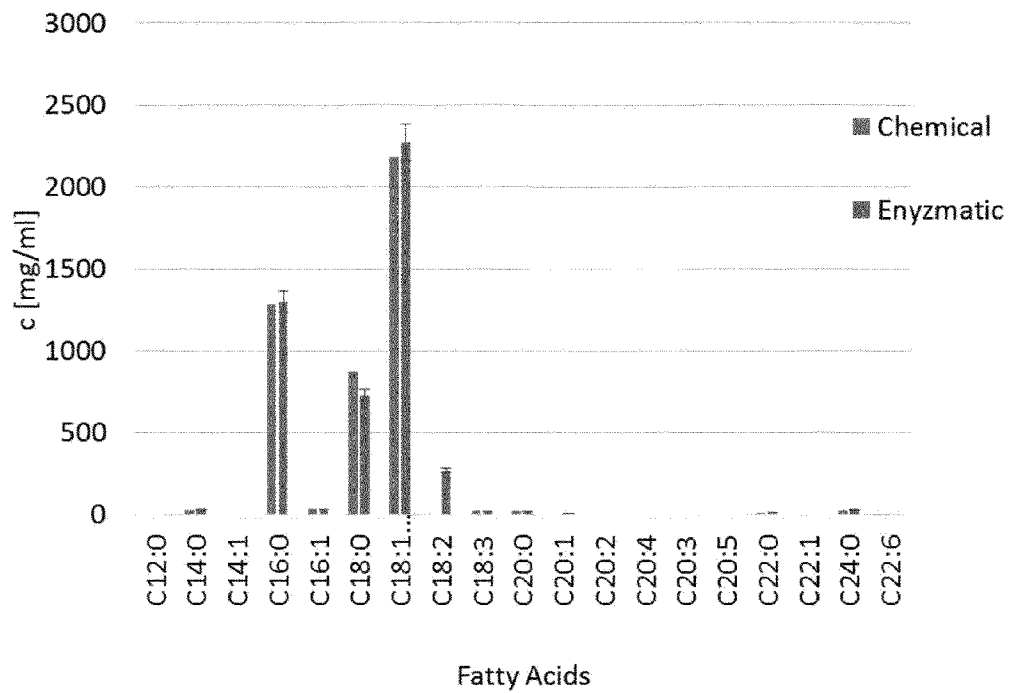


Fig. 21: Hydrolysate analysis

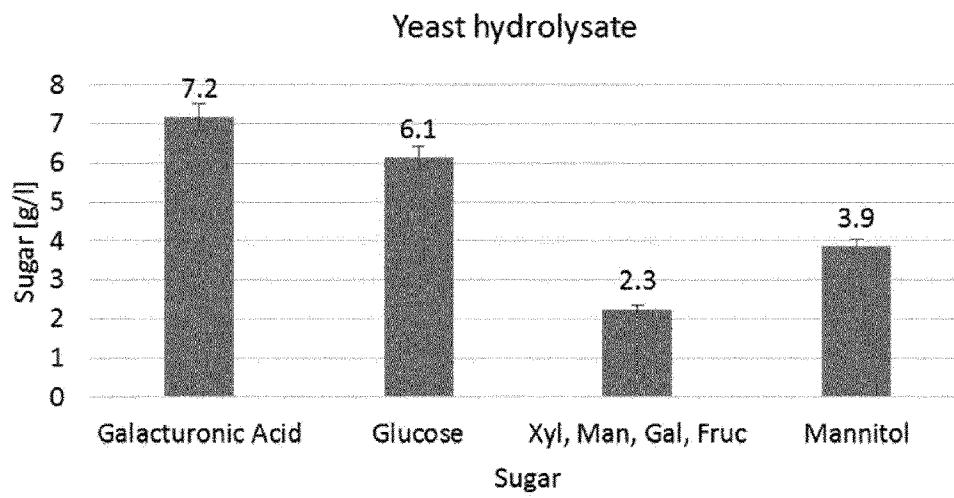


Fig. 22A to 22C: Layer formation and analysis

