

QUANTIFICATION AND PHYSICOCHEMICAL CHARACTERIZATION OF
STARCH IN MALTED BARLEY

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7 **ABSTRACT**

8

9 Sixteen samples of malted barley -grown in Buenos Aires Province
10 (Argentina)- were selected for this study. The starch was isolated and purified
11 using a modified version of Morrison Method. The starch concentration in the
12 samples ranged from 53.2 to 63.3 %. The starch samples were characterized
13 physicochemically, obtaining the following results: a) the concentration of lipids,
14 phosphorus and nitrogen was too low; b) the values of apparent amylose
15 ranged from 19.0 to 23.9 % whereas the values of total amylose ranged from
16 23.6 to 31.2; c) starch presents a bimodal granule size distribution: type A (big
17 and lenticular) and type B (small and irregular or spherical); d) the gelatinization
18 temperature ranged from 62.18° C to 64.68°C; e) the amylopectin is the
19 responsible for the crystallinity of starch granules; f) granules are birefringent.
20 This property disappears when starch is heated above its gelatinization
21 temperature.

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23 **Key words:** malted barley, starch, quantization, physicochemical
24 characteristics.

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32 INTRODUCTION

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34 Malted barley is one of the most important crops in the world, occupying
35 the fourth position after wheat, corn and rice. MERCOSUR produces
36 approximately 1% of the world's total production, Argentina being the country
37 that makes the greatest contribution, followed by Uruguay, Brazil and Bolivia.
38 The province of Buenos Aires concentrates more than 90% of the national
39 production as its climate and soils are favorable for the harvest of this crop.
40 Besides, the presence of a thriving malting industry contributes to the
41 production of malted barley in this area (1).

42 As many other cereals, malted barley is extremely important in the
43 primary production of foods. In Argentina, the most important application of this
44 cereal is the production of malt.

45 Malted barley belongs in the family of the gramineae, which produce
46 one-seeded cereal grains, called caryopsides. In their structure, caryopsides
47 present a pericarp, a testa, an aleurone layer, an endosperm and an embryo or
48 germ (Figure 1). The endosperm makes up 70% of the total weight of the
49 caryopsis. Having the greatest capacity to store the grain, this organ becomes
50 the main host for the accumulation of carbohydrates, presenting 65-70% of its
51 weight in the form of starch (2).

52 Starch constitutes a potential source of energy for the plant. It occurs in
53 the form of granules, which are synthesized in the amyloplasts. There are two
54 kinds of granules: Type A (big and lenticular) and Type B (small and spherical).
55 When the grain is fully ripe, granules B considerably outnumber granules A, at a
56 rate of 10:1. Being much smaller (<10 μm) than granules A (20-45 μm),

57 granules B represent less than 30% of the total weight of accumulated starch
58 (3).

59 Starch granules are anisotropic due to the presence of crystalline regions
60 in their mass, which is preeminently amorphous. As a result of this, the
61 phenomenon of birefringence takes place. Birefringence allows for the
62 possibility of looking at the starch granule through the polarizing microscope.
63 Under the microscope, the starch granule appears as two different gray zones
64 which resemble a Maltese cross. When starch is heated in water, its structure
65 absorbs the water, becoming “swollen”. At a certain temperature, this swelling
66 becomes irreversible and birefringence is lost because of the destruction of the
67 crystalline state. This temperature is called gelatinization temperature.

68 Starch is fundamentally made up of two polymers: a polymer of amylose
69 glucose (lineal) and a polymer of amylopectin glucose (strongly ramified). It also
70 presents a series of minor constituents such as polar lipids, nitrogen and
71 phosphorus in the form of phospholipids (4). As it has been mentioned before,
72 the starch granule is found partially crystallized as a result of the presence of
73 the amylopectin molecule. There is a relatively constant relation between
74 amylose and amylopectin (23:77).

75 The aim of this study is twofold: to establish an accurate quantitative
76 methodology which enables the isolation and quantification of starch in malted
77 barley and to provide a physical and chemical characterization of the isolated
78 starch.

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82 MATERIALS AND METHODS

83

84 Grain samples

85 Sixteen samples of malted barley were processed from Quilmes Palomar
86 cultivar (liberated in Argentina and registered in 1994). The samples were
87 collected in six cities of Buenos Aires Province: Alberti (S35°08'-W60°13'),
88 Bordenave (S37°51'-W63°01'), Cascallares (S38°30'-W60°28'), Coronel Suárez
89 (S37°28'-W61°56'), Puán (S37°33'-W62°46') and San Mayol (S38°23'-
90 W60°17'). These samples were quartered to obtain representative samples of
91 each site.

92 Starch isolation and purification

93 Applying the technique proposed by McDonald and Stark in 1988 (5),
94 barley grains were triturated using a small mill so that grains would only be
95 reduced to parts avoiding powder formation. Then smaller parts were steeped
96 for 17 hours in 0.02 M HCl at 4° C (10 mL / 1 g of grain).

97 The steeped grains were neutralized using 0.2 M NaOH and then filtered
98 to recover the solids. A solution of 0.1 M TRIS HCl; pH 7.6; with 0.5 % of
99 Na₂SO₃ and 0.01 % of thiomersal (10 mL / 1 g of grain) was added to the
100 recovered solids, which were then agitated for 1 hour at room temperature.
101 After that, Proteasa Sigma type XIV (5 mg / 1 g of grain) was added to the
102 grains, which were constantly agitated at 4° C for a period of 12 hours. Once
103 the time for the enzymatic action had passed by, the remaining solids were
104 rubbed with a pestle to release the starch as a suspension, which was next
105 filtered, recovering the filtered liquid. The solids which remained in the funnel
106 were put back in the mortar with distilled water to ensure the full release of

107 starch. A new filtering process was carried out. This process was repeated until
108 the total release of starch was achieved.

109 The solution obtained was centrifuged for 5 minutes at 5000 rpm,
110 producing two layers: a lower layer of starch (white) and an upper very thin
111 layer of protein (brown). The brown proteid layer was softly removed and
112 reserved for later treatment. The white layer was washed in distilled water and
113 centrifuged again. Once more, two layers were formed: the upper layer was
114 removed and set apart. This procedure was repeated until the brown layer no
115 longer formed at the moment of centrifuging.

116 The layers of starch and protein were washed separately, three times in
117 distilled water and once in acetone. Then they were put to dry at room
118 temperature. The brown layer was purified to separate the starch granules from
119 the protein matrix.

120 The brown layer was weighed before starting the purification process and
121 a solution 0.1 M TRIS HCl; pH 7.6, containing 0.5 % of Na_2SO_3 and 0.01 % of
122 thiomersal, and proteinase K were added, knowing that for 1 g of brown layer,
123 30 mL of the solution and 1.25 mg of proteinase K are required. The solution
124 was agitated for 24 hours at room temperature. The resulting solution was
125 centrifuged for 5 minutes (5000 rpm). The supernatant was discarded and the
126 precipitate obtained was washed six times in distilled water and once in
127 acetone. Then it was dried at room temperature.

128 The brown layer, dry and treated with the enzyme, was weighed and 0.2
129 M NaCl and toluene were added to the solution, knowing that for every 5 g of
130 brown layer, 500 mL of solution NaCl and 71.5 mL toluene are required. This
131 suspension was agitated for 12 hours at room temperature and centrifuged,

132 forming three layers: a layer of toluene, an aqueous layer and a precipitate of
133 starch. The toluene layer and the aqueous layer were removed and set apart.

134 The toluene layer was washed in distilled water and centrifuged to
135 recover starch granules. The aqueous layer was centrifuged directly to obtain
136 the same result.

137 The layers of starch obtained were dried at room temperature and
138 weighed.

139 All procedures were conducted in duplicate in all the samples.

140 **Physicochemical characterization of starch**

141 **Lipids concentration**

142 The concentration of lipids was determined using the technique devised
143 by King in 1980 (6). Starch was agitated for 4 hours at room temperature, with a
144 mixture of chloroform- methanol (2:1), at a rate of 27 mL/500 mg of starch. The
145 solution was centrifuged for 5 minutes at 5000 rpm, then it was filtered and
146 transferred into a tared distillation balloon flask. The mixture of solvents
147 evaporated in a rotary evaporator and the distillation balloon flask was placed in
148 a vacuum furnace for 2 hours at 100° C and 6.66×10^2 Pa (5 Torr). The balloon
149 flask was next weighed again and the percentage of lipids in the sample was
150 estimated by the difference of weight registered.

151 **Nitrogen concentration**

152 The concentration of nitrogen was determined by means of the method
153 Kjeldahl (7). Starch was weighed and introduced into the digestion tube.
154 Concentrated H₂SO₄ (8 mL / 0.05 g of starch) and a catalytic mixture of salts
155 (10 g K₂SO₄: 1 g CuSO₄: 0.1 g Se) were added and the digestion process was
156 carried out. 40 mL of distilled water and some drops of Tashiro Indicator (a

157 mixture of methyl red and methylene blue) were added to the solution. Then, a
158 given volume of 0.1000 M NaOH was added to neutralize the solution. The
159 mixture was distilled for 5 minutes in a distillation unit including an automatic
160 steam generator. The distillate was received in a 50 mL Erlenmeyer which
161 contained 10 mL of 0.1000 M HCl and some drops of Tashiro Indicator. Finally,
162 the distillate was titrated using 0.1000 M HCl until the indicator turned to bright
163 green.

164 The following formulae were used to make the calculation:

$$165 \quad (10 \text{ mL HCl} - \text{mL HCl used}) \times [\text{HCl}] \times [\text{NaOH}] \times 14 = \text{mg N}$$

$$166 \quad \% \text{ total N} = \frac{\text{mg de N}(\text{sample}) - \text{mg de N}(\text{control})}{\text{mg sample}}$$

167 **Phosphorous concentration**

168 Following the method devised by Johnson and Ulrich in 1959 (8), starch
169 was introduced into a 50 mL tube, and a mixture of HNO₃ and HClO₄ (2:1), at a
170 rate of 1 mL / 0.1 g of starch, was added. Then the mixture was digested.
171 Distilled water was added until the solution reached 25 mL. The content (ppm)
172 of phosphorous (P) was determined using a spectrometer of atomic absorption
173 with inductive coupling plasma (ICP).

174 The following formulae were used to make the calculation:

$$175 \quad (\text{ppm P in plasm}) \times \left(\frac{25 \text{ mL}}{\text{starch weight}} \right) = \text{ppm P sample}$$

$$176 \quad \text{ppm P in sample} \times 10^4 = \% \text{ P sample}$$

177 **Amylose concentration**

178 Following the method devised by Morrison and Laignelet in 1983 (9), 70-
179 80 mg of starch were weighed in a 20 mL tube placed on a magnetic shaker. 10

180 mL of a urea-dimethyl sulfoxide solution (9 volumes of dimethyl sulfoxide : 1
181 volume of 6M urea) were added and the tube containing the suspension was
182 placed in a calefactor plate with agitation until homogenization was achieved.
183 Then the suspension was introduced into a furnace at 100° C for 1 hour, after
184 which it was cooled at room temperature. (*).

185 *Concentration of apparent amylose*

186 0.5 mL of the solution (*) were taken and transferred into a 50 mL flask.
187 This step was made in triplicate. The 0.5 mL added to each flask were weighed.
188 After that, 25 mL of distilled water and 1 mL of solution I₂/IK (2 mg of I₂, 20 mg
189 of IK/mL) were added to the solution. Distilled water provided the required
190 volume and the solutions were mixed until they became homogeneous.
191 Simultaneously, the control sample was prepared with distilled water. The
192 samples were settled for 15 minutes for stabilization. In order to read the
193 absorbency, the spectrophotometer was adjusted to zero with the control
194 sample. The absorbency was read at 635 nm and the “blue value” and the
195 percentage of apparent amylose were calculated.

196 *Total amylose concentration*

197 0.5 mL of the solution (*) were transferred into a 10 mL tube and
198 weighed. This step was made in triplicate. 5 mL of ethanol 99.5 % (v/v) were
199 added to remove the lipids. Then the content of the tube was mixed in a vortex
200 mixer, centrifuged for 30 minutes at 5000 rpm and the supernatant was
201 discarded. 1 mL of the urea- dimethyl sulfoxide was added and mixed in a
202 vortex mixer and a clear solution was obtained 10 seconds later. The content
203 was transferred into a 50mL flask and 25 mL of distilled water and 1 mL of I₂/IK
204 were added. Distilled water provided the required volume and the solution was

205 mixed. After 15 minutes the absorbency was read at 635 nm and the “blue
206 value” and the percentage of total amylose were calculated.

207 The following formulae were used to make the calculation:

$$208 \quad \text{Blue value} = \frac{\text{Absorbency} \times 100}{2 \times \text{g solution} \times \text{mg starch}}$$

$$209 \quad \text{Percentage of amylose} = 28,414 \times \text{blue value}$$

210 **Scanning Electron Microscopy (SEM)**

211 The microscope used in this study was a scanning electron microscope
212 (JEOL 35 CF) equipped with a detector of secondary electrons, with a nominal
213 resolution of 60 Å. An acceleration voltage of 15 KV was used with a
214 magnification of 1000 X. The images were obtained with IDX, a software
215 program designed to acquire images digitally (IDX), with a resolution of 1024 x
216 800 pixels. The statistic treatment was conducted applying AnalySis Pro 3.0, a
217 software program used for the processing and analysis of images.

218 **Determination of gelatinization temperature by differential scanning 219 calorimetry (DSC)**

220 The tests were made in a DSC Polymer Laboratories (Rheometric
221 Scientific Surrey, UK) with a PL-V5.41 software program, using a heating
222 program of 10°C/minute from 10 to 120°C. Suspensions of starch were
223 prepared. The samples were weighed in aluminum capsules and then they were
224 closed hermetically. An empty capsule was used as reference. The enthalpy of
225 gelatinization was determined in mJoule/mg of the dry sample, and the initial
226 and peak temperatures (°C) were measured using the software mentioned
227 before. The dry weights of the samples were obtained using a 105° C furnace
228 until a constant weight was achieved.

229 **X ray diffraction spectroscopy**

230 The tests were made in a diffractometer equipped with an X Ray tube
231 with a copper anode (PW1710 BASED), which produces a radiation of 1.54 Å,
232 and is operated at 45 KV and 30 mA.

233 **Polarizing microscopy**

234 A suspension of starch was prepared, presenting a 5% concentration.
235 The suspension was then centrifuged and a drop from the bottom of the tube
236 was removed and observed under the polarizing microscope. The suspension
237 was next heated above its gelatinization temperature and a drop of the solution
238 was removed and observed under the polarizing microscope.

239

240 **RESULTS AND DISCUSSION**

241

242 **1. Starch concentration**

243 Previous research (10) proved that a considerable number of small
244 starch granules is lost if the brown protein layer is removed from the surface of
245 suspensions of raw starch during the isolation process. Following the method
246 selected for this study, the brown protein layer was purified in order to recover
247 the starch granules which are associated with the protein matrix, obtaining
248 representative samples.

249 The percentage of starch found in the dry samples ranged from 53.2% to
250 63.3%, with an average value of 59.7%. This variation is similar to that reported
251 in the bibliography (2), and is probably close to the real values.

252

253

254 **Starch chemical composition**

255 **Phosphorous, lipids and nitrogen concentration**

256 The concentration of phosphorous (P), lipids and nitrogen (N) was
257 determined with the sole aim of showing the purity of the starch samples under
258 study.

259 The method selected for the determination of P is a modified version of
260 the method used for determining micronutrients. The percentages of P ranged
261 from 0.060 to 0.075, with an average value of 0.067.

262 The method employed in the determination of lipids is based on the
263 premiss that lipids associated with starch are essentially polar and require polar
264 solvents so that they can later be extracted and quantified. The percentages of
265 lipids ranged from 0.73 to 0.97, with an average value of 0.86. This range is
266 correspondent with the values found in the bibliography (0.5 – 1 %).

267 In order to determine the concentration of N, all N in the sample was
268 converted to ammonium through a digestion process made with concentrated
269 sulfuric acid. Also, K_2SO_4 was used to increase the digestion temperature and
270 catalysts such as Se were employed to increase the rate of oxidation. The
271 ammonium was determined by the quantity of ammonia released by the
272 distillation of the digest with an alkali. The advantage of this method is that it
273 requires only a few samples and reagents and that it offers results which are
274 highly reproducible. In all cases, the samples presented a very low level of N (<
275 0.05 %), part of which belongs to the lipids. The rest might be proteid, probably
276 the remains of enzymes involved in the synthesis of starch.

277 In order to corroborate that the enzymatic treatment with proteinase K -
278 developed in the purification of starch- can effectively separate proteins from

279 granules, the percentage of N in one of the samples was determined before and
280 after its purification. It was confirmed that the concentration of N in the sample
281 which was not purified was greater than that found in the sample purified with
282 the enzyme, the results being 0.513 and 0.042 % respectively.

283 The percentages of P, lipids and N found allow us to conclude that the
284 method used for isolating the starch led to starch samples which were highly
285 purified.

286 **Amylose concentration**

287 The method selected to determine the concentration of amylose is based
288 on the premiss that amylose fraction has affinity with iodine to form complexes,
289 which can be quantified colorimetrically.

290 Amylose forms complexes with the lipids present in starch granules.
291 These complexes hinder the bond between amylose and iodine, impeding the
292 determination of total amylose at this stage of the process (2). The value of
293 apparent amylose was determined, which corresponds with the amylose found
294 in starch without the separation of lipids. The study also determined the value of
295 total amylose, which corresponds with the real value of amylose in starch given
296 that lipids had previously been separated from starch. The values of apparent
297 amylose ranged from 19.0 and 23.9 %, with an average value of 21.3 % and the
298 values of total amylose ranged from 23,6 to 31,2 %, with an average value of
299 26.4 %.

300 Table 1 shows the chemical composition of starch in malted barley.

301 **Morphology and size distribution of starch granules**

302 The study conducted with SEM showed two types of granules: type A,
303 corresponding to big granules, and type B, to small ones (Figure 2). Some of

304 the small granules presented an irregular shape while others were practically
305 spherical. In contrast, big granules presented a lenticular shape with better
306 defined rims (Figure 3).

307 In order to study the size distribution of starch granules, a histogram was
308 made (Figure 4). Each rectangle represents the amount of particles counted for
309 each class and each class corresponds with a certain range of average
310 diameters of starch granules (class 1: 0–2 μm ; class 2: 2–4 μm , etc.). A
311 bimodal distribution is observed. Granules A present average diameters greater
312 than 20 μm , whereas granules B have average diameters smaller than 10 μm
313 and represent 83% of the total number of granules.

314 **Gelatinization temperature**

315 Diverse changes are observed when starch is hydrated and heated. The
316 process of gelatinization implies the loss of molecular order which is revealed in
317 the starch granule. This transformation is accompanied by certain irreversible
318 changes such as water absorption, grain swelling, crystalline part fusion, loss
319 of birefringence, increment of viscosity and solubility of the granule. The
320 differential scanning calorimetry (DSC) is a thermo-analytical technique which
321 monitors how the physical or chemical properties of materials are affected when
322 temperature is modified and detects changes in heat. The principle underlying
323 the procedure is based on the comparison between the influence of the heat
324 flux on the sample and on some inert material of reference, both of which are
325 heated and cooled at the same rate (11).

326 Figure 5 shows a thermogram of the starch samples under study.
327 Thermograms show how the heat flux varies with temperature. The beginning of

328 the peak is correspondent with the beginning of the loss of birefringence and
329 the area below the curve represents the energy (enthalpy) necessary for the
330 loss of molecular order. Concerning these parameters, Table 2 shows the
331 values of starch in the samples under study.

332 **X Ray diffraction spectroscopy**

333 As starches are crystalline, they have the capacity of diffracting X rays,
334 which allows for the possibility of obtaining information about their structure
335 (11). In fact, starch is a semi-crystalline material which produces different
336 responses when subject to the action of X Ray. In general, four different
337 patterns can be observed (Figure 6).

338 Pattern A: starch in cereals.

339 Pattern B: starch in tubercles.

340 Pattern C: an intermediate form between A and B.

341 Pattern V: complexes of helicoidal inclusion of crystalline amylose.

342 The X Ray diffraction specters of amylose and of commercial
343 amylopectin were made in order to show their crystalline quality (Figure 7). The
344 specter of the amylose presents some peaks, probably due to the small
345 ramifications of its structure. The amylopectin specter is similar to the pattern of
346 X ray diffraction registered in type A cereals. Therefore, crystallinity in the starch
347 granule should be the product of amylopectin.

348 The specter of X Ray diffraction of one of the starch samples under study
349 is shown in Figure 8.

350 A study using Correlation Coefficients was carried out in order to
351 establish statistic correlations between the X Ray diffraction specters of all
352 starch samples and the patterns of amylose and amylopectin. It was found that

353 all samples present a high correlation of crystallinity with amylopectin, as all
354 coefficients were greater than 0.9. On the other hand, the correlation with
355 amylose was very low, smaller than 0.25 in all cases. This clearly shows that
356 the crystallinity of the starch granule is a consequence of the amylopectin
357 polymer.

358 **Polarizing microscopy**

359 Given their high degree of structuring, starch granules showed
360 birefringence under the polarizing microscope. The birefringent material is seen
361 as bright areas when the granules are observed through the polarizing
362 microscope. Figure 9 shows a microscopy of one of the starch samples under
363 study. Birefringence was destroyed when the samples were heated above their
364 gelatinization temperatures and the bright areas were no longer observed.
365 Figure 10 shows a microscopy of one of the starch samples after it was heated
366 above its gelatinization temperature.

367

368 **CONCLUSIONS**

369

370 The method selected for the isolation and purification led to the isolation
371 of starch samples from malted barley grains, which are both representative and
372 quantitative.

373 The variation of starch found (53.2 and 63.3 %) was similar to that
374 reported in the bibliography, showing that the technique used for isolating the
375 starch was appropriate to produce quantitative samples. Besides, the values of
376 concentration of lipids, phosphorous and nitrogen allow us to conclude that the
377 method of isolation used led to highly purified samples.

378 The starch studied presented a bimodal granule size distribution,
379 evidencing small granules (type B) and big granules (type A). Type B granules
380 present an irregular or spherical shape, while most granules in Type A have a
381 lenticular shape.

382 The gelatinization temperature of the starch studied coincided with the
383 data reported in the bibliography. X-Ray diffraction spectroscopy determined
384 that amylopectin is the responsible for the crystallinity of the starch granule.

385 Besides, the use of polarizing microscopy allowed us to prove that
386 starch granules are birefringent. This characteristic disappears when the
387 samples are heated above their gelatinization temperature.

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403 **LITERATURE CITE**

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453 **CAPTIONS FIGURES**

454 **Figure 1.** Structure of malted barley grain.

455 **Figure 2.** Scanning Electron Micrography of starch granules in malted barley,
456 Quilmes Palomar cultivar.

457 **Figure 3.** Scanning Electron Micrography of starch granules in malted barley,
458 .Quilmes Palomar cultivar.

459 **Figure 4.** Size Distribution of Starch granules in malted barley, Quilmes
460 Palomar cultivar.

461 **Figure 5.** Thermogram of starch in malted barley, Quilmes Palomar cultivar.

462 **Figure 6.** X Ray Specters of different starches: **A:** cereals, **B:** tubercles, **C:**
463 intermediate form between A and B and **V:** complexes of helicoidal inclusion of
464 crystalline amylose.

465 **Figure 7.** X Ray Specters of commercial amylose and amylopectin.

466 **Figure 8.** X ray Diffraction Specter of starch in malted barley, Quilmes Palomar
467 cultivar.

468 **Figure 9.** Polarizing Micrography of starch granules in malted barley, Quilmes
469 Palomar cultivar, before the sample reached its gelatinization temperature.

470 **Figure 10.** Polarizing Micrography of starch granules in malted barley, Quilmes
471 Palomar cultivar, heated above its gelatinization temperature.

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478 **TABLES**

479 **Table 1.** Chemical composition of starch in malted barley, Quilmes Palomar
480 cultivar.

Phosphorous ^a (%)	0.067 ± 0.004
Lipids ^a (%)	0.86 ± 0.10
Nitrogen ^a (%)	0.042 ± 0.000
Apparent amylose ^b (%)	21.3 ± 1.46
Total amylose ^b (%)	26.4 ± 2.19

481 ^a Average of two determinations

482 ^b Average of three determinations

483

484 **Table 2.** Enthalpies, initial temperature of peaks and gelatinization
485 temperatures, determined by Differential Scanning Calorimetry (DSC) of starch
486 in malted barley, Quilmes Palomar cultivar.

ΔH^a (mJ/mg)	Initial temperature of peak ^a (°C)	Gelatinization temperature ^a (°C)
9.24 ± 0.38	55.99 ± 0.76	63.43 ± 0.64

487 ^a Average of two determinations

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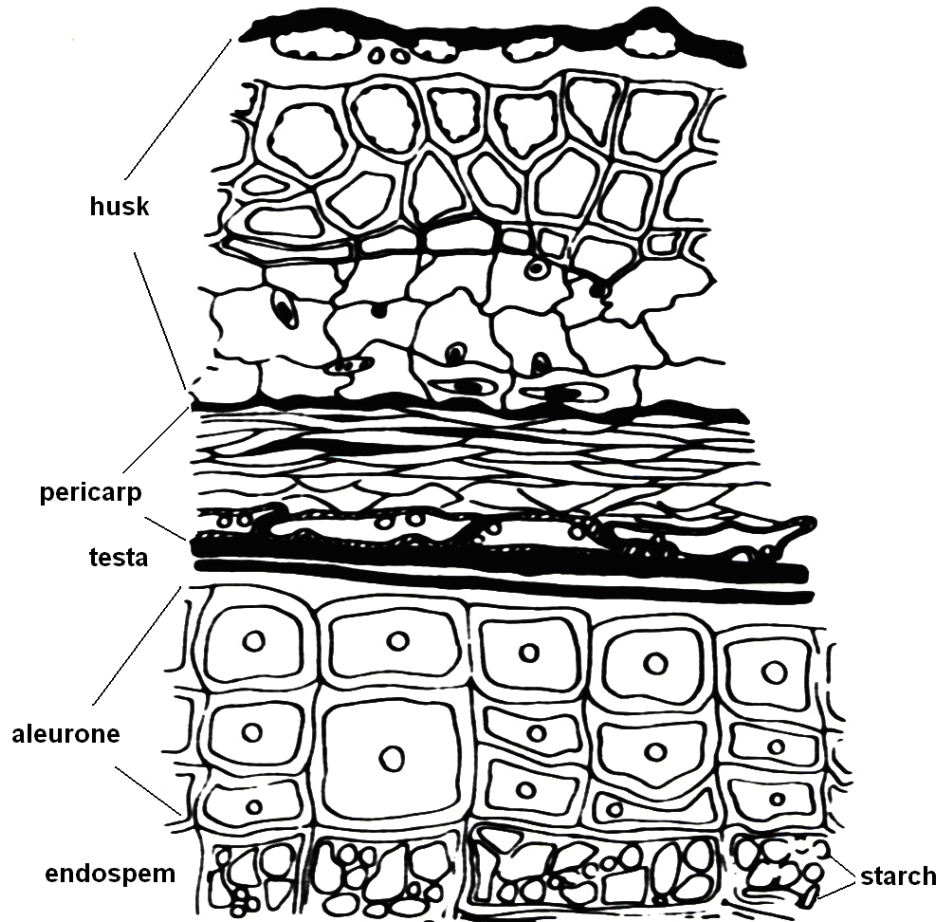
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Figure 1

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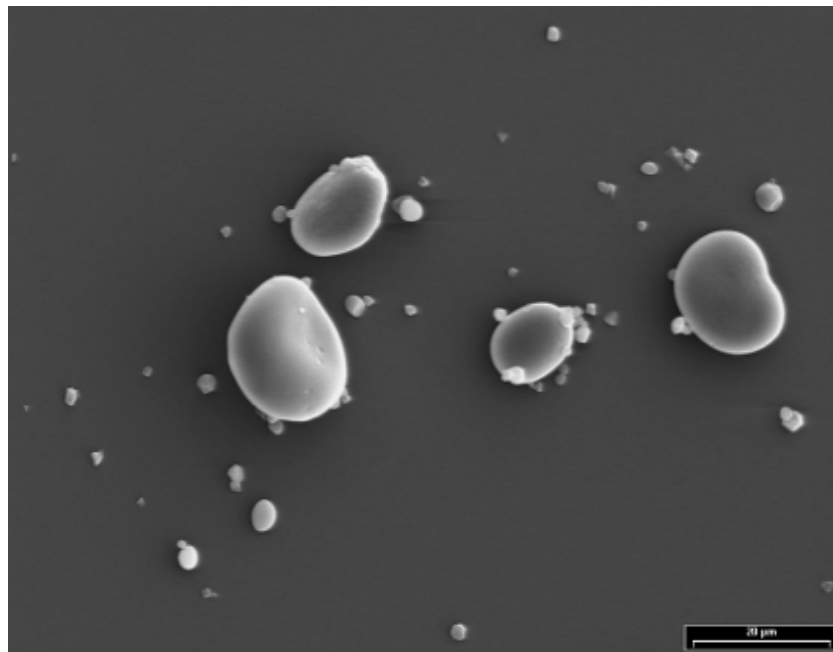
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Figure 2

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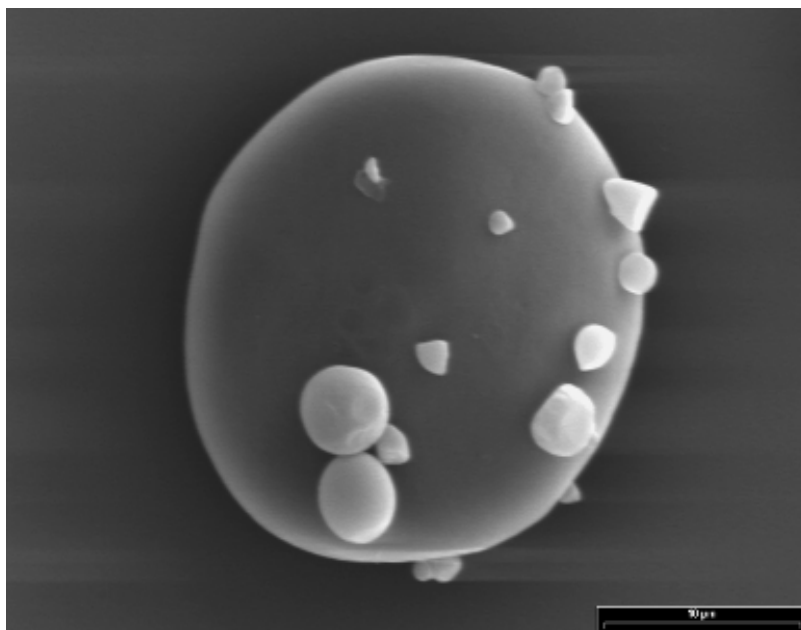
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Figure 3

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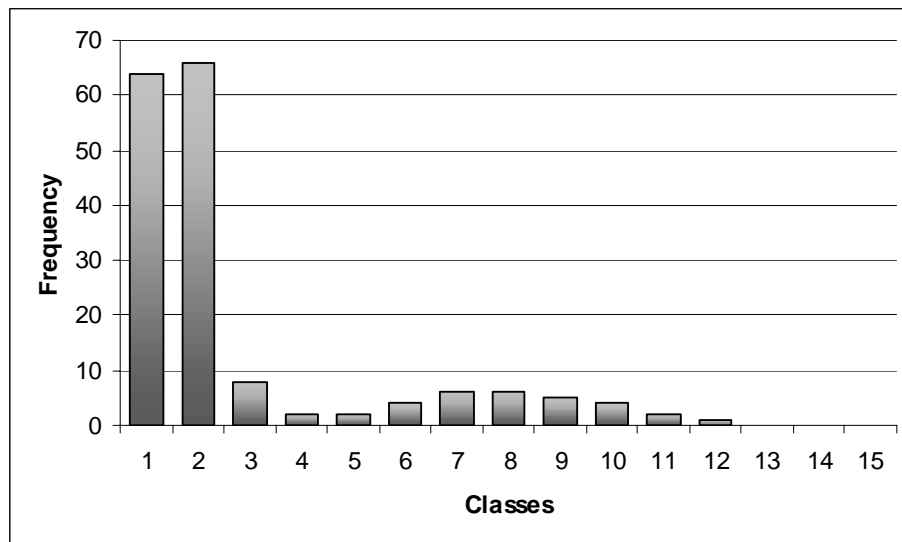
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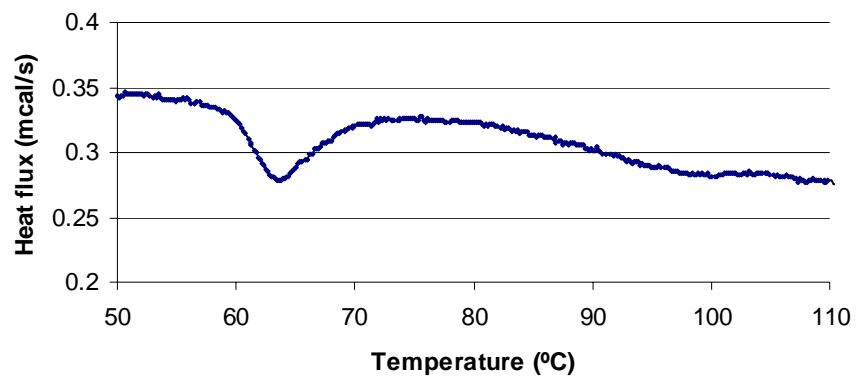
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Figure 4

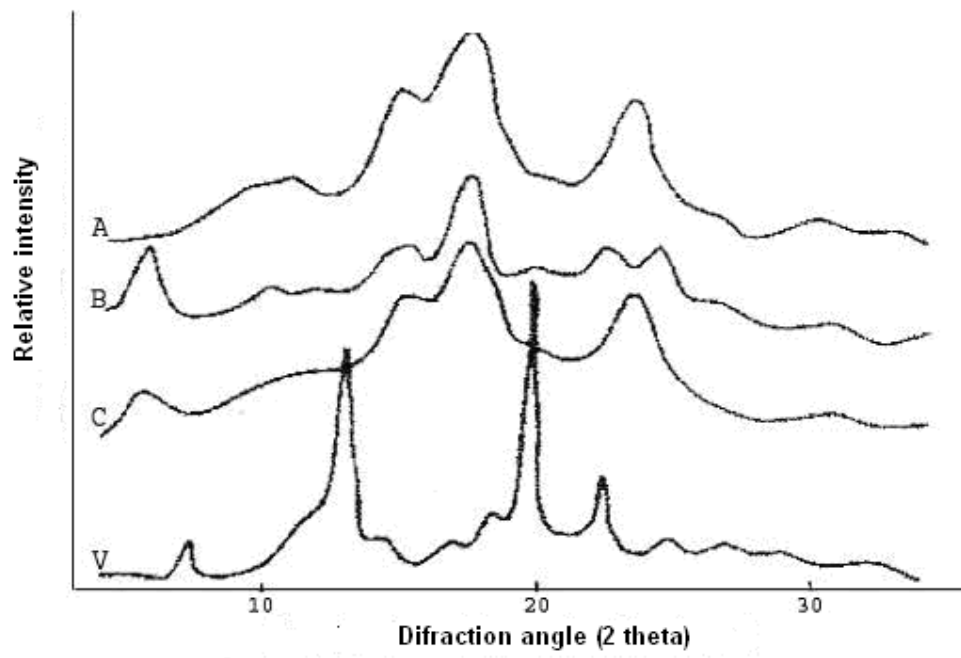
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Figure 5

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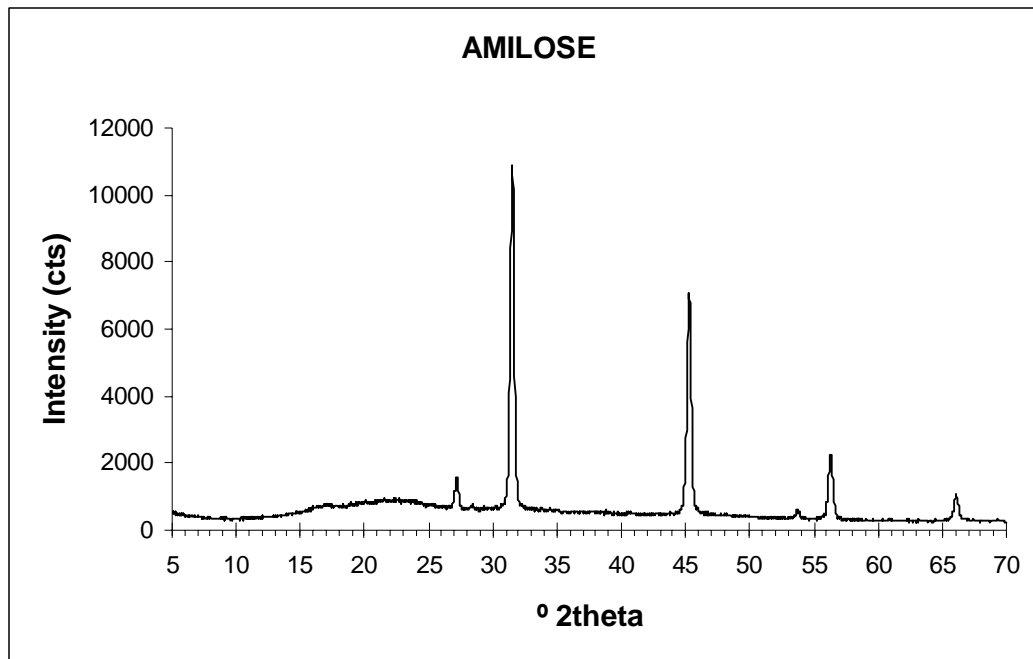
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Figure 6

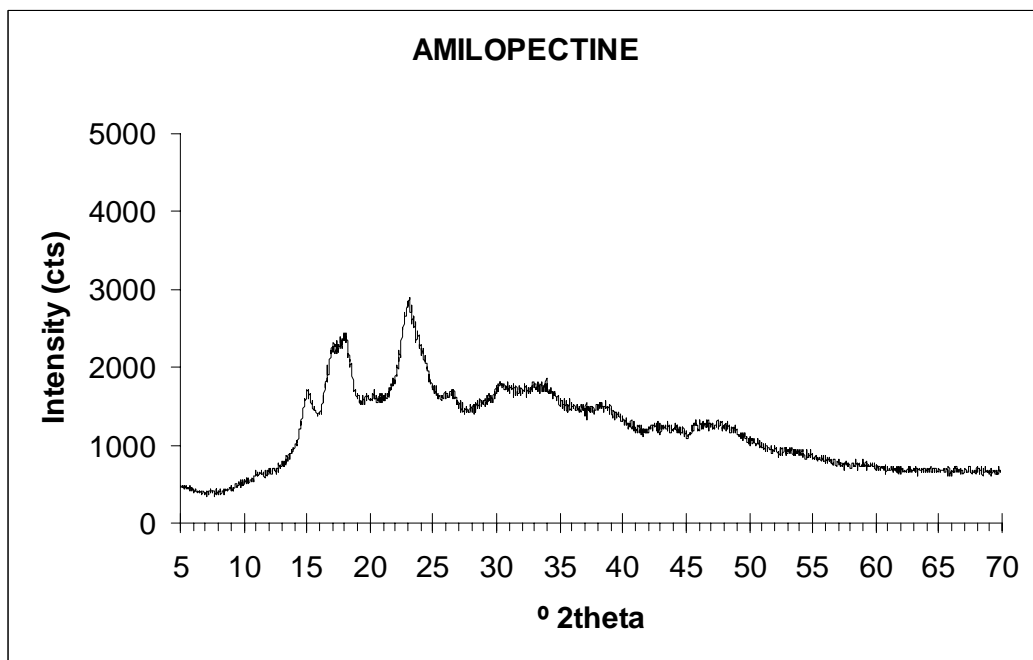
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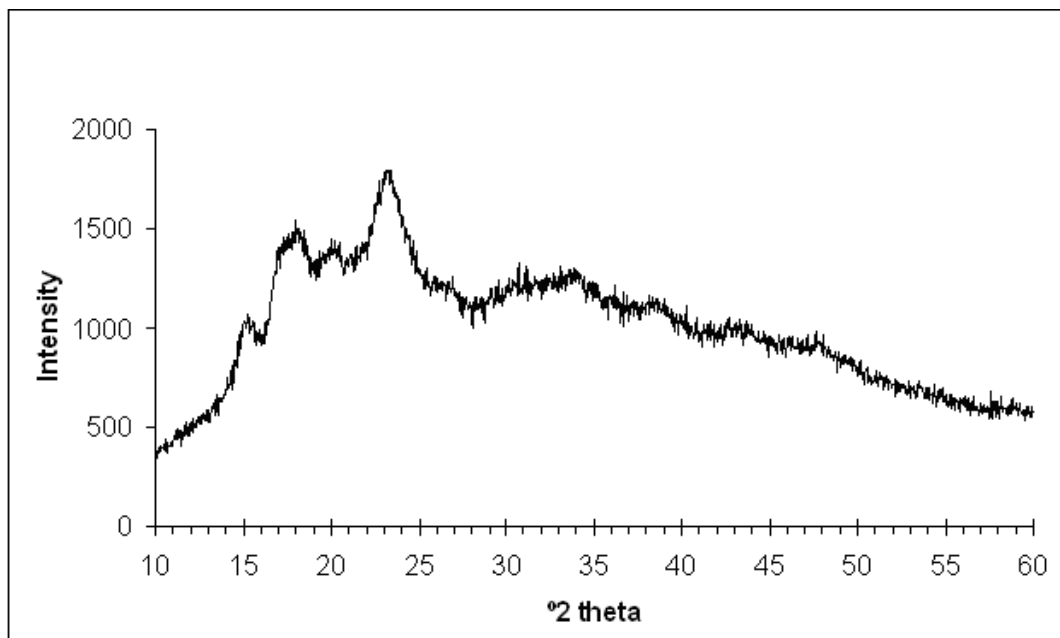
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Figure 7

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Figure 8

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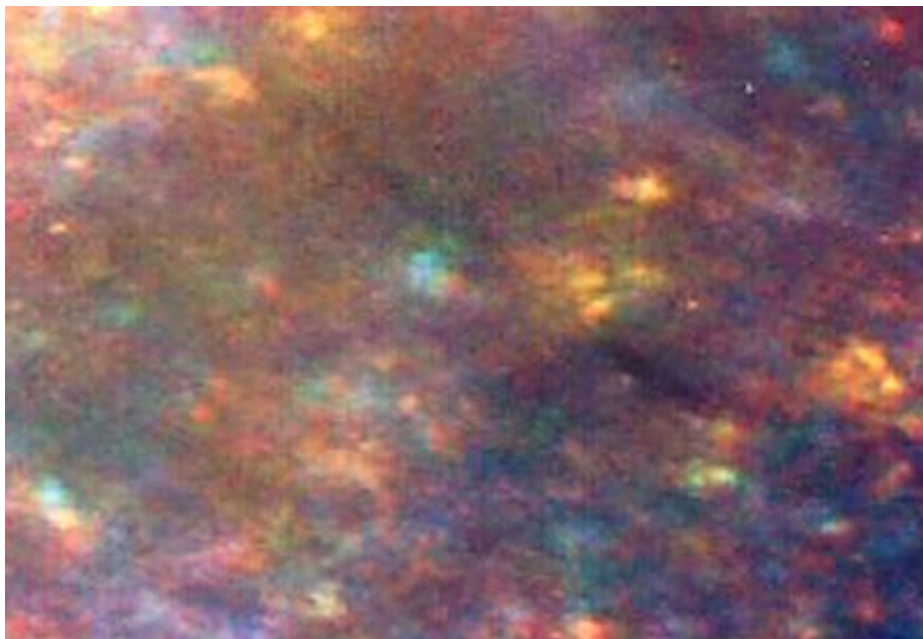
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Figure 9

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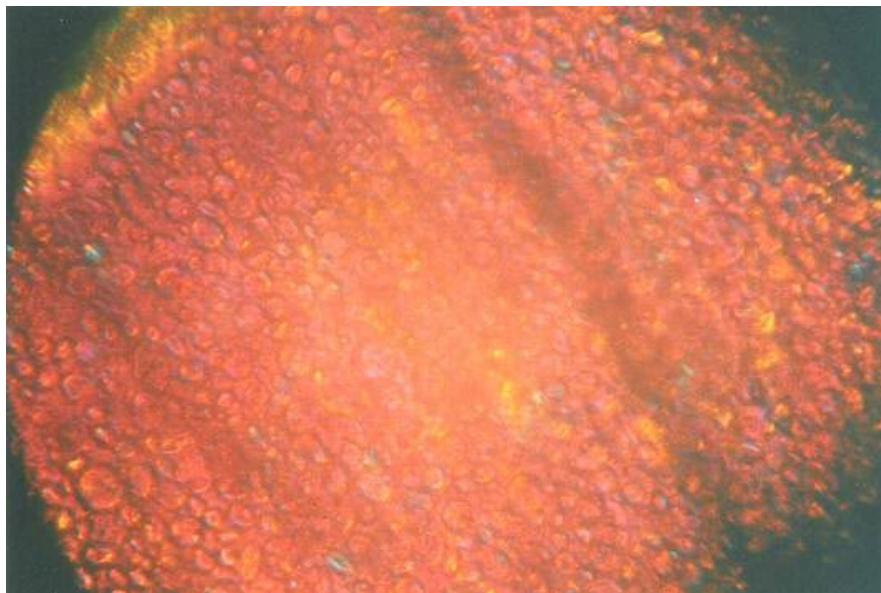
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Figure 10

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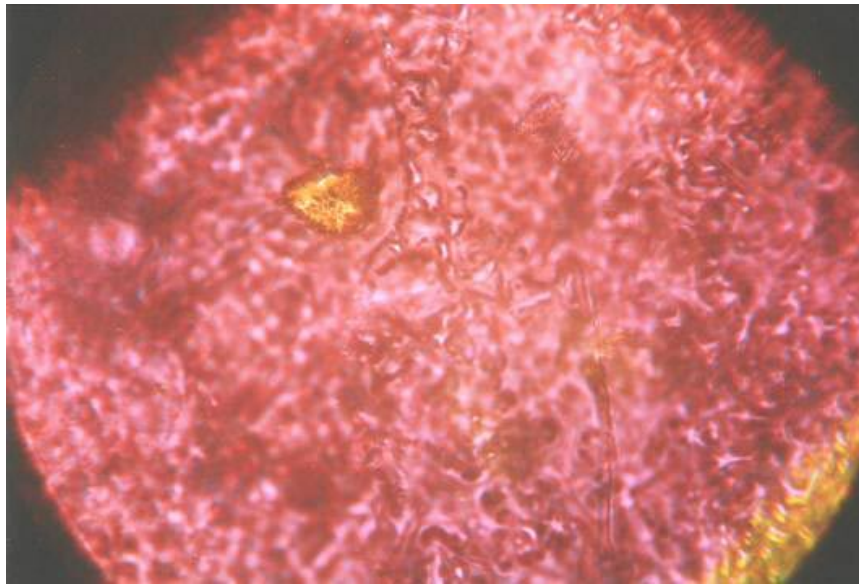
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Figure 11