Microbiological Characteristics of Dungeness Crab
(Cancer magister)  

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Aerobic, heterotrophic microorganisms of Dungeness crab (Cancer magister) were isolated from raw crab, cooked crab, crab meats obtained during commercial processing, and from retail crab meat samples. Each microbial isolate was then identified to the genus level employing the revised replica plating procedure. Microbial groups most commonly isolated from crab meat were, in the order of predominance, Moraxella, Pseudomonas, Acinetobacter, Arthrobacter, Micrococcus, Flavobacterium-Cytophaga, and Bacillus sp. Proteus, Staphylococcus, yeasts, Vibrio, and Lactobacillus sp. were found less frequently in some samples. Distribution patterns of microbial flora in crab meat revealed the presence of three classes of microorganisms. Microorganisms that originated from the raw crab and gained predominance by growth during refrigerated storage were Moraxella, Pseudomonas, Acinetobacter, and Flavobacterium-Cytophaga sp. Those that originated from the crab but did not grow in meat were Arthrobacter and Bacillus sp. Micrococcus, Staphylococcus, and Proteus sp. were introduced during processing, but they did not grow in the refrigerated crab meat.

Phillips and Peeler (17) examined the bacteriological survey data of the blue crab industry and reported, among others, that the aerobic plate count of cooked crab changed characteristically at each processing step. The counts alone, however, could not reveal whether the change was due to bacterial growth during improper storage or due to contamination during processing.

Loaharanu and Lopez (16) examined the microbial flora of pasteurized crab cake mix and reported that the psychrophilic spoilage bacteria rarely survived the pasteurization treatment of 85 to 87 C for 110 min, and the shelf-life of the product was dramatically increased from 4 days at 18 C to 6 months at 2 C.

Dungeness crab is harvested and processed throughout the year on the Northern Pacific coast, but the peak commercial season is during the winter months of December through April. Live crabs are placed in a 5.0 to 7.8 C cooler immediately after landing. This is done to prevent the active crabs from damaging each other. Within 24 h the docile crabs are graded for size and physical condition. The crabs of certain size and intact legs are sold as whole crabs, either before or after cooking. The crabs that do not meet the above criteria or the surplus landings are then processed at the plant. The usual procedure for the extraction of Dungeness crab meat is as follows. The carapace of the crab is first removed. The gills and the intestinal content are next removed with brush and water, and the crab is cut into two equal parts. The crab sections are cooked in boiling water for 10 to 15 min and air cooled for approximately 1 h. The crab meat is hand extracted by shaking and squeezing. The body meat is picked first, followed by the claw, then the leg meat. The picked meat is weighed, floated in brine solution to remove the shell fragments by density difference, washed, and desalted under running water. Upon draining, the meat is hand sorted and hand packed in 5-lb (no. 10; about 2.267.5 g) cans. Each can contains approximately equal parts of body and leg meats in two paper-partitioned compartments. The sealed cans are frozen and shipped frozen. The retailer then thaws and repackages the frozen crab meat for sale.

This investigation was undertaken to examine the microbiological characteristics of Dungeness crab (Cancer magister) processed and retailed in Oregon. The identities of microorganisms isolated from the raw crab, cooked crab, crab meat obtained at various processing
steps, and the crab meat obtained from the retail shelves are reported. Each processing step in terms of its influence on the microbial composition of the crab meat was then examined and evaluated.

MATERIALS AND METHODS

Samples. (i) Retail crab meat. Sixteen samples of crab meats were purchased at random from the local supermarkets throughout a year. The microbial counts, as well as the generic identification of the isolates, were made by the procedure described below.

(ii) Intestinal contents. The intestinal contents of both raw and cooked crabs were obtained through a hole drilled in the carapace with a sterile knife, which was previously swabbed with 70% ethanol and air dried. A sterile, 10-ml wide-mouth serological pipette was inserted into this hole and stirred, and the mixed content was drawn out by suction. The intestinal contents of 12 raw crabs and 12 cooked crabs were pooled for June and October 1973 samplings. Seven raw crabs and nine cooked crabs were used for February 1974 sampling due to scarcity of the crabs.

(iii) Processing samples. At the same plant where the October 1973 samples for raw and cooked crabs were taken, equal weights of body and leg meat samples were obtained from the picking tables, from the draining tray after the picked meats had been brined and rinsed, and finished product from the packaging tables. The brine was also sampled at the same time. Sampling was made at the midpoint of morning coffee and lunch breaks. Samples were obtained from all representative processing areas and pooled, iced, and transported to the laboratory located within 20 miles (about 32 km) of the plant. The time lapse between the sampling and the microbial analysis was less than 1 h.

Microbiological analytical procedures. (i) Plating and enumeration. The pooled sample was thoroughly mixed with a sterile spatula and 50 g was blended in 450 ml of Butterfield's phosphate buffer (21) for 2 min at 2,000 rpm in an Osterizer. The appropriate dilutions in the same buffer were then spread plated in triplicate on TPE agar (13). After incubation at 25 C for 48 h, the plates were counted and the isolated colonies were picked for identification.

(ii) Differentiation by replica plating. The microbial identification scheme and the procedure have been reported earlier (6). Since that time, several modifications and improvements have been incorporated into the procedure and the method presently employed is described below.

(a) Select two plates containing well-isolated colonies of 50 to 100 from the same dilution. Transfer all colonies from the plates onto one of 30 marked spots on TPE master plates, using a sterile toothpick for each colony. Care should be taken to transfer colonies of similar sizes on each master plate to insure uniform growth. Incubate the master plates at 25 C until each colony has grown at least 2 mm in diameter (24 to 72 h).

(b) Flame sterilize the wires of the replicators (a wooden cylinder of 7.5 cm in diameter and 7.0 cm in height, one end of which has 30 22-gauge nichrome wires of 4.5 cm inserted in a pattern so that the distance from one wire tip is approximately equal to another). Upon cooling, replicate the growth on the master plates onto the following daughter plates in the listed order. All agar plates should contain at least 0.5% NaCl to ensure the growth of moderate halophiles.

1. TPE (13)—For microscopic and cytochrome oxidase tests.
2. TPE—For ultraviolet florescence and colony pigmentation tests.
3. Hugh-Leifson glucose medium (9) with 1.5% agar—Test for oxidative utilization of glucose.
4. Same as (3)—Test for fermentative utilization of glucose upon anaerobic incubation.
5. Peptone iron agar (Difco)—For H₂S production.
6. Penicillin agar (3.0 IU of penicillin G in TPE agar)—For identification of Pseudomonas (19) and differentiation of Moraxella and Acinetobacter (1, 2).
7. Staphylococcus 110 (S110, Difco)—For selection of NaCl (7.5%)-tolerant microorganisms.
8. EMB agar (Difco)—Selective isolation and differentiation of Enterobacteriaceae.
9. Potato dextrose agar (Difco) acidified to pH 3.5 with 10% lactic acid—For selection of yeasts.
10. TPE—For transfer confirmation and for further examination.

(e) Incubate all plates at 25 C aerobically except plate no. 4, which is to be incubated in the Anaerojar (Baltimore Biological Laboratories) at 25 C and plate no. 8, which is to be incubated aerobically at 35 C. Examine plates 1, 2, 5, 6, 8, and 10 within 24 to 48 h. Read plates 3 between 12 and 24 h. Read plates 4, 7, and 9 after 5 days.

(d) Slide preparation and the cytochrome oxidase test are performed simultaneously as follows. Using the broad portion of the sterile flat toothpick, transfer the colony growth on a Pathotec-Co test strip (General Diagnostics, Morris Plains, N.J.) and smear on the strip. Next, bring the same toothpick on one of the five designated spots on the microscopic slide and smear along the width of the slide on a drop of buffer. Fix the slide by heat and place in a slide tray (Scientific Products S7650). Each tray accommodations 10 slides and each slide accommodates five smears.

(e) Gram stain 10 slides or 50 smears simultaneously by successively dipping the trays into tanks containing the Gram reagents.

Comments on the procedure. No difference in response was observed by changing the order of replication. Nevertheless, the present order of replication was established to minimize the potential carryover of the inhibitory agent to the least number of plates and also to maintain procedural uniformity.

Differentiation of oxidase versus fermentative utilization of glucose on agar was tested with the original tube method of Hugh-Leifson (9). The plate modification compared favorably with the responses in the tubes. The oxidative response on agar was from 12 to
24 h faster than in the tube, and the fermentative response was comparable to that of the deep tube. In addition, the strict aerobes did not grow on the anaerobic plates.

Cytochrome oxidase test by Pathotec-Co was more sensitive and convenient than the original Kovacs procedure (10). Custom-made filter paper disk impregnated with the Pathotec-Co ingredients (General Diagnostics) were tested by directly placing the disk on the agar. This eliminated the need for testing individual colonies on the strip. A shortcoming of this method, besides the unavailability of such a disk, and heat at 60°C for 1 h. Incubate the tubes at 25°C for 5 days and check for the growth of the survivors. Catalase test is done by mixing the loopful of agar growth with 3% of H₂O₂ on a glass slide.

Three genera of gram-positive rods commonly found in seafoods are then differentiated as follows (20). Bacillus: survives 65°C/30 min, catalase positive, spores sometimes are microscopically visible. Arthrobacter: fails to survive 65°C/30 min, catalase positive, microscopically pleomorphic rods and the cells from the older cultures appear spherical. Lactobacillus: fails to survive 65°C/30 min, catalase negative, slow growth on TPE agar or in both.

(b) Gram-negative microorganisms: Rods.

*Pseudomonas*: resistant to 3.0 IU of penicillin G. Fails to grow on Hugh-Leifson anaerobic plate, cytochrome oxidase positive, usually slender and uniform-sized rods. *Pseudomonas* sp. are further differentiated into (19):

*Pseudomonas* I: ultraviolet fluorescent.
*Pseudomonas* II: Hugh-Leifson glucose oxidative and ultraviolet fluorescence negative.
*Pseudomonas* III: Hugh-Leifson glucose alkaline or no change.

Among *Pseudomonas* sp., *P. putrefaciens* is identified by H₂S production on Peptone iron agar (Difco; 14).

*Moraxella*: cytochrome oxidase-positive cocccacilli. Sensitive to penicillin. "*Moraxella*-like" - cytochrome oxidase positive but resistant to penicillin.

*Acinetobacter*: cytochrome oxidase-negative cocccacilli. Penicillin resistant. "*Acinetobacter*-like" - cytochrome oxidase negative but sensitive to penicillin.

*Flavobacterium*: bright yellow to orange colonies. Inoculate the soft agar and confirm negative motility. "*Cytophaga*: bright yellow to orange colonies with thin spreading edges.

*Vibrio*: all cytochrome oxidase-positive and Hugh-Leifson glucose-fermentative, gram-negative rods are differentiated as follows (18):

*Flavobacterium* luminous.
*Vibrio*: sensitive to vibriostatic agent 0/129 (3,4-diamino-6,7-di-isopropylpteridine, Calbiochem 267316). Lysine decarboxylase positive and arginine dihydrolase negative.
*Moraxella*: sensitive to vibriostatic agent 0/129. Lysine decarboxylase negative and arginine dihydrolase positive.

*Enterobacteriaceae*: cytochrome oxidase negative, fermentative on Hugh-Leifson glucose and growth on EMB at 35°C. Inoculate Enterotube (Roche Diagnostics, Nutley, N.J.) and differentiate according to the manufacturer's published scheme.

Comments on the key. The identification procedures were divided into two steps. The replica plating and the microscopic examination will establish identities of *Staphylococcus*, *Micrococcus*, *Pseudomonas*, *Moraxella*, *Acinetobacter*, and *Cytophaga*.

The second, or the confirmation steps, were needed for identification of *Bacillus*, *Arthrobacter*, *Lactobacillus*, *Flavobacterium*, *Vibrio*, and *Enterobacteriaceae*.

The generic identification key was prepared before the 8th edition of *Berger's Manual of Determinative Bacteriology* (3) became available. Many of the differential features employed in the key, however, agreed well with those of the manual.

*Micrococcus* and *Staphylococcus* were differentiated in the manual and the key essentially by the mode of carbohydrate metabolism (see reference 3, Table 14). *Moraxella* and *Acinetobacter* were differentiated on the basis of cytochrome oxidase and penicillin sensitivity both in the manual and in the key (see reference 3, p. 443 and p. 436). Agreement was also found for the differentiation of genera in the family *Vibrio* and the differential scheme of gram-positive rods.

Modifications to be made according to the manual are the differentiation of *Flavobacterium* and *Cytophaga* which we had grouped together in this study. The nonmotile, gram-negative, yellow- to orange-pigmented rods are to be placed under *Flavobacterium*, and the colonies that exhibited thin and spreading edges are to be placed under *Cytophaga* (see reference 3 for comments, p. 357). We had differentiated *Moraxella* from *Acinebacter* in this study on the basis of cytochrome oxidase reaction, irrespective of resistance or sensitivity to penicillin. This is apparently acceptable as a screening criterion (see reference 3 for further comments, p. 433). If required, the cyto-
chrome oxidase-positive coccobacilli that are resistant to penicillin and the cytochrome oxidase-negative but penicillin-sensitive coccobacilli may be placed under "Moraxella-like" and "Acinetobacter-like" groups, respectively.

The major variance in the key from the manual is the classification scheme for *Pseudomonas*. We adhered to the differentiation scheme of Shewan et al., (19) and Shewan (18) because the scheme provided an indirect means for differentiating the proteolytic property of *Pseudomonas* sp. (group III/IV). Recognition of such functional property is important in the study of microbial flora of seafoods.

**RESULTS AND DISCUSSION**

**Microbial flora of retail crab meat.** Microbial counts of 16 crab meat samples purchased at random from the local supermarket ranged from $2.1 \times 10^4$ to $8.2 \times 10^7$ with the geometric mean of $9.0 \times 10^4$. The count was obtained by spread plating on TPE and by incubating the plates at 25°C. This, according to our previous experience, would yield a count at least a log higher than that obtained by pour plating with standard plate count agar and incubating the plates at 35°C (11, 13).

The microbial flora of six of these samples were identified to the genus level (Table 1). To facilitate comparison, the data are arranged in the order of ascending counts.

*Moraxella* sp. were found consistently in highest proportions in all samples (Table 1).

**Table 1. Microbial flora of Dungeness crab meat obtained from retail stores**

| Microorganisms (%) | Crab meat samples* |
|--------------------|--------------------|
|                    | I      | II     | III    | IV     | V      | VI     |
| *Pseudomonas*      | ——    | 8     | 10     | 12     | 32     | 46     |
| *Moraxella*        | 24    | 39    | 59     | 35     | 22     | 22     |
| *Acinetobacter*    | 5     | 14    | 13     | 22     | 16     | 12     |
| *Flavobacterium*   | 5     | 6     | 4      | 8      | —      | —      |
| *Cytophaga*        | —      | 2     | —      | —      | —      | —      |
| *Vibrio*           | —      | 3     | 2      | —      | —      | —      |
| *Bacillus*         | 3      | 1     | —      | —      | —      | —      |
| *Lactobacillus*    | 12    | 6     | 8      | 4      | 14     | —      |
| *Arthrobacter*     | 29    | 12    | 3      | 2      | —      | —      |
| *Micrococcus*      | 33    | 1     | —      | 5      | —      | —      |
| *Staphylococcus*   | 22    | 2     | 2      | —      | —      | —      |
| *Proteus*          | —      | —     | 4      | 22     | —      | —      |
| Unidentified       | None  | 3     | 2      | 2      | 4      | 5      |

*The numbers of colonies identified for each meat sample I to VI were 122, 147, 137, 107, 125, and 170, respectively. The microbial counts per gram for each sample I to VI were $2.1 \times 10^4$, $4.3 \times 10^4$, $8.1 \times 10^4$, $3.2 \times 10^7$, and $8.2 \times 10^7$, respectively.  
*— Not detected.

*Acinetobacter* and *Arthrobacter* sp. were also found in all samples. *Pseudomonas* sp. were found in five out of six samples, but more significantly, the high count samples contained a greater proportion of *Pseudomonas* sp. Other microbial groups found in some but not all samples were, in the order of frequency, *Flavobacterium-Cytophaga*, *Bacillus*, yeasts, *Staphylococcus*, *Vibrio*, and *Lactobacillus* sp.

Table 1 did not show the further differentiation of *Pseudomonas* sp. into three types as described by Shewan et al. (19). This was done for the sake of simplicity and such breakdown is presented in Table 2.

*Moraxella* sp. were differentiated from *Acinetobacter* on the basis of positive cytochrome oxidase reaction and included the penicillin-resistant coccobacilli. Conversely, *Acinetobacter* included cytochrome oxidase-negative and penicillin-sensitive coccobacilli. If the narrow differential criteria of the 8th edition of Bergey's manual is followed (3), they could be placed under intermediate groups such as "Moraxella-like" and "Acinetobacter-like" categories. Table 2 also shows the distribution of these intermediate groups in the six crab meat samples. *Flavobacterium-Cytophaga* sp. were also differentiated into *Flavobacterium* and "Cytophaga" in Table 2 by using the criteria proposed in the manual. Since the taxonomic status of these microbial groups is still uncertain, no further attempt will be made in this paper to differentiate them.

The main purpose of microbial flora identification is to determine the proportional contribution of each microbial type to the total population. The more rapidly growing types would be closely correlated with the higher microbial counts. *Pseudomonas*, *Moraxella*, *Acinetobacter*, and *Flavobacterium-Cytophaga*
counts are positively correlated with the total microbial count (Table 3). The predominance by the *Moraxella* sp. was due to its high initial numbers and rapid growth, while the predominance by *Pseudomonas* sp. was due more to the high initial number than to the growth. Conversely, the growth of *Acinetobacter* and *Flavobacterium-Cytophaga* sp. contributed more to their predominances than the respective sizes of the initial numbers.

*Arthrobacter* and *Micrococcus* sp. were not significantly associated with the higher microbial counts.

*Flavobacterium-Cytophaga* and *Micrococcus* sp. in seafoods are known to decrease during refrigeration storage (7). *Pseudomonas* sp. are also known to increase in greater proportion at low temperatures (4). The microbial flora composition shown in Table 1 generally paralleled these observations, indicating that the high microbial count of the retail crab meat was due to growth of psychrotrophic microorganisms during storage. Certain deviation from the expectation, such as the slight increase of *Flavobacterium-Cytophaga* sp. instead of decrease noted in Table 3, might have been due to improper refrigeration or mishandling.

**Microbial flora of intestinal contents of crab.** The intestinal contents of pooled raw and cooked crabs were obtained from three processing plants in summer, fall, and winter, and the microbial flora were identified (Table 4 and 5).

The microbial flora of the intestinal contents of raw crabs contained, in the order of predominance, *Moraxella*, *Pseudomonas*, *Acinetobacter*, *Arthrobacter*, and *Flavobacterium-Cytophaga* sp. *Vibrio* and *Micrococcus* sp. were found in two out of three pooled samples, and *Staphylococcus* and *Bacillus* sp. were found in one such sample (Table 4). Gram-negative, large spherical rods that formed thin filmy colony on TPE agar and resembled *Azotobacter* sp. were also found in raw crab samples. There was very little seasonal variation.

The microbial flora of the intestinal content of the cooked crabs showed a noticeable increase in the population of *Moraxella* sp. (Table 5). The order of predominace was also shifted slightly from that of raw crab. *Arthrobacter* sp. replaced *Pseudomonas* sp. as the second most predominant microbial group. *Acinetobacter* and *Pseudomonas* sp. were still found in all

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**Table 3. Relationship of specific microbial groups to the total microbial population found in retail crab meat (linear regression of group as the total microbial count increases)**

| Microorganisms     | m  | b          | r       | P    |
|--------------------|----|------------|---------|------|
| *Pseudomonas*      | 0.090 | 12.448     | 0.894   | ≤0.05|
| *Moraxella*        | 0.183 | 11.425     | 0.986   | ≤0.01|
| *Acinetobacter*    | 0.120 | 3.244      | 0.953   | ≤0.01|
| *Flavobacterium-Cytophaga* | 0.092 | -11.149   | 0.995   | ≤0.01|
| *Arthrobacter*     | 0.054 | 17.296     | 1.363   | NS   |
| *Micrococcus*      | -0.087 | -79.672   | -1.864  | NS   |

*Percentage converted to respective counts.  
NS, Not significant.

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**Table 4. Microbial flora of intestinal content of raw crab**

| Microorganisms (%) | Raw crab samples* |
|--------------------|-------------------|
|                    | I (June 1973)     | II (October 1973) | III (February 1974) |
| *Pseudomonas*      | 16                | 18               | 26               |
| *Moraxella*        | 31                | 45               | 44               |
| *Acinetobacter*    | 13                | 15               | 12               |
| *Flavobacterium-Cytophaga* | 6           | 6                | 1                |
| *Vibrio*           | 5                 | 7                | -                |
| *Bacillus*         | 2                 | -b               | -                |
| *Arthrobacter*     | 15                | 3                | 11               |
| *Micrococcus*      | 9                 | -                | -                |
| *Staphylococcus*   | 2                 | -                | -                |
| "Azotobacter-like" | 2                 | 4                | 6                |

*The numbers of colonies identified in raw crab samples I, II, and III were 133, 129, and 125, respectively.  
, Not detected.

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**Table 5. Microbial flora of intestinal content of cooked Dungeness crab**

| Microorganisms (%) | Cooked crab samples* |
|--------------------|----------------------|
|                    | I (June 1973)        | II (October 1973)  | III (February 1974) |
| *Pseudomonas*      | 2                    | 8                  | 8                 |
| *Moraxella*        | 68                   | 65                 | 47                |
| *Acinetobacter*    | 2                    | 9                  | 9                 |
| *Flavobacterium-Cytophaga* | 2           | -                 | 11                |
| *Bacillus*         | 2                    | 3                  | -                 |
| *Lactobacillus*    | -                    | -                  | 4                 |
| *Arthrobacter*     | 14                   | 10                 | 19                |
| *Micrococcus*      | 10                   | 6                  | -                 |
| *Aeromonas*        | 0                    | 0                  | 2                 |

*The numbers of colonies identified in cooked crab samples I, II, and III were 64, 77, and 53, respectively.  
, Not detected.

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three samples, while two out of three samples contained Micrococcus, Flavobacterium-Cytophaga, and Bacillus sp., Lactobacillus sp., and Aeromonas sp. were found in one of the samples. Vibrio and Staphylococcus sp. that were found in some raw crab intestinal contents were no longer detectable after the crabs had been cooked.

The hemolymph of healthy blue crab was reported to be not sterile and yielded V. para-haemolyticus cultures (5). We subcultured 121 Dungeness crab blood samples asexpctically obtained from live intact crabs via pinched-off leg tips, in brain heart infusion broth (Difco) and glucose salt teepol broth (GSTB, 8). Both subcultures were negative after 7 days incubation at 25 and 35°C, respectively.

**Microbial flora change during processing.**

Samples of crab meats at various processing steps and a brine sample were taken from one of the plants, and the microbial flora of these samples were identified. Table 6 shows the microbial counts and the changes in the flora as the crab meats are picked, brined, washed, and packaged.

*Arthrobacter* and *Micrococcus* sp. appeared to increase in proportion during processing while *Moraxella* and *Pseudomonas* sp. seemed to decrease during this period. The brine, to which all picked meats were subjected to prior to rinsing and packaging, contained the most diverse microbial flora. It also appeared that the *Micrococcus* sp. had accumulated in the brine.

Most of the microbial groups found in raw and cooked crab intestinal contents were found in the processed crab meat (Table 6). This may indicate that some of the microorganisms found in the processed crab meat have originated from the gills and the guts of the crab. Each processing step, however, distinctly influenced the microbial flora compositions. The cooking decreased the microbial number by approximately one-fifth, reducing *Vibrio, Flavobacterium-Cytophaga, Pseudomonas*, and *Acinetobacter* sp. in greater proportion than *Bacillus, Arthrobacter, Micrococcus, and Moraxella* sp.

The microbial load of picked and sorted crab meats increased by a factor of 30. This is one major step in crab processing that required an extensive human handling. *Staphylococcus* sp. were first detected in this sample, and *Micrococcus, Acinetobacter, and Flavobacterium-Cytophaga* sp. increased in greater proportion than *Moraxella, Bacillus, and Pseudomonas* sp.

The brine, which is used repeatedly, is an apparent microbial depository and may serve as the secondary source of contamination. Gram-positive cocci were shown to accumulate in brines used for smoked salmon industry (12). Since the brine could accumulate the coagulase-positive staphylococci, special attention should be given to monitor, improve, or modify this operation.

The microbial composition of the Dungeness

### Table 6. Microbial flora of Dungeness crab during a processing operation

| Microorganisms (%) | Raw crab | Cooked crab | Picked crab meat | Brine | Meat brined and washed | Meat ready to can |
|--------------------|----------|-------------|------------------|-------|-----------------------|------------------|
| *Pseudomonas*      | 18       | 8           | 1                | 4     | 6                     | 9                |
| *Moraxella*        | 45       | 65          | 31               | 24    | 20                    | 27               |
| *Acinetobacter*    | 15       | 8           | 15               | 17    | 15                    | 18               |
| *Flavobacterium-Cytophaga* | 6 | —          | 5                | 6     | 8                     |                  |
| *Vibrio*           | 7        | —           | —                | 1     | —                     | —                |
| *Bacillus*         | —        | 3           | 2                | 3     | 4                     | 2                |
| *Lactobacillus*    | —        | —           | —                | 1     | —                     | —                |
| *Arthrobacter*     | 3        | 10          | 28               | 6     | 14                    | 8                |
| *Micrococcus*      | 2        | 6           | 16               | 25    | 30                    | 19               |
| *Yeasts*           | —        | —           | —                | —     | —                     | 1                |
| *Staphylococcus*   | —        | —           | 2                | 7     | 5                     | 2                |
| *Proteus*          | —        | —           | —                | 2     | —                     | 4                |
| *Unidentified*     | 4        | 0           | 0                | 1     | 0                     | 2                |

*See text for explanation. The numbers of colonies identified in samples of raw crab, cooked crab, picked crab meat, brine, brined meat, and meat ready to can were 129, 77, 123, 234, 44, and 103, respectively. The microbial counts per gram or per milliliter (from pooled samples) for each sample were $2.6 \times 10^4$, $4.3 \times 10^4$, $1.3 \times 10^3$, $2.5 \times 10^3$, $3.3 \times 10^3$, and $3.4 \times 10^3$, respectively.*

*Intestinal contents.*

— Not detected.

*Coagulase negative.*
Micrococcus, and Staphylococcus sp. did not multiply in the refrigerated crab meat and their proportions progressively decreased. The growth of psychrotrophic microorganisms of Pseudomonas, Moraxella, and Acinetobacter sp. during refrigerated storage was the major contributory factor for the high microbial count of the retail crab meat.

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