A Study on the Composition and Microbiology of Raw Milk from Three Breeds of Buffalo in Thailand

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ABSTRACT

The objective of this study is to investigate the milk quality parameters and microbiological status of raw buffalo milk. Seventy nine samples of raw buffalo milk were collected from three types of buffalo including swamp buffalo (n=10), river buffalo (Murrah) (n=55) and crossbreed buffalo (Murrah x swamp buffalo; F1) (n=14). Average milk compositions were; fat 6.35%, protein 4.13%, lactose 4.79%, solid not fat (SNF) 9.8% and total solid (TS) 16.22% with freezing point (FP) at -0.61 °C and pH 6.72. Instead of lactose that was higher in Murrah milk rather than in swamp buffalo milk, most of other parameters; fat, protein, SNF, TS, FP and pH of milk from swamp buffalo were higher than those of Murrah milk. Moreover, those parameters of the crossbreeds were presented in between those of milk from swamp buffalos and Murrah. Average of electrical resistance (ER) and somatic cell counts (SCC) were 659 units and 147,494 cells/ml respectively. Microbiological analysis of an average total plate count (TPC) was 4.43 x 10⁵ cfu/ml, which was not shown any significantly different among three types of samples. Some pathogenic microorganisms were isolated such as Staphylococcus aureus, Pseudomonas spp., Enterobacter spp. and Escherichia coli which most presented in milk samples of Murrah. All milk quality and microbiological values reveal the need of upgrade breeding to improve the quality and hygienic status of buffalo milk production in Thailand.

Keywords: Milk, Milk composition, Microbiology, Murrah, Swamp, Buffalo

INTRODUCTION

Thailand is one of the countries that breed buffaloes. Most of them are Swamp type. A study on buffalo rising situation and attitude of farmers raising buffalos in the northeastern part of Thailand indicated that the primary objective of buffalo used is to produce the fertilizer made from buffaloes’ feces for 80.70 % instead of considering for work. However, the farmer sales buffaloes for their beneficial income. Moreover another study reveals that primary purpose of buffaloes rising of farmers is to be used as a heritage which accounted for 75.8%. Recently, Thai people start to pay attention in buffalo milks by more consumption. Occurrence of buffalo dairy farm will make buffalo become an economic livestock in the future. River type buffaloes are breed. In addition, crossbreeding the native swamp buffalo with river buffalo breeds such as Murrah and Thai local swamp buffalos are thought to be an improvement of production and feeding management. To awareness of food safety and quality, the microbial and chemical composition of buffalo milks need to be investigated. Even though those general data and knowledge from the studies in others countries are available (Han and Ding., 1994; Fundora et al., 2001; Supino et al., 2004; Han et al., 2007), the information reported in Thailand will be great significance for further development of higher quality buffalo milk production.

MATERIALS AND METHODS

Animal and milk sampling

Samples of buffalo milk were obtained from a Murrah farm in Chachoengsao province of Thailand. A total of 79 samples of buffalo milk, tested with California Mastitis test (CMT) did not exceed +1 score, were collected from three types of buffalo. These included 10 samples from...
swamp buffalo, 55 samples from pure river buffalo (Murrah) and 14 samples from crossbreed (murrah buffalo x swamp buffalo; F1).

**milk pH, Electrical resistance (ER) and California Mastitis Test (CMT)**

A part of each sample was used to be measured for pH, electrical resistance (ER) and California Mastitis Test (CMT) parameters immediately. A digital pH meter and a mastitis detector (Draminski®) were utilized to detect the pH and the ER respectively. CMT was conducted according to Gomes et al. (2006).

**Milk composition analysis and SCC**

The composition of fat, protein, lactose, solid not fat (SNF), total solids (TS) and freezing point (FP) were measured using automated infrared analysis (MilkoScan™, IDF and AOAC approved), while SCC was analyzed using Fossomatic milk cell counter (Fossomatic™, AOAC approved).

**Microbiological analysis**

A tenfold serial dilution of each milk sample was prepare in sterile NSS 0.9% up to \(10^{-3}\) dilution. Subsequently, 1 ml of each dilution was spread onto Plate Count agar and 1 ml of milk was spread onto sheep blood-agar plate and MacConkey. The plates were incubate aerobically at 37°C and examined at 24 h post-seeding. The colonies were provisionally identified based on morphology, haemolysis pattern and Gram stain. The number of each distinct colony type were recorded. Representative colonies were subculture on sheep blood agar plate and incubated aerobically at 37°C, 24 h to obtain pure colony. Gram positive cocci were tested for catalase and coagulase production.

**Statistical analysis**

All data were subjected to one way ANOVA according to a completely randomized design. The multiple comparisons were used for significant differences among each parameter from three types of buffalos.

**RESULTS AND DISCUSSIONS**

**Milk composition analysis**

Fat, protein, Solid not fat (SNF), Total solid (TS), and pH of swamp buffaloes were significantly higher \((P<0.05)\) than those of river buffalo Murrah. The lactose content of Murrah was significantly higher \((P<0.05)\) than swamp buffalo. Interestingly that protein, SNF and TS of F1 were higher than the value of Murrah but lower than those of swamp buffalo. Even though the fat content of Murrah and F1 milk were not difference but F1 also show the lower value than swamp buffalo (Table 1). These results are in agreement with the previous study that reported by Han et al. (2007). Their results show the content of multi-crossbreed-buffalo milk were higher than those of river buffalo Murrah but lower than crossbreed F1 and F2 buffaloes. This ranking was to be expected that the swamp buffalo milk has more nutritive value than river buffalo milk (Amarjit and Toshihiko, 2003). Considering this investigation with the others, it can be reported that most of the nutrients in swamp buffalo milk has higher levels than the river buffalo milk which in between of those milk composition values is expected to be Crossbreed F1. Concerning of breeding Murrah in Thailand, Murrah milk in this study had lower fat, protein, lactose and total solid contents than other reported of other countries such as China, Cuba, Bulgaria and Pakistan (Petrova and Tzankova, 2000; Han et al., 2007; Mahmood and Usman, 2010). According to fat (%), protein (%), lactose (%), total solid (%) of F1 buffalo in this study indicated that the lower nutrient of Murrah milk that breed in Thailand can be improved by cross breeding between River buffalo Murrah and Thai local swamp buffalo.

**Electrical Resistance (ER) and Somatic cell count (SCC)**

There is no significant statistical difference of ER and SCC’s values among three types of buffalo milk were observed. Normally, the mastitis detector that equipped for cows was assigned the range of 250 to 300 units for milk quality interpretation, however, all ER values in this study were exceed 600 units. This result indicated that the standard range used with cows was not
appropriate for buffalo milk determination, thus the further study can be conducted to adjust the new range for buffalo milk.

**Microbiology analysis**

There is no significant statistical difference of total plate count (TPC) values among three types of buffalo milk were observed. Buffalo milk contained an average TPC of $4.43 \pm 1.45 \times 10^5$ cfu/ml which is lower than the maximum level of the EU specification (EU Directive 92/46/EEC), $5 \times 10^5$ cfu/ml. There are 13 types of bacteria were isolated from 79 buffalo milk samples such as *Acinetobacter spp.*, *Acinetobacter baumannii*, Group D *Streptococcus*, *Streptococcus* not Group A,B,D, *Viridans streptococcus*, *Pseudomonas aeruginosa*, *Enterococcus spp.*, *Enterobacter spp.*, *Moraxella spp.*, *S.aureus*, Coagulase-negative *staphylococcus* and *E.coli*. The majority of bacterial isolates were Coagulase-negative *Staphylococcus* (83.54%), Group D streptococcus (25.32%) and *Staphylococcus aureus* (18.99%) with most encountered in Murrah milk. In addition, 3 majorities of bacterial isolated from Murrah milk were Coaulase-negative *Staphylococcus* (85.45%), Group D streptococcus (30.91%) and *Enterobacter spp.* (20.00%). Concerning pathogenic microorganism, *S.aureus*, *Enterobacter spp.*, *Pseudomonas spp.* and *E.coli* founded in this study are in accordance with those of previous finding (Gupta, 1987; Han et al., 2007; Maniruzzaman et al., 2010). *E.coli* is microorganism indicates contamination of fecal. The presence of pathogenic and indicator bacteria, such as *E. coli*, *Enterobacter spp.*, *Pseudomonas spp.* and *S. aureus* indicate a public health problem. As most of the microorganisms were isolated from Murrah milk, this evidence indicated that pure breed murrah breeding in Thailand was susceptible to infection rather than swamp buffalo and those crossbreed.

**IMPLICATIONS**

Upgraded crossbreed (Murrah×Swamp) should be recommended to improve immunity and milk quality of milking buffalo in Thailand. This investigation also indicated the safety of raw buffalo milk production in Thailand.

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**REFERENCES**


### Table 1. Milk compositions analysis of buffalo milk.

<table>
<thead>
<tr>
<th>Breed</th>
<th>Fat (%)</th>
<th>Protein (%)</th>
<th>Lactose (%)</th>
<th>SNF (%)</th>
<th>TS (%)</th>
<th>FP</th>
<th>pH</th>
</tr>
</thead>
<tbody>
<tr>
<td>S (n=10)</td>
<td>8.30±0.46$^a$</td>
<td>5.41±0.18$^a$</td>
<td>4.61±0.05$^b$</td>
<td>10.75±0.14$^a$</td>
<td>19.30±0.55$^a$</td>
<td>-0.61±0.00</td>
<td>6.83±0.02$^a$</td>
</tr>
<tr>
<td>M (n=55)</td>
<td>5.90±0.18$^b$</td>
<td>3.79±0.08$^b$</td>
<td>4.83±0.03$^a$</td>
<td>9.51±0.07$^b$</td>
<td>15.44±0.20$^b$</td>
<td>-0.62±0.00</td>
<td>6.69±0.02$^b$</td>
</tr>
<tr>
<td>F1 (n=14)</td>
<td>6.74±0.54$^b$</td>
<td>4.60±0.25$^c$</td>
<td>4.75±0.10$^{ab}$</td>
<td>10.19±0.16$^c$</td>
<td>17.10±0.66$^c$</td>
<td>-0.62±0.01</td>
<td>6.75±0.04$^{ab}$</td>
</tr>
<tr>
<td>Average</td>
<td>6.35±0.19</td>
<td>4.13±0.09</td>
<td>4.79±0.03</td>
<td>9.80±0.08</td>
<td>16.22±0.24</td>
<td>-0.61±0.00</td>
<td>6.72±0.01</td>
</tr>
</tbody>
</table>

S (Swamp buffalo), M (Murrah), F1 (Murrah×Swamp buffalo) $^{abc}$ different letters in the same column show significant statistical difference ($P<0.05$) *Mean±SEM