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| **Joint Biotechnology Master Program** | | |
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| Palestine Polytechnic University  Deanship of Higher Studies and Scientific Research |  | Bethlehem University  Faculty of Science |

Isolation of Two Serovars of *Salmonella*, with Microbial Studies of *E.coli* and Coliforms, Found in Municipal Solid Wastes (MSW) at Yatta Landfill

By

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In Partial Fulfillment of the Requirements for the Degree

Master of Science

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The undersigned hereby certify that they have read and recommend to the Faculty of Scientific Research and Higher Studies at the Palestine Polytechnic University and the Faculty of Science at Bethlehem University for acceptance a thesis entitled:

**Isolation of Two Serovars of *Salmonella*, with Microbial Studies of *E.coli* and Coliforms, Found in Municipal Solid Wastes (MSW) at Yatta Landfill**

**by**

**Maryam Mohammad Amr**

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In partial fulfillment of the requirements for the degree of Master of Science in biotechnology

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**Isolation of Two Serovars of *Salmonella*, with Microbial Studies of *E.coli* and Coliforms, Found in Municipal Solid Wastes (MSW) at Yatta Landfill**

**by (Maryam Mohammad Amr)**

**ABSTRACT**

Landfill sites are potential risks for the environment, as microbes and toxic substances may find their way into water sources and, via agriculture or direct contact with humans, re-enter the human food chain. The Yatta landfill site, which serves the Hebron and Bethlehem directorates, is not lined, which constitutes a special hazard because of the possibility of leachates entering the environment. Nevertheless, its use continues while a new site is being prepared at al Menya (World Bank, 2009).

The municipal solid waste coming into the Yatta landfill site was assessed for possibly harmful microbes, which might pose an environmental health risk. Furthermore, the hypothesis that this microbial examination of the municipal solid waste arriving at the site could serve a useful function as an indicator of public health was also tested. To that end, samples of food, human feces, organic matter, toilet paper and cardboard in the municipal solid waste of nine separate waste skips, from a representative selection of villages and towns that arrived at the site over a two week period were examined for bacterial contamination.

The nine towns and villages from which samples were obtained were grouped into three different socioeconomic metrics, and “most probable number” (MPN) data on *Salmonella sp* and “colony forming units” (CFU) data for *E.coli* and total coliforms in the various categories of solid waste were calculated from each of the nine town and village samplings. It was found that the highest bacterial loads depend on the source, but not on the socioeconomic metric. CFU/g for *E.coli* and coliforms from feces reached the order of 108 with on average a single log reduction for food, while MPN for *Salmonella* of 104 - 105 were found in food waste from 8 of the 9 sites.

A small, random sample of the isolated bacteria were tested for antibiotic susceptibility, and only 50% were clearly susceptible to ampicillin, while all were fully susceptible to nitrofurantoin and 3 third generation cephalosporins, with intermediate sensitivities for combined amoxicillin and clavulanic acid, ciprofloxacin, and cefoxitin.

The *Salmonella* test results were confirmedby microbiology and molecular techniques. Microbial techniques were used to identify *Salmonella* positive clones isolated on XLD plates from 11 different samples of food and feces from 6 distinct regions of Hebron and Bethlehem. A portion of the *invA* gene of each of these was amplified by PCR and sequenced. All of the 11 sequences were variants of two serovars: 9 were *Salmonella enterica* serovar Heidelberg and two were serovar Newport. Both of these serovars, and especially Heidelberg, have been implicated as important causes of public health concern throughout the world.

**عزل نوعين من السالمونيلا، ودراسة في الأحياء الدقيقة لل *E.coli* و Coliforms الموجودة في نفايات البلديات الصلبة/ مكب نفايات يطا**

**مريم محمد يوسف عمرو**

**ملخص**

تشكل مواقع دفن النفايات مخاطر محتملة على البيئة، فالميكروبات والمواد السامة قد تجد طريقها إلى مصادر المياه، والزراعة أو عن طريق الاتصال المباشر مع البشر، ودخولها إلى السلسلة الغذائية للإنسان. موقع مكب يطا، والذي يخدم محافظتي الخليل وبيت لحم، غير مجهز بشبكة حماية مما يشكل خطرا خاصة بسبب رشح المياه الملوثة وتأثيرها البيئي. ولا يزال المكب مستخدما في حين يجري إعداد موقع جديد في المنيا.

لقد تم في هذه الدراسة تقييم الميكروبات الضارة في النفايات البلدية الصلبة القادمة إلى موقع المكب، والتي قد تشكل خطرا على الصحة البيئية. كذلك تم اختبار فرضية أن هذا الفحص الميكروبي للنفايات الصلبة البلدية الذاهبة الى الموقع يمكن أن تكون مؤشر على الصحة العامة. ولهذه الغاية، تم فحص عينات من المواد الغذائية، براز الإنسان، والمواد العضوية، وورق التواليت والكرتون في النفايات البلدية الصلبة خلال تسعة زيارات منفصلة لمكب النفايات، ​​لتمثل مجموعة القرى والمدن التي وصلت نفاياتها الى الموقع خلال فترة أسبوعين. حيث تم فحص التلوث البكتيري فيها.

وقد جمعت العينات من تسعة مناطق مختلفة قسمت إلى ثلاث مستويات حسب المقاييس الاجتماعية والاقتصادية. بعد ذلك تم فحص جميع العينات من فئات النفايات الصلبة التي جمعت من المدن والقرى المختلفة وحساب و " عدد الأكثر احتمالا " (MPN) للسالمونيلا و "وحدة تشكيل مستعمرة (CFU)" لبكتيريا *E.coli* وColiform. وجد أن أعلى الاعداد البكتيرية تعتمد على المصدر، و ليس على المستويات الاجتماعية والاقتصادية. وصل CFU / G لبكتيريا *E.coli* وColiform من البراز 108 في المتوسط ​​مع انخفاض بدرجة واحدة للغذاء، في حين MPN للسالمونيلا عثر على 104 - 105 في فضلات الطعام في عينات 8 مواقع من 9.

تم اختبار عينة عشوائية من البكتيريا المعزولة للمضادات الحيوية، وكانت 50٪ فقط حساسة للأمبيسلين بوضوح، في حين كانت جميع العينات شديدة التأثر من نتروفورانتوين و 3 السيفالوسبورينات الجيل الثالث، وكانت الحساسيات متوسطة للأموكسيسيلين المشتركة وحمض الكلافولانيك، سيبروفلوكساسين، وسيفوكسيتين.

وقد تم إثبات ​​نتائج اختبار السالمونيلا باستخدام تقنيات الأحياء الدقيقة والجزيئية. وقد نجحت هذه التقنيات في عزل واستنساخ السالمونيلا على XLD من 11 عينة مختلفة من المواد الغذائية والبراز من 6 مناطق مختلفة من الخليل وبيت لحم. وتم تكثير جزء من الجين *invA* بواسطة PCR كانت جميع العينات من نوعين من السالمونيلا. حيث كان تسعة منها Heidelberg واثنين Newport. وقد تسببت كل من هذه serovars، وخاصة Heidelberg بعدة حالات من الهلع لذلك تعد أسباب مهمة للقلق حول الصحة العامة في جميع أنحاء العالم.

**DECLARATION**

I declare that the Master Thesis entitled "dissertation title" is my own original work, and hereby certify that unless stated, all work contained within this thesis is my own independent research and has not been submitted for the award of any other degree at any institution, except where due acknowledgment is made in the text.

Name and signature: \_\_\_\_\_\_\_\_\_\_"Maryam Mohammad Yousef Amr"\_\_\_\_

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**Dedication**

To the best supporters I ever had, whose support knows no bounds, my father, mother, and husband.

To the best kids in my life for their patience with me: Leen, Mu’ath and Mohammad.

To My first family; brothers and sisters - especially Iyad (Abu Ahmad).

To My second family; father and mother in law, and brothers and sisters in law - especially Raed (Abu Tamer).

To every person who stood with me, supported me, and encouraged me to go on from amongst my family circle, friends, and others.

To all these, I dedicate this thesis.

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I reserve special thanks to Dr. Ashraf Abdeen who continues to provide me with the online access to most journals and publications that has enabled me to keep constantly up to date with developments in my field of research.

**Abbreviations:**

|  |  |
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| **BLAST** | **Basic Local Alignment Search Tool** |
| **BRC** | **Biotechnology Research Center** |
| **CFU** | **Colony Forming Unit** |
| **EEC** | **European Economic Community** |
| **EMBL- EBI** | **European Molecular Biology Laboratory– European Bioinformatics Institute** |
| **LB** | **Luria Broth** |
| **MEGA** | **Molecular Evolutionary Genetics Analysis** |
| **MPN** | **Most Probable Number** |
| **MSW** | **Municipal Solid Wastes** |
| **NCBI** | **National Center of Biotechnology Information** |
| **PCR** | **Polymerase Chain Reaction** |
| **SW** | **Solid Wastes** |
| **TT Hajna** | **Tetrathionate Hajna** |
| **WHO** | **World Health Organization** |
| **XLD** | **Xylose Lysine**  **Desoxycholate** |

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**CHAPTER 1**

1. **Introduction:** 
   1. **Municipal Solid Waste**

Municipal solid waste (MSW) includes any solid waste produced by industries, institutions and households that are dumped in landfills (Gerba et al., 2011). Landfills hold wastes containing organic materials of both natural and unnatural origin. Municipal solid waste landfills often contain animal remains and feces, hospital wastes and domestic sewage sludge that pose a potentially significant health hazard (Nagendran. et al., 2006). The main pathways of exposure to MSW hazards are inhalation due to emissions from incinerators and landfills, the food-chain due to consumption of food contaminated with bacteria and viruses from land spreading of sewage and manure, consumption of water in the case of water supplies contaminated with landfill leachate, as well as occupational hazards for those working with MSW during collection and on landfill sites (Giusti, 2009).

In many developing countries MSW is dumped in an uncontrolled way, without special precautions for pathogenic microorganisms, gas formation, and leachates (Nagendran. et al., 2006). All these threaten the environment and there can be a significant bacterial population associated with municipal landfill leachates, which varies with the age and the chemical properties of the leachate (Nagendran. et al., 2006).

* 1. **Municipal Solid Wastes in Palestine**

Unsanitary and uncontrolled solid wastes disposal became a serious public health and environmental hazard of great concern to the Palestinian people in the West Bank and Gaza from the time of the second intifada (Muslih, 2002). The number of dumpsites in Palestine has been estimated to range from 189 to 419 and the proliferation of these sites increases the risk. The majority of solid waste produced by the Palestinian population in the West Bank has historically been disposed of at unregulated dump sites. Burning, which causes air pollution, and potential infiltration of polluted leachate into the water supply aquifers causes pollution of valuable agricultural land and the natural landscape and creates a habitat for breeding disease-transmitting vectors (Tuffaha, 2006). The total population of the West Bank, estimated at 2.27 million, generates a solid waste load of about 690,000 tons per year (t/yr), which is primarily of domestic and commercial origin (JSC, 2010). The total municipal waste load is expected to increase to about 316,600 t/yr by 2020 and 370,500 t/yr by 2030, currently, the average waste collection rate is estimated at 85%, and about 60-70% of the waste consists of organic matter (JSC, 2010).

Over the past years, the Palestinian Authority has tried to strengthen the municipal service delivery capacity by enhancing the management of local governments; encouraging municipalities to establish Joint Service Councils as regional institutions for the delivery of MSW services to realize economies of scale; and establish three regional sanitary landfill sites to effectively service the entire West Bank (JSC, 2010). Funding from external donors to support Palestinian Joint Service Councils to deal more efficiently and safely with MSW is continuing with a special emphasis on the Bethlehem and Hebron area (European Union, 2012).

* 1. **Municipal Solid Wastes in Yatta Landfill**

Yatta landfill is an example of the open landfills in the developing countries. The landfill is located 166833° east – 95929° north with an elevation ranging from 620-650 meters above sea level. The landfill started operation in 1996 on an area of 14.4 hectares purchased by Hebron Municipality. From 1996 until 1999, most of the MSW used to be burned by landfill pickers to recycle metals. The practice of burning was stopped in the year 2000.

Between 1996 and 2005, the landfill served Hebron Municipality with a population of 200,000 inhabitants. From 2005 until recently, the landfill served Hebron Directorate (Hebron Municipality and the surrounding towns and villages) with a population of approximately 500,000 inhabitants. Since May 1, 2010, the landfill has served the Hebron and Bethlehem Directorates which have a population of more than 800,000 inhabitants. Daily MSW load averaged 450 metric tons prior to May 1, 2010. Starting May 1, 2010, the landfill has been receiving an average of 600 metric tons per day and has been operating 6 days per week.

For the last 7 years, significant improvements have taken place through better management practices and through spreading and covering the waste on a daily basis. However, leachate can be seen in the adjacent wadis (i.e. a valley or stream-bed that remains dry except during the rainy season) due to the fact that the landfill is not lined. Because of the lack of landfill lining, causing the leachate problems, it was decided by Hebron Municipality to close the landfill. A new landfill with new standards and modern design is in the works (European Union, 2012) and is being funded by the World Bank and the European Union. Until that time, and even after, the problem of random dumping of the solid wastes would be still standing (JSC, 2010).

* 1. **Pathogens in Municipal Solid Waste**

Improper MSW management leads to public concern about the environmental and human health impact, and MSW poses a risk of human exposure to pathogenic bacteria and viruses (Giusti, 2009).

Certain components of MSW entering landfills may contain pathogenic bacteria, viruses and parasites capable of causing disease in man (Hossain et al., 2011). Pathogenic micro-organisms in landfills may more often originate from food waste and diapers containing feces, and common enteric pathogens associated with feces include *Salmonella* and *E.coli*, which can be transmitted via the fecal-oral route by contaminated food, water or fomites (Gerba et al., 1995; Gerba et al., 2011).

Most studies about *Salmonella* have been about methods of detecting it in food and beverages (Radji et al., 2010), especially in eggs and chicken products (Moussa et al., 2010), as well as meat (Hassanein et al., 2011). However, *Salmonella* also survives in the feces of both chickens ( Tayfun et al., 2001) and humans (Konstantia et al., 2006) as well as in solid wastes (Andreas et al., 2009). It has been isolated from solid wastes, but is thought to originate from contaminated food or feces of infected individuals (Gerba. et al., 1995). The concentration of *Salmonella* according to Geldreich can range from 104 – 1011 /g in the stools of infected individuals (Geldreich, 1978).

Therefore, sensitive and rapid detection of *Salmonella* is considered one of the priorities in the fields of food safety, SW management and public health.

The health and safety performance of the waste management industry is likely to vary significantly across the world, with major differences between developed and developing countries. In developed countries, workers’ protection and health and safety measures have substantially reduced the likelihood of fatal or major accidents resulting from contamination (Giusti, 2009).

In developing countries, however the likelihood of contaminated solid waste posing a hazard is expected to be greater than in developed countries. In addition to the use of unlined landfills, such as the Yatta site that is the subject of this study, it is noted that in developing countries large numbers of young, poor workers pick their way through landfill sites in search of metals, plastic, and glass items to sell, and the Yatta landfill workers (Figure 1.1) were no exception. Indeed, they were so at home on the landfill site that they were offering their guests tea, brewed on a gas stove supplied by gas that was collecting in pockets within the landfill site as a result of bacterial metabolism of the wastes dumped there. Surveillance of solid wastes in the developing world for pathogens and antibiotic resistance lags behind that in the developed world, but countries such as Brazil, which is known for its poor slum dwellers making a living picking through solid waste, are beginning to take an interest (Vieira et al., 2011).

Figure 1.1: Two views of the Yatta landfill site showing: (A) one of the workers, walking past a mound of freshly delivered municipal waste, appears in the left corner, and (B) a resting tent at the left edge of the photo with piles of waste in the vicinity (marked by dashed arrows). Behind the tent, and to the right of the view, a larger mound of refuse appears as a small hill.

Surveillance of solid wastes for pathogenic organisms usually focuses upon specific indicator organisms for assessing the contamination level. The most commonly tested indicator organisms are total coliform and fecal coliform (Staley et al., 2012), but in addition to these, the European Economic Community (EEC) has, since 1976, required testing for *Salmonella* along with the other indicator organisms (Sahar et al., 2009). While *E.coli,* coliforms and *Salmonella* may all be found in human waste, *Salmonella* are a particular concern, as they are not part of the natural flora of the human digestive tract, and indeed, persistent carriage of *Salmonella* in humans requires colonization of other parts of the body, outside the digestive tract, (Monack, 2012). Therefore, the presence of *Salmonella* in human waste indicates a greater health concern than the other indicator bacteria.

* 1. ***Salmonella***

*Salmonella* isa common pathogen of food borne disease worldwide and is responsible for a large number of infections in both humans and animals. The infective dose of *Salmonella* can be as low as 15-20 cells depending on the age and health of the host (FDA, 2003), and it is estimated that *Salmonella* causes 93.8 million human infections and 155,000 deaths annually worldwide (Li et al., 2012a).

*Salmonella enterica* serovars, capable of causing human infection, also have exceptional abilities for adapting to, and surviving in, harsh and changing environmental conditions (Spector and Kenyon, 2012), which makes them well suited to survival in MSW. While the Yatta landfill workers are at risk of contracting *Salmonella* during their work, they are not alone in being able to potentially reintroduce these hardy bacteria to their local communities in the Hebron governate, as many species of wild animals and birds have been reported to serve as reservoirs for infection and have been implicated in re-introducing *Salmonella* to humans (Hilbert et al., 2012).

Regarding nomenclature, the *Salmonella* are divided into two species: *S.enterica* and *S.bongori*, and *S.enterica* is further divided into six subspecies (Brenner et al., 2000). *S.enterica* subspecies I, also confusingly named subsp. ‘*enterica*’, is responsible for 99% of clinical infections, and accounts for 1,504 of the total 2,541 total serovars (serotypes) that have been identified (McQuiston et al., 2008). The World Health Organization keeps tables of antigen combinations for serovar determination, which depends on the mix of 46 O group antigens and 114 H group antigens where the H group are flagellar antigens that are commonly expressed in two phases for *S.enterica* subspecies I (McQuiston et al., 2008; WHO, 2007).

* 1. **This Study**

This study will first address three indicators of contamination (total coliform, *E.coli*, and *Salmonella*) since they are widely spread, and, taken together, they provide both an indicator of the overall degree of contamination and its risk for human health and life (Jillson et al., 2001).

As stated by the World Health Organization, the increasing emergence of antibiotic resistance in human pathogenesis is a concern, not only for treating infectious disease, but also for other pathologies in which antibiotic prophylaxis is needed for avoiding associated infections (WHO, 2001). Furthermore, increasing antibiotic resistance of bacteria in the environment is a worldwide phenomenon (Bürgmann et al., 2009), and this study seeks to provide a measure, albeit on a small scale, of the level of antibiotic resistance in the MSW locally at the Yatta landfill site.

This study focuses mostly, however, on *Salmonella,* because of the special public health concerns reviewed above, in this introduction. The detection of *Salmonella* in MSW will be done using the commercially available ‘RapidCheck’ system, in which liquid culture in an enrichment media followed be a selective media will be used to generate a rich culture of *Salmonella* (if present initially in the sample) to be applied to a strip test kit that provides a simple positive/ negative result. Quantification of infectious *Salmonella* will be possible by initial serial dilution of samples before liquid culture, in order to calculate the MPN based upon the greatest dilution at which samples test positive following the liquid culture stages. At the molecular level, specific primers for *Salmonella* detection will be used to confirm the RapidCheck detection system, as it has been licensed for detection of *Salmonella* in food but not solid wastes.

Primers used for the detection of *Salmonella* species are specific for the *invA* gene, which is located on the *Salmonella* pathogenicity island 1 and encodes a type III secretion system that exports proteins in response to bacterial contact with epithelial cells, and is necessary for invading mammalian cells (Galán et al., 1992). It is highly conserved in *Salmonella* species (Malorny et al., 2003), making it a good target for identification of unknown *Salmonella sp* in MSW samples. Indeed, in one study of 12 virulence genes, *invA* was the most prevalent (99.5%) of all (Dione et al., 2011) and it remains the target of choice for developing detection systems, including real-time PCR (González-Escalona et al., 2012), pyrosequencing (Li et al., 2012b) and surface Plasmon resonance (Zhang et al., 2012). This study will use standard PCR, whose products of the correct size will also be used as a sequencing template, both for confirmation of the PCR result and in order to identify the serovar of any *Salmonella* found at the site, and it is hoped that this research contributes to establishing a picture of the public health status across the two directorates that are served by the Yatta landfill site.

**CHAPTER 2**

1. **Objectives**
   1. **The Main Goal of the Current Study**

To evaluate the bacterial content of the Municipal Solid Wastes as a public health factor using different techniques

* + 1. **Specific Goals**
* To evaluate MSW categories for three groups of bacteria (coliform*, E.coli, Salmonella).*
* To isolate the *Salmonella* serovars that are present in the MSW, and, based on comparison with the existing literature on these serovars, make a partial assessment of the public health situation that gave rise to the presence of these serovars.
* To evaluate the feasibility of correlating the socioeconomic metric with bacterial load present in the MSW of this study.
* To test the hypothesis that source correlates with the bacterial load in the MSW.
* To validate the RapidChek® *Salmonella* Test Kit for detecting *Salmonella* in MSW.

**CHAPTER 3**

1. **Materials and Methods**
   1. **Materials**
      1. **Reagents:**

This is the list of the main materials that were used in the research:

* 3M™ Petrifilm™ *E.coli* /ColiformCount Plates (Catalog no.6404) from 3M company; USA
* RapidChek® SELECT™ *Salmonella* (Part# 7000192) from sdix; USA
* Tetrathionate Broth Base Hajna (TT Broth) (Part#: 95021-682) from HiMedia; USA
* Iodine solution from AlHekma pharmacy, Hebron
* RapidChek® *Salmonella* Test Kit (Part#7000183) One step strip tests from sdix; USA.
* Xylose Lysine Desoxycholate Agar (XLD Catalog no. 278850) from BD; Jerusalem.
* MacConkey Agar 281810 from BD; Jerusalem.
* Muller-Hinton from OXOID; Jerusalem.
* Agar European Bacteriological from Hylabs; Jerusalem.
* Yeast Extract (7184A) from Accumedia; Jerusalem.
* Tryptone (7351A) from Accumedia; Jeursalem.
* NaCl from Frutarom.
* Antibiotic discs for antibiotic susceptibility testing from Oxoid. Eight different antibiotic discs were used: Cefotaxime (CTX) 30µg, Ceftazidime (CAZ) 30µg, Ceftriaxone (CRO), Cefoxitin (FOX) 30µg, Nitrofurantoin (F300) 300µg, Ampicillin (Amp10) 10µg, Amoxicillin and Clavulanic acid (Amc30) 30µg, and Ciprofloxacin (Cip5) 5µg.
* PCR master mix catalogue number AB-0575/DC/LD/A from Thermo Fisher Scientific; Jerusalem.
* Agarose (A9539) from SIGMA; Jerusalem.
* Tris-EDTA buffer (T7527) from SIGMA; Jerusalem.
* Gel loading buffer (TBE: Tris/Borate/EDTA) from SIGMA; Jerusalem.
* Sterile water was obtained by autoclaving deionized water at 121°C for 15 minutes.
* Molecular weight markers:

. (pUC18 Hae III digested) from Sigma Aldrich; Jerusalem.

* Sterile Glycerol (0854) from AMRESCO; Jerusalem.
* Wizard® SV Gel and PCR Clean-Up System (Catalog no. A 9281) from Promega; Jerusalem**.**
* AccuPrep® PCR Purification Kit (Catalog no. 3034) from Bioneer; Jerusalem.
  + 1. **Oligonucleotide Primers**

Primer sequences, specificity, Tm, and size of the amplified product are given in (Table 3.1).

Table 3.1: Primers set table, shows the sequences, the target gene, Tm and the amplified product size (Rahn et al., 1992).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Primer | Target gene | Primer Specificity | Sequence (5'-3') | Tm  /0C | Size of amplified  product |
| Forward  Reverse | *invA*  *invA* | *Salmonella* species | TCATCGCACCGTCAAAGGAACC GTGAAATTATCGCCACGTTCGGGCAA | 55 | 284 |

* + 1. **Bacterial Growth Media and Preparation**

Different types of media were used and prepared as follows.

* + - 1. **The RapidChek® SELECT™ *Salmonella***

This is an enrichment media, used as the first of 2 steps in testing for the presence of S*almonella*.

It was prepared according to the manufacturer’s instructions. Briefly, one liter of sterile water was prepared by autoclaving deionized water at 121°C for 15 minutes before it was placed into a sterile 2 liter beaker. The sterilized deionized water was equilibrated to 42 ± 0.5°C on a hotplate stirrer. A weight of 27.0 ± 0.2 grams of RapidChek® SELECT™ *Salmonella* Medium was then added to the sterilized deionized water and stirred until the media dissolved.

* + - 1. **Tetrathionate TT Broth Base Hajna**

This is a selective media, used as the second culturing step for *Salmonella* detection*.*

The media was prepared according to the manufacturer’s instructions. Briefly, one liter of sterile deionized water was prepared by autoclaving deionized water at 121°C for 15 minutes, and 908.5 ml of this was placed into a 2 liter beaker, and brought to the boil on a stirrer hotplate. After that, 91.5g of the TT Hajna medium was added to the sterile deionized water and left stirring, with continued boiling, until it dissolved completely. The medium was allowed to cool down to 45°C, whereupon 40ml/L of iodine solution was added.

* + - 1. **Xylose Lysine Desoxycholate (XLD) Agar**

This is a selective agar medium for *Salmonella.* It was prepared according to the manufacturer’s instructions. Briefly, 27.5g of the media powder was added to a 1L flask. The volume was completed to 500 ml by adding 472.5 ml of sterile deionized water. Then the mixture was heated on a hot plate stirrer until boiling and then directly moved to a 50°C water bath. The medium was poured into plates after it cooled to 50°C.

* + - 1. **TT Hajna Agar**

One liter of sterile deionized water was prepared by autoclaving deionized water at 121°C for 15 minutes. Then 895 ml of the sterilized deionized water placed into a 2 liter beaker and boiled on a stirrer hotplate. A weight of 91.5g of TT Hajna media and 13.5 g of agar were added to the sterile deionized water and left stirring with the boiling deionized water for a few seconds until fully dissolved. The mixture was left to cool down to 45°C before 40ml/L of iodine solution was added, whereupon the agar medium was poured directly into plates.

* + - 1. **MacConkey Agar Media**

This medium is selective for gram negative bacteria, and differentiates lactose fermenting from non-fermenting bacteria. To prepare, 50g of the media powder was dissolved in 1 liter of deionized water, boiled for one minute and then autoclaved at 121°C for 15 minutes. The medium was poured into petri dishes.

* + - 1. **Non Selective Agar Media (Laura Agar, LB)**

This medium was used for gram negative cultures, after prior selection, and before antibiotic testing. In 1 liter of de-ionized water, 5g of yeast extract, 10g of tryptone, 10g of NaCl , and 13g of agar were dissolved, boiled and then autoclaved at 121°C for 15 minutes.

* + - 1. **Muller Hinton Agar**

This medium was used for antibiotic susceptibility testing and was prepared by adding 38g of the media powder in 1 liter of deionized water, which was boiled for 1 minute and then autoclaved for 15minutes at 121°C. Agar plates were then prepared.

* + 1. ***Salmonella* Reference Sample**

The *Salmonella* reference sample, which would be used for establishing a PCR assay for *Salmonella* from MSWs, was *Salmonella enterica* serovar Newport, which was kindly donated by the Central Laboratory of Public Health (CLPH) in Ramallah with the code *Newport*: 011-010. It was supplied in lyophilized form and was reconstituted using sterile saline, as recommended by the donor lab, then plated on a MacConkey agar plate and incubated overnight at 37°C. Then it was checked for growth.

* 1. **Methods**
     1. **MSW Work**

The MSW work began in the landfill with sorting and categorizing the samples, which were then taken to the BRC laboratory.

* + - 1. **MSW Sorting in the Landfill**

Samples were collected from Yatta landfill by Dr. Akrum Tamimi and Dr. Charles Gerba during five different visits, spread over a period of 2 weeks in the summer of 2011. Nine different samples were collected, such that two samples covered Hebron city, while each of the others represented a different location from the Hebron and Bethlehem governates. Table 3.2 shows the categorization of the areas surveyed according to socioeconomic metrics as high, medium, and low depending on Socio-Economic and Food Security (Sarhan, 2010).

Table 3.2: The table shows the categorization of the regions according to the socioeconomic level and specifies the sampling area. Bold type indicates the specific source of MSW sampled within each given region (Sarhan, 2010).

|  |  |  |  |
| --- | --- | --- | --- |
| **No.** | **Region** | **Socioeconomic**  **Metrics** | **Cities & Towns in Region** |
| 1 | Hebron City | Medium | ***Hebron*** |
| 2 | Hebron South and East Towns | Low | Beni Naeem, Samoe, ***Dura***, Yatta, Saeer, Ithna, Halhoul |
| 3 | Hebron North and West Towns | Low | Shoyouk, Tarkomya, ***Beit Omar***, Sureef, Beit Kahel, Rural Dura, Rural Yatta |
| 4 | City of Bethlehem | High | ***Bethlehem*** |
| 5 | Bethlehem Eastern Towns | High | ***Bet Sahour*** & Bet Jala |
| 6 | Bethlehem Western Towns | Low | ***Bateer***, Hosan, Nahaleen |
| 7 | Bethlehem Southern Towns | Low | ***Bet Fajjar*** |
| 8 | UNRWA (Refugee Camps) | Low | ***Fawar***, Dhaisheh, Aroub, Aydeh |

In the landfill, a truck from a specific area was chosen randomly to represent that region. A random sample from the truck was taken, sorted to different categories and subcategories of MSW. Figures 3.1 to 3.2 illustrate the sorting process.



Figure 3.1: The MSW from a random truck, waiting to be sorted in the containers.



Figure 3.2: Example of MSW sorting in the containers. Organic matter appeared in the right of the picture.

Between 50 and 100 grams were sampled from human feces, food, organic matter, toilet papers, and corrugated cardboard categories and were placed in sterile bags and were stored on ice until taken to the Biotechnology Research Center (BRC), Palestine Polytechnic University, at the end of the sampling day. This sampling method allowed collection of a uniform portion of material that was sufficiently small in volume to be transported and processed in the laboratory while still representing the material being sampled such that the relative concentration of the entire component will be the same in the sample as in the material being sampled, and that the sample will be handled in a manner that will cause no significant changes in composition before the appropriate tests are completed (Coropration, 1993).

* + - 1. **MSW Samples Processing**

The following procedures were performed for the sorted samples from each of the nine MSW sample regions.

Human feces were collected in 25 gram aliquots from six soiled diapers, selected at random from the dumped soiled diapers collected. Food scraps were collected in 100 gram representative samples and appeared to represent bread; rice; fruits; vegetables; chicken and lamb meats, skins and bones. Twenty five grams were randomly selected from food samples and were used for bacterial quantification. Organic matter included yard, garden and park waste; agricultural residues such as chicken feather; manure; wood and textiles. For bacterial quantification25 grams were used. Different colors, sizes and textures of toilet papers samples were collected with size of about 50 grams. The samples were shredded in the laboratory and 25 grams of representative material were selected and processed for bacterial quantification. Corrugated cardboards of different thickness, color and size were collected. The samples were cut into small pieces using sterilized scissors and 25 grams were randomly selected for bacterial testing in the laboratory.

* + 1. **Microbiology:**

This section describes the microbiology procedures that were used in the laboratory to test the MSW samples that were previously collected from Yatta landfill in order to detect the bacteria that represent the core of the whole study.

* + - 1. ***E.coli* and ColiformSamples Processing**
         1. ***E.coli* and ColiformSamples Preparation**

Twenty five grams of each solid waste composition sample were mixed with 225ml of sterile deionized water and were homogenized using a sterile blender for 30 seconds providing a 1:10 dilution. Dilutions of 10-2 down to 10-8 were prepared from the suspended samples in sterile deionized water for plating.

* + - * 1. ***E.coli* and ColiformSamples Plating**

Commercially available 3M™ Petrifilm™ *E.coli* / Coliform Count Plates (3M Food Safety, 3M Center) were used to quantify *E.coli* and Coliform in human feces, food, organic matter, toilet papers, and corrugated cardboards.

The 3M Petrifilm plate was placed on a leveled counter and with a pipette perpendicular to the Petrifilm plate, 1 ml of the prepared homogenized sample was placed on top of the plate. The top film was rolled carefully down to avoid entrapping air bubbles. A spreader was placed on top of the film over the inoculum and pressure was gently applied on the spreader to distribute the inoculum evenly over the entire circular area under the viewing window. When the gel was solidified, plates were incubated for 24 hours at 37° C. After the incubation period, Petrifilm plates were counted (Vail et al., 2003).

The colonies were counted on each Petrifilm in order to estimate the (colony forming unit per gram) CFU/g of each solid waste type. According to the manufacturer, the confirmed coliforms are red colonies without associated gas bubbles, while confirmed *E.coli* are blue colonies with associated gas bubbles. (Figure 3.3) shows the bacterial growth on the 3M Petrifilm plate.

|  |
| --- |
| Figure 3.3: *E.coli/* Coliform plates. Coliforms are the red colonies without associated gas bubbles while *E.coli* are the blue colonies with associated gas bubbles. |

As a negative control, 1ml of sterile water was plated on a Petrifilm plate and incubated with the samples. After 24 hour the plate was checked for possible contamination by noting presence or absence of colonies.

* + - 1. **Antibiotic Susceptibility Test**

The antibiotic susceptibility tests were performed to indicate the degree of bacterial resistance to antibiotics in MSW. Gram negative bacteriathat were isolated from two feces samples were used to perform the tests. Six isolated clones from each of the two feces sample were tested for antibiotic susceptibility. The test was done according to the Kirby-Bauer Disk Diffusion Susceptibility Test Protocol (Hudzicki, 2012).

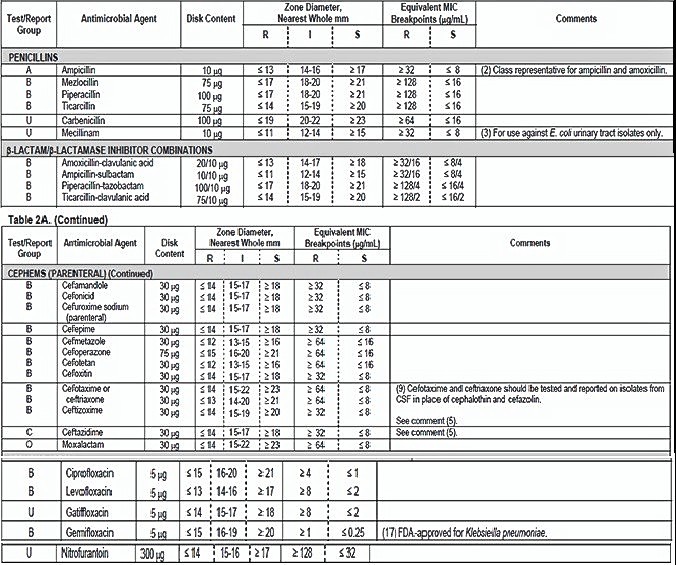
* + - * 1. **Bacterial Isolation**

Scratches from two frozen MSW samples were taken and plated on MacConkey agar plates. The plates were incubated overnight at 37°C and isolated colonies that appeared the next day were picked for re-plating to obtain bacterial clones from the mixed colonies on the plate. Touches of different colonies (red colonies) were transferred onto fresh MacConkey plates and incubated overnight at 37°C. Isolated bacterial colonies that appeared the next day were transferred to non-selective agar to be then tested for antibiotic susceptibility.

* + - * 1. **Bacterial Susceptibility Test for Antibiotic**

The 0.5 McFarland standard is an established standard for bacterial plating density during antibiotic resistance testing and was achieved using a spectrophotometer at 625nm wavelength to measure when the absorbance was 0.09. From each plate, 3 inocula were prepared by adding 4 colonies to 2ml sterile saline. Two inocula for the duplicates of the (amp10, Amc30, Cip5, and F300) group was prepared and one for the (FOX, CTX, CAZ, and CRO) group and spread onto Muller Hinton agar plates. The antibiotic discs (4 discs per plate) were added. For the first group, duplicate inocula were prepared and from each inoculum a duplicate of plates were prepared. The total number of antibiotics used was eight for each inoculum. The plates were incubated at 37°C. The inhibition zones were measured and then compared to the tables from the “Performance Standards for Antimicrobial Susceptibility Testing” (CLSI, 2007) as shown in (Table 3.3) to judge the results.

Table 3.3: Zone diameter interpretive standards and equivalent minimal inhibitory concentration breakpoints for enterobactereoceae (CLSI, 2007).



* + - 1. ***Salmonella* Sample Preparation**

RapidChek® SELECT™ *Salmonella* Test Kits (Strategic Diagnostics Inc., SDIX, USA) were used to test for the presence of *Salmonella* in food scraps and human feces sampled from Yatta MSW landfill after a two step enrichment and selection process for *Salmonella*.

* + - * 1. ***Salmonella* Enrichment in Liquid Culture**

Approximately 25 grams of the MSW sample and 225 ml of rehydrated RapidChek® SELECT™ *Salmonella* medium (pre-warmed to 42°C) were homogenized in blender for 30 seconds providing a 1:10 dilution. Ten fold dilutions, down to 10-8 with a volume of 1 ml were prepared in 1.5ml Eppendorf tubes and incubated for 24 hours at 42 ± 0.5°C, according to the manufacturer’s instructions, for preliminary enrichment. The media is specific for *Salmonella* enrichment, but it does not inhibit other bacteria. Three replicates of each dilution were prepared.

The remaining samples in the original serial tubes were kept in -80°C freezer for subsequent PCR confirmation.

* + - * 1. ***Salmonella* Selection in Liquid Culture**

After the 24 hr incubation at 42°C, the Eppendorf tubes were removed from the incubator and were vigorously vortexed. For each dilution, 1 ml of the enriched sample was added to a tube containing 10 ml of pre-warmed (42°C) TT Hajna medium, and all tubes with the different dilutions were incubated at 42°C for 24 hours. The TT Hajna medium is selective for *Salmonella* and inhibits the other bacteria.

* + - * 1. **Test Strip Detection for *Salmonella***

After the 24 hours selection step in TT Hajna medium, the RapidChek® SELECT™ *Salmonella* detection procedure was used to determine the presence or the absence of *Salmonella* for each dilution. Aliquots of 0.5 ml of enriched broth were aspirated into plastic tubes supplied with the kit. Each plastic tube was labeled with the sample ID and dilution and a test strip was inserted with arrows facing down into the plastic tube. The strip remained in contact with the aliquot for 10 minutes, in accordance with the manufacturer’s instructions. The appearance of one red line (control) on the strip indicated a negative result, while the appearance of two red lines on the strip indicated a positive result.

For each sample tested for *Salmonella*, three tubes of each dilution were tested resulting in a negative or positive result. Utilizing the different dilution levels, enough data points were generated to use the most probable number (MPN) method outlined in Margareat & Roscoe (Margareat and Roscoe, 1983). The MPN method involves taking the original sample, and serially diluting it, in replicates, by orders of magnitude 10× and assessing presence or absence of bacteria in each dilution.

* + - 1. **Clonal Isolation of *Salmonella*:**
         1. **Isolation of *Salmonella* Directly on XLD Plates**

Frozen MSW samples, as well as positive and negative control samples, were tested by XLD agar media, which is selective for *Salmonella* and *Shigella* spp.

The frozen samples were kept on ice during handling to prevent the thawing of the samples, which would lead to cells loss with each thawing freezing cycle. A scratch from each sample was taken using a sterile loop and directly streaked on an XLD agar plate. All the plates were incubated overnight at 37°C. The following day they were checked for growth.

The positive control was *S.enterica* serovar Newport donated from the Central Labs of Public Health in Ramallah. A colony was streaked onto a new XLD agar plate. As a negative control, a standard laboratory strain of *E.coli* (DH5α) wasused. Another plate was used as a true negative control, which was incubated without bacteria with the other plates. All the plates were incubated overnight at 37°C and following overnight incubation checked for growth.

The positive controls and MSW samples were checked for black colonies, which indicate *Salmonella* growth, without change in the color of the media while the *E.coli* negative control was checked for yellow colonies and change of the media color to yellow, which indicates *E.coli*.

* + - * 1. **Isolation of *Salmonella* Using TT Hajna**

Scratches from the frozen samples were taken and suspended directly in 5ml of RapidChek® SELECT™ *Salmonella* broth and incubated overnight at 42°C. The next day, 100µl of the enriched samples were spread on TT Hajna agar plates, and another 100µl was added to 10ml TT Hajna broth base, and both the plates and the tubes were incubated overnight at 42°C. After colonies appeared on the TT Hajna plates, some colonies were taken and streaked on XLD media plates, while 80µl from the TT Hajna tubes were also plated on XLD plates. In order to obtain pure *Salmonella* colonies after the first growth on the XLD plates, a colony was replated on a new XLD agar plate.

* + - 1. **Positive Control Culture:**

In order to better ensure work from a true clonal isolate, a colony touch from the previously mentioned MacConkey plates (section 3.1.4) was re-plated on a fresh XLD agar plate and was also used to prepare DNA for PCR authentication. The plates were incubated overnight at 37°C. A new colony was picked from the plate and suspended in 5ml LB and re-incubated overnight at 37°C. 500µl of each overnight culture was added to a 1.5ml tube and mixed with a 1:1 volume of sterile glycerol for long term storage at -80°C.

* + 1. **Statistical Analysis**

The data generated from the microbiology tests for detection of coliforms*, E.coli,* and *Salmonella* were subjected to appropriate statistical analyses. Two types of analyses were used; descriptive analysis was used for all of the three pathogens results (CFU/g and MPN). The second type of analysis was the hypothesis testing. The data were also represented on charts and graphs as appropriate. The analyses used the socioeconomic metric and the MSW categories as factors of comparison. The data analysis and presentation were generated on SPSS 16.0.

Previously mentioned data in (Tables 4.1 and 4.2) were tested first for a relationship between the socioeconomic metric and the bacterial load. The second test was for a relationship between the source of the bacteria and the CFU/g. Also the *Salmonella* MPN in (Table 4.13) was used to test the hypotheses that were generated to correlate between the socioeconomic metric and the MPN of *Salmonella* in both samples (food and feces)*.* The tested hypotheses are (the lower socioeconomic metric regions have the highest MPN of *Salmonella* in feces, while the other one is that the higher socioeconomic metric has the highest *Salmonella* number in food).

The first hypothesis was tested using One-Way ANOVA because the tested factor –socioeconomic metric- is of three groups while the *E.coli* and coliform were tested using the Kruskal-Wallis test because the data were not normalized even after the transformation. The test determines if there is a relationship between more than two different groups when the data is not normally distributed. The hypotheses that were tested for both bacteria were in similar format to each other. The hypotheses were written as follows for each bacteria type on its own:-

* **Coliforms/Socioeconomic**

The hypothesis for the relationship between coliform and the socioeconomic metric group.

H0: there is no difference in coliformbetween the different socioeconomic metric regions.

H1: the regions with the lower socioeconomic metrics are the highest in coliform.

α: 0.05

* **Coliforms/Source**

The hypothesis of the relationship between the coliformand the source categories.

H0: there is no difference in coliformbetween the different source categories.

H1: the coliformcontent depends on the source.

α: 0.05

* ***E.coli*/Socioeconomic**

The hypothesis for the relationship between *E.coli* and the socioeconomic metric group.

H0: there is no difference in *E.coli* between the different socioeconomic metric regions.

H1: the regions with the lower socioeconomic metrics are the highest in *E.coli*.

α: 0.05

* ***E.coli/*Source**

The hypothesis of the relationship between the *E.coli* and the source categories.

H0: there is no difference in *E.coli* between the different source categories.

H1: the *E.coli* content depends on the source.

α: 0.05

The *Salmonella* hypotheses were the same as for the other types of bacteria. They were used for testing the relationship between the *Salmonella* MPN and the socioeconomic metric and the source category.

* ***Salmonella* MPN/Socioeconomic**

The first *Salmonella* hypothesis was for the relationship between the socioeconomic metric and *Salmonella* MPN. This hypothesis was tested by the One-Way ANOVA, generated on the transformed data.

H0: there is no difference in *Salmonella* between the different socioeconomic metric regions.

H1: the regions with the higher socioeconomic metrics are the highest in *Salmonella*.

α: 0.05

* **MPN Food/MPN Feces**

The second hypothesis was tested using the independent samples T-test because it was comparing two groups only and was generated on the transformed data.

The second hypothesis:

H0: there is no difference in *Salmonella* occurrence between food and feces.

H1: the food has a higher *Salmonella* number than feces.

α: 0.05

* + 1. **Molecular Work**

# MSW samples were stored at -80°C until required for PCR confirmation using specific primers, which were also used on the *Salmonella* reference samples. After the PCR, DNA amplification products were subjected to agarose gel electrophoresis and purified from the gel and sequenced at Bethlehem University; Hereditary Research Laboratory.

* + - 1. **DNA Extraction:**

DNA was extracted using the boiling method for all the samples. A colony touch was taken from the agar plates and suspended in 1.5ml tubes that contain 400µl 1X TE buffer. The tubes were incubated in a water bath at 100°C for 15-20 min, and then left to cool down to room temperature. Lastly, they were centrifuged at 13000 rpm in a benchtop centrifuge for 10min and 5µl of the supernatant was used as the template for the PCR.

* + - 1. **DNA Amplification:**

The PCR reaction was performed using the *invA* gene primers; the general *Salmonella* specific primers. It was made for each DNA template. PCR amplifications were performed in a final volume of 20µl in micro-amplification tubes (PCR tubes). The reaction mixtures consisted of 5µl of the DNA template, 1 µl (25 pmol) from each of the forward and reverse primers, 10µl of 2x PCR master mix, and the volume of the reaction mixture was completed to 20µl using sterile ultra pure water.

Optimal thermal cycler conditions were: initial denaturation at 95°C for 5 min, followed by 35 cycles of (denaturation at 94°C for 1 min, annealing at 55°C for 30 sec and extension at 72°C for 30 sec.). Final extension was carried out at 72°C for 7 min and the PCR products were stored at 4°C until they were needed.

* + - 1. **Agarose Gel Electrophoresis:**

PCR products were visualized using 1.5% agarose gel electrophoresis. The voltage ranged from 90-110 volts depending on the tray size. The running time was 1 hour. The markers used were *HaeIII*-digested pUC18, from Sigma Aldrich.

* + - 1. **DNA Sequencing:**

The sequencing was performed two times. The purification of DNA was different each time. It was purified from gel and from PCR product.

* Gel Purification.

The target bands for sequencing were cut from the gel, and then the DNA was purified using the Promega protocol (Wizard® SV Gel and PCR Clean-Up System) kit instructions. Briefly, the gel containing the DNA was dissolved to get rid of it. Then a mini-column was used to separate the DNA from the degraded gel fragments. DNA was washed and then collected using DNAse-RNAse free water.

* PCR product purification

The PCR products were purified using AccuPrepTM PCR Purification Kit instructions. Briefly, buffers were added in proportion to the PCR reaction volume as detailed in the kit. The mixture was transferred to binding columns, which were used to adsorb the target DNA and get rid of other residues such as excess primers. The DNA was washed using the buffers from the kit and then collected.

* + - 1. **Sequence Analysis**

The resulting sequences were processed using the Sequencher 4.1.4 software in order to produce a consensus sequence from the two sequences that were generated from each of the forward and reverse primers. The raw data for the sequences are in the appendices: the FASTA format sequences are in appendix A and the traces of the sequences are in appendix B. The sequences were aligned using BLAST on NCBI to check for significant similarities with the known strains. Also, they were aligned against each other using the ClustalW2 from EMBL-EBI databases. Phylogenetic and molecular evolutionary analyses were conducted using MEGA version 5 (Tamura et al., 2011).

**CHAPTER 4**

**Results:**

* 1. **Microbiology Results**
     1. **Coliformand *E.coli***

The results of counting the coliforms in MSW samples are shown in Table 4.1, which is organized according to the socioeconomic metric. The table shows that the highest coliform content was in feces, with a mean of 1.65X108 CFU/g, followed by toilet paper, food organic matter and, lastly, cardboard with a mean 6.68X106 CFU/g. In addition, there seems to be a possible relationship between socioeconomic metric and mean coliform content.

Table 4.1: The coliform CFU/g numbers. The numbers for each category from all of the different regions ordered according to the socioeconomic metric.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Location | Socioeconomic metric | Feces | Toilet Paper | Food | Organic Matter | Cardboard | Means |
| Coliform  (CFU/g) | Coliform  (CFU/g) | Coliform  (CFU/g) | Coliform  (CFU/g) | Coliform  (CFU/g) |
| Fawwar | Low | 1.58X107 | 6.34X107 | 1.24X108 | 2.50X107 | 4.94X106 | 9.44X107 |
| Dura | Low | 1.61X108 | 1.22X107 | 2.28X107 | 6.08X107 | 2.23X107 |
| Batteer | Low | 4.56X108 | 1.21X108 | 1.07X107 | 3.99X107 | 4.06X105 |
| Beit Fajjar | Low | 3.43X108 | 2.84X107 | 4.23X107 | 9.36X107 | 4.82X106 |
| Beit Ommar | Low | 2.39X108 | 3.75X108 | 7.06X107 | 1.65X107 | 7.70X106 |
| Hebron-1- | Medium | 2.72X107 | 5.85X106 | 9.38X106 | 1.81X105 | 3.20X106 | 5.20X107 |
| Hebron -2- | Medium | 1.62X108 | 9.65X107 | 2.08X108 | 5.31X106 | 2.29X106 |
| Beit Sahour | High | 2.77X107 | 1.19X107 | 1.21X108 | 1.75X107 | 3.02X106 | 3.54X107 |
| Bethlehem | High | 5.64X107 | 6.06X107 | 3.10X107 | 1.24X107 | 1.25X107 |
| Mean | | 1.65X108 | 8.61X107 | 7.11X107 | 3.01X107 | 6.68X106 |  |

These results are illustrated, with statistical indications of significance, in two graphs: one to show the difference according to the category and the other according to the socioeconomic metric.

Figure 4.1 shows that there is no significant difference between the feces and the toilet paper, but there is a difference between the feces and the food. Cardboard and organic matter had lower coliform counts than the other three categories (food, feces, toilet paper) and hence the coliform content in the landfill depends on its source.

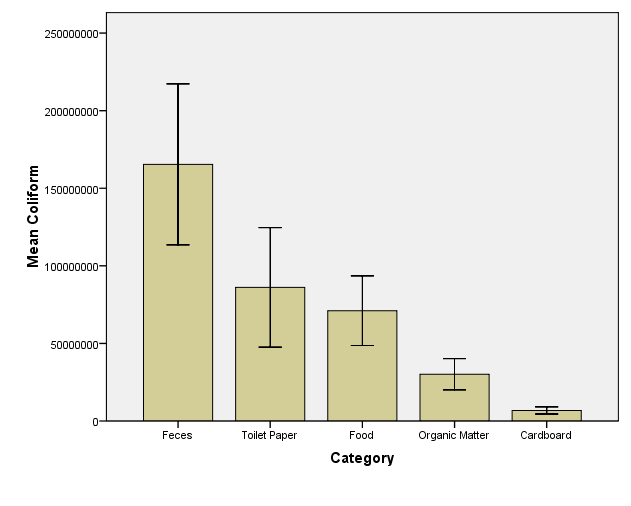


Figure 4.1: The comparison of the coliform means according to the waste category of the source.

Figure 4.2 appears to show that the regions with the high socioeconomic metric are the lowest contributor of coliforms and that the regions with the lowest socioeconomic metric are the highest contributors, but the statistical analysis for the data showed that these differences were not significant, so the hypothesis was rejected.

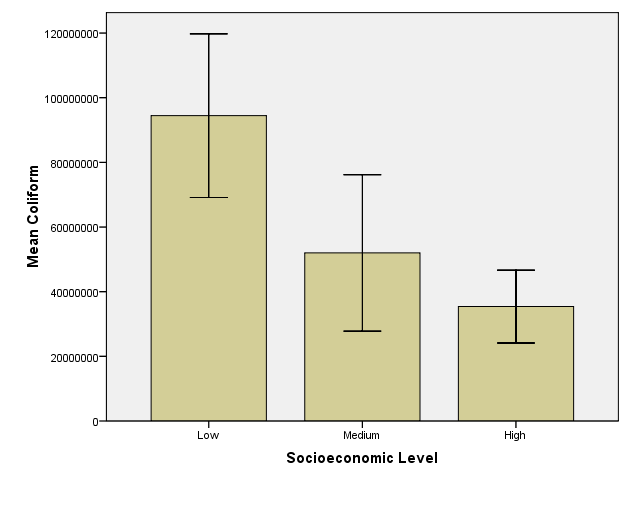


Figure 4.2: The coliform means comparison according to the socioeconomic metric.

The results of counting the *E.coli* in MSWare shown in Table 4.2, which is organized according to the socioeconomic metric. Inspection of Table 4.2 shows that the highest *E.coli* content was in feces with a mean 7.32X106 CFU/g, also that when the socioeconomic metric is low with mean 3.27X106 CFU/gwhile the least was in the cardboard with a mean of 9.23X104 CFU/g. These results are illustrated in two graphs: one to show the difference according to the category, the other according to the socioeconomic metric.

Table 4.2: The CFU/g for the *E.coli.* The numbers for each category from all of the different regions are ordered according to the socioeconomic metric.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Location | Socioeconomic metric | Feces | Toilet Paper | Food | Organic Matter | Cardboard | Means |
| *E.coli*  (CFU/g) | *E.coli*  (CFU/g) | *E.coli*  (CFU/g) | *E.coli*  (CFU/g) | *E.coli*  (CFU/g) |
| Fawwar | Low | 1.56X106 | 6.25X105 | 1.56X106 | 2.50X107 | 4.94X106 | 9.44X107 |
| Dura | Low | 3.13X105 | 8.75X104 | 8.13X105 | 6.08X107 | 2.23X107 |
| Batteer | Low | 2.81X107 | 2.59X106 | 1.88X105 | 3.99X107 | 4.06X105 |
| Beit Fajjar | Low | 2.81X107 | 8.13X105 | 6.50X104 | 9.36X107 | 4.82X106 |
| Beit Ommar | Low | 5.63X106 | 9.38X106 | 2.69X105 | 1.65X107 | 7.70X106 |
| Hebron-1- | Medium | 1.88X105 | 9.00X105 | 6.06X105 | 1.81X105 | 3.20X106 | 5.20X107 |
| Hebron -2- | Medium | 1.56X106 | 9.00X105 | 2.19X105 | 5.31X106 | 2.29X106 |
| Beit Sahour | High | 3.13X105 | 5.00X104 | 2.50X103 | 1.75X107 | 3.02X106 | 3.54X107 |
| Bethlehem | High | 1.56X106 | 2.63X104 | 6.75X104 | 1.24X107 | 1.25X107 |
| Mean |  | 7.32X106 | 1.71X106 | 4.21X105 | 3.01X107 | 6.68X106 |  |

Figure 4.3 shows that there are significant differences between the different categories. The tested hypothesis that was used to analyze the results proved the correlation between the source and the amount of *E.coli* present. This means that the *E.coli* content in the landfill depends on its source.

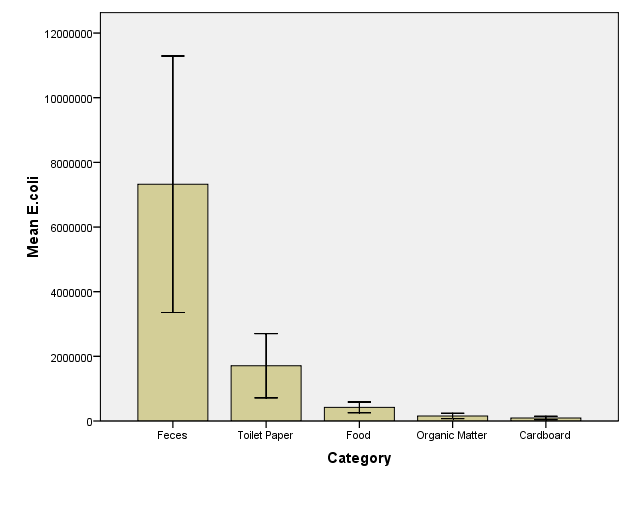


Figure 4.3: The *E.coli* mean CFU/g comparison according to the category source.

Figure 4.4 appears to show that the highest socioeconomic metric regions are the lowest contributor of *E.coli* and the lowest socioeconomic metric regions are the highest contributors. However, statistical analysis for the data showed that any differences according to the socioeconomic metric are not significant.

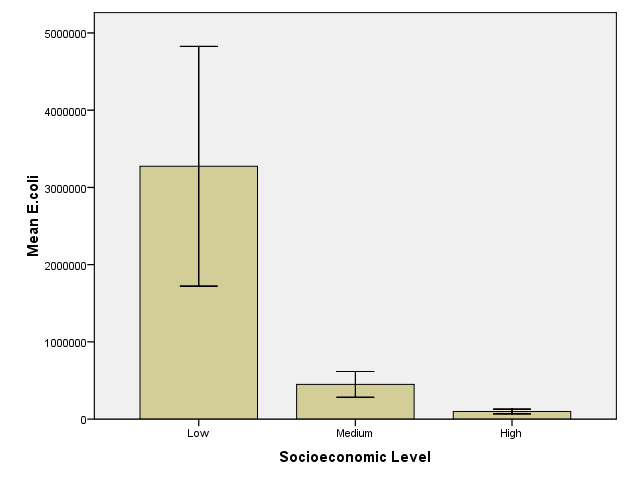


Figure 4.4: The *E.coli* CFU/g comparison of means according to the socioeconomic metric.

The results for bacterial counting from *E.coli*, coliforms and *Salmonella* are summarized together in Table 4.3. The percentage of contribution of each bacterial group, from the total counted, according to the source is shown in the table. The highest percentage in feces is the coliform (44.8%) and the lowest is the *Salmonella* (0.01%).

Table 4.3: The contribution of bacteria by source.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Feces | Food | Organic Matter | Toilet Paper | Cardboard |
| Colifom | 44.80% | 19.30% | 8.01% | 23.30% | 1.85% |
| *E.coli* | 2% | 0.11% | 0.05% | 0.50% | 0.03% |
| *Salmonella* | 0.01% | 0.04% | Not tested | Not tested | Not tested |

* + 1. **Antibiotic Susceptibility Test Result**

The diameter was measured for each zone of inhibition. Figure 4.5 is an example for the antibiotic inhibition zones.

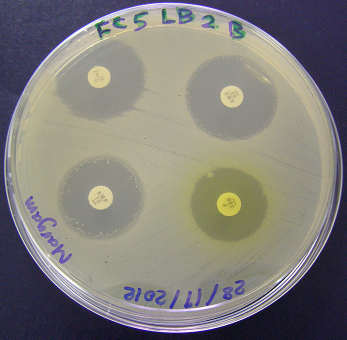


Figure 4.5: Example of an antibiotic susceptibility test plate result. The antibiotics on the plate are Nitrofurantoin, Ampicillin, Amoxicillin and Clavulanic acid, and Ciprofloxacin.

* + - 1. **Ampicillin Results**

From two feces samples, six different clones were made and from each of the six clones, two inocula were made. Furthermore, for each inoculum two antibiotic test plates were made. Four antibiotic discs used on each plate. Table 4.4 shows the Ampicillin antibiotic results for each inoculum of a clone and its duplicate. The table shows that 4 out of 12 samples were resistant to ampicillin; 1-2 were intermediate while the rest were susceptible.

Table 4.4: The result of the susceptibility test of the Ampicillin antibiotic; (R: resistant, I: Intermediate, S: susceptible) the zone diameter is in mm.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Ampicillin 10µg/disc | | | | | |  |  |
| 1st inoculum | | Average | Result | 2nd inoculum | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 0 | 0 | 0 | R | 0 | 0 | 0 | R |
| MSW/2011/**B.Umar**/feces-2 | 21 | 22 | 21.5 | S | 20 | 21 | 20.5 | S |
| MSW/2011/**B.Umar**/feces-3 | 0 | 0 | 0 | R | 0 | 0 | 0 | R |
| MSW/2011/**B.Umar**/feces-4 | 0 | 0 | 0 | R | 0 | 0 | 0 | R |
| MSW/2011/**B.Umar**/feces-5 | 18 | 20 | 19 | S | 16 | 12 | 14 | I |
| MSW/2011/**B.Umar**/feces-6 | 16 | 14 | 15 | I | 18 | 16 | 17 | S |
| MSW/2011/**Hebron**/feces-1 | 0 | 0 | 0 | R | 0 | 0 | 0 | R |
| MSW/2011/ **Hebron** /feces-2 | 18 | 20 | 19 | S | 20 | 21 | 20.5 | S |
| MSW/2011/ **Hebron** /feces-3 | 25 | 25 | 25 | S | 28 | 28 | 28 | S |
| MSW/2011/ **Hebron** /feces-4 | 28 | 27 | 27.5 | S | 28 | 26 | 27 | S |
| MSW/2011/ **Hebron** /feces-5 | 19 | 19 | 19 | S | 14 | 17 | 15.5 | I |
| MSW/2011/ **Hebron** /feces-6 | 28 | 27 | 27.5 | S | 25 | 30 | 27.5 | S |

* + - 1. **Amoxicillin and Clavulanic Acid Results**

From two feces samples, six different clones were made and from each of the six clones, two inocula were made; also from each inoculum, two antibiotic test plates were made. None of the tested bacteria was resistant to the Amoxicillin & Clavulanic acid, though four or five show intermediate susceptibility. The detailed results are shown in Table 4.5.

Table 4.5: The result of the Amoxicillin and Clavulanic acid antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible) the zone diameter in mm.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Amoxicillin & Clavulanic acid 30µg/disc | | | | | |  |  |
| 1st inoculum | | Average | Result | 2nd inoculum | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 16 | 16 | 16 | I | 16 | 15 | 15.5 | I |
| MSW/2011/**B.Umar**/feces-2 | 25 | 24 | 24.5 | S | 25 | 24 | 24.5 | S |
| MSW/2011/**B.Umar**/feces-3 | 16 | 16 | 16 | I | 16 | 16 | 16 | I |
| MSW/2011/**B.Umar**/feces-4 | 17 | 17 | 17 | I | 17 | 17 | 17 | I |
| MSW/2011/**B.Umar**/feces-5 | 16 | 20 | 18 | S | 18 | 14 | 16 | I |
| MSW/2011/**B.Umar**/feces-6 | 15 | 17 | 16 | I | 17 | 18 | 17.5 | I |
| MSW/2011/**Hebron**/feces-1 | 20 | 17 | 18.5 | S | 18 | 20 | 19 | S |
| MSW/2011/ **Hebron** /feces-2 | 28 | 21 | 19.5 | S | 25 | 24 | 24.5 | S |
| MSW/2011/ **Hebron** /feces-3 | 28 | 28 | 28 | S | 34 | 33 | 33.5 | S |
| MSW/2011/ **Hebron** /feces-4 | 40 | 38 | 39 | S | 36 | 36 | 36 | S |
| MSW/2011/ **Hebron** /feces-5 | 22 | 20 | 21 | S | 18 | 22 | 20 | S |
| MSW/2011/ **Hebron** /feces-6 | 38 | 36 | 37 | S | 32 | 36 | 34 | S |

* + - 1. **Ciprofloxacin Results**

From two feces samples, six different clones were made and from each of the six clones, two inocula were made; also, from each inoculum two antibiotic test plates were made. Some of the bacteria that were of intermediate susceptibility to the combined Amoxicillin and Clavulanic acid were resistant to the Ciprofloxacin. Table 4.6 shows the results for each clone and its duplicates. 2-3 were resistant to the Ciprofloxacin; 1-2 were intermediate, where the rest were susceptible.

Table 4.6: The result of Ciprofloxacin antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible) the zone diameter is in mm.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Ciprofloxacin 5µg/disc | | | | | |  |  |
| 1st inoculum | | Average | Result | 2nd inoculum | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 12 | 11 | 11.5 | R | 10 | 11 | 10.5 | R |
| MSW/2011/**B.Umar**/feces-2 | 24 | 25 | 24.5 | S | 24 | 25 | 24.5 | S |
| MSW/2011/**B.Umar**/feces-3 | 10 | 11 | 10.5 | R | 18 | 16 | 17 | I |
| MSW/2011/**B.Umar**/feces-4 | 11 | 10 | 10.5 | R | 11 | 11 | 11 | R |
| MSW/2011/**B.Umar**/feces-5 | 37 | 38 | 37.5 | S | 38 | 36 | 37 | S |
| MSW/2011/**B.Umar**/feces-6 | 38 | 40 | 39 | S | 40 | 36 | 38 | S |
| MSW/2011/**Hebron**/feces-1 | 40 | 34 | 37 | S | 32 | 32 | 32 | S |
| MSW/2011/ **Hebron** /feces-2 | 20 | 20 | 20 | I | 22 | 21 | 21.5 | S |
| MSW/2011/ **Hebron** /feces-3 | 29 | 30 | 29.5 | S | 32 | 32 | 32 | S |
| MSW/2011/ **Hebron** /feces-4 | 40 | 40 | 40 | S | 42 | 42 | 42 | S |
| MSW/2011/ **Hebron** /feces-5 | 21 | 21 | 21 | S | 20 | 19 | 19.5 | I |
| MSW/2011/ **Hebron** /feces-6 | 34 | 34 | 34 | S | 32 | 32 | 32 | S |

* + - 1. **Nitrofurantoin Results**

From two feces samples, six different clones were made and from each of the six clones, two inocula were made; also, from each inoculum two antibiotic test plates were made. All of the 12 isolates were sensitive to Nitrofurantoin. The results of both inocula of each clone and their duplicates are listed in Table 4.7.

Table 4.7: The result of the Nitrofurantoin antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible) the zone diameter is in mm.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Nitrofurantoin 300µg/disc | | | | | |  |  |
| 1st inoculum | | Average | Result | 2nd inoculum | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 22 | 23 | 22.5 | S | 25 | 25 | 25 | S |
| MSW/2011/**B.Umar**/feces-2 | 18 | 20 | 19 | S | 19 | 19 | 19 | S |
| MSW/2011/**B.Umar**/feces-3 | 26 | 24 | 25 | S | 25 | 24 | 24.5 | S |
| MSW/2011/**B.Umar**/feces-4 | 22 | 22 | 22 | S | 22 | 21 | 21.5 | S |
| MSW/2011/**B.Umar**/feces-5 | 26 | 25 | 25.5 | S | 26 | 24 | 25 | S |
| MSW/2011/**B.Umar**/feces-6 | 25 | 25 | 25 | S | 25 | 25 | 25 | S |
| MSW/2011/**Hebron**/feces-1 | 24 | 24 | 24 | S | 25 | 24 | 24.5 | S |
| MSW/2011/ **Hebron** /feces-2 | 25 | 25 | 25 | S | 24 | 24 | 24 | S |
| MSW/2011/ **Hebron** /feces-3 | 28 | 27 | 27.5 | S | 32 | 32 | 32 | S |
| MSW/2011/ **Hebron** /feces-4 | 32 | 30 | 31 | S | 32 | 23 | 27.5 | S |
| MSW/2011/ **Hebron** /feces-5 | 24 | 23 | 23.5 | S | 23 | 23 | 23 | S |
| MSW/2011/ **Hebron** /feces-6 | 31 | 25 | 28 | S | 24 | 23 | 23.5 | S |

* + - 1. **Ceftriaxon Results**

From two feces samples, five different clones were isolated and from each clone, one inoculum was made; also from each inoculum two antibiotic test plates were made. Since the results for the first four antibiotics were reproducible, the second group was tested just in a duplicate for one inoculum of each bacterial clone. All the tested clones were sensitive to the Ceftriaxone. The detailed results are listed in Table 4.8.

Table 4.8: The results Ceftriaxone antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Ceftriaxone 30µg/disc | | | |
|  | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 26 | 27 | 26.5 | S |
| MSW/2011/**B.Umar**/feces-2 | 30 | 30 | 30 | S |
| MSW/2011/**B.Umar**/feces-3 | 30 | 30 | 30 | S |
| MSW/2011/**B.Umar**/feces-4 | 31 | 31 | 31 | S |
| MSW/2011/**B.Umar**/feces-5 | 36 | 36 | 36 | S |
| MSW/2011/**Hebron**/feces-1 | 28 | 35 | 31.5 | S |
| MSW/2011/ **Hebron** /feces-2 | 32 | 32 | 32 | S |
| MSW/2011/ **Hebron** /feces-3 | 36 | 37 | 36.5 | S |
| MSW/2011/ **Hebron** /feces-4 | 30 | 30 | 30 | S |
| MSW/2011/ **Hebron** /feces-5 | 36 | 36 | 36 | S |

* + - 1. **Ceftazidime Results**

From two feces samples, five different clones were isolated and from each clone one inoculum was made; also from each inoculums, two antibiotic test plates were made. Table 4.9 shows the result of the clones tested against Ceftazidime. All of the tested clones were susceptible to the Ceftazidime.

Table 4.9: The result of the Ceftazidime antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Ceftazidime 30µg/disc | | | |
| 1 | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 26 | 30 | 28 | S |
| MSW/2011/**B.Umar**/feces-2 | 28 | 30 | 29 | S |
| MSW/2011/**B.Umar**/feces-3 | 30 | 28 | 29 | S |
| MSW/2011/**B.Umar**/feces-4 | 29 | 28 | 28.5 | S |
| MSW/2011/**B.Umar**/feces-5 | 34 | 34 | 34 | S |
| MSW/2011/**Hebron**/feces-1 | 33 | 30 | 31.5 | S |
| MSW/2011/ **Hebron** /feces-2 | 30 | 30 | 30 | S |
| MSW/2011/ **Hebron** /feces-3 | 34 | 34 | 34 | S |
| MSW/2011/ **Hebron** /feces-4 | 27 | 28 | 27.5 | S |
| MSW/2011/ **Hebron** /feces-5 | 32 | 34 | 34 | S |

* + - 1. **Cefotaxim Results**

From two feces samples five different clones were isolated and from each clone one inoculum was made; also from each inoculum two antibiotic test plates were made. All the tested clones were susceptible to the Cefotaxime. The detailed results are shown in Table 4.10.

Table 4.10: The results of the Cefotaxim antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Cefotaxime 30µg/disc | | | |
|  | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 30 | 31 | 30.5 | S |
| MSW/2011/**B.Umar**/feces-2 | 31 | 32 | 31.5 | S |
| MSW/2011/**B.Umar**/feces-3 | 33 | 33 | 33 | S |
| MSW/2011/**B.Umar**/feces-4 | 31 | 32 | 31.5 | S |
| MSW/2011/**B.Umar**/feces-5 | 34 | 34 | 34 | S |
| MSW/2011/**Hebron**/feces-1 | 35 | 41 | 38 | S |
| MSW/2011/ **Hebron** /feces-2 | 32 | 34 | 33 | S |
| MSW/2011/ **Hebron** /feces-3 | 38 | 35 | 36.5 | S |
| MSW/2011/ **Hebron** /feces-4 | 31 | 32 | 31.5 | S |
| MSW/2011/ **Hebron** /feces-5 | 40 | 40 | 40 | S |

* + - 1. **Cefoxitin Results**

From two feces samples, five different clones were isolated and from each clone one inoculum was made; also from each inoculum two antibiotic test plates were made. Table 4.11 shows that one of the clones that tested by Cefoxitin was resistant to the antibiotic while the rest were susceptible.

Table 4.11: The results of Cefoxitin antibiotic susceptibility test (R: resistant, I: Intermediate, S: susceptible).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Cefoxitin 30µg/disc | | | |
|  | | Average | Result |
| MSW/2011/**B.Umar**/feces-1 | 22 | 20 | 21 | S |
| MSW/2011/**B.Umar**/feces-2 | 24 | 23 | 23.5 | S |
| MSW/2011/**B.Umar**/feces-3 | 23 | 24 | 23.5 | S |
| MSW/2011/**B.Umar**/feces-4 | 24 | 24 | 24 | S |
| MSW/2011/**B.Umar**/feces-5 | 10 | 10 | 10 | R |
| MSW/2011/**Hebron**/feces-1 | 26 | 26 | 26 | S |
| MSW/2011/ **Hebron** /feces-2 | 26 | 28 | 27 | S |
| MSW/2011/ **Hebron** /feces-3 | 29 | 29 | 29 | S |
| MSW/2011/ **Hebron** /feces-4 | 26 | 26 | 26 | S |
| MSW/2011/ **Hebron** /feces-5 | 18 | 18 | 18 | S |

The overall results for the antibiotics are summarized in Table 4.12. The highest percentage of resistance is for the Ampicillin with 33.3%, followed with the Ciprofloxacin with 21%. All the third generation cephalosporins tested here showed 100% susceptibility.

Table 4.12: The antibiotic susceptibility test summary table.

|  |  |  |  |
| --- | --- | --- | --- |
| Antibiotic | Resistance | Intermediate | Susceptible |
| Ampicillin | 33.3% | 17% | 50% |
| Amoxicillin & Clavulanic Acid | 0 | 40% | 60% |
| Ciprofloxacin | 21% | 12.5% | 76.5% |
| Nitrofurantoin | 0 | 0 | 100% |
| Ceftriaxone | 0 | 0 | 100% |
| Cefotaxime | 0 | 0 | 100% |
| Ceftazidime | 0 | 0 | 100% |
| Cefoxitin | 8% | 0 | 92% |

* + 1. ***Salmonella* Results**
       1. **Results of *Salmonella* MPN Analysis**

The *Salmonella* MPNs (Table 4.13) are shown for both food and feces samples from each different location in order according to the socioeconomic metric group. The Table shows that the highest *Salmonella* number was in the food, with a mean of 1.28X105. When compared according to the socioeconomic metric the high socioeconomic metric group appeared to have the highest *Salmonella* number with a mean count of 1.84X105.

Table 4.13: The *Salmonella* MPN’s for both food and feces samples, from each location, ordered according to the socioeconomic metric.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Location | Socioeconomic metric | Human Feces | Food | Mean |
| *Salmonella* (MPN/g) | *Salmonella*  (MPN/g) |
| Fawwar | Low | 2.30X103 | 2.31X103 | 3.35X104 |
| Dura | Low | 2.34X104 | 2.34X104 |
| Batteer | Low | 2.12X104 | 1.46X105 |
| Beit Fajjar | Low | 9.17X104 | 2.76X104 |
| Beit Ommar | Low | 2.34X104 | 2.34X104 |
| Hebron -1- | Medium | 1.00X101 | 1.31X104 | 6.35X104 |
| Hebron -2- | Medium | 2.34X104 | 2.17X105 |
| Beit Sahour | High | 9.36X103 | 2.42X104 | 1.84X105 |
| Bethlehem | High | 2.37X104 | 6.78X105 |
| Mean | | 2. 48X104 | 1.28X105 |  |

The means of the numbers in Table 4.13 were compared using the socioeconomic metric and the category source as comparison factors. The results are illustrated in the following graphs.

Figure 4.6 shows the mean comparison according to the source. Although the mean MPN for *Salmonella* in food is higher than in feces, the statistical test showed that the difference between the two source groups (food and feces) is not significant.

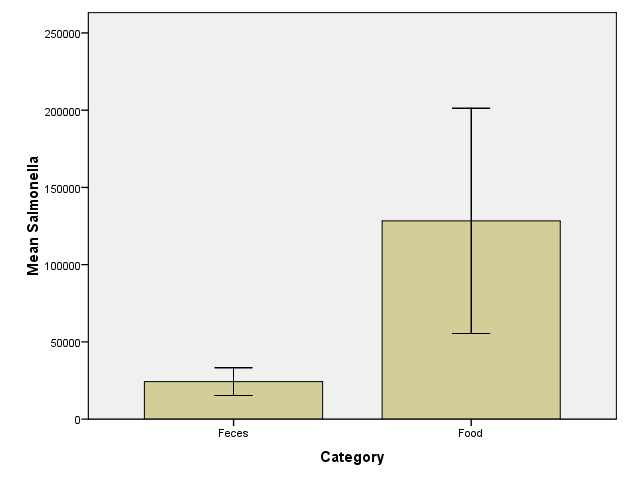


Figure 4.6: The *Salmonella* MPN means comparison according to the source category.

The mean comparison according to the socioeconomic metric (Figure 4.7) shows that the high socioeconomic metric group has higher *Salmonella* MPN than the other two groups, but when tested using one-way ANOVA the difference was not significant.

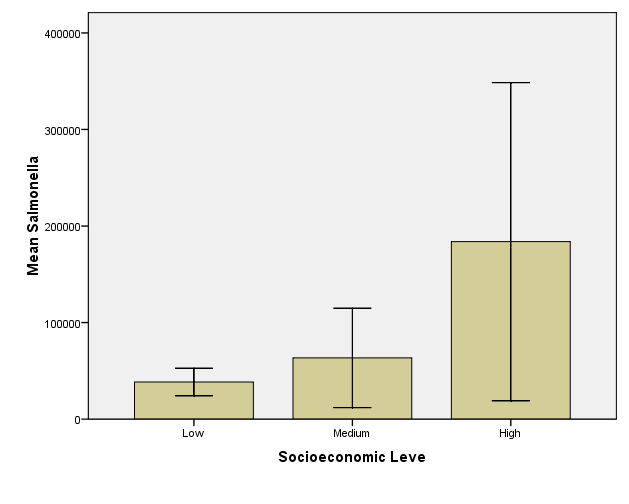


Figure 4.7: The *Salmonella* MPN mean comparison according to the socioeconomic metric.

* + - 1. ***Salmonella* Colony Isolation:**

This section shows the results of the microbiology work for isolating a reference sample of *Salmonella,* and the testing of the MSW samples on the XLD agar media, not for generating numbers of *Salmonella,* but for confirmation of the *Salmonella* existence in the MSW and also to isolate pure colonies of *Salmonella* for molecular work.

* + - * 1. ***Salmonella* Positive Control:**

XLD agar was validated for use on the MSW samples by plating a known sample of *Salmonella*. The sample used for testing the XLD media was a reference sample of *S.enterica* serovar Newport, which was kindly provided by the Central Laboratory of Public Health in Ramallah. The growth of the *Salmonella* on XLD media is known to be indicated by colonies with black centers. Figure 4.8 shows the positive growth of the sample.

|  |  |
| --- | --- |
| **Figure 4.8: The positive control: *S.enterica* serovar Newport on an XLD plate.** |  |

* + - * 1. **MSW on XLD Media and Isolation *Salmonella* from MSW:**

After testing the XLD medium using the positive *Salmonella* strain *S.enterica* serovar Newport and negative control (*E.coli DH5α*), XLD plates were used to test the MSW to confirm the existence of *Salmonella,* which was previously indicated by the RapidChek® SELECT™ *Salmonella* method, and also to isolate pure colonies of *Salmonella*.

**Testing the MSW Samples on XLD Medium**

The samples from the MSW, which had been stored at -80°C, failed to show growth of *Salmonella* when plated directly on XLD plates. The bacterial growth that was recorded, based upon morphology and color, varied between *E.coli, Shigella*, and other types of bacteria such as *Enterobacter/Klebsiella*. As previously mentioned, the indicator of *E.coli* growth is yellow colonies and the change in the medium color to yellow, while *Salmonella* growth is indicated by black centers of the transparent red colonies with no change in the medium color. The *Shigella* growth indicator is red colonies, while the *Enterobacter/Klebsiella* growth indicator is yellow mucoid colonies. Table 4.14 shows the description of colonies, along with bacterial type concluded from examination of the plates in Figure 4.9 from both feces and food samples, and the origin of the MSW samples.

Table 4.14: The result of the bacterial growth on the XLD media plates.

|  |  |  |  |
| --- | --- | --- | --- |
| Serial | Sample description | Colony description | Bacteria |
| A | MSW2011/**Dura**/feces | Large flat yellow growth, and some red colonies | *E.coli and Shigella* spp. |
| B | MSW2011/**Dura**/food | Large flat yellow growth, and some red colonies | *E.coli and Shigella* spp. |
| C | MSW2011/**Hebron**/feces | Large flat yellow growth | *E.coli* |
| D | MSW2011/**Hebron**/food | Large flat yellow growth | *E.coli* |
| E | MSW2011/**B.Umar**/feces | Large flat yellow growth, and some red colonies | *E.coli and Shigella* spp. |
| F | MSW2011/**B.Umar**/food | Large flat yellow growth, and some red colonies | *E.coli and Shigella* spp. |
| G | MSW2011/**B.Sahour**/feces | Large flat yellow growth, and some mucoid colonies | *E.coli and Enterobacter/Klebsiella* |
| H | MSW2011/**B.Sahour**/food | Large flat yellow growth, and some mucoid colonies | *E.coli and Enterobacter/Klebsiella* |
| I | MSW2011/**Batir**/food | Large flat yellow growth, and some mucoid colonies | *E.coli and Enterobacter/Klebsiella* |
| J | MSW2011/**Batir**/feces | Large flat yellow growth, and some mucoid colonies | *E.coli and Enterobacter/Klebsiella* |
| K | MSW2011/**B.Fajar**/feces | Large flat yellow growth, red and some mucoid colonies | *E.coli, Shigella and Enterobacter/Klebsiella* |
| L | MSW2011/**B.Fajar**/food | Large flat yellow growth, red and some mucoid colonies | *E.coli, Shigella and Enterobacter/Klebsiella* |

|  |  |  |
| --- | --- | --- |
| C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FC 3.jpg | C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FD 3.jpg | FC4.jpg |
| C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FD4.jpg | C:\Users\DELL\Desktop\maryam\Salmonella culture pictures\FC5.JPG | C:\Users\DELL\Desktop\maryam\Salmonella culture pictures\FD5.JPG |
| C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FC7.jpg | C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FD7.jpg | C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FC8.jpg |
| C:\Users\DELL\Desktop\maryam\Salmonella culture pictures\FD8.JPG | C:\Users\DELL\Desktop\maryam\PICTURES THESIS\FC9.jpg | C:\Users\DELL\Desktop\maryam\Salmonella culture pictures\FD9.JPG |
| **Figure 4.9: The plates of the MSW food and feces samples from the different locations; A:** MSW2011/**Dura**/feces **shows *E.coli* and *Shigella* growth B:** MSW2011/**Dura**/food **shows growth of *E.coli* and *Shigella*. C:** MSW2011/**Hebron**/feces **shows high growth of *E.coli.* D:** MSW2011/**Hebron**/food **shows high growth of *E.coli.* E:** MSW2011/**B.Umar**/feces **shows growth of *Shigella* and *E.coli*. F:** MSW2011/**B.Umar**/food **shows growth of *Shigella* and *E.coli*. G:** MSW2011/ **B.Sahour**/feces **shows high growth of *E.coli* and suspected of *Enterobacter*/*Klebsiella* H:** MSW2011/**B.Sahour**/food **shows *E.coli* growth and suspected of *Enterobacter*/*Klebsiella* I:** MSW2011/**Batir**/feces **show growth of *E.coli*, suspected E*nterobacter* /*Klebsiella* J:** MSW2011/**Batir**/food **shows growth of *E.coli*, and suspected growth of *Enterobacter*/ *Klebsiella*K:** MSW2011/**B.Fajar**/feces **shows growth of *E.coli, Shigella* and suspected of *Enterobacter*/*Klebsiella*  L:** MSW2011/**B.Fajar**/food **shows growth of *E.coli, Shigella* and suspected of *Enterobacter*/*Klebsiella.*** | | |

**Isolation of *Salmonella* from MSW**

Following the failure of plating MSW samples directly onto XLD agar, an intermediate selection step using TT Hajna media was introduced. Both plating onto TT Hajna agar plates and inoculation with growth in TT Hajna broth was performed. Both methods were successful with subsequent plating on XLD agar. Figure 4.10 shows growth of *Salmonella* on XLD plates from a second round of colony isolation in order to better ensure pure clonal isolates in each case. Note that in addition to *Salmonella*, growth of *E.coli* was also observed.

|  |  |  |
| --- | --- | --- |
| C:\Users\DELL\Desktop\maryam\Thesis\مريم\مريم\fc3.jpg | C:\Users\DELL\Desktop\maryam\Thesis\مريم\مريم\fd3.jpg | C:\Users\DELL\Desktop\maryam\Thesis\مريم\مريم\fc4.jpg |
| C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\fd4.jpg | C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\fc5.jpg | C:\Users\DELL\Desktop\maryam\Thesis\مريم\مريم\fd5.jpg |
| C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\P1010258.JPG | C:\Users\DELL\Desktop\maryam\Thesis\مريم\مريم\fd7.jpg | C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\fc8.jpg |
| C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\fd8.jpg | C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\FC9.jpg | C:\Users\DELL\Desktop\maryam\Thesis\1-7-2012\Fd9.jpg |
| **Figure 4.10: *Salmonella* growth on XLD plates from both food and feces samples originated from the different locations; A:** MSW2011/**Dura**/feces**. B:** MSW2011/**Dura**/food**. C:** MSW2011/**Hebron**/feces***.* D:** MSW2011/**Hebron**/food**. E:** MSW2011/**B.Umar**/feces**. F:** MSW2011/**B.Umar**/food**. G:** MSW2011/**B.Sahour**/feces**. H:** MSW2011/**B.Sahour**/food **I:** MSW2011/**Batir**/feces**. J:** MSW2011/**Batir**/food. K**:** MSW2011/**B.Fajar**/feces. **L:** MSW2011/**B.Fajar**/food. | | |

* 1. **Molecular Detection of *Salmonella* Isolates from MSW**
     1. **PCR Results:**

The PCR was conducted several times to determine the optimal reaction condition for the primers against the reference sample as well as the MSW samples.

* + - 1. **Reference Sample:**

The PCR that was run using the *Salmonella* reference strain, *S.enterica* serovar Newport, gave the expected band of 284 nucleotides for the *invA* primer pair against the reference sample and no band for the negative control (Figure 4.11).

Figure 4.11: The *invA* gene primers result. Neg Cntrl = negative control, Newport = *Salmonella enterica* serovar Newport. The ladder used is pUC18 (*HaeIII* digest) from Sigma Aldrich.

* + - 1. **MSW Samples**

Despite the primers against the reference sample working moderately well, the first few sets of PCR failed (data not shown) before it was realized that isolation of *Salmonella* on selective plates would be required as previously described (see Discussion). The primers were then tested again on the MSW samples after isolation of *Salmonella*.

* + - * 1. **PCR Results of the Isolated *Salmonella***

The PCR with *invA* specific primers for the isolated *Salmonella* was successful as shown in Figure 4.12. The 12 different samples show the expected 284bp band, although sample FC4 was poorly amplified and the negative control in the middle of the gel produced no band.

Figure 4.12: The 1.5% agarose gel of PCR products from six different pairs (food and feces) of MSW samples. M: the marker (pUC 18; Hae III digest). FD9: MSW2011/**B.Fajar**/food, FD8: MSW2011/**Batir**/food, FD7: MSW2011/**B.Sahour**/food, FD5: MSW2011/**B.Umar**/food, FD4: MSW2011/**Hebron**/food, FD3: MSW2011/**Dura**/food, FC9: MSW2011/**B.Fajar**/feces, FC8: MSW2011/**Batir**/feces, FC7: MSW2011/**B.Sahour**/feces, FC5: MSW2011/**B.Umar**/feces, FC4: MSW2011/**Hebron**/feces, FC3: MSW2011/**Dura**/feces.

* + 1. **Sequencing Results**

Two separate sequencing reactions were performed for each gel purified amplicon, once using the PCR forward primer and once the PCR reverse primer. This was done for the reference sample and for eleven of twelve MSW samples.

* + - 1. **The Reference Sample BLAST Result**

The amplicon that gave the band for the reference sample shown in Figure 4.12 was shown to be a perfect match with the *invA* gene of *Salmonella* from the NCBI database, thereby confirming the specificity of the PCR.

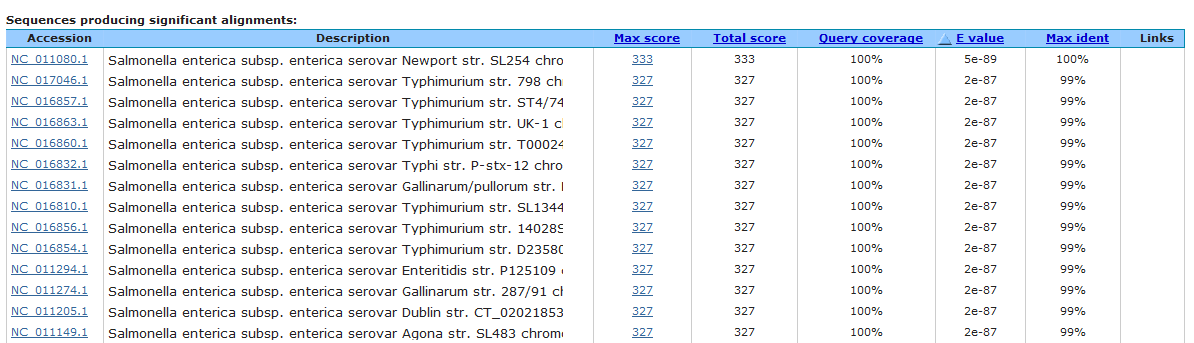
The result of aligning the sequences using BLAST confirmed also that the *Salmonella* serovar used as a reference sample was correct. Figure 4.13 shows that all resulting sequences with significant score were *Salmonella* and the identity was 100% with the *S.enterica* Newport. 

Figure 4.13: The BLAST results of the *S.enterica* Newportthat produced significantalignment.

The BLAST results also confirmed the specificity of the primer toward the *invA* gene. Figure 4.14 illustrates that result.

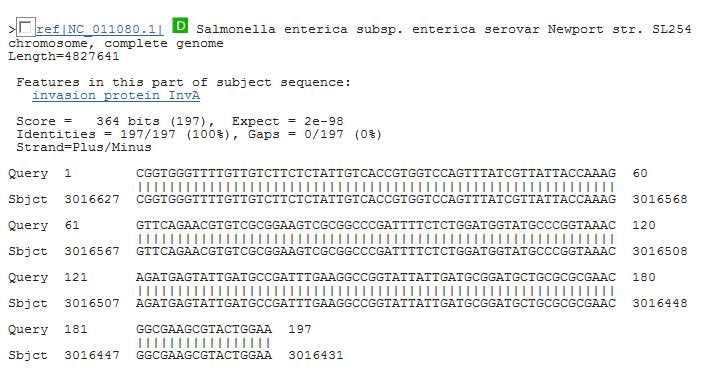


Figure 4.14: Alignment results confirm that the sequence was for the *invA* gene, which was related to Newport serovar.

* + - 1. **The MSW Samples BLAST Results**

The results of sequencing MSW PCR amplicons, shown in Figure 4.12, all produced identical BLAST results; identifying *invA*. The full data of the BLAST are presented in appendix C. The significant alignment results with 100% identity are listed in Table 4.15; the differences among sequences were in *Salmonella* serovars.

Table 4.15: The most significant results of sequencing MSW samples.

|  |  |  |  |
| --- | --- | --- | --- |
| Sample ID | Identity | The highest similarity sequence | The gene name / gene product |
| MSW2011/ **Dura**/feces | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/**B.Umar**/feces | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/**B.Sahour**/feces | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/ **Batir**/feces | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/**B.Fajar**/feces | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/ **Dura**/food | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Newport str. SL254 | invasion protein *invA* |
| MSW2011/ **Hebron**/food | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Newport str. SL254 | invasion protein *invA* |
| MSW2011/**B.Umar**/food | 99% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/**B.Sahour**/food | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/ **Batir**/food | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |
| MSW2011/**B.Fajar**/food | 100% | *Salmonella* *enterica* subsp. *enterica* serovar Heidelberg str. B182 | Type III secretion inner membrane channel protein |

* + - 1. ***Salmonella* Serovars and Their Regional Distribution**

The sequences in appendix D were aligned together and the tree generated from the alignment is shown in (Figure 4.15); the boot strap values are shown in the graph. *Salmonella bongori* sequence was used as an out-group, as it represents a different species of *Salmonella* to the ones found in the MSW.

|  |  |
| --- | --- |
|  | MSW2011/**Dura**/feces  MSW2011/**B.Fajar**/feces  MSW2011/**B.Sahour**/feces  MSW2011/**B.Fajar**/food  MSW2011/**Batir**/feces  MSW2011/**Batir**/food  MSW2011/**B.Umar**/feces  MSW2011/**B.Sahour**/food  MSW2011/**B.Umar**/food  MSW2011/**Dura**/food  MSW2011/**Hebron**/food  *Salmonella bongori* |

Figure 4.15: The UPMGA phylogenic tree for the *Salmonella* sequences using *Salmonella bongori* as an out-group. The main two clades represent the two serovars. Heidleberg with boot strap 71 and Newport with boot strap 93

The graph shows the two main clades, which represent the two main serovars that resulted from the BLAST of the MSW *Salmonella* sequences.

The regional distribution of serovars, displayed in (Figure 4.16), makes it clear that *Salmonella* serovar Heidelberg was widely distributed from north to south of the sampled area in all fecal samples, but, for food waste, it was restricted to samples from the north and east (Batir, Bayt Sahour and Bayt Fajar). *Salmonella* serovar Newport, on the other hand, was absent in all fecal samples and was limited to food samples in the two southern-most areas (Hebron and Dura), while the *Salmonella* from the food sample from Bayt Umar, which is the next northerly sample location along the main north-south route in the West Bank, has an intermediate sequence assignment between the main Heidelberg and Newport clades shown in the phylogenetic tree of Figure 4.15.

Figure 4.16: The geographical distribution of *Salmonella* serovars in food and feces of MSW. The serovar Heidelberg samples that group as a single clade in Figure 4.15 are shown in blue text and blue O, while the samples from the serovar Newport clade are shown in green ▲, and the single sample that is intermediate between the two clades is shown in purple ●.

**CHAPTER 5**

**Discussion**

* 1. **Bacterial Counting for *E.coli* and Coliforms**

The results (Table 4.3) show that the coliforms made up the highest percentage of bacteria, from those counted, in the MSW, and the largest contributor to these is feces, with 44.8%, followed by the toilet paper with 23.3%. This is to be expected, as the coliforms are generally used as a sensitive indicator for fecal contamination of water supplies and food (Bitton, 2005). In this study, the food scraps were the third in order, with 19.3%, but interestingly the food scraps were the highest contributor (80.62%) in a previous study (Gerba. et al., 2011). That study was done on MSW in the U.S. and the much higher contribution of food waste to the proportion of coliforms may reflect the excess wasteage of foods in the U.S. that may provide a rich environment for bacteria to propagate, compared with lower food wastage of Palestinian culture.

It can be inferred from table 4.3 that *E.coli* made up a much higher relative proportion of the bacteria in feces and toilet paper, compared to food, than do the coliforms. This is understood as *E.coli* inhabit the human digestive tract in huge abundance, while the coliforms are a diverse group of bacteria that come from the human digestive system as well as other sources. Indeed, this is one reason that much research is ongoing into identifying the best indicators of fecal contamination as well as correlation of indicator organisms with pathogenicity (Wu et al., 2011), and some are favoring direct estimates of *E.coli* content, rather than coliforms, when checking the environment for possible sources of human fecal contamination (Ferguson et al., 2012).

Statistical hypotheses were used to correlate between the contribution of the bacteria and the socioeconomic metric, and between the contribution and the source. The hypothesis that was accepted correlates with the source, but not with the socioeconomic metric. The lack of correlation between the socioeconomic metric and bacterial quantity may reflect the unsuitability of the metric adopted for this study, that there truly is no meaningful distinction within the sampled area and the nature and bacterial content of the waste being disposed of, or that the low sample size for each of the three socioeconomic levels was insufficient to draw a conclusion from. Considering the 9 sample areas together, however, did allow comparison between local Palestinian MSW and published data on MSW from the U.S. In terms of public health, the lower levels of *E.coli* and coliform contamination in Palestinian food waste, compared to that of U.S. food waste, is encouraging.

* 1. **Bacterial Counting for *Salmonella***

The presence of relatively large amounts of *Salmonella*, however, in most of the food samples is indicative of problems in local food safety, despite the fact that the lowest pathogen percentage was for *Salmonella.* One possible concern in comparing levels of bacterial contamination is that *Salmonella* contamination was counted using a different method (MPN) to that employed for *E.coli* and coliforms (CFU). This was necessitated by the fact that *Salmonella* counting took place after a culturing step, in order to reach a threshold of detection. Nevertheless, although the amount of *Salmonella* in the samples was estimated by a different technique than *E.coli* and coliforms: MPN versus CFU, the two methods of bacterial counting have been shown to be comparable, with any differences being a simple consequence of the probabilistic basis of the MPN method that can lead to greater variability, rather than a skewed representation of bacterial numbers (Gronewold and Wolpert, 2008). The percentage of *Salmonella* was lower than that of *E.coli* and coliforms, but this is little comfort to those concerned with public health, because *E.coli* and coliforms are common enteric bacteria in healthy individuals, while *Salmonella* is an opportunistic pathogen.

Looking at the *Salmonella* numbers by themselves leads to concern about two things. First, high numbers in both studied sources (food and feces with 1.28X105 and 2.43X104 , MPN respectively), and second the widespread finding of *Salmonella* in MSW from all the examined sites and its confirmation by PCR and sequencing in 11 of 12 selected food and feces samples drawn from 6 of the sites. As for the twelfth sample, for which no sequencing data was obtained, it nevertheless gave a positive result by PCR, but the product was simply too weak to be sent for sequencing. That *Salmonella* was so widespread in high numbers, in both food scrapes and feces of local MSW, is a heightened concern when it is considered that *Salmonella* has a great capacity for survival in the environment. Indeed, a previous study showed that *Salmonella* can survive even after 175 days of composting (Gerba. et al., 1995). So if it can survive after composting, then it could more likely survive and grow in large numbers in the solid wastes, and perhaps find its way to the agricultural fields or even to the ground water aquifers, especially that the Yatta landfill site is not lined.

* 1. **Antibiotic Susceptibility Test**

The overall bacterial load is not the only matter of public health and environmental concern. Another factor of worldwide concern, is antibiotic resistance in bacteria, which has been increasing in recent years (Bürgmann et al., 2009). Relaxed prescribing of antibiotics and poor public awareness in Palestine may be expected to correlate with greater antibiotic resistance.

Bacteria, for antibiotic susceptibility testing, were chosen from human waste as a downstream indicator of the level of resistance in the human body, and baby feces from diapers was chosen to represent a sample from a group at greater risk than adults. The antibiotics used were from different groups: ampicillin from the penicillin group, the amoxicillin and clavulanic acid from the β-lactamase inhibitor group, the ciprofloxacin from the flouroquinlones group, nitrofurantoin from the nitrofurantoins group, and from the cephalosporins group: cefoxitin, the second generation and Cefotaxime, ceftriaxon, and ceftazidime from the third generation cephalosporins (CLSI, 2007).

The antibiotic results (Table 4.12) showed that there was no resistance against third generation cephalosporins and minimal resistance (8%) to second generation cephalosporins. This is a cause for hope that the later generations of cephalosporins are still highly effective and indicate that these antibiotics are not being widely misused in infants. At the other end of the generational spectrum of antibiotics it is a matter of concern, but no great surprise, that ampicillin susceptible bacteria accounted for only half of the sampled bacteria. According to one study (Achudume and Olawale, 2009) result might change seasonally with antibiotic resistance for ampicillin being greater in the wet seasons than in the dry seasons. Since samples in this study were collected during Summer, the percentage of ampicillin resistant bacteria may be somewhat higher during Palestinian winters than the results reported here.

The degree of resistance to the combined amoxicillin and clavulanic acid was somewhat lower than ampicillin as expected. Perhaps of greatest concern, however, is the finding that only three quarters of the tested bacteria from baby fecal samples were clearly sensitive to ciprofloxacin, as ciprofloxacin is not recommended to be prescribed for babies except in very limited circumstances.

While the numbers of bacteria tested in this study were relatively small, they do indicate meaningful trends worthy of a large scale study.

**5.3. Confirmation of *Salmonella* inSWby PCR**

Previous studies used the RapidChekTM   *Salmonella* assay to detect confidently *Salmonella* in raw ground chicken, chicken carcass rinse, sliced cooked turkey, and liquid eggs (Muldoon et al., 2009), but the manufacturer has not validated the kit for SW, and for this reason additional confirmation was sought. The first confirmation trial used direct PCR for the previously tested positive samples, and the results were disappointing because no *Salmonella* band appeared after PCR. The results of the above-mentioned Muldoon study (Muldoon et al., 2009) showed that there were no false positives or false negatives in *Salmonella* detection, so the initial failure to detect *Salmonella* by PCR was unexpected and further confirmation of the *Salmonella* by microbiology techniques was sought*.* Generally, isolation of *Salmonella* from samples, such as feces, that contain >107 aerobic bacterial cells/g requires a selective enrichment medium that permits the growth of *Salmonella*, while inhibiting the growth of other aerobic bacteria (Madigan et al., 1997). Then PCR was used to test isolated *Salmonella* from the MSW samples, which delivered positive results.

Using the XLD media directly to detect *Salmonella* showed other types of bacteria instead of *Salmonella.* (Figure 4.8)shows some examples of the detected organisms that appeared instead of *Salmonella*; they were *Shigella, Enterobacter/ Klebsiella.* It is normal to have such variety of bacteria, since the subject of the search is the MSW and these bacteria are part of the coliform bacilli (Guentzel, 1996). Having failed to detect *Salmonella* after direct plating on XLD it was postulated that the *E.coli* load, being 2 logs higher than that of the *Salmonella,* was in some way forming an obstacle. Perhaps, *E coli* metabolites had swamped the media’s capacity to support and detect *Salmonella* metabolism as others have suggested (Chen et al., 1993). Indeed, fermentation of xylose, lactose, and sucrose by *E.coli* generates acidic products that change the media pH to acidic, so *Salmonella* growth would have been inhibited. *Salmonella* metabolism decarboxylates lysine in XLD leading to alkaline conditions, but it seems most likely that this was prevented by an excess of acid production from the fermentation of lactose and sucrose by bacterial competitors (Becton, 2007).

After understanding the likely cause of failure in detecting *Salmonella* directly on the XLD, the next step was to do two selections. The first selection was on the first time prepared TT Hajna agar side by side with TT Hajna broth, and the second was using the grown colonies to be tested on the XLD because it is a differential medium. The TT Hajna was used with agar to make plates, not just as broth, which was a novel application in the hope of observing colonies. The TT Hajna was inhibitory for *E.coli* and other Coliforms*,* while it enriched *Salmonella.*

In *Salmonella* detection procedures, when the TT Hajna was used it was always incubated at 42°C, despite that most studies and media’s manuals indicated that the best temperature is 35±2°C (Difco, 2011). The reason for this innovation is that the *Salmonella* came from MSW samples with high numbers of contaminants (France, 2003). When the samples were plated on the TT Hajna agar first, *Salmonella* could be confirmed later on. Therefore, as expected, using the TT Hajna led to inhibition of *E.coli* by the Tetrathionate while other coliforms and gram-positive organisms were inhibited by the Brilliant green and Sodium desoxycholate. Only the organisms that contain the enzyme tetrathionate reductase could survive (Difco, 2011).

Feces and food were the only categories that were tested for *Salmonella,* because they are the most likely sources for it in the MSW. Feces may commonly have *Salmonella* if obtained from an infected person (De´portes et al., 1998) or food, especially if it has a poultry or meat origin*.*

* 1. **Sequences of *Salmonella* Isolates**

The isolated *Salmonella* from the SW were inferred by sequencing and BLAST searching to be from two different serovars: *Heidelberg* and *Newport*. The more common of the two serovars was the Heidelberg. Both isolated serovars are known to be human pathogens, and have caused several outbreaks in the recent years (CDC, 2012). According to the Centers for Disease Control and Prevention, USA, (Liu et al., 2011) these two serovars are classified amongst the top 9 human *Salmonella* that cause salmonellosis.

The sequences in the raw traces (appendix B) appear to have more variation than when they were aligned (appendix D). This is because the alignment is based on a consensus sequence, which was generated from both the forward and reverse primers using the SEQUENCHER program. In addition to not accepting the SEQUENCHER results blindly, it should be mentioned that the BLAST alignment ignored some sequence diversity at the ends of some of the aligned sequences. Nevertheless, the BLAST alignment (appendix D) was accepted as the very ends of the alignments are less reliable than core parts of the sequences and they lack confirmation by the complementary sequencing reaction.

In the MSW2011/B.Sahur/food sequence in (appendix B) there is an (A) insertion in the forward sequence but not in the reverse. SEQUENCHER built this insertion in its alignment, but it would likely be a lethal mutation if it were really there as it would shift the reading frame. After investigation of the forward and the reverse sequences, it becomes obvious that the forward sequence is weak in this region. Therefore, the (A) insertion was manually edited out of the SEQUENCHER consensus sequence on the basis that the apparent insertion was simply an error in the forward sequencing reaction.

* 1. ***Salmonella* Serovars Regional Distribution**

The phylogenetic tree (Figure 4.15) and the geographical distribution (Figure 4.16.) demonstrate that there is a geographical correlation between *Salmonella* sequences in the food waste. *Salmonella* serovar Newport was found in food from the south and *Salmonella* serovar Heidelberg was found in the food waste from the north, with food waste from Bayt Umar, which is intermediate between the northern and southern parts of the sample range, having an intermediate location on the phylogenetic tree. In order to understand the implication of these data, it helps to ask, what are the factors that support *Salmonella* presence in food and feces? All the feces samples studied contained serovar Heidelberg, and so it would seem that serovar Heidelberg is more entrenched within the sample range than is serovar Newport. *Salmonella* found in feces demonstrates adaptation and survival in humans, while its presence in food demonstrates risk to humans, and not necessarily infection. It is suggested, therefore, that serovar Heidelberg is widespread in the human population as the dominant serovar, and that it has either been present for a long time, or the area was experiencing an acute outbreak in the summer of 2011 when the samples were collected. Serovar Newport appears to have been a contaminant of food at that time, but its lack of representation in the sequenced food samples from the north indicates that either it was not able to compete with Heidelberg in the human population, or was a very recent newcomer to the region. Its small range in the very south of the region indicates that it is a newcomer, while the existence of an intermediate sequence at a half way point between the south and north allows for the possibility that it has been present for long enough for genetic recombination to take place between Newport and Heidelberg in the sample range. The sectional analysis below (Figure 5.1) shows the locations of the three mutations within the sequenced region of the *invA* gene that distinguish serovar Heidelberg from Newport, and also shows that the food sample from Bayt Umar is identical to the Heidelberg sequence at nucleotides 1525 and 1555, while it is identical to the sequence of Newport at nucleotide 1654, which is the basis for speculation that recombination may have occurred here between nucleotide 1555 and 1654 within the *invA* gene of the food sample from Bayt Umar. With data available, however, it cannot be known with any certainty, whether the isolated sequence found in Bayt Umar’s food waste was indeed the result of recombination, or arose due to another mechanism.

Figure 5.1: Schematic representation from the start of the *Salmonella* *invA* gene to its end at nucleotide 2058. Forward (FP) and reverse (RP) primer locations are shown and the sequenced region between them is shaded. The three sites within the sequenced region, where serovar Heidelberg (blue) and Newport (green) can be differentiated, are shown (\*) with the specific nucleotides for serovar Heidelberg and Newport also given above and below the schematic respectively.

**CHAPTER 6**

**Conclusions**

* *Public health concerns are raised by this study.*
  1. *Salmonella* was detected in high numbers from both of the tested source types; feces and food. The presence of *Salmonella* throughout the widely separated and distinct Hebron and Bethlehem regions, that were tested, was of particular concern.
  2. The two serovars of *Salmonella* were *Newport* and *Heidelberg*, and both are foodbornes. They are amongst the top nine human *Salmonella* that cause salmonellosis, according to the Centers for Disease Control and Prevention, and their presence in food, rather than any of the many hundreds of other less harmful serovars indicates a need for better food safety surveillance in Palestine.

* 1. The antibacterial results showed a high percent of ampicillin resistant bacteria in the MSW and intermediate percent of ciprofloxacin comparing both with the Cephalosporin’s group.
* The difficulty in isolating *Salmonella* from SW during this research, led to the development of a successful sequential isolation procedure. It is concluded, therefore, that other researchers are likely underestimating the *Salmonella* content when studying *Salmonella* from highly contaminated sources.
* The statistical results correlate between the bacterial count and the source, but fail to support a relationship between the bacterial count and the socioeconomic metric.
* The RapidCheck assay was demonstrated to give 100% correlation with the subsequent *Salmonella* specific PCR and is thereby validated as specific for *Salmonella* in MSW.

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**Appendix A**

***Salmonella* Sequences:**

>Newport

CGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGTGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCTGCGCGCGAACGGCGAAGCGTACTGGAA

> MSW2011/**Dura**/feces

TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**B.Umar**/feces

TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**B.Sahour**/feces

TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACGG

> MSW2011/**Batir**/feces

TTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**B.Fajar**/feces

ATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACGTGGC

> MSW2011/**Dura**/food

CGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGTGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCTGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGCCAGCTTTACGGTTCCTTTGACGG

> MSW2011/**Hebron**/food

AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGTGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCTGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGCCAGCTTTACGGTTCCTTTGACGGG

> MSW2011/**B.Umar**/food

AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**B.Sahour**/food

AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**Batir**/food

ATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGGGTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACCAAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGGTATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTATTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGCCAGCTTTACGGTTCCTTTGACG

> MSW2011/**B.Fajar**/food

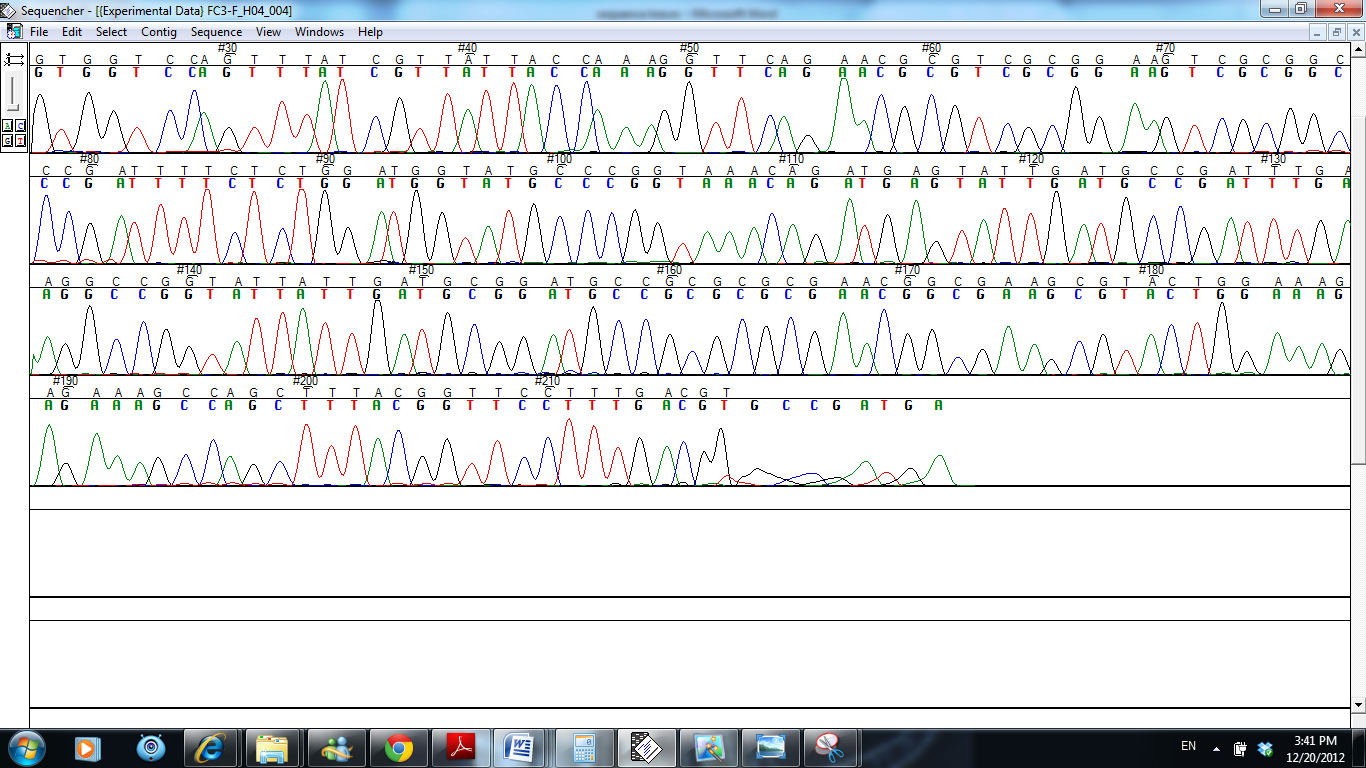
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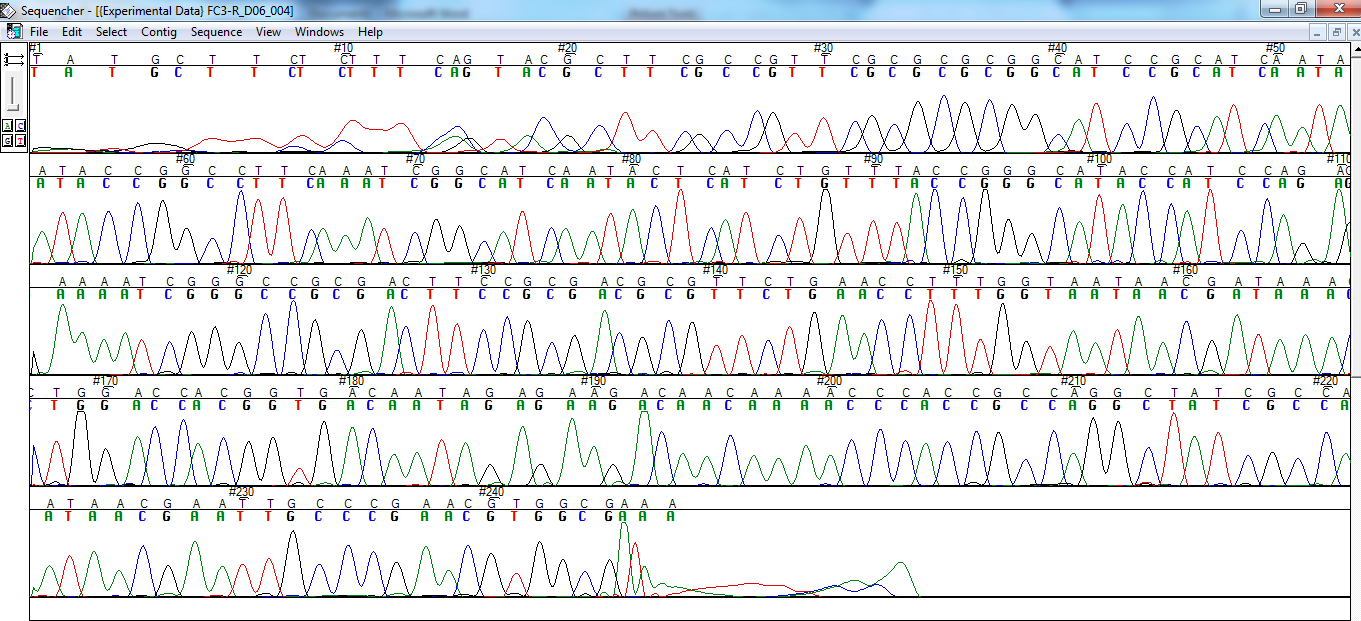
>*Salmonella* bongori

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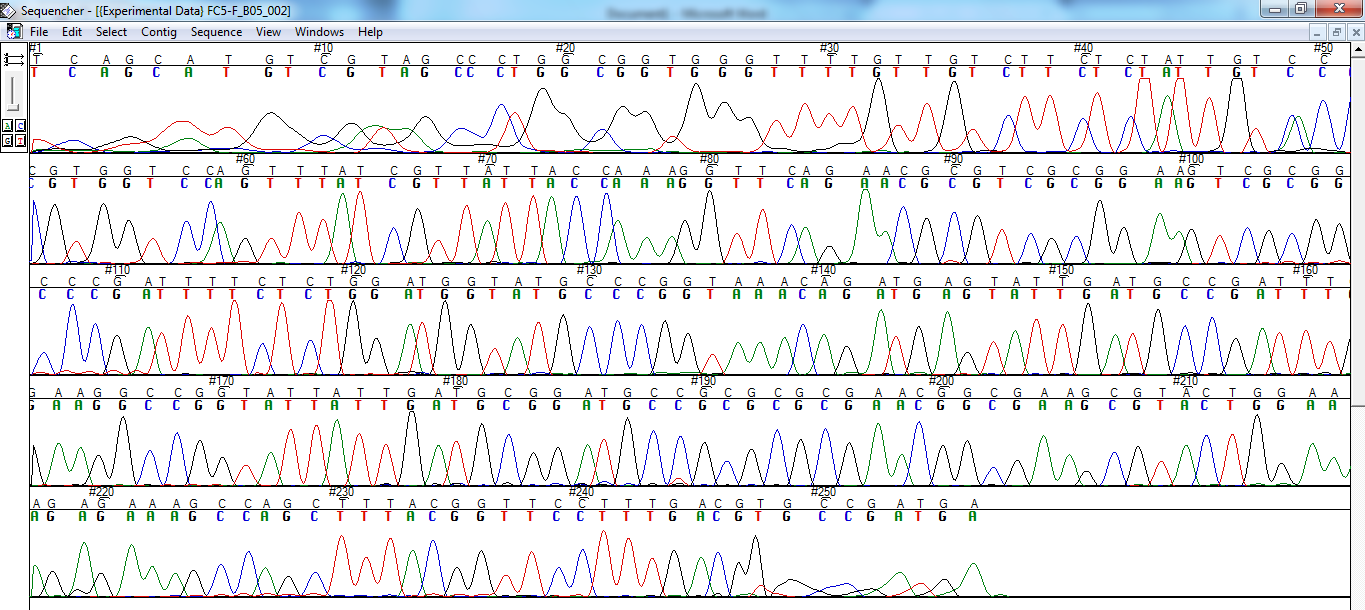
**Appendix B:**

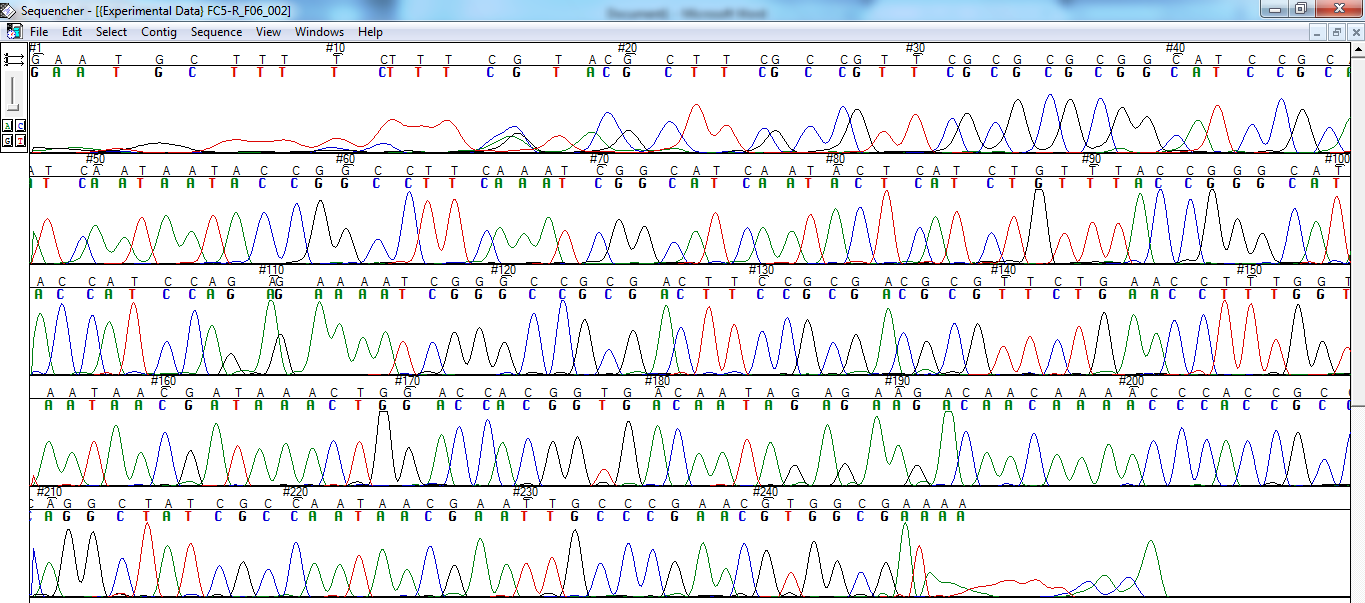
MSW2011/**Dura**/feces Forward & Reverse



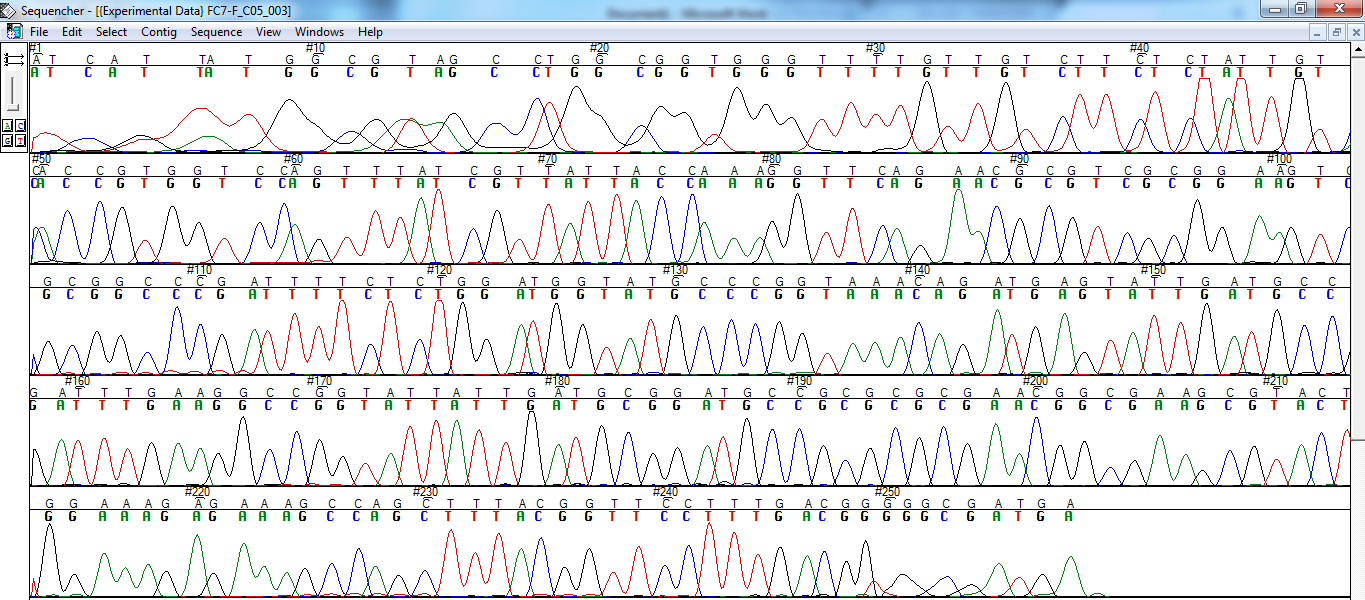


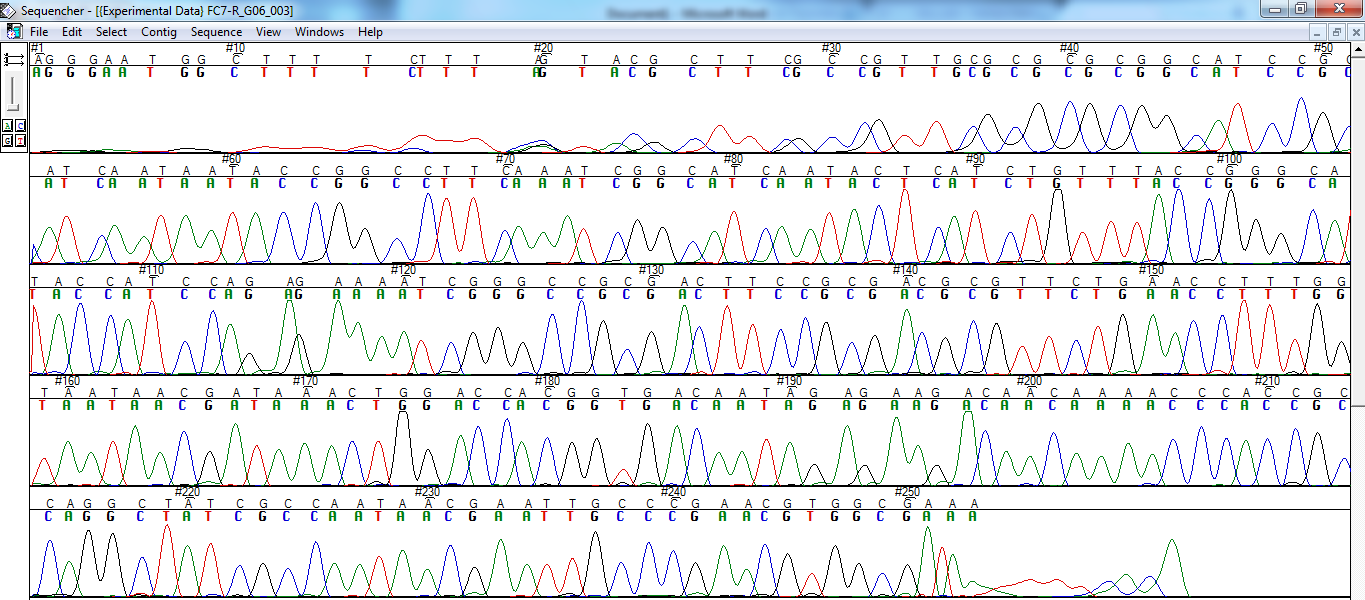
MSW2011/**B.Umar**/feces Forward & Reverse



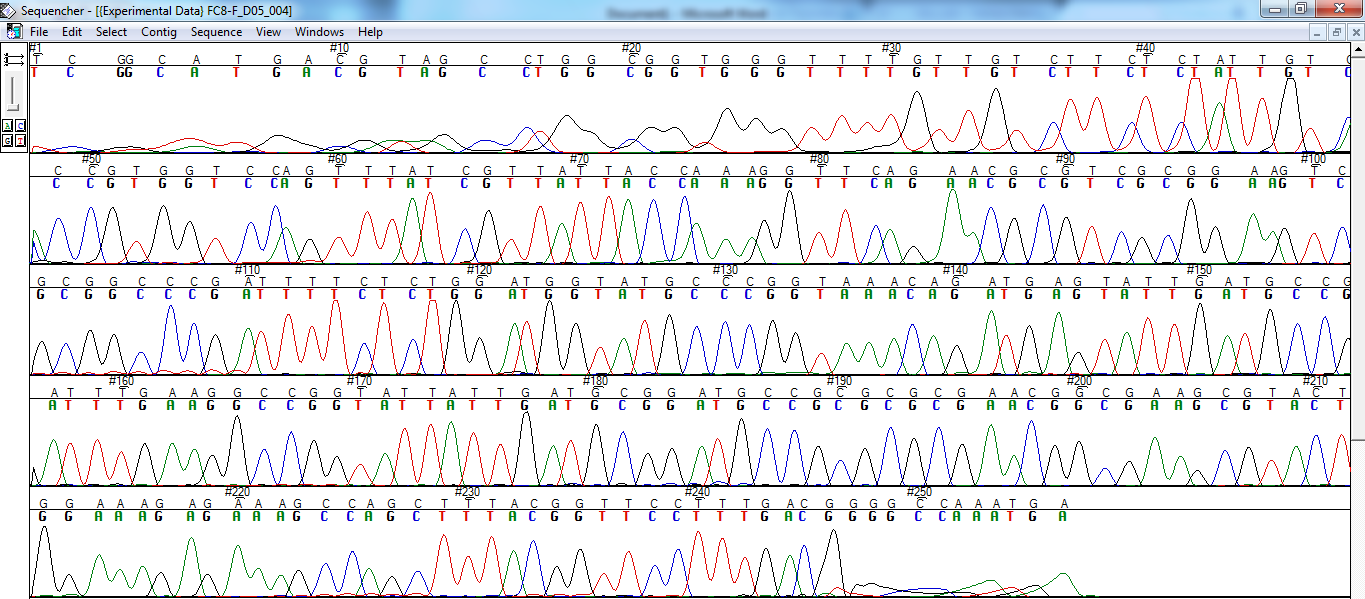


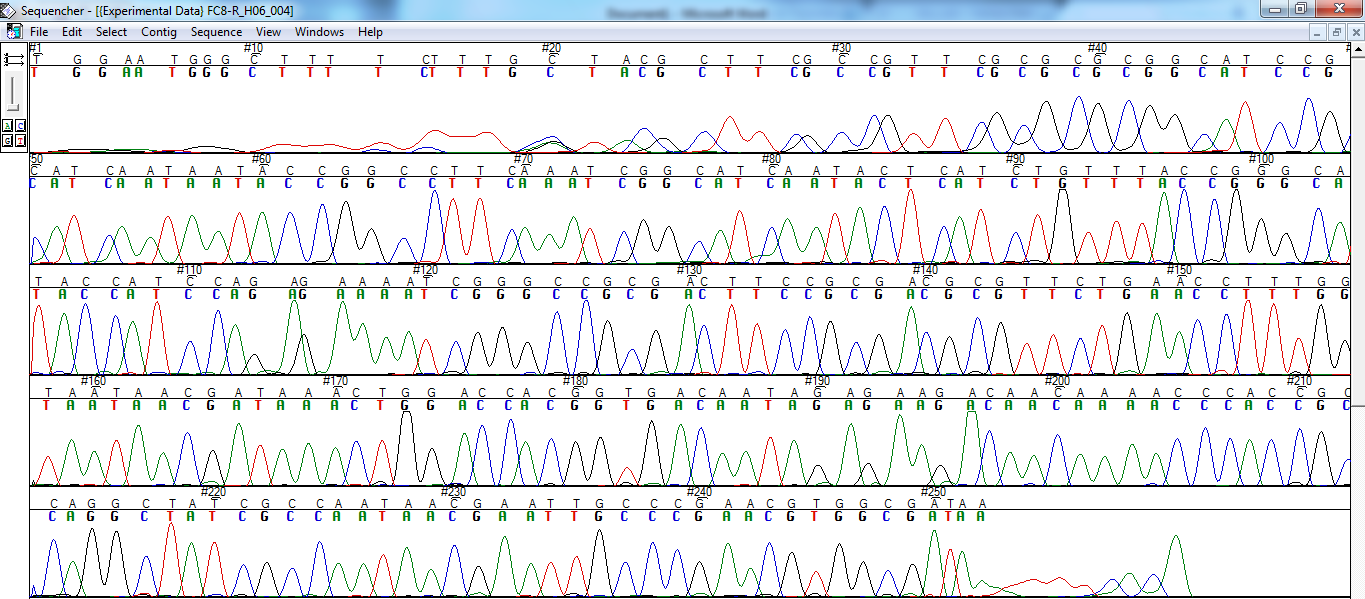
MSW2011/**B.Sahour**/feces Forward & Reverse



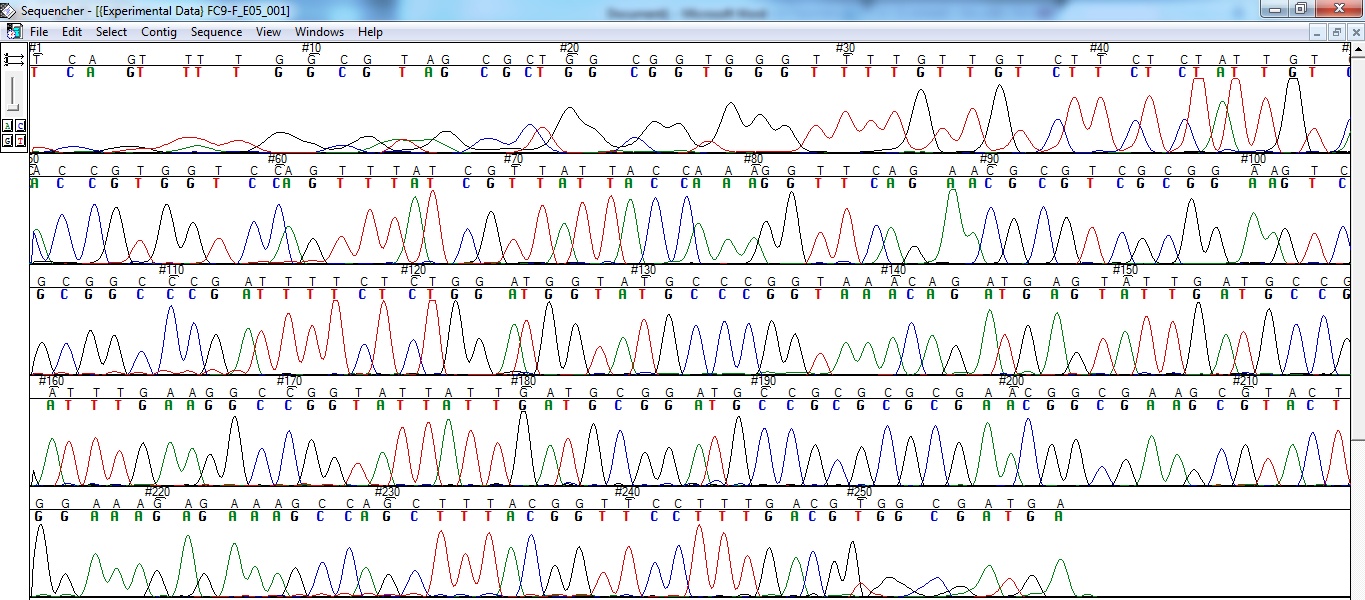


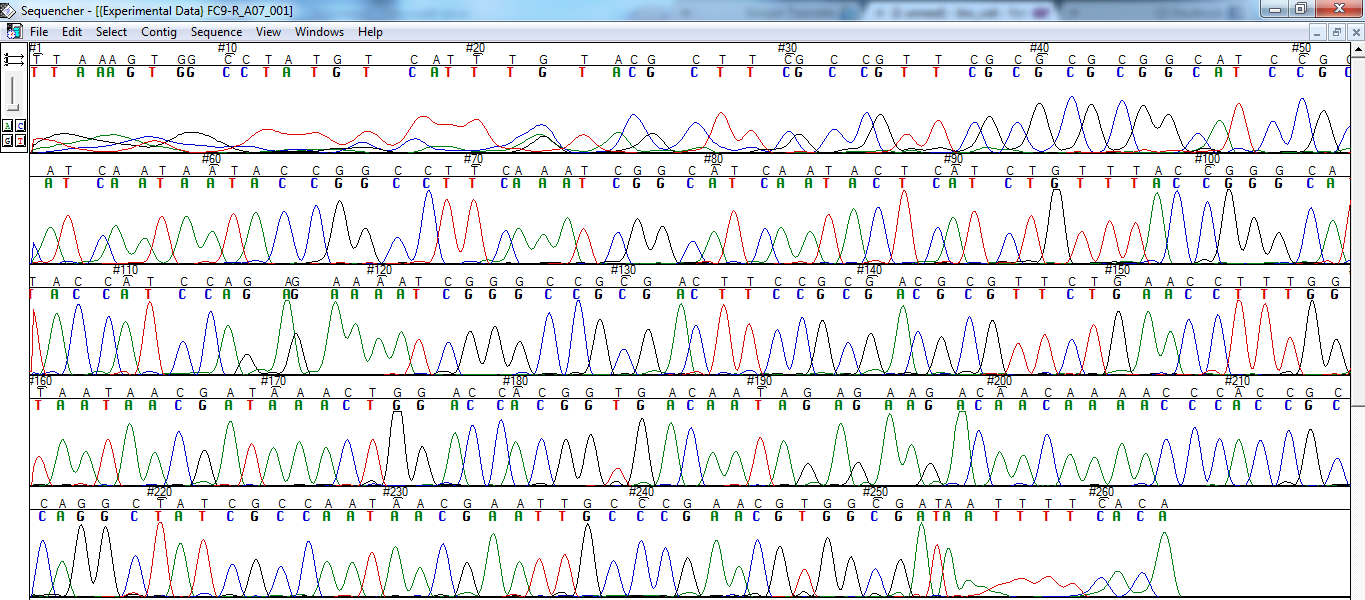
MSW2011/**Batir**/feces Forward & Reverse



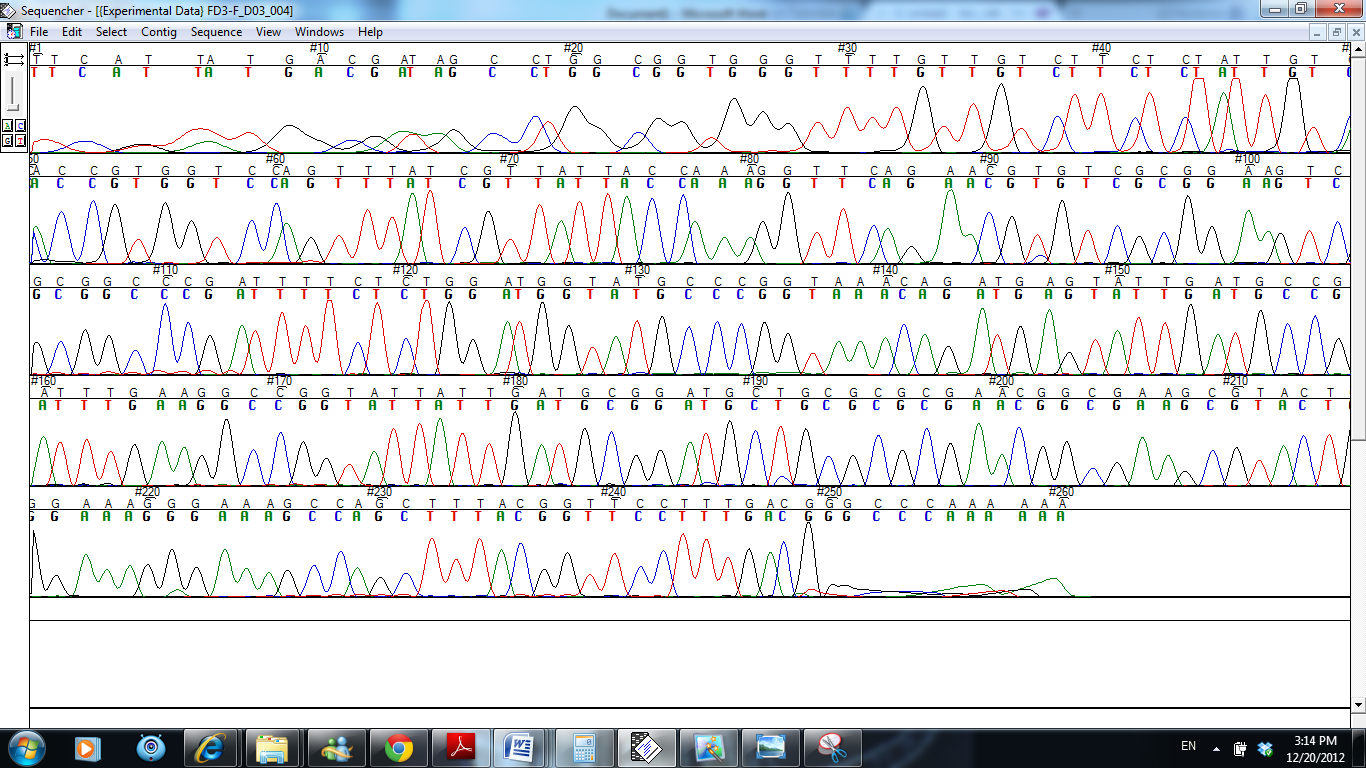


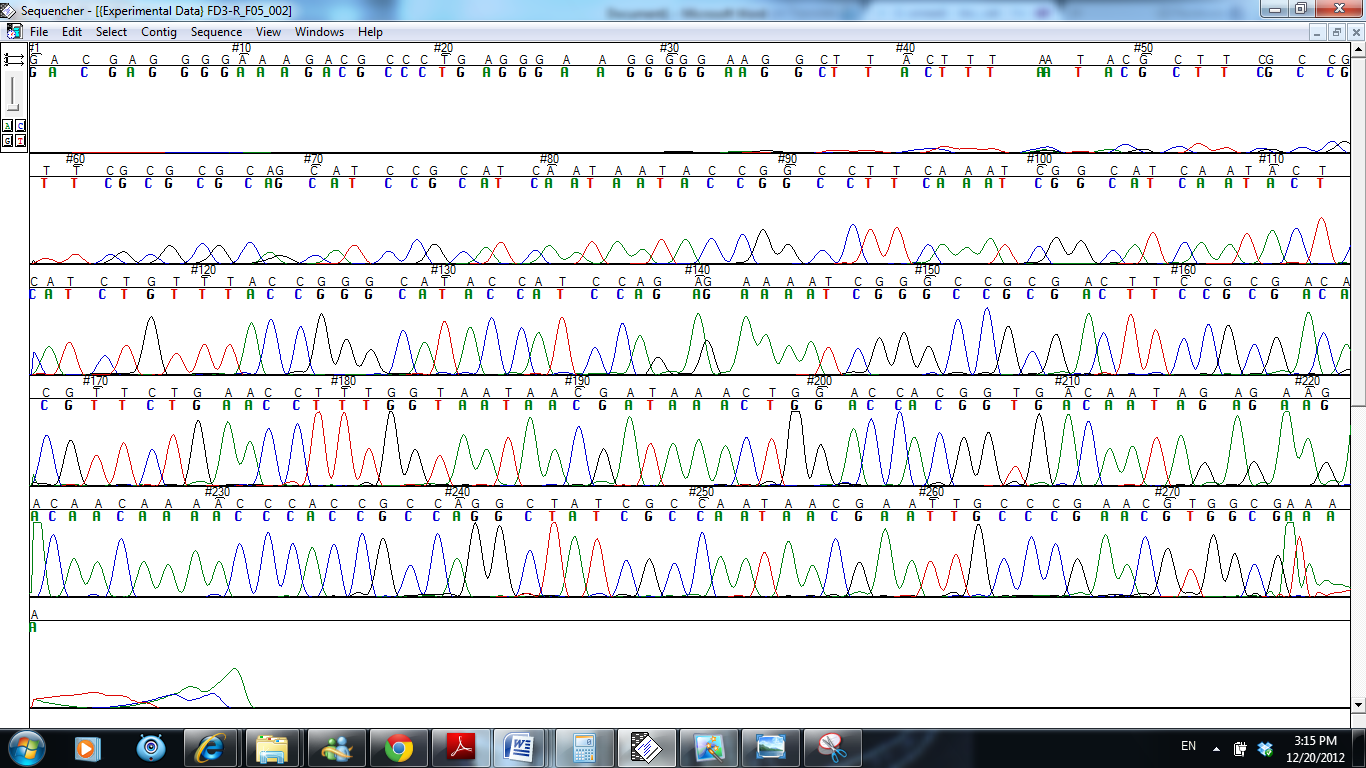
MSW2011/**B.Fajar** /feces Forward & Reverse



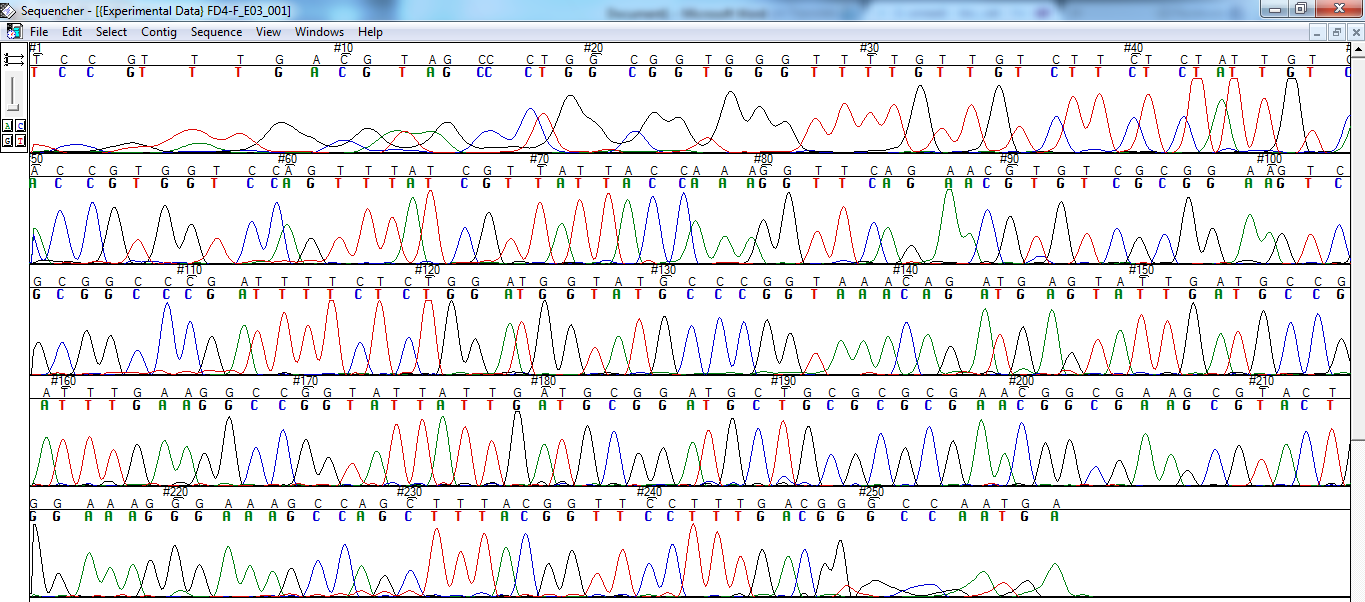


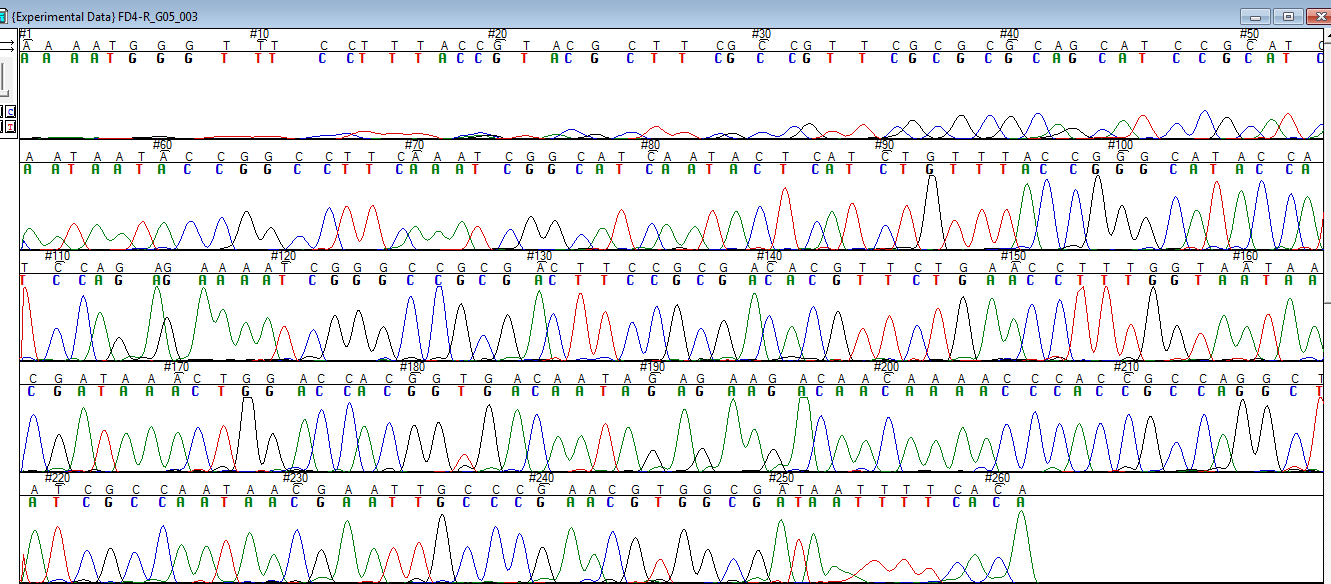
MSW2011/**Dura**/food Forward & Reverse



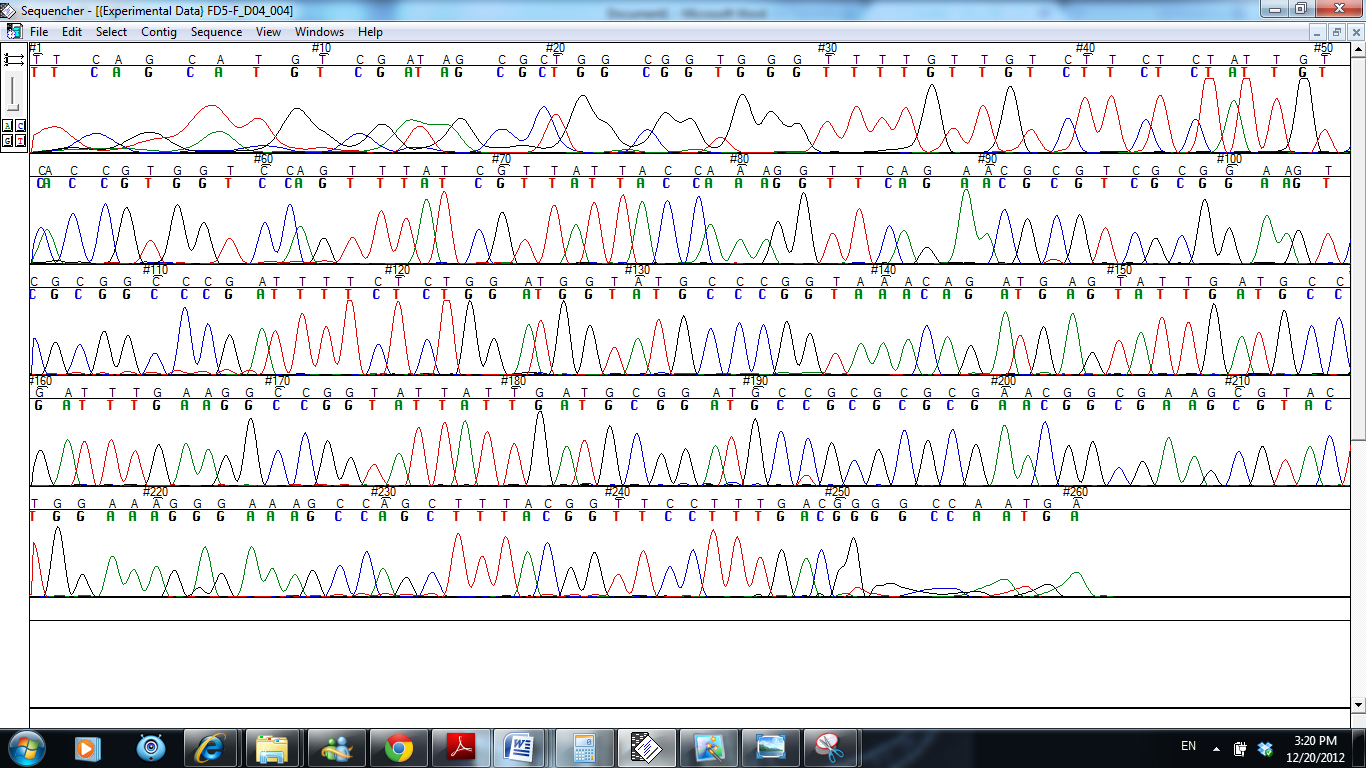


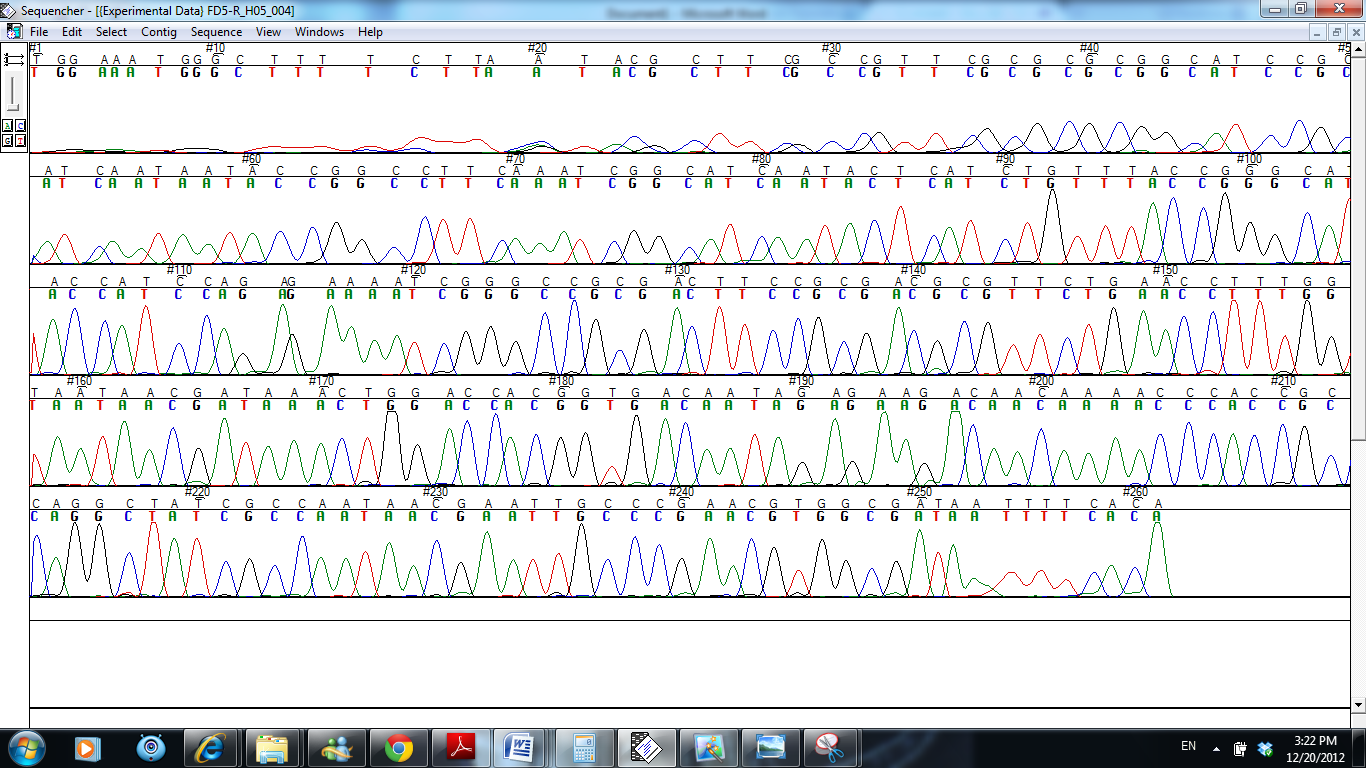
MSW2011/**Hebron**/food Forward & Reverse



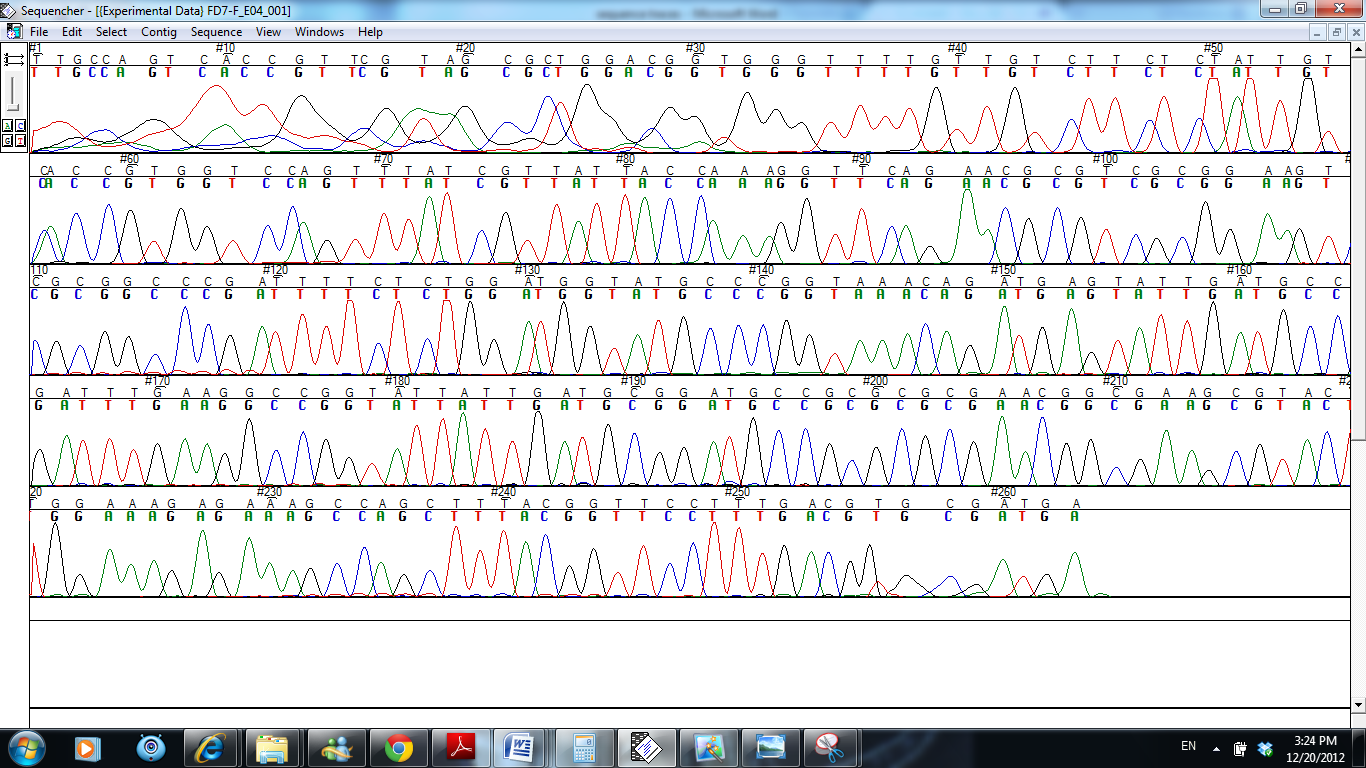


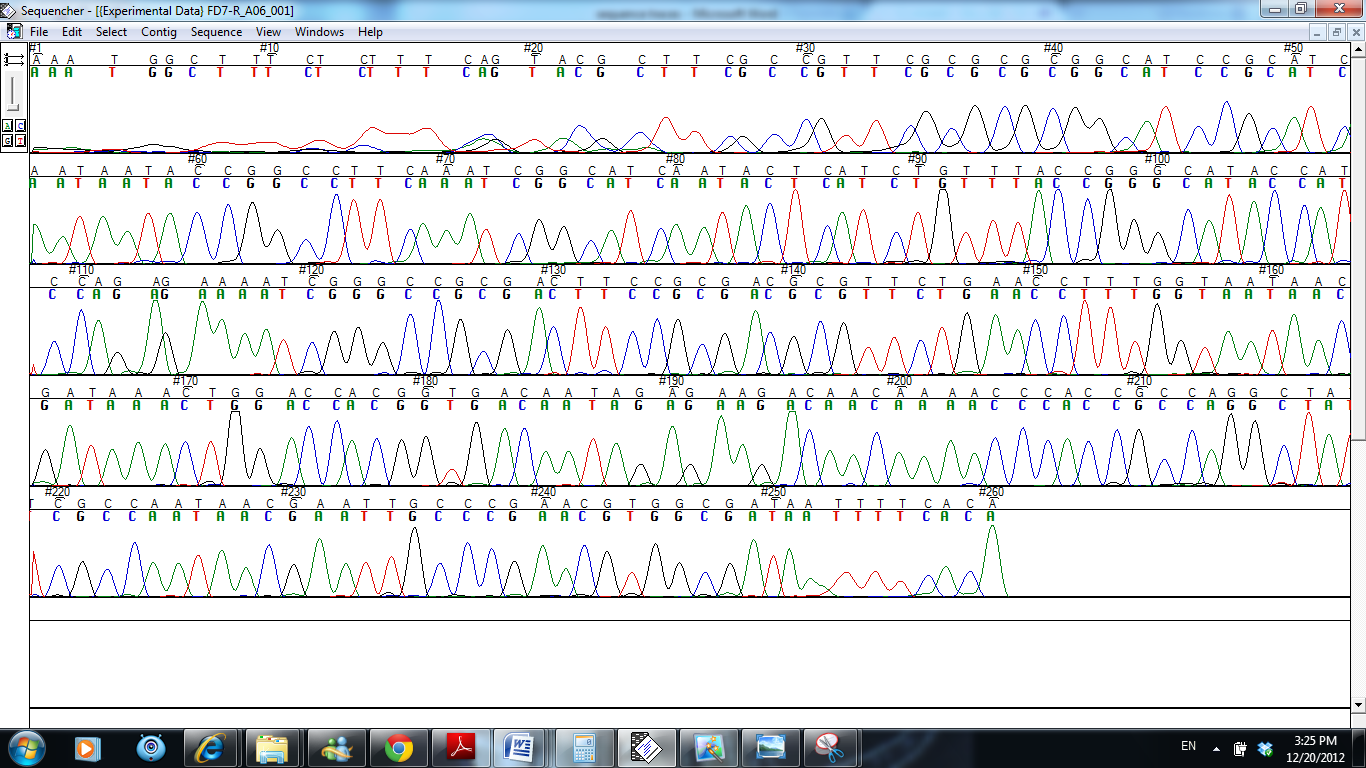
MSW2011/**B.Umar**/food Forward & Reverse



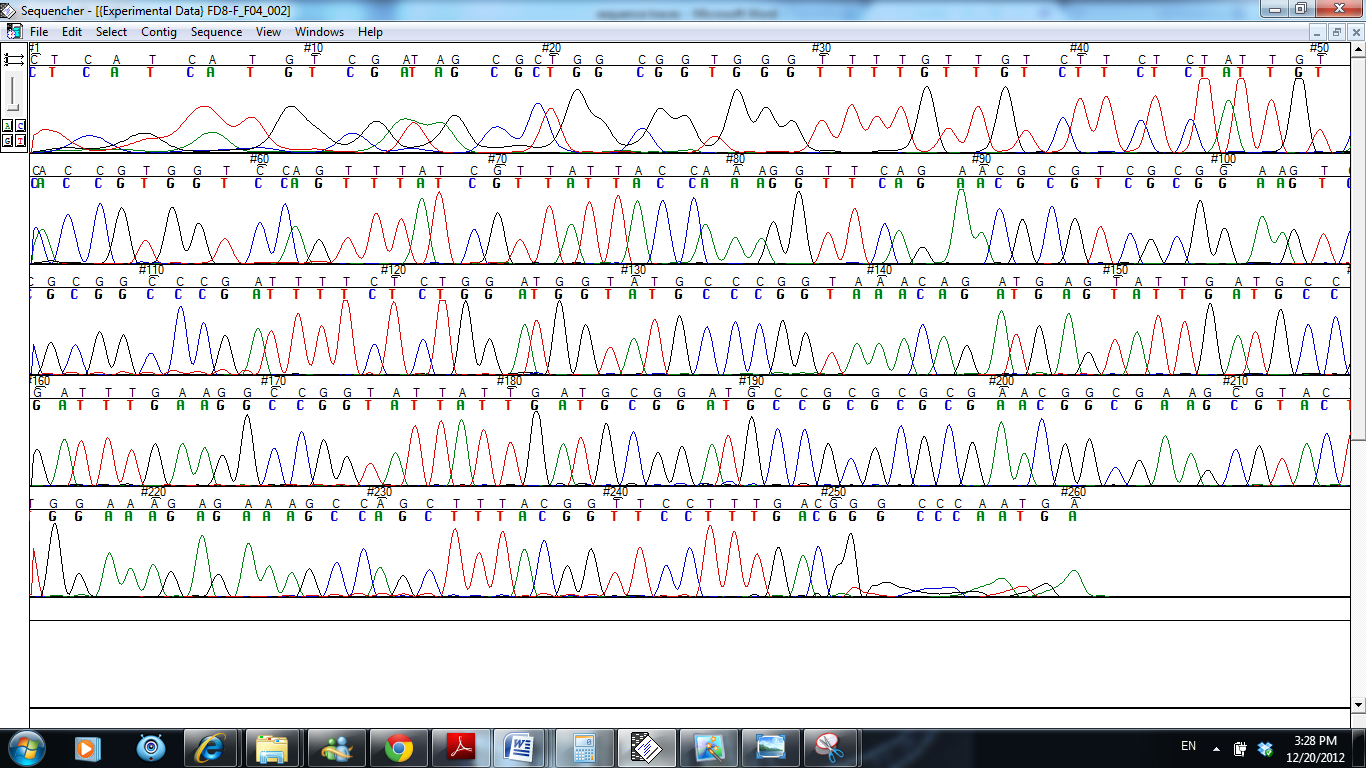


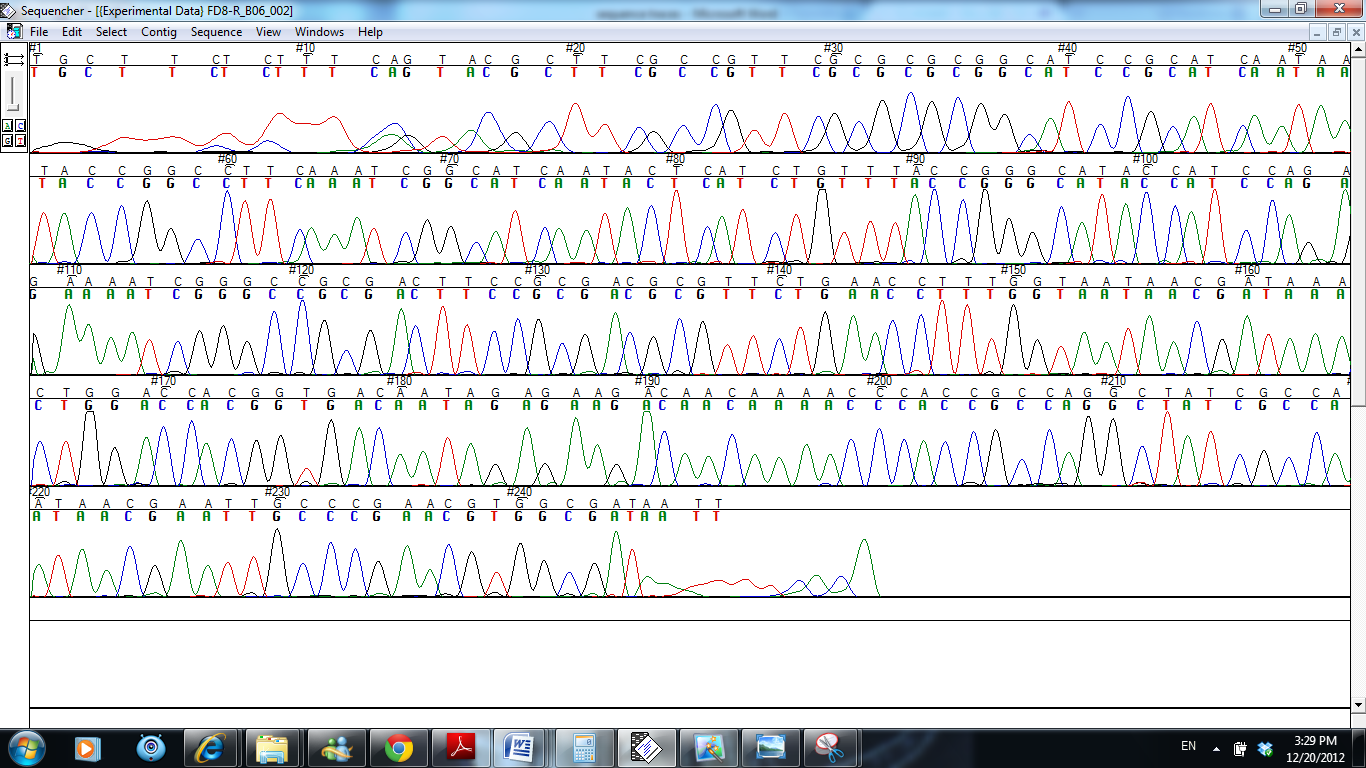
MSW2011/**B.Sahour**/food Forward & Reverse



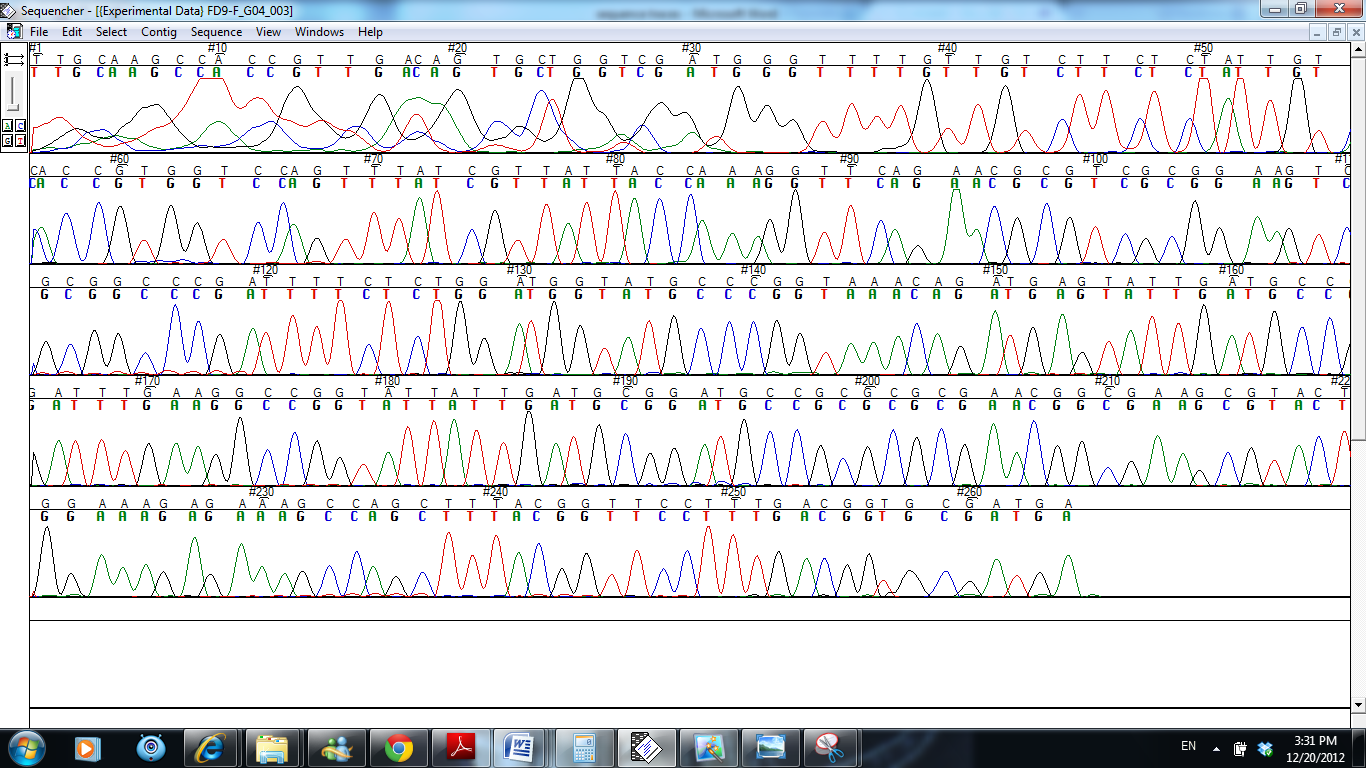


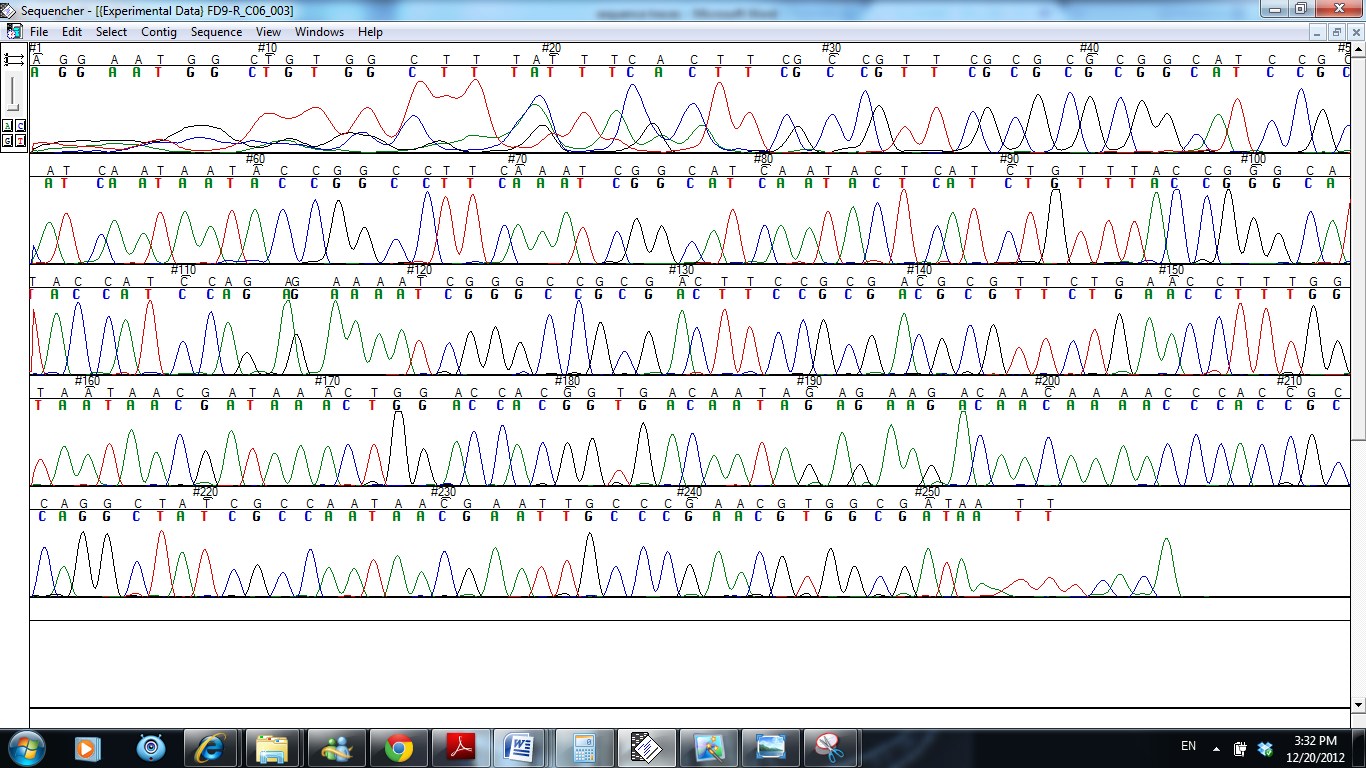
MSW2011/**Batir**/food Forward & Reverse





MSW2011/**B.Fajar**/food Forward & Reverse





**Appendix C**

**BLAST Tables**

| Sequences producing significant alignments for Newport reference sample: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CTZ8N08N01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CTZ8N08N01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CTZ8N08N01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CTZ8N08N01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CTZ8N08N01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) | Links |
| [NC\_011080.1](http://www.ncbi.nlm.nih.gov/nucleotide/194442203?report=genbank&log$=nucltop&blast_rank=1&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Newport str. SL254 chromosome, complete genome | [364](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194442203) | 364 | 100% | 3e-98 | 100% |  |
| [CP001113.1](http://www.ncbi.nlm.nih.gov/nucleotide/194400866?report=genbank&log$=nucltop&blast_rank=2&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Newport str. SL254, complete genome | [364](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194400866) | 364 | 100% | 3e-98 | 100% |  |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=3&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=4&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=5&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=6&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=7&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=8&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=9&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 359 | 100% | 2e-96 | 99% |  |
| [NC\_016856.1](http://www.ncbi.nlm.nih.gov/nucleotide/378448274?report=genbank&log$=nucltop&blast_rank=10&RID=CTZ8N08N01R) | *Salmonella* enterica subsp. enterica serovar Typhimurium str. 14028S chromosome, complete genome | [359](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378448274) | 359 | 100% | 2e-96 | 99% |  |

| Sequences producing significant alignments for MSW2011/**Dura**/feces Sample: | | | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDPH7YD01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDPH7YD01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDPH7YD01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDPH7YD01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDPH7YD01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=BUDPH7YD01R) | *Salmonella* enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 494 | 100% | 3e-137 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 494 | 100% | 3e-137 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 494 | 100% | 3e-137 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 483 | 100% | 7e-134 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 483 | 100% | 7e-134 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 483 | 100% | 7e-134 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 483 | 100% | 7e-134 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 483 | 100% | 7e-134 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Gallinarum/ pullorum str. RKS5078 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 483 | 100% | 7e-134 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 483 | 100% | 7e-134 | 99% |
| [NC\_016856.1](http://www.ncbi.nlm.nih.gov/nucleotide/378448274?report=genbank&log$=nucltop&blast_rank=11&RID=BUDPH7YD01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378448274) | 483 | 100% | 7e-134 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Umar**/feces Sample: | | | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDMPP1X01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDMPP1X01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDMPP1X01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDMPP1X01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUDMPP1X01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 494 | 100% | 3e-137 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 494 | 100% | 3e-137 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 494 | 100% | 3e-137 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 483 | 100% | 7e-134 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 483 | 100% | 7e-134 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 483 | 100% | 7e-134 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 483 | 100% | 7e-134 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 483 | 100% | 7e-134 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 483 | 100% | 7e-134 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=BUDMPP1X01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [483](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 483 | 100% | 7e-134 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Sahour**/feces: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUD4ZJSE01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUD4ZJSE01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUD4ZJSE01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUD4ZJSE01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=BUD4ZJSE01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 496 | 100% | 9e-138 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 496 | 100% | 9e-138 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 496 | 100% | 9e-138 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 484 | 100% | 2e-134 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 484 | 100% | 2e-134 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 484 | 100% | 2e-134 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 484 | 100% | 2e-134 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 484 | 100% | 2e-134 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 484 | 100% | 2e-134 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=BUD4ZJSE01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 484 | 100% | 2e-134 | 99% |

| Sequences producing significant alignments for MSW2011/**Batir**/feces: | | | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2V8MDS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2V8MDS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2V8MDS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2V8MDS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2V8MDS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 499 | 100% | 7e-139 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 499 | 100% | 7e-139 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 499 | 100% | 7e-139 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 488 | 100% | 2e-135 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 488 | 100% | 2e-135 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 488 | 100% | 2e-135 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 488 | 100% | 2e-135 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 488 | 100% | 2e-135 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 488 | 100% | 2e-135 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=CD2V8MDS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 488 | 100% | 2e-135 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Fajar**/feces: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD38H0CJ014&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD38H0CJ014&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD38H0CJ014&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD38H0CJ014&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD38H0CJ014&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 496 | 100% | 9e-138 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 496 | 100% | 9e-138 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 496 | 100% | 9e-138 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 484 | 100% | 2e-134 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 484 | 100% | 2e-134 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 484 | 100% | 2e-134 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 484 | 100% | 2e-134 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 484 | 100% | 2e-134 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Gallinarum/ pullorum str. RKS5078 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 484 | 100% | 2e-134 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=CD38H0CJ014) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 484 | 100% | 2e-134 | 99% |

| Sequences producing significant alignments for MSW2011/**Dura**/food: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2WJ65H01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2WJ65H01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2WJ65H01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2WJ65H01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2WJ65H01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_011080.1](http://www.ncbi.nlm.nih.gov/nucleotide/194442203?report=genbank&log$=nucltop&blast_rank=1&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Newport str. SL254 chromosome, complete genome | [494](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194442203) | 494 | 100% | 3e-137 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=2&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 488 | 100% | 2e-135 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=3&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 488 | 100% | 2e-135 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=4&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 488 | 100% | 2e-135 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=5&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 488 | 100% | 2e-135 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=6&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 488 | 100% | 2e-135 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=7&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 488 | 100% | 2e-135 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=8&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 488 | 100% | 2e-135 | 99% |
| [NC\_016856.1](http://www.ncbi.nlm.nih.gov/nucleotide/378448274?report=genbank&log$=nucltop&blast_rank=9&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S chromosome, complete genome | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378448274) | 488 | 100% | 2e-135 | 99% |
| [NC\_016854.1](http://www.ncbi.nlm.nih.gov/nucleotide/378443454?report=genbank&log$=nucltop&blast_rank=10&RID=CD2WJ65H01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 | [488](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378443454) | 488 | 100% | 2e-135 | 99% |

| Sequences producing significant alignments for MSW2011/**Hebron**/food: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD371WCV01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD371WCV01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD371WCV01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD371WCV01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD371WCV01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_011080.1](http://www.ncbi.nlm.nih.gov/nucleotide/194442203?report=genbank&log$=nucltop&blast_rank=1&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Newport str. SL254 chromosome, complete genome | [505](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194442203) | 505 | 100% | 2e-140 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=2&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 499 | 100% | 7e-139 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=3&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 499 | 100% | 7e-139 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=4&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 499 | 100% | 7e-139 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=5&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 499 | 100% | 7e-139 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=6&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 499 | 100% | 7e-139 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=7&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 499 | 100% | 7e-139 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=8&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 499 | 100% | 7e-139 | 99% |
| [NC\_016856.1](http://www.ncbi.nlm.nih.gov/nucleotide/378448274?report=genbank&log$=nucltop&blast_rank=9&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378448274) | 499 | 100% | 7e-139 | 99% |
| [NC\_016854.1](http://www.ncbi.nlm.nih.gov/nucleotide/378443454?report=genbank&log$=nucltop&blast_rank=10&RID=CD371WCV01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378443454) | 499 | 100% | 7e-139 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Umar**/food: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YHC2R01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YHC2R01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YHC2R01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YHC2R01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YHC2R01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 497 | 100% | 3e-138 | 99% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=2&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 497 | 100% | 3e-138 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=3&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 497 | 100% | 3e-138 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=4&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 497 | 100% | 3e-138 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=5&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 497 | 100% | 3e-138 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=6&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 497 | 100% | 3e-138 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=7&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. RKS5078 chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 497 | 100% | 3e-138 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=8&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 497 | 100% | 3e-138 | 99% |
| [NC\_016856.1](http://www.ncbi.nlm.nih.gov/nucleotide/378448274?report=genbank&log$=nucltop&blast_rank=9&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S chromosome, complete genome | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378448274) | 497 | 100% | 3e-138 | 99% |
| [NC\_016854.1](http://www.ncbi.nlm.nih.gov/nucleotide/378443454?report=genbank&log$=nucltop&blast_rank=10&RID=CD2YHC2R01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 | [497](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378443454) | 497 | 100% | 3e-138 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Sahour**/food: | | | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YVJCG01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YVJCG01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YVJCG01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YVJCG01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2YVJCG01R&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | 503 | 503 | 100% | 6e-140 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | 503 | 503 | 100% | 6e-140 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | 503 | 503 | 100% | 6e-140 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Gallinarum/ pullorum str. RKS5078 chromosome, complete genome | 492 | 492 | 100% | 1e-136 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=CD2YVJCG01R) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | 492 | 492 | 100% | 1e-136 | 99% |

| Sequences producing significant alignments for MSW2011/**Batir**/food: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2Z8GCS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2Z8GCS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2Z8GCS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2Z8GCS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2Z8GCS016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 496 | 100% | 9e-138 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 496 | 100% | 9e-138 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [496](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 496 | 100% | 9e-138 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 484 | 100% | 2e-134 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 484 | 100% | 2e-134 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 484 | 100% | 2e-134 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 484 | 100% | 2e-134 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 484 | 100% | 2e-134 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Gallinarum/ pullorum str. RKS5078 chromosome, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 484 | 100% | 2e-134 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=CD2Z8GCS016) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [484](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 484 | 100% | 2e-134 | 99% |

| Sequences producing significant alignments for MSW2011/**B.Fajar**/food: | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | [Max score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2U8EMU016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=1&HSP_SORT=1#sort_mark) | [Total score](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2U8EMU016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=2&HSP_SORT=1#sort_mark) | [Query coverage](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2U8EMU016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=4&HSP_SORT=0#sort_mark) | [E value](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2U8EMU016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=0&HSP_SORT=0#sort_mark) | [Max ident](http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=MicrobialGenomes&DATABASE_SORT=0&DESCRIPTIONS=100&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&MASK_CHAR=2&MASK_COLOR=1&NUM_OVERVIEW=100&OLD_BLAST=false&PAGE=MegaBlast&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CD2U8EMU016&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WWW_BLAST_TYPE_URL=&DISPLAY_SORT=3&HSP_SORT=3#sort_mark) |
| [NC\_017623.1](http://www.ncbi.nlm.nih.gov/nucleotide/386589256?report=genbank&log$=nucltop&blast_rank=1&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Heidelberg str. B182 chromosome, complete genome | [510](http://blast.ncbi.nlm.nih.gov/Blast.cgi#386589256) | 510 | 100% | 3e-142 | 100% |
| [NC\_011083.1](http://www.ncbi.nlm.nih.gov/nucleotide/194447306?report=genbank&log$=nucltop&blast_rank=2&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 chromosome, complete genome | [510](http://blast.ncbi.nlm.nih.gov/Blast.cgi#194447306) | 510 | 100% | 3e-142 | 100% |
| [NC\_010102.1](http://www.ncbi.nlm.nih.gov/nucleotide/161612313?report=genbank&log$=nucltop&blast_rank=3&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 chromosome, complete genome | [510](http://blast.ncbi.nlm.nih.gov/Blast.cgi#161612313) | 510 | 100% | 3e-142 | 100% |
| [NC\_017046.1](http://www.ncbi.nlm.nih.gov/nucleotide/383494824?report=genbank&log$=nucltop&blast_rank=4&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhimurium str. 798 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#383494824) | 499 | 100% | 7e-139 | 99% |
| [NC\_016857.1](http://www.ncbi.nlm.nih.gov/nucleotide/379699217?report=genbank&log$=nucltop&blast_rank=5&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#379699217) | 499 | 100% | 7e-139 | 99% |
| [NC\_016863.1](http://www.ncbi.nlm.nih.gov/nucleotide/378987404?report=genbank&log$=nucltop&blast_rank=6&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378987404) | 499 | 100% | 7e-139 | 99% |
| [NC\_016860.1](http://www.ncbi.nlm.nih.gov/nucleotide/378982542?report=genbank&log$=nucltop&blast_rank=7&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhimurium str. T000240, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378982542) | 499 | 100% | 7e-139 | 99% |
| [NC\_016832.1](http://www.ncbi.nlm.nih.gov/nucleotide/378958130?report=genbank&log$=nucltop&blast_rank=8&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378958130) | 499 | 100% | 7e-139 | 99% |
| [NC\_016831.1](http://www.ncbi.nlm.nih.gov/nucleotide/378953804?report=genbank&log$=nucltop&blast_rank=9&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Gallinarum/ pullorum str. RKS5078 chromosome, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378953804) | 499 | 100% | 7e-139 | 99% |
| [NC\_016810.1](http://www.ncbi.nlm.nih.gov/nucleotide/378697983?report=genbank&log$=nucltop&blast_rank=10&RID=CD2U8EMU016) | Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344, complete genome | [499](http://blast.ncbi.nlm.nih.gov/Blast.cgi#378697983) | 499 | 100% | 7e-139 | 99% |

**Appendix D:**

**The Multiple Sequence Alignment Results:**

MSW2011/Dura/food ------CGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 44

MSW2011/Hebron/food AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 50

MSW2011/B.Umar/food AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 50

MSW2011/B.Sahour/feces -----TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 45

MSW2011/B.Fajar/food -----TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 45

MSW2011/Dura/feces -----TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 45

MSW2011/B.Fajar/feces ----ATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 46

MSW2011/Batir/food ----ATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 46

MSW2011/B.Umar/feces -----TCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 45

MSW2011/Batir/feces --TTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 48

MSW2011/B.Sahour/food AATTATCGCCACGTTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 50

Salmonella -----TCGCCACATTCGGGCAATTCGTTATTGGCGATAGCCTGGCGGTGG 45

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MSW2011/Dura/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 94

MSW2011/Hebron/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 100

MSW2011/B.Umar/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 100

MSW2011/B.Sahour/feces GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 95

MSW2011/B.Fajar/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 95

MSW2011/Dura/feces GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 95

MSW2011/B.Fajar/feces GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 96

MSW2011/Batir/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 96

MSW2011/B.Umar/feces GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 95

MSW2011/Batir/feces GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 98

MSW2011/B.Sahour/food GTTTTGTTGTCTTCTCTATTGTCACCGTGGTCCAGTTTATCGTTATTACC 100

Salmonella GGTTTGTTGTCTTTTCTATTGTTACTGTCGTTCAGTTTATCGTTATTACA 95

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MSW2011/Dura/food AAAGGTTCAGAACGTGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 144

MSW2011/Hebron/food AAAGGTTCAGAACGTGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 150

MSW2011/B.Umar/food AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 150

MSW2011/B.Sahour/feces AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 145

MSW2011/B.Fajar/food AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 145

MSW2011/Dura/feces AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 145

MSW2011/B.Fajar/feces AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 146

MSW2011/Batir/food AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 146

MSW2011/B.Umar/feces AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 145

MSW2011/Batir/feces AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 148

MSW2011/B.Sahour/food AAAGGTTCAGAACGCGTCGCGGAAGTCGCGGCCCGATTTTCTCTGGATGG 150

Salmonella AAAGGTTCAGAGCGTGTCGCTGAAGTTGCGGCCCGTTTTTCTCTGGATGG 145

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MSW2011/Dura/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 194

MSW2011/Hebron/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 200

MSW2011/B.Umar/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 200

MSW2011/B.Sahour/feces TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 195

MSW2011/B.Fajar/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 195

MSW2011/Dura/feces TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 195

MSW2011/B.Fajar/feces TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 196

MSW2011/Batir/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 196

MSW2011/B.Umar/feces TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 195

MSW2011/Batir/feces TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 198

MSW2011/B.Sahour/food TATGCCCGGTAAACAGATGAGTATTGATGCCGATTTGAAGGCCGGTATTA 200

Salmonella TATGCCCGGTAAACAGATGAGTATTGATGCCGAT-CGAAAGCCGGTATTA 194

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MSW2011/Dura/food TTGATGCGGATGCTGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGC 244

MSW2011/Hebron/food TTGATGCGGATGCTGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGC 250

MSW2011/B.Umar/food TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGGGAAAGC 250

MSW2011/B.Sahour/feces TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 245

MSW2011/B.Fajar/food TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 245

MSW2011/Dura/feces TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 245

MSW2011/B.Fajar/feces TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 246

MSW2011/Batir/food TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 246

MSW2011/B.Umar/feces TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 245

MSW2011/Batir/feces TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 248

MSW2011/B.Sahour/food TTGATGCGGATGCCGCGCGCGAACGGCGAAGCGTACTGGAAAGAGAAAGC 250

Salmonella TTGATGCGGATGCCGCGCGTGAACGGCGAAGCGTACTGGAAAGAGAAAGT 244

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MSW2011/Dura/food CAGCTTTACGGTTCCTTTGACGG-------- 267

MSW2011/Hebron/food CAGCTTTACGGTTCCTTTGACGGG------- 274

MSW2011/B.Umar/food CAGCTTTACGGTTCCTTTGACG--------- 272

MSW2011/B.Sahour/feces CAGCTTTACGGTTCCTTTGACGG-------- 268

MSW2011/B.Fajar/food CAGCTTTACGGTTCCTTTGACGGTGCGATGA 276

MSW2011/Dura/feces CAGCTTTACGGTTCCTTTGACG--------- 267

MSW2011/B.Fajar/feces CAGCTTTACGGTTCCTTTGACGTGGC----- 272

MSW2011/Batir/food CAGCTTTACGGTTCCTTTGACG--------- 268

MSW2011/B.Umar/feces CAGCTTTACGGTTCCTTTGACG--------- 267

MSW2011/Batir/feces CAGCTTTACGGTTCCTTTGACG--------- 270

MSW2011/B.Sahour/food CAGCTTTACGGTTCCTTTGACG--------- 272

Salmonella CAGCTTTACGGTTCTTTTGACG--------- 266

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