



UNIVERSITI PUTRA MALAYSIA

***EFFECTS OF CONDENSED TANNIN FRACTIONS FROM LEUCAENA
LEUCOCEPHALA (LAM.) DE WIT HYBRID ON METHANE MITIGATION,
RUMEN FERMENTATION AND DIVERSITY OF METHANOGENS,
PROTOZOA AND BACTERIA IN VITRO***

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By

SAMINATHAN MOOKIAH

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in
Fulfillment of the Requirements for the Degree of Doctor of Philosophy**

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DEDICATION

*This thesis is dedicated to my parents and brothers
for their love, endless support,
and encouragement*



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in Fulfillment of the Requirement for the Degree of Doctor of Philosophy

EFFECTS OF CONDENSED TANNIN FRACTIONS FROM *LEUCAENA LEUCOCEPHALA* (LAM.) DE WIT HYBRID ON METHANE MITIGATION, RUMEN FERMENTATION AND DIVERSITY OF METHANOGENS, PROTOZOA AND BACTERIA *IN VITRO*

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December 2015

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Methane (CH₄) emission is a primary environmental concern due to its contribution to global warming and climate change. Methane gas released from livestock, in particular the ruminants accounts to about one-third of global anthropogenic CH₄ emission. Condensed tannins (CTs) are secondary plant metabolites that have shown methanogenic toxicity, resulting in reduced CH₄ formation in ruminants. Condensed tannins are also known to bind proteins. The CTs produced by plants vary in molecular weights (MWs). The effects of CTs on protein-binding affinity and rumen methanogens may be dependent on the size of the CTs molecules. At the moment, it is not clearly understood whether CTs of different MWs would exert these effects differently. Thus, it was hypothesised that higher MWs, would be more efficient in binding protein and mitigating CH₄ than CTs with lower MWs. Therefore, the objectives of the present study were to determine the effects of CT fractions of different MWs from a *Leucaena leucocephala* hybrid-Rendang (LLR) on protein binding affinity and CH₄ mitigation by rumen microbes *in vitro*. In conjunction to these, the effects of CTs of different MWs on rumen microbial fermentation activities and microbial species were also determined. Condensed tannins were extracted from LLR and fractionated into five fractions (F1–F5) using size exclusion chromatography procedure. The degrees of polymerization (DP) of the CT fractions were measured by a modified vanillin assay, the MWs of the fractions were determined by Q-TOF LC/MS, and their structures were investigated using ¹³C-NMR. The protein-binding affinities of CT fractions were measured using a protein precipitation assay. The *in vitro* gas production test was used to investigate the effects of CT fractions on CH₄ production, rumen microbial fermentation and populations (methanogens, protozoa and bacteria) *in vitro*. Based on the vanillin assay, it was found that the DP of the five CT fractions (fractions F1–F5) ranged from 4.86 to 1.56. The number-average MWs (M_n) of the different fractions were 1265.8, 1028.6, 652.2, 562.2, and 469.6 for fractions F1, F2, F3, F4, and F5, respectively. The ¹³C-NMR results showed that the CT fractions possessed monomer unit structural heterogeneity. The *b* values representing the CT quantities needed to bind half of the maximum precipitable bovine serum albumin

increased with decreasing MWs from fraction F1 to fraction F5, with values of 0.216, 0.295, 0.359, 0.425, and 0.460, respectively. This indicated that higher MWs fractions had higher protein-binding affinity. The total gas [ml/g dry matter (DM)] and CH₄ (ml/g DM) productions decreased significantly ($P < 0.05$) with increasing MWs of the CT fractions, with no significant reduction in DM digestibility. However, the *in vitro* nitrogen disappearance decreased significantly ($P < 0.05$) with the inclusion of CT fraction F1 (highest MW) when compared with the control (without CTs) and other fractions (F2–F5). The inclusion of CT fraction F1 also significantly ($P < 0.05$) decreased total volatile fatty acid, acetic acid concentrations and acetic/propionic acid ratio when compared with that of the control. The real-time PCR assay showed that higher MWs CT fractions (fractions F1 and F2) significantly ($P < 0.05$) decreased the total methanogens and methanogens from the order *Methanobacteriales*, and total protozoa than the lower MWs CT fractions (fractions F3–F5). Inclusion of higher MWs CT fractions F1 and F2 significantly ($P < 0.05$) increased the *Fibrobacter succinogens* population compared to CT fractions F3–F5. Whereas, inclusion of CT fractions (F1–F5) significantly ($P < 0.05$) decreased the *Ruminococcus flavefaciens* population compared with that of the control. Amplification of archaeal V3 regions of 16S rRNA genes using Illumina MiSeq sequencer showed that the relative abundance of the predominant unclassified *Thermoplasmata*-associated group (VadinCA11 gut group) increased significantly ($P < 0.05$), corresponding with increasing MWs of the CT fractions, whereas the predominant methanogen genus *Methanobrevibacter* was significantly ($P < 0.05$) decreased. The partial 18S rRNA gene analysis of the rumen protozoa using Illumina sequencer showed that the relative abundance of the predominant genus *Entodinium* significantly ($P < 0.05$) decreased with inclusion of CT fractions F1, F2 and F3 as compared with the control. In contrast, significant ($P < 0.05$) increases in second predominant rumen protozoa genus, *Anoplodinium-Diplodinium* were observed with CT fractions F1–F4 than that of the control. Illumina MiSeq sequencing of the V3 region of the bacterial 16S rRNA genes illustrated that the relative abundance of predominant genus *Prevotella* and unclassified *Clostridiales* were significantly ($P < 0.05$) decreased, corresponding with increasing MWs of CT fractions, whereas the cellulolytic bacteria *Fibrobacter* genus was significantly ($P < 0.05$) increased. In conclusion, CTs of different MWs have varying ability to bind proteins and decreased ruminal CH₄ production by altering the populations and diversities of rumen methanogens and protozoa, and the effects were more pronounced for CTs with higher-MWs. The bacterial population and fermentation activities were also influenced by CT fractions, but the changes had no adverse effect on DM degradability. The strong binding affinity of higher MWs CTs to proteins may be beneficial in reducing degradation of feed protein by rumen microbes, thus enhancing bypass protein in ruminants. Moreover, higher MWs CTs could be potential methanogen inhibitors, which can be incorporated in ruminant diet to mitigate the CH₄ emission, thus improving the feed efficiency and animal productivity, and at the same time reducing the contribution of ruminant livestock to global CH₄ inventory.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk Ijazah Doktor Falsafah

KESAN PECAHAN TANIN TERKONDENSASI DARIPADA *LEUCAENA LEUCOCEPHALA* (LAM.) DE WIT HIBRID TERHADAP MITIGASI METANA, FERMENTASI RUMEN SERTA DIVERSITI METHANOGEN, PROTOZOA DAN BAKTERIA *IN VITRO*

Oleh

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Pengeluaran gas metana (CH_4) adalah salah satu keprihatinan utama terhadap alam sekitar disebabkan sumbangannya kepada pemanasan global dan perubahan iklim. Pengeluaran CH_4 daripada ruminan adalah lebih kurang satu pertiga pengeluaran CH_4 antropogen global. Tanin terkondensasi (CTs) adalah metabolik sekunder tumbuhan, menunjukkan ketoksikan methanogenic, mengakibatkan kekurangan pembentukan CH_4 dalam ruminan. Tanin terkondensasi juga dapat mengikat protein. Tanin terkondensasi dihasilkan oleh tumbuhan adalah berbeza dari segi berat molekul (MWs). Kesan CTs terhadap afiniti ikatan-protein dan methanogens rumen bergantung kepada saiz molekul. Ketika ini, adalah tidak dapat ditentukan sama ada CTs yang berbeza MWs akan menunjukkan pengaruh ke atas kesan-kesan yang berlainan. Justeru, ia dihipotesiskan bahawa CTs yang mempunyai MWs lebih tinggi akan lebih cekap mengikat protein dan mengurangkan CH_4 daripada CTs yang mempunyai MWs lebih rendah. Justeru, kajian ini bertujuan menyiasat kesan pecahan-pecahan CT yang mempunyai MW yang berbeza daripada *Leucaena leucocephala* hybrid-Rendang (LLR) dalam afiniti ikatan-protein dan pengurangan CH_4 oleh mikrob rumen *in vitro*. Rentetan itu, kesan CTs yang mempunyai MWs berbeza dalam fermentasi mikrob rumen aktiviti dan spesies mikrob juga ditentukan. Tanin terkondensasi telah diekstrak daripada LLR, ditulen dan dipemeringkatkan kepada lima pecahan dengan menggunakan teknik kromatografi penyisihan saiz. Darjah pempolimeran (DP) pecahan-pecahan CT diukur dengan ujian vanilin yang telah diubah suai, MWs pecahan CT telah ditentukan melalui Q-TOF LC/MS, dan struktur-struktur pecahan CT disiasat menggunakan ^{13}C -NMR. Afiniti ikatan-protein bagi pecahan-pecahan CT ditentukan dengan menggunakan ujian pemendakan protein. Ujian pengeluaran gas *in vitro* digunakan untuk menyiasat kesan pecahan-pecahan CT dalam pengeluaran CH_4 , fermentasi rumen, serta populasi dan diversiti methanogens, protozoa dan bakteria *in vitro*. Kajian berdasarkan ujian vanilin mendapati bahawa DP lima pecahan CT (pecahan F1–F5) adalah antara 4.86 hingga 1.56. Nombor purata berat molekul (M_n) bagi pecahan-pecahan CT ialah 1265.8, 1028.6, 652.2, 562.2 dan 469.6, masing-masing untuk pecahan F1, F2, F3, F4 dan F5. Keputusan ^{13}C -NMR menunjukkan bahawa

pecahan-pecahan CT berbeza antara satu sama lain dengan unit konstituen yang berlainan. Nilai b yang mewakili kuantiti CT yang diperlukan untuk mengikat separuh daripada albumin serum bovin bertambah dengan penurunan MW daripada pecahan F1 ke pecahan F5, masing-masing dengan nilai 0.216, 0.295, 0.359, 0.425 dan 0.460. Keputusan ini menunjukkan bahawa pecahan-pecahan CT yang terdiri daripada MW lebih tinggi mempunyai afiniti ikatan-protein yang lebih tinggi. Jumlah gas [ml / g bahan kering (DM)] dan pengeluaran CH_4 (ml / g DM) menurun secara ketara ($P < 0.05$) dengan penambahan MW pecahan-pecahan CT, tetapi tidak ada perbezaan ketara antara pecahan-pecahan CT dalam degradasi DM. Bagaimanapun, kehilangan nitrogen *in vitro* menurun dengan ketara ($P < 0.05$) dengan kemasukan pecahan CT F1 berbanding dengan kawalan (tanpa CT) dan pecahan-pecahan CT yang lain (F2–F5). Kemasukan pecahan CT F1 didapati mengurangkan ($P < 0.05$) jumlah asid lemak meruap, konsentrasi asid asetik dan nisbah asid asetik/propionik berbanding dengan kawalan. PCR masa nyata menunjukkan bahawa pecahan-pecahan CT yang terdiri daripada MW yang lebih tinggi (pecahan F1 and F2) mengurangkan jumlah methanogen dan methanogens dalam order *Methanobacteriales* dan jumlah protozoa berbanding dengan pecahan-pecahan CT yang mempunyai MW yang lebih rendah (pecahan F3–F5). Pecahan-pecahan CT MW yang lebih tinggi F1 and F2 dapat meningkatkan ($P < 0.05$) populasi *Fibrobacter succinogens* dengan ketara berbanding dengan pecahan-pecahan CT F3–F5. Manakala, kemasukan pecahan-pecahan CT (F1–F5) mengurangkan ($P < 0.05$) populasi *Ruminococcus flavefaciens* dengan ketara apabila dibandingkan dengan kawalan. Amplifikasi rantau V3 gen 16S rRNA archaeal daripada semua sampel rumen dengan menggunakan penjujuk Illumina MiSeq menunjukkan bahawa kelimpahan relatif dominan kumpulan dikaitkan-*Thermoplasmata* yang tidak diklasifikasikan (kumpulan VadinCA11) bertambah dengan ketara ($P < 0.05$), sepadan dengan peningkatan MW pecahan-pecahan CT, manakala dominan methanogen genus *Methanobrevibacter* menurun dengan ketara ($P < 0.05$). Analisis sebahagian gen 18S rRNA protozoa menggunakan penjujuk Illumina menunjukkan bahawa kelimpahan relatif dominan genus *Entodinium* berkurangan secara ketara ($P < 0.05$) dengan kemasukan pecahan-pecahan CT seperti F1, F2 and F3 berbanding dengan kawalan. Bagaimanapun, peningkatan ketara ($P < 0.05$) dalam kelimpahan relatif protozoa rumen yang kedua dominan, iaitu *Anoploidium* *Diplodinium* telah diperhatikan dengan pecahan-pecahan CT F1–F4 berbanding dengan kawalan. Penjujukan Illumina MiSeq rantau V3 gen-gen 16S rRNA bakteria menunjukkan bahawa kelimpahan relatif dominan *Prevotella* dan *Clostridiales* yang tidak diklasifikasikan berkurangan secara ketara ($P < 0.05$), selaras dengan penambahan MW pecahan-pecahan CT, manakala bakteria selulosa jenis *Fibrobacter* meningkat dengan ketara ($P < 0.05$). Secara kesimpulannya, CTs yang berbeza MWs mempunyai keupayaan berlainan dalam afiniti ikatan-protein dan mengurangkan pengeluaran CH_4 dengan mengubah populasi methanogen rumen dan protozoa, dan kesanya lebih ketara untuk CT dengan MW yang lebih tinggi. Populasi bakteria dan aktiviti fermentasi juga dipengaruhi oleh pecahan-pecahan CT, tetapi perubahannya tidak menjejaskan degradasi DM. Afiniti ikatan-protein yang kuat untuk CT yang mempunyai MWs yang tinggi mungkin bermanfaat dalam mengurangkan degradasi protein tumbuhan oleh mikrob rumen, justeru meningkatkan “bypass protein” dalam ruminan. Tambahan lagi, CTs yang mempunyai MWs yang tinggi berpotensi sebagai perencat methanogen, yang boleh digabungkan dalam diet ruminan bagi mengurangkan pemancaran CH_4 , seterusnya meningkatkan kecekapan makanan dan produktiviti haiwan, dan juga mengurangkan sumbangan ternakan ruminan kepada inventori CH_4 global.

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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

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LIST OF ABBREVIATIONS

BLAST	- Basic Local Alignment Search Tool
Bp	- basepair
BSA	- Bovine Serum Albumin
BW	- Body Weight
Cm	- Centimeter
CH ₄	- Methane
CO ₂	- Carbon dioxide
CP	- Crude protein
Ct	- threshold cycle
CT	- Condensed Tannin
CTs	- Condensed Tannins
°C	- Degree Celsius
Da	- Dalton
DM	- Dry matter
DNA	- deoxyribonucleic acid
dNTP	- deoxyribonucleotide triphosphate
DP	- Degree of polymerization
Es	- amplification efficiency
F	- Fraction
FAO	- Food and Agriculture Organization
G	- gram
G	- gravity
GPC	- Gel Permeation Chromatography
H	- Hydrogen
H	- hour
HCl	- Hydrochloric acid
HPLC	- High performance liquid chromatography
H ₂ SO ₄	- sulphuric acid
HT	- Hydrolysable Tannins
IPCC	- Intergovernmental Panel on Climate Change
IVDMD	- <i>In vitro</i> DM degradability
IVND	- <i>In vitro</i> nitrogen degradability
K	- Potassium
Kb	- kilo basepair
Kg	- Kilogramme
L	- Liter
LLB	- <i>Leucaena leucocephala</i> hybrid-Bahru
LLR	- <i>Leucaena leucocephala</i> hybrid-Rendang
M _w	- weight average molecular weight
M _n	- number average molecular weight
M	- molar / molarity

Mg	- milligram
Min	- minutes
mL	- milliliter
Mm	- millimetre
µg	- microgram
µL	- microliter
µm	- micrometre
N	- nano
N	- Nitrogen
Na	- Sodium
ND	- nitrogen degradability
NH ₄	- Ammonium
Nm	- nanometre
NTC	- No-template control
OH	- Hydroxyl
PCR	- polymerase chain reaction
PDI	- Polydispersity index
PEG	- Polyethylene glycol
pH	- Puissance Hydrogen
Q-TOP LC/MS	- Liquid chromatograph-quadrupole time-of-flight mass spectrometer
R ²	- correlation coefficient
SEM	- Standard Error Mean
TAE	- Tris-acetate EDTA
U	- Unit
V	- Volt
v/v	- Volume per volume
w/v	- Weight per volume

CHAPTER 1

INTRODUCTION

In the past century, the ruminant sector has played a major role in human nutrition. This sector contributed about 30% of global meat production (equivalent to 81 million tonnes) and about 83% of global milk production (equivalent to 717 million tonnes) in 2013 (FAOSTAT, 2014). The demand for ruminant products is expected to increase due to the growth of the human population, in which the global ruminant meat and milk production is forecasted to grow at a rate of 1.2% and 1.1%, respectively, during the period 2006–2050 (FAOSTAT, 2014).

At present, the productivity of ruminants is under ever increasing pressure from the public to improve the environmental sustainability of ruminant meat production and dairy farming. Apart from maintaining the productivity, the latest challenge for ruminant nutritionist is to minimise the excretion of environmentally hazardous wastes by ruminants. Methane (CH₄) emissions from ruminants have been identified as a primary environmental concern because of the contribution to the greenhouse effect and global warming (Moss *et al.*, 2000). Methane is the end-product of feed fermentation to dispose of hydrogen (H₂) produced by microbes in the rumen. It is a potent greenhouse gas (GHG) and has a heat trapping potential of 34 times more than carbon dioxide (CO₂) (IPCC, 2013). Ruminants typically lose 3 to 12% of their ingested energy as eructated CH₄ (Johnson and Johnson, 1995).

Enteric CH₄ emission from cattle is greatly influenced by the ruminant diet. Modification of rumen fermentation offers a potential approach to minimize waste excretion from animals. In ruminants, the rumen is an important site of digestion, owing to complex microbial communities including bacteria, archaea, fungi and protozoa (Zened *et al.*, 2013). A better understanding of the effects of the modifiers on rumen microbial populations could maintain the animal productivity and decrease environmental pollution. Increasing the dry matter (DM) intake and the feeding of more digestible forage and legume have been reported to improve digestibility and reduce CH₄ production (Iqbal *et al.*, 2008). On contrary, rumen modification approaches such as defaunation, the use of ionophores, dicarboxylic acid, oils, antibiotic and analogues are not permanent solutions to ruminal CH₄ mitigation due to the adaptation of rumen microbes (Cottle *et al.*, 2011). Therefore, recent research has focused on investigating strategies at the plant and plant extract level, which might offer a long-term solution of CH₄ production and a promising approach for future research.

Forages and legumes containing condensed tannins (CTs) have been shown to mitigate enteric ruminal CH₄ emission (Hess *et al.*, 2003a; Tavendale *et al.*, 2005; Soltan *et al.*, 2012). It has been suggested that using the CTs extract to reduce CH₄ emissions may be a better alternative than feeding tannin-rich forages (Beauchemin *et al.*, 2007). Condensed tannins, also known as proanthocyanidins, are heterologous compounds that vary in structure and size, with free phenolic groups. They are complexes of oligomers

and polymers built up of flavan-3-ols (catechins) and/or flavan-3,4-diol (epigallocatechins), with molecular weights (MWs) ranging from 500 to 20,000 Daltons (Da) (Hagerman and Butler, 1991). The different combination of monomeric units and carbon-carbon bonds lead to differences in MWs and structures of CTs that could play key roles in biological activities (Rakhmani *et al.*, 2005).

The mechanism by which CTs reduce CH₄ production is not well understood, although a reduction in ruminal methanogens and protozoa could be a main factor in the suppression of CH₄ production (Animut *et al.*, 2008a). In many of the studies, supplementation of CTs resulted in reduced CH₄ emissions accompanied by detrimental effects on DM digestibility (Woodward *et al.*, 2001; Hess *et al.*, 2003b, Animut *et al.*, 2008b). Condensed tannins have also been found to exhibit protein binding ability (Kumar and Horigome, 1986; Osborne and McNeill, 2001; Huang *et al.*, 2010). Depending on their molecular weights, CT fractions vary in their capability to bind proteins. They are able to protect feed protein from being degraded by rumen microorganisms through formation of CT-protein complexes. The CT-protein complexes are then dissociated under the acidic condition of the abomasum releasing proteins for digestion and absorption (McNabbl *et al.*, 1993), presumably increasing the N utilisation and reducing NH₃ emissions from manure (Woodward *et al.*, 2009). Furthermore, CTs also reduce protein degradation in the rumen through binding to extracellular protein-degrading enzymes (Smith *et al.*, 2005). A study by Khamseekhiew (2006) on *Leucaena* hybrid, which was used as a feed supplement for sheep in Malaysia, found that the CTs extracted from *Leucaena* hybrid had a strong binding affinity for proteins.

Leucaena leucocephala, a tropical scrub legume with high crude protein (CP) content ranging from 200 to 300 g/kg DM (Khamseekhiew, 2006), has been widely used as a feed additive to overcome nutrient deficiencies in ruminants in the tropics and sub-tropical regions. In Malaysia, several generations of crossing between *L. leucocephala* and *L. diversifolia* for acid tolerance resulted in two new *L. leucocephala* hybrids, namely 62-2-8 *L. leucocephala* hybrid-Bahru (LLB) and 40-1-18 *L. leucocephala* hybrid-Rendang (LLR) (Wong *et al.*, 1998). These two hybrids have adaptability for high soil aluminium, are acid tolerant and resistant to psyllid attack. They also have a high content of secondary metabolite compounds, such as CTs. Khamseekhiew (2006) reported that the *L. leucocephala* hybrids exhibited lower DM digestibility and nitrogen (N) degradability than the local *L. leucocephala* in ruminants, owing to the higher content of CTs.

The MWs and chemical structures of CTs may be the primary factors determining their beneficial effects on CH₄ mitigation and improving the utilisation of feed proteins by ruminants (Aerts *et al.*, 1999; Vidal *et al.*, 2003). Recently, Tan *et al.* (2011a) found that the inclusion of 30–40 mg CTs/g DM of unfractionated pure CTs from LLR reduced CH₄ production and populations of methanogens and protozoa with no adverse effects on DM digestibility and nitrogen degradability *in vitro*. Later studies indicated that unfractionated pure CTs from LLR could alter the diversities of bovine rumen methanogens and protozoa (Tan *et al.*, 2011b; 2103). However, the latter studies conducted by Tan *et al.* (2011a; 2011b; 2013), used a preparation containing a mixture of CTs with different MWs. At present, it is not known whether CTs of different MWs

from LLR would differ on their effects on protein-binding affinity, CH₄ production, rumen fermentation parameters and populations and diversities of rumen microorganisms.

Therefore, the present study was conducted to investigate the effects of CT fractions of different MWs from *Leucaena leucocephala* hybrid-Rendang (LLR) on protein binding affinity and rumen microbial activities. The specific objectives of this study were:

1. To extract, purify and fractionate CTs from *Leucaena leucocephala*-hybrid Rendang (LLR) and to determine their molecular weights (MWs), degree of polymerisation (DP) and structure of the CT fractions.
2. To determine the protein binding affinity of unfractionated CTs and CT fractions from LLR using a protein precipitation assay.
3. To evaluate the effects of CT fractions of different MWs from LLR on *in vitro* CH₄ production, *in vitro* DM degradability and N disappearance, and volatile fatty acid (VFA) production using the *in vitro* gas production test.
4. To determine the effects of CT fractions of different MWs from LLR on the population and diversity of bovine rumen archaea, protozoa and bacteria *in vitro* using real-time PCR and Illumina MiSeq sequencing approaches.

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