

UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL – UFRGS

**Síndrome anual da abelha mandaia (*Melipona quadrifasciata*) - o papel de simbiotes,
sistema imune e ambiente.**

Lílian Caesar

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Orientadora: Dr^a Karen Luisa Haag

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LISTA DE ABREVIATURAS E UNIDADES

+ssRNA: RNA fita simples de sentido positivo (*positive-sense single-stranded RNA*)

°C: graus Celsius

ABPV: vírus da paralisia aguda de abelha (*Acute bee paralysis virus*)

AMPs: peptídeos antimicrobianos

ANOVA: análise de variância

ARV-1: *Apis mellifera rhabdovirus-1*

BL: Boqueirão do Leão - RS

BLAST: ferramenta básica de busca de alinhamento local (*Basic Local Alignment Search Tool*)

BP: Bom princípio - RS

bp: pares de base (*base pairs*)

BQCV: vírus da célula de rainha negra (*Black queen cell virus*)

BU: teste incondicional de Barnard (*Barnard's Unconditional test*)

CBPV: vírus da paralisia crônica das abelhas (*Chronic bee paralysis virus*)

CCD: desordem do colapso das colônias (*Colony collapse disorder*)

CDS: sequência codificante (*Coding sequence*)

CMH: teste de Cochran-Mantel-Haenszel

CNRQ: quantidade relativa calibrada e normalizada (*Calibrated Normalized Relative Quantity*)

Cq: ciclo de quantificação (*quantification cycle*)

DEG: genes diferentemente expressos (*differentially expressed genes*)

dsDNA: DNA de fita dupla

DWV: vírus deformador da asa (*Deformed wing virus*)

E: eficiência do primer (*primer efficiency*)

fem: gene feminizador

g: gramas

GE: expressão gênica (*gene expression*)

GOX: glicose oxidase

H: saudável (*healthy*)

HDNA: amostra de DNA de abelhas saudáveis (*DNA sample from healthy bees*)

HJ: hormônio juvenil

HRNA: amostra de RNA de abelhas saudáveis (*RNA sample from healthy bees*)

IAPV: vírus da paralisia aguda israelense (*Israeli acute paralysis virus*)

Imd: via da imunodeficiência (*Immune deficiency*)

Jak/STAT: Janus quinase / transdutor de sinal e ativador da transcrição (*Janus kinase/Signal Transducer and Activator of Transcription*)

KBV: vírus de abelha da caxemira (*Kashmir bee virus*)

LSV: vírus do lago Sinai (*Lake Sinai virus*)

Ma: milhões de anos

min: minutos

mL: mililitros

mm: milímetros

mM: milimolar

MqC: *Melipona quadrifasciata cyclovirus*

MqC1: *Melipona quadrifasciata cyclovirus 1*

MqC2: *Melipona quadrifasciata cyclovirus 2*

MqD: *Melipona quadrifasciata densovirus*

MqV1a: *Melipona quadrifasciata virus 1a*

MqV1b: *Melipona quadrifasciata virus 1b*

MqV2: *Melipona quadrifasciata virus 2*

NF- κ B: fator nuclear kappa-B

NGE: expressão gênica normalizada (*normalized gene expression*)

nm: nanômetros

NMDS: escala multidimensional não métrica (*non-metric multidimensional scaling*)

nt: nucleotídeos

OcNV: *Osmia cornuta nudivírus*

OTUs: unidades taxonômicas operacionais (*Operational Taxonomic Units*)

p450: citocromo p450

PA: Porto Alegre - RS

PAMPs: Padrões Moleculares Associados a Patógenos

PCA: análise de componentes principais (*Principal Component Analysis*)

PCR: reação em cadeia da polimerase (*Polymerase Chain Reaction*)

PERMANOVA: análise multivariada permutacional de variância (*Permutational Multivariate Analysis of Variance*)

PO: fenoloxidase

r.p.m: rotações por minuto

RFU: unidade de fluorescência relativa (*Relative Fluorescence Unit*)

RL: Rolante – RS

RT-qPCR: PCR quantitativa de transcrição reversa (*quantitative reverse transcription PCR*)

SBPV: vírus da paralisia lenta das abelhas (*Slow bee paralysis virus*)

SBV: vírus de abelha *Sacbrood* (*Sacbrood bee virus*)

SGE: similaridade de expressão gênica (*gene expression similarity*)

ssDNA: DNA de fita simples

–ssRNA: RNA fita simples de sentido negativo (*negative-sense single-stranded RNA*)

U: doente (*unhealthy*)

UDNA: amostra de DNA de abelhas doente (*DNA sample from unhealthy bees*)

uL: microlitros

URNA: amostra de RNA de abelhas doentes (*RNA sample from unhealthy bees*)

VDV1: *Varroa destructor virus-1*

Vg: vitelogenina

Δ : delta

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RESUMO

Todos os anos ao final do verão, no sul do Brasil, colônias manejadas da abelha sem ferrão *Melipona quadrifasciata* manifestam uma síndrome que eventualmente leva-as ao colapso. Abelhas de colônias afetadas podem apresentar sintomas como tremores e paralisia, mas a principal característica da síndrome é a repentina morte de operárias, cujos corpos são encontrados em frente ou mesmo dentro da colméia. Nesta tese descrevemos nossos achados sobre as possíveis causas dessa mortalidade avaliando os diferentes níveis de complexidade de uma abelha social, desde o indivíduo e seus microrganismos associados até o nível da colônia. Mostramos que a microbiota de *M. quadrifasciata* é altamente variável, com grandes diferenças na composição bacteriana de abelhas de diferentes colônias. Bactérias patogênicas não foram detectadas em abelhas afetadas e o padrão na composição da microbiota não indicou uma correlação entre disbiose e a ocorrência da síndrome. Mostramos também que os sintomas observados em forrageiras doentes não são causados por vírus conhecidos como patogênicos em outras abelhas. Entretanto, novos vírus que nós identificamos no viroma da *M. quadrifasciata* são mais frequentemente diagnosticados em determinados meliponários durante a síndrome, e podem estar relacionados à intensidade dos sintomas e ao colapso de certas colméias. Por fim, num monitoramento temporal feito ao longo de cinco meses no verão de 2018/2019, mostramos que a síndrome foi resultado da incapacidade de expressar genes envolvidos na detoxificação de xenobióticos e resposta imune cerca de dois meses antes da síndrome, seguido da perda de peso das forrageiras, troca nos recursos polínicos utilizados e perda da capacidade de controle do clima interno da colônia. Além da divulgação e discussão no meio científico, elaboramos também, com base nestas investigações, um guia com recomendações de manejo aos meliponicultores que, se aplicadas, podem contribuir para a prevenção da síndrome anual de *M. quadrifasciata*, bem como da perda de outras abelhas nativas.

palavras-chave: abelha, abelha sem ferrão, simbiose, microbiota, vírus, sistema imune, comportamento, saúde das abelhas.

ABSTRACT

Every year at the end of summer, in southern Brazil, managed colonies of the stingless bee *Melipona quadrifasciata* manifest a syndrome that eventually leads to their collapse. Bees from affected colonies may show symptoms such as tremors and paralysis, but the main feature of the syndrome is the sudden death of workers, whose bodies are found in front or inside the hives. In this thesis we describe our discoveries on the possible causes of this mortality evaluating the different complexity levels of an eusocial bee, from the individual and its associated microorganisms until colony level. We show that the *M. quadrifasciata* microbiota is highly variable, with large differences in community composition among bees from different colonies. Pathogenic bacteria were not detected in affected bees, and the pattern of microbiota composition did not indicate a correlation between dysbiosis and syndrome occurrence. We have also shown that the symptoms observed in unhealthy foragers are not caused by viruses known to be pathogenic in other bees. However, novel viruses that we identified in the *M. quadrifasciata*-associated virome are more often diagnosed in some meliponaries during the outbreak, and may be related to the intensity of observed symptoms and to the collapse of some colonies. Finally, on a temporal survey performed for five months during the summer of 2018/2019, we show the syndrome resulted from the inability to express genes involved in the detoxification of xenobiotics and immune response about two months before the outbreak, followed by foragers weight loss, a shift in pollen resources used, and a decrease in performance to control the nest environment. In addition to reporting our results to the scientific community, we have also prepared, based on our investigations, a guide with recommendations for the management of stingless bees that may contribute to the prevention of the *M. quadrifasciata* annual syndrome, as well the loss of other native bees.

key words: bee, stingless bee, symbiosis, microbiota, virus, immune system, behavior, bee health.

CAPÍTULO 1

Introdução e objetivos

1. Introdução

1.1 Abelhas neotropicais

Polinizadores prestam um serviço importante na manutenção de ecossistemas naturais e também para a agricultura. As abelhas fazem parte das 100.000 espécies polinizadoras de mais de 200.000 espécies de plantas. Quanto às espécies de plantas cultivadas pelo homem, as abelhas são o grupo mais importante de polinizadores (Heard 1999; Klein et al. 2007; Giannini et al. 2015).

A região neotropical é reconhecida por suportar uma fauna rica em espécies de abelhas. Estima-se para a região um número total de mais de 15.000 espécies e para o Brasil a riqueza de espécies de abelhas pode chegar a 3.000 (Silveira et al. 2002). As abelhas fazem parte da ordem Hymenoptera e, dentre as sete famílias que a compõe, Apidae é a mais rica e abundante na Mata Atlântica. Espécies da tribo Meliponini são as mais registradas neste bioma (Gonçalves e Brandão 2008). A tribo agrupa as abelhas sociais encontradas nos trópicos e regiões subtropicais, conhecidas popularmente como abelhas sem ferrão por possuírem o ferrão atrofiado. Abelhas do gênero *Melipona*, reconhecidamente monofilético, fazem parte de um clado que inclui apenas abelhas sem ferrão neotropicais (Figura 1) (Ramírez et al. 2010; Rasmussen e Cameron 2010).

1.1.2 A abelha mandaçaia

A mandaçaia (*Melipona quadrifasciata*, Lepeletier 1836, Figura 2) é a segunda espécie de abelha sem ferrão mais cultivada por meliponicultores (aqueles que criam abelhas da tribo Meliponini) (Jaffé et al. 2015). As colônias de mandaçaia são compostas por 300 a 400 indivíduos (Tóth et al. 2003) e colônias selvagens costumam nidificar em troncos ocos. O período de desenvolvimento do ovo ao adulto é de em média 40 dias. Quando adultas, operárias medem 10 a 11 mm e são mais robustas que as abelhas melíferas. A determinação das castas em abelhas do gênero *Melipona* é diferente da maioria das abelhas sem ferrão, em que as larvas determinadas a desenvolverem-se como rainhas recebem e consomem uma quantidade maior de alimento comparado aos demais ovos depositados (Kerr 1969; Hartfelder et al. 2006).

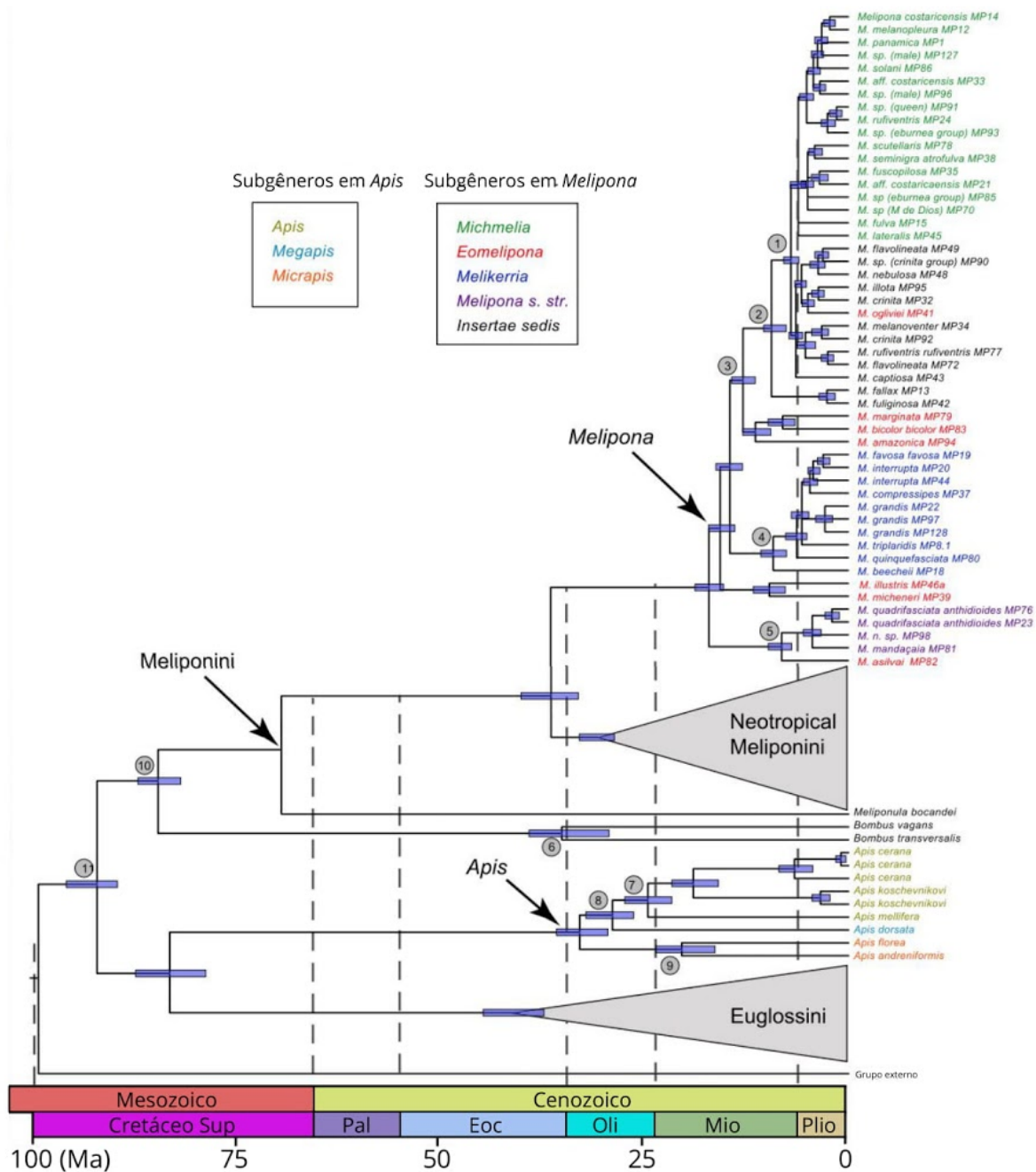


Figura 1. Análise filogenética Bayesiana baseada em cinco *loci* e cronograma com relógio-relaxado do gênero *Melipona* e grupos relacionados. Os tempos de divergência são apresentados em milhões de anos (Ma). *Melipona* compartilhou um ancestral comum durante o Mioceno, 14–17 milhões de anos atrás (adaptado de Ramírez et al. 2010).

Em *Melipona* a determinação de castas se dá por predisposição genética, seguindo um modelo de dois *loci*/dois alelos ainda não determinados (Kerr 1950; Hartfelder et al. 2006). Estudos mais recentes mostram que os níveis de transcritos do gene feminizador (*fem*) em abelhas fêmeas são provavelmente aumentados pelo hormônio juvenil (HJ), mais expresso em larvas

que irão se desenvolver como rainhas, sugerindo que *fem* atua como componente de interação entre vias de determinação do sexo e das castas (de Oliveira Campos et al. 1975; Bonetti et al. 1995; Brito et al. 2015).

As abelhas sem ferrão são consideradas polinizadoras generalistas da flora nativa e também fundamentais para polinização de cultivares agrícolas. Uma característica marcante das mandaiaias, assim como outras abelhas do gênero *Melipona*, é sua capacidade de coletar pólen por vibração especialmente em flores com anteras poricidas (onde o pólen sai da antera através de poros apicais), como da família de plantas Solanaceae. A abelha pousa sobre o ápice da antera, agarra-se ao estame e contrai os músculos torácicos de forma a vibrar e liberar o pólen (Nunes-Silva et al. 2010). Devido a este comportamento, a mandaiaia é uma importante polinizadora de cultivares como o de tomate, pimentão e berinjela (Cruz et al. 2005; dos Santos et al. 2009; Nunes-Silva et al. 2013; Bartelli e Nogueira-Ferreira 2014).

A mandaiaia ocorre na Argentina, Paraguai e Brasil. No Brasil a espécie *M. quadrifasciata* é dividida em duas subespécies. No nordeste, sudeste e centro-oeste do Brasil encontra-se a subespécie *M. q. anthidioides*, com bandas amarelas interrompidas no dorso do abdômen; enquanto no centro-oeste, sudeste e sul ocorre a subespécie *M. q. quadrifasciata*, na qual as bandas dorsais são contínuas (Batalha-Filho et al. 2009). Marcadores moleculares, como regiões polimórficas do DNA (Waldschmidt et al. 2000) e regiões do DNA mitocondrial com padrões diferentes de clivagem por enzimas de restrição (Souza et al. 2008; Batalha-Filho et al. 2010) já foram descritos para auxiliar na diferenciação das subespécies e para estudos de zonas híbridas, encontradas em São Paulo e Minas Gerais. As mandaiaias híbridas possuem um padrão de coloração intermediário, com bandas dorsais interrompidas e contínuas no abdômen. A subespécie *M. q. quadrifasciata* é classificada como em perigo na lista mais atual de espécies ameaçadas do Rio Grande do Sul, elaborada pela Fundação Zoobotânica (2014) e tentativas de encontrar ninhos selvagens na região não tiveram sucesso.

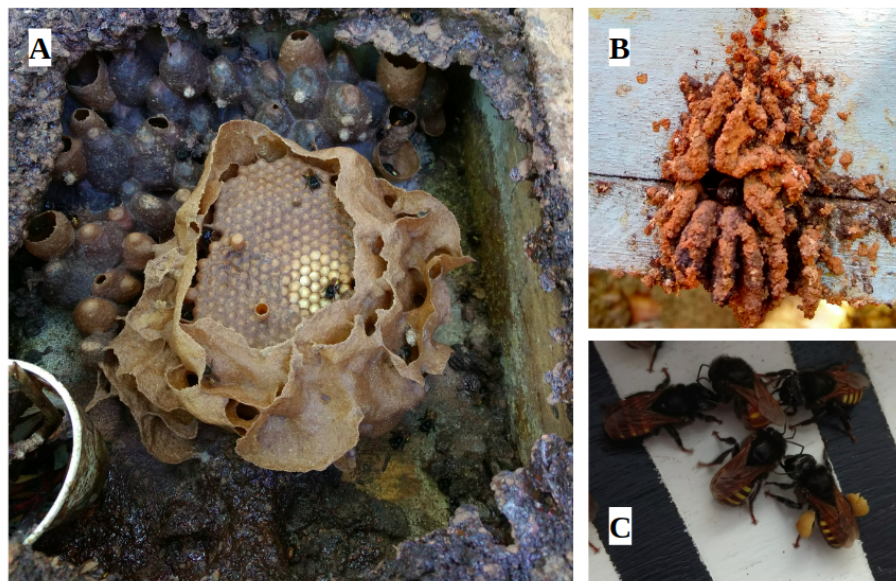


Figura 2. Características da abelha mandaçaia. (A) Parte interna de uma colônia manejada de mandaçaia, com discos de cria envoltos por cerume e no canto da caixa os potes de mel e pólen. (B) Entrada típica de um ninho de mandaçaia, feito de barro coletado por operárias. (C) Abelhas operárias da subespécie *M. q. quadrifasciata* do Rio Grande do Sul. (Fotos: Lílian Caesar)

1.2 Ameaças às abelhas e o colapso de colônias

Nas últimas décadas tem sido relatada a diminuição das populações de abelhas. Na América do Norte e Europa perdas anuais de populações de abelhas manejadas têm aumentado, podendo chegar até 40% do total de colônias (Genersch et al. 2010; Kulhanek et al. 2017). Em 2005 e 2006 apicultores dos Estados Unidos da América começaram a relatar o que passou-se a chamar de desordem do colapso de colônias (CCD, *colony collapse disorder*) (Stokstad 2007). A CCD é caracterizada pela repentina perda da população adulta de abelhas, sem que se encontrem indivíduos mortos no interior ou na proximidade das colônias. O grande número de colônias perdidas após o aparecimento da CCD levou a esforços de pesquisa principalmente voltados a gerar informações sobre cargas de patógenos em polinizadores, permitindo a identificação de possíveis ameaças emergentes à saúde das abelhas (Cox-Foster et al. 2007; Evans e Schwarz 2011; Schwarz, Huang, et al. 2015). Esse processo, no entanto, levou à conclusão de que as perdas de colônias são o resultado de vários estressores em interação, como aquecimento global e perda de habitat, má nutrição, ação de

patógenos e práticas agrícolas como a utilização de pesticidas (vanEngelsdorp e Meixner 2010).

O declínio de populações selvagens de abelhas é um fato (Koh et al. 2016; Meeus et al. 2018). Na região tropical, os fatores que têm influenciado o baixo *status* de conservação de abelhas selvagens incluem a disseminação de espécies de abelhas exóticas, que competem por recursos e podem transmitir patógenos às abelhas nativas, a perda de habitat e o uso de pesticidas (Freitas et al. 2009; Guzman-Novoa et al. 2015; Ueira-Vieira et al. 2015; Maggi et al. 2016; Santos et al. 2018). A meliponicultura, por sua vez, pode ser uma atividade benéfica ao criar e manejar abelhas nativas em risco de extinção, como a *M. q. quadrifasciata* (Jaffé et al. 2015). No entanto, meliponicultores do sul do Brasil relatam uma síndrome de ocorrência anual, geralmente no final do verão, que culmina com o colapso das colônias da espécie. A síndrome difere da conhecida CCD uma vez que são encontrados indivíduos mortos nas proximidades ou até dentro das colônias. A principal característica desta síndrome é a quantidade anormal de operárias mortas em frente a colônia (Figura 3). Em alguns meliponários indivíduos de colônias afetadas podem também apresentar um comportamento alterado e tremores, incapacidade de voo e a eversão da probóscide. O colapso da colônia ocorre devido à falta de operárias para a manutenção e proteção, de modo que a colônia acaba por fim sendo invadida por parasitas como fungos e moscas. A síndrome ocorre em meliponários com ambientes heterogêneos, situados em áreas urbanas à regiões cercadas por mata conservada. Há também diferenças na intensidade dos sintomas observados nos diferentes locais, assim como nem todas as colônias de mandaçaia ficam doentes. Portanto, assim como sugerido para o declínio das populações globais de abelhas e mesmo para a CCD, esta também pode ser uma síndrome multifatorial.

1.2.1 Bactérias

Diversas bactérias patogênicas são conhecidas por infectar principalmente abelhas melíferas, dentre elas as bactérias *Paenibacillus larvae* e *Melissococcus plutonius* são as mais bem caracterizadas (Fünfhaus et al. 2018). *P. larvae* é o agente causador da cria pútrida americana (*American Foulbrood*). O sintoma típico observado após a infecção das larvas por esporos da bactéria é a degradação da larva morta (J. Brødsgaard et al. 1998; Genersch 2010),

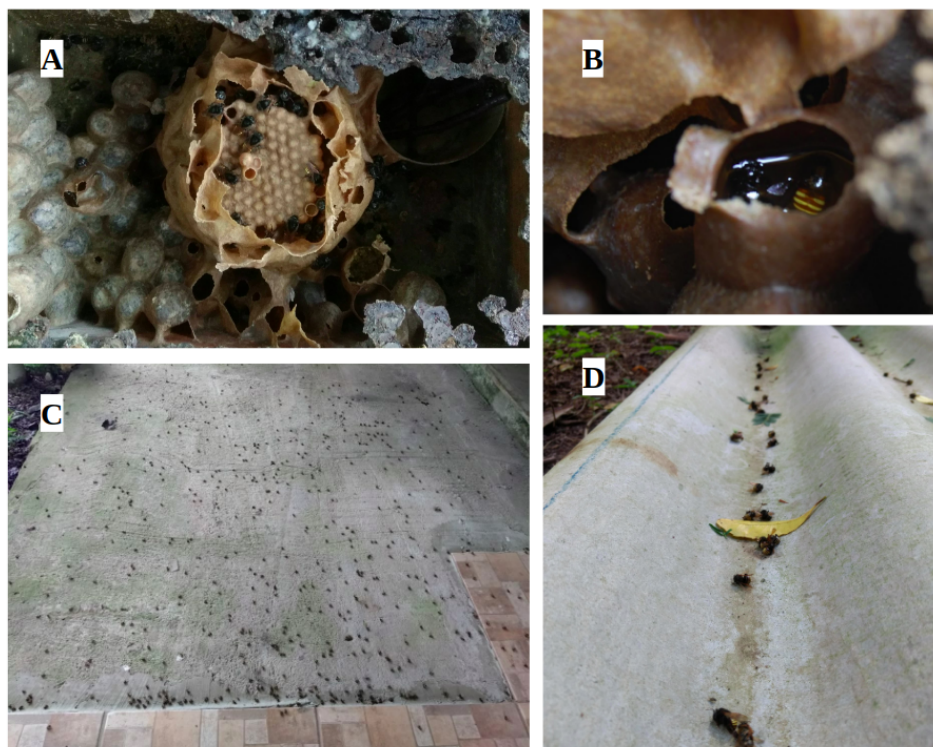


Figura 3. Imagens da síndrome anual das mandaçaias. (A) Parte interna de uma colônia manejada de mandaçaia no início da síndrome. Os discos de cria, potes de pólen e mel permanecem intactos, mas no fundo da colônia começam a acumular operárias mortas ou com sintomas da síndrome, como tremores e paralisia (Foto: Lílian Caesar). (B) Nos potes de mel também passam a ser observadas operárias afogadas que não são removidas por falta de operárias para desempenhar as atividades de limpeza dentro da colônia (Foto: Lucas Kehl). (C, D) A característica mais marcante da síndrome é o grande número de operárias mortas em frente às suas colônias (Foto C: Daniel Iochims; D: Lílian Caesar).

essencial para a transmissão de esporos para larvas saudáveis, bem como para a transmissão da doença dentro e entre colônias. Já *M. plutonius* é o agente causador da doença conhecida como cria pútrida européia (*European Foulbrood*). As larvas são infectadas ao ingerirem alimento larval contaminado e quando mortas são encontradas torcidas dentro da célula de cria aberta. Sua decomposição ocorre também pela presença de invasores secundários como *P. alvei* ou *Enterococcus faecalis* (Nakamura et al. 2016; Lewkowski e Erler 2018). Ambas bactérias já foram diagnosticadas em abelhas melíferas brasileiras em estudos de monitoramento (Maggi et al. 2016), mas não há detalhes sobre os sintomas da infecção. Recentemente *M. plutonius* foi também diagnosticado em abelhas sem ferrão do gênero *Melipona* que apresentavam os sintomas da cria pútrida européia e em alguns casos estava

levando ao colapso de colônias (Teixeira et al. 2020). No estudo mostram que a infecção ocorreu por meio da suplementação alimentar das colônias de abelhas sem ferrão com pólen de *Apis* contaminado.

A bactéria *Lysinibacillus sphaericus* é um conhecido patógeno de insetos, sendo inclusive usada em programas de controle de insetos vetores de doenças humanas (Lacey 2007). Apesar desta bactéria não ser, a princípio, patogênica à abelhas melíferas (West Davidson et al. 1977), ela é o agente causador da perda da prole de colônias manejadas da abelha sem ferrão australiana *Tetragonula carbonaria* (Shanks et al. 2017). Colônias afetadas parecem não ter rainhas, tem uma população reduzida de abelhas adultas e pouca atividade na entrada do ninho. As larvas infectadas apresentam descoloração ou aspecto apodrecido. No Brasil não há registros de abelhas sem ferrão infectadas por tal bactéria.

Outras bactérias patogênicas à abelhas são *Spiroplasma apis* e *S. melliferum*, que vivem intracelularmente nos tecidos do hospedeiro ou extracelularmente na hemolinfa. Abelhas infectadas por *S. apis* são incapazes de voar, rastejam no chão e tremem, além de ficarem com o abdômen inchado devido ao intestino cheio de pólen não digerido (Mouches et al. 1982; Mouches et al. 1983). A infecção por *S. melliferum* se dá na hemolinfa causando patologia em diversos tecidos e diminuindo a longevidade de abelhas adultas (Clark et al. 1985; Zheng e Chen 2014). Abelhas melíferas brasileiras, sem sintomas evidentes, já foram diagnosticadas para a infecção por ambas espécies de *Spiroplasma*, inclusive com infecções concomitantes de *S. apis* e *S. melliferum* (Schwarz et al. 2014).

A bactéria *Serratia marcescens*, encontrada tanto em plantas como animais, é também um patógeno oportunista de abelhas (Raymann et al. 2018). Está frequentemente presente em baixa densidade no intestino de abelhas adultas e já foi também isolada de ácaros parasitas e da hemolinfa de abelhas doentes ou mortas (El Sanousi et al. 1987; Burritt et al. 2016; Raymann et al. 2017). No Brasil não há relatos e falhas em colônias relacionado a infecção por esta bactérias.

1.2.2 Vírus

Até pouco tempo podíamos contar facilmente o número de vírus identificados em abelhas, principalmente em *A. mellifera* (Chen e Siede 2007; McMenamin e Genersch 2015).

Mas as recentes técnicas de sequenciamento de nova geração tem facilitado o sequenciamento de alto rendimento de transcriptomas, metagenomas e viromas, o que tem contribuído significativamente para a caracterização da diversidade de vírus associados às abelhas (Grozinger e Flenniken 2019). A maioria dos vírus de abelhas são de RNA fita simples de sentido positivo (+ssRNA). A família *Dicistroviridae* inclui vírus como: vírus da paralisia aguda israelense (IAPV, *Israeli acute paralysis virus*), vírus de abelha da caxemira (KBV, *Kashmir bee virus*), vírus da paralisia aguda de abelha (ABPV, *Acute bee paralysis virus*) e vírus da célula de rainha negra (BQCV, *Black queen cell virus*). Na família *Iflaviridae* fazem parte vírus como: vírus deformador da asa (DWV, *Deformed wing virus*), vírus *Varroa destructor*-1/DWV-B, vírus de abelha *Sacbrood* (SBV, *Sacbrood bee virus*) e vírus da paralisia lenta das abelhas (SBPV, *Slow bee paralysis virus*). Há também vírus +ssRNA taxonomicamente não classificados, como: vírus da paralisia crônica das abelhas (CBPV, *Chronic bee paralysis virus*) e vírus do lago Sinai (LSVs, *Lake Sinai virus*) (McMenamin e Flenniken 2018; Grozinger e Flenniken 2019).

Alguns destes vírus são conhecidos por causar paralisia em abelhas. O vírus SBPV acumula-se nos tecidos da parte anterior do corpo das abelhas causando a paralisia das pernas anteriores do inseto, sintoma observável apenas 12 dias após a inoculação do vírus, não sendo tão agressivo de imediato (Bailey e Woods 1974). O vírus CBPV causa sintomas semelhantes, podendo também ser observadas abelhas incapazes de voar, aglomeradas e rastejando próximas à colmeia, sem pelos e com o abdômen inchado (Bailey et al. 1983; Blanchard et al. 2007). Este vírus acumula-se principalmente no sistema nervoso da abelha melífera e infecta/aumenta sua carga viral particularmente no verão, podendo infectar e levar apenas algumas colônias de apiários ao colapso.

Em meliponários de Minas Gerais e Pernambuco, onde ocorreu uma alta mortalidade de *M. scutellaris*, o vírus ABPV foi detectado em abelhas operárias (Ueira-Vieira et al. 2015). Este vírus é considerado praticamente assintomático, mas leva rapidamente à morte de abelhas infectadas (Miranda et al. 2013). Análises filogenéticas mostraram que a linhagem de ABPV desta abelha sem ferrão derivou de sequências de ABPV de *A. mellifera* da Europa e da América do Sul (Ueira-Vieira et al. 2015). O vírus DWV e BQCV também já foi detectado em abelhas melíferas do Brasil, assim como em cinco diferentes espécies de abelhas sem ferrão (de Souza et al. 2019; Guimarães-Cestaro et al. 2020). Nestas espécies de abelha sem

ferrão em que o vírus foi detectado não há evidência de sintomas, mas quando a infecção é sintomática, como observado principalmente em abelhas melíferas, este vírus leva abelhas a desenvolverem-se com asas amassadas/vestigiais e abdômen inchado, levando à morte logo após o indivíduo emergir da pupa. A transmissão deste vírus por um vetor, como o ácaro *Varroa*, leva a infecções mais virulentas e com sintomas observáveis (Ryabov et al. 2014; Wilfert et al. 2016). O DWV também já foi detectado na abelha sem ferrão *Scaptotrigona mexicana*, espécie na qual também foi detectado o vírus BQCV (Guzman-Novoa et al. 2015), que costuma causar sintomas mais evidentes nos estágios iniciais do desenvolvimento, como pré-pupas mortas em células com paredes escurecidas ou larvas com aparência pálida e o tecido endurecido (Miranda et al. 2013). Devido ao compartilhamento do ecossistema com *A. mellifera*, o próprio contato físico entre as abelhas exóticas e nativas, ou o contato com pólen de plantas visitadas por ambas as espécies, é sugerido como possível via de transmissão destes vírus (Guzman-Novoa et al. 2015).

Outros vírus identificados em abelhas incluem vírus de RNA fita simples de sentido negativo (-ssRNA), como o *Apis mellifera* rhabdovirus-1 (ARV-1) e *Apis mellifera* rhabdovirus-2 (ARV-2) (Remnant et al. 2017). Quanto aos vírus de DNA, dois vírus de DNA de fita dupla (dsDNA) foram já descritos, o Vírus filamentososo de *Apis mellifera* (Gauthier et al. 2015) e o *Osmia cornuta* nudivírus (OcNV) (Schoonvaere et al. 2018). Também foram já identificados sequências virais correspondentes a vírus de DNA de fita simples (ssDNA) das famílias *Circoviridae* e *Parvoviridae* (Galbraith et al. 2018; Schoonvaere et al. 2018). A patogenicidades destes vírus em abelhas infectadas ainda precisa ser investigada.

1.2.3 Outros inimigos naturais

Além de bactérias e vírus, outros inimigos naturais das abelhas são os ácaros, fungos e tripanossomatídeos. O ácaro *Varroa destructor*, que foi transmitido da abelha *A. ceranae*, tolerante ao parasita, à *A. mellifera*, é hoje um dos mais importantes parasitas desta espécie de abelha (Rosenkranz et al. 2010; Evans e Cook 2018). Ele se beneficia da ampla distribuição da abelha melífera, juntamente com as práticas de manejo, como a alta densidade de colônias nos apiários, para ser transmitido horizontalmente entre colônias (Seeley e Smith 2015). *Varroa* causa danos pelos efeitos diretos do seu parasitismo, como malformações durante o desenvolvimento e diminuição da performance das colônias (Garedew et al. 2004; Dainat et

al. 2012). O ácaro também atua como vetor de vírus como KBV, IAPV e DWV (Chen et al. 2004; Shen et al. 2005; Di Prisco et al. 2011) e seu parasitismo tem contribuído para a emergência de estirpes virais, como do DWV, ao suprimir a resposta imune do hospedeiro desestabilizando a dinâmica de controle da infecção (Yang e Cox-Foster 2005; McMahon et al. 2016; Erban et al. 2019). Este ácaro já está espalhado por diferentes países da América Latina, incluindo o Brasil, mas até o momento não causa danos aparentes ou há evidências de sua atuação na transmissão de vírus (Strapazzon et al. 2009; de Mattos et al. 2016; Brettell e Martin 2017).

Nosema ceranae é um microsporídeo parasita intracelular obrigatório de abelhas melíferas (Fries et al. 1996; Fries 2010). Nosemoses afetam larvas e abelhas adultas, causando mortalidade de abelhas e podendo levar ao colapso de colônias (Higes et al. 2007; Higes et al. 2008; Higes et al. 2009; Bromenshenk et al. 2010; Paxton 2010), apesar de ser também diagnosticada em colônias assintomáticas (Cox-Foster et al. 2007; Fernández et al. 2012). A infecção por *Nosema* pode comprometer o sistema imune, forrageamento, produção de feromônios e hormônios e síntese lipídica (Kralj e Fuchs 2010; Goblirsch et al. 2013; Mayack et al. 2015; Badaoui et al. 2017; Li et al. 2018). O parasita é transmitido por via oral pelo mel, néctar, pólen e matéria fecal das abelhas (Smith 2012). Um estudo realizado em colônias de *A. mellifera* de 20 apiários do estado de São Paulo detectou esporos do parasita em indivíduos de todas colônias, mas nenhuma evidência clara de correlação da quantidade de esporos com o declínio das colônias foi observado (Teixeira et al. 2013). Esporos de *Nosema* já foram também detectados em abelhas sem ferrão, provavelmente adquiridos em flores também visitadas por *A. mellifera* parasitadas (Porrini et al. 2017; Purkiss e Lach 2019). Em um estudo recente o patógeno, no entanto, não foi encontrado no intestino das abelhas sem ferrão, sugerindo que essas abelhas não são afetadas (Guimarães-Cestaro et al. 2020).

Os tripanossomatídeos *Crithidia mellificae* e *Lotmaria passim* são parasitas obrigatórios unicelulares que costumam infectar abelhas melíferas (Schwarz et al. 2015). *L. passim* é atualmente a espécie de tripanossomatídeo predominante em *A. mellifera* de grande parte do mundo. Para a América do Sul as informações sobre a distribuição dos tripanossomatídeos permanecem escassas, apesar de já terem sido diagnosticados (Arismendi et al. 2016; Castelli et al. 2019). Apesar de *L. passim* ter sido associado à mortalidade de abelhas (Ravoet et al. 2013), os efeitos de sua infecção ainda são pouco conhecidos. Já *C.*

bombi é um tripanossoma parasita de *Bombus* sp., e sua infecção já foi melhor caracterizada. Ele reduz drasticamente a produção de machos, o sucesso na fundação de novas colônias e tamanho delas, além de prejudicar processos cognitivos nas abelhas parasitadas (Brown et al. 2003; Gegear et al. 2006). Também induz a expressão de genes relacionados ao sistema imunológico, como os codificadores de Relish e peptídeos antimicrobianos (AMPs) (Schlüns et al. 2010; Riddell et al. 2011; Riddell et al. 2014).

1.2.5 Agroquímicos

O Brasil é o maior consumidor mundial de agroquímicos, representando aproximadamente 20% do uso total (Albuquerque et al. 2016). Em um estudo de caso recente, 90% dos apicultores brasileiros entrevistados relataram perda de colônias que acreditam ser causadas por causa do uso de agroquímicos em culturas próximas a seus apiários (Cerqueira e Figueiredo 2017). Mas enquanto países desenvolvidos têm reduzido o uso de agroquímicos na agricultura, o Brasil tem ido na contramão, facilitando ainda mais o seu uso (Santos et al. 2018). Altas doses de agroquímicos podem ter efeito letal para as abelhas, levando colônias inteiras ao colapso. Mas o efeito subletal dos agroquímicos, aquele que não leva a morte imediata das abelhas, pode também ser muito prejudicial e contribuir para falha da colônias (Desneux et al. 2007).

Agroquímicos já foram detectados em níveis residuais na prole, pólen, mel e cera de colônias de abelhas melíferas (Wu et al. 2011; Calatayud-Vernich et al. 2018; Tosi et al. 2018). Estes resíduos influenciam negativamente no crescimento, força e sobrevivência das colônias de abelhas por comprometerem o retorno de forrageiras ao lar, habilidades cognitivas e de forrageamento (Mommaerts et al. 2010; Henry et al. 2012), a motilidade espermática em machos (Thompson et al. 2005; Ciereszko et al. 2017) e a emergência, sobrevivência e reprodução de rainhas (Thompson et al. 2005; Sandrock et al. 2014; dos Santos et al. 2016). O efeito de doses subletais de agroquímicos pode também ser acentuado ao agir de forma sinérgica com agroquímicos de outras classes (Spurgeon et al. 2016; Sgolastra et al. 2017), contribuir para o aumento da susceptibilidade a infecção por patógenos como *Nosema* sp. ou DWV (Alaux, Brunet, et al. 2010; Prisco et al. 2013; Aufauvre et al. 2014) e reduzir ainda mais a longevidade e sobrevivência de abelhas sob estresse nutricional (Tosi et al. 2017).

Diversos estudos experimentais têm mostrado os efeitos tóxicos de agroquímicos sob abelhas sem ferrão (Valdovinos-Núñez et al. 2009; Dorneles et al. 2017; Tomé et al. 2017; Padilha et al. 2020). Abelhas do gênero *Melipona* contaminadas sofrem uma diminuição na longevidade e mudanças no comportamento que influenciam a capacidade de forrageamento (Del Sarto et al. 2014; de Moraes et al. 2018; Nocelli et al. 2019). Um estudo que investigou a suscetibilidade de *M. quadrifasciata* e *A. mellifera* aos agroquímicos Deltametrina, Metamidofós e Abamectina mostrou que a abelha nativa é, inclusive, mais suscetível do que a abelha exótica comumente usada como parâmetro para estudos de toxicidade (Del Sarto et al. 2014). Um padrão similar foi observado para a abelha sem ferrão *Partamona helleri*, mais suscetível à ação sinérgica de misturas da Deltametrina e uma formulação combinada de fungicidas comparado à *A. mellifera* (Tomé et al. 2017)

1.2.6 Perda de habitat

Cerca de um terço do território nacional já foi convertido em produção agrícola, o que tem levado à perda de grandes áreas de vegetação natural (Ferreira et al. 2012). Essa expansão está relacionada principalmente à crescente quantidade de terra usada para o cultivo de monoculturas, como a da soja, observada nos últimos anos no Brasil e outros países da América do Sul (Pacheco 2012). A invasão das florestas pelo cultivo de monoculturas afeta a saúde das abelhas pelo aumento no uso de pesticida nestes cultivares, por fragmentar habitats de nidificação e estabelecimento das colônias, e por comprometer a nutrição das abelhas uma vez que leva à perda da flora nativa que fornece diversas fontes de néctar e pólen às abelhas. Uma boa nutrição é essencial para a saúde das abelhas (Brodschneider e Crailsheim 2010). O consumo de pólen diverso, polifloral, e de boa qualidade é fisiologicamente mais saudável, contribuindo para uma maior tolerância a infecções patogênicas por garantir a disponibilidade de micronutrientes necessários e estimular a expressão de genes do sistema imune inato da abelha (Alaux, Ducloz, et al. 2010; Perry et al. 2015; Pasquale et al. 2016; Filipiak et al. 2017). Por exemplo, a alimentação com pólen polifloral aumenta a longevidade de abelhas melíferas parasitadas por *Nosema* comparado a abelhas que se alimentaram de pólen monofloral (Pasquale et al. 2013). Esta resposta também é observadas na infecção por IAPV, em que uma dieta polifloral tem o potencial de reduzir a mortalidade de abelhas infectadas (Dolezal et al. 2019).

1.3 Sistema imune e saúde da abelha

A saúde da abelha não é um tópico trivial e quando se trata de abelhas sociais, como a mandaçaia, uma colônia saudável não pode ser reduzida à ausência de patógenos ou colônias populosas. Ao estudar a saúde das abelhas deve se respeitar os diferentes níveis de complexidade do superorganismo (Figura 4), a saúde deve ser medida e investigada a nível individual, da colônia e populacional (López-Urbe et al. 2020). É o resultado da interação destes diferentes níveis que possibilitará um estado de bem-estar onde a energia é adquirida, alocada e utilizada da maneira ideal, permitindo que os indivíduos vivam mais e/ou se reproduzam mais. Nesta tese investigamos a síndrome das mandaçaia sob uma perspectiva multinível, medindo aspectos individuais (microbioma intestinal, diagnóstico de patógenos, viroma e expressão gênica), assim como medindo características da colônias (peso dos indivíduos, temperatura e umidade dentro das colônias e comportamento imune social).

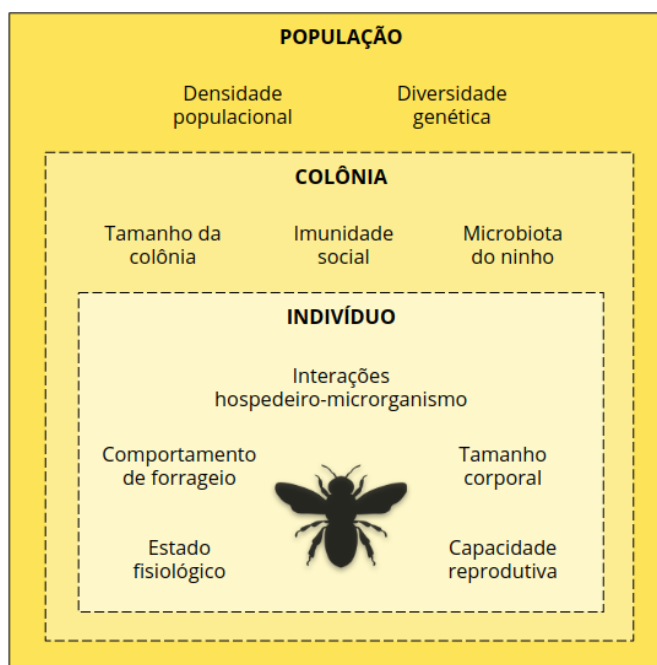


Figura 4. Os três níveis de organização biológica importantes para o estudo e discussões sobre a saúde das abelhas e, dentro de cada um, algumas das diferentes maneiras avaliá-los. As linhas pontilhadas entre os níveis representam o fluxo de informações de níveis mais específicos aos mais amplos. Por exemplo, avaliações a nível de indivíduo informam também sobre a saúde da colônia, e avaliações a nível de colônia informam também sobre a saúde a nível de população (adaptado de López-Urbe et al. 2020, ilustração da abelha de www.kindpng.com).

1.3.1 Imunidade social

A imunidade social é uma forma de defesa coletiva contra parasitas e patógenos, onde os indivíduos da colônia realizam pequenas tarefas que coletivamente têm um impacto na saúde da colônia (Cremer et al. 2007). A auto-higiene e higienização de outras abelhas da colônia é um comportamento imune social para remoção de pólen, partículas estranhas e parasitas, como ácaros, do corpo das abelhas (Jander 1976; Büchler et al. 1992; Danka e Villa 1998; Boecking e Spivak 1999). Comportamentos termorregulatórios, como a febre social gerada por abelhas operárias, são importantes no combate a patógenos sensíveis ao calor, como fungos (Simone-Finstrom et al. 2014). O comportamento higiênico envolve a detecção de células de cria com larvas mortas ou infectadas e sua remoção da colônia, evitando a disseminação de ácaros, vírus e fungos na colônia (Spivak e Gilliam 1998; Bigio et al. 2014; Toufaily et al. 2014; Al Toufaily et al. 2016). Quando a abelha adulta é quem está infectada, ela também pode abandonar a colônia para morrer fora dela, evitando a disseminação de doenças (Rueppell et al. 2010; Shorter e Rueppell 2012). Em abelhas sem ferrão podemos observar que as células de cria são preenchidas com alimento larval logo após a construção e antes da oviposição pela rainha, sendo seladas imediatamente após a oviposição (Lindauer 1976). Diferente das abelhas melíferas, em que o alimento é dado progressivamente às larvas em células de cria abertas, este comportamento impede que parasitas, como ácaros, tenham acesso à prole em desenvolvimento.

Outros comportamentos relacionados à imunidade social envolvem a auto-medicação, como o uso de resinas antimicrobianas coletadas nas plantas visitadas, que são misturadas à cera ou solo e então usadas na construção dos ninhos (Simone et al. 2009; Drescher et al. 2014; Popova et al. 2014; Drescher et al. 2017). Abelhas nutrizas também podem usar a glicose oxidase (GOX), produzida pelas abelhas que processam o néctar, no alimento larval e estoques de mel servindo como um agente antimicrobiano (Bucekova et al. 2014). A produção de GOX tem sido inclusive usada como um biomarcador de defesa imune social, apesar de sua expressão também poder variar devido a fatores genéticos e ambientais (Alaux, Ducloz, et al. 2010; López-Urbe et al. 2017; Jones et al. 2018).

1.3.2 Imunidade individual

Cada abelha de uma colônia possui resposta imune individual, podendo ser mecânica, fisiológica e imunológica. A cutícula e a membrana peritrófica revestindo o trato digestivo servem como uma primeira barreira mecânica impedindo a aderência ou entrada de microrganismos no corpo. Inibidores fisiológicos à invasão microbiana incluem alterações no pH e outras condições químicas do intestino de insetos tornando-o inóspito (Evans e Spivak 2010). Quando estas barreiras são ultrapassadas, as abelhas contam então com o sistema imune humoral (Evans et al. 2006; Wilson-Rich et al. 2008). Ele é ativado uma vez que reconhece motivos estruturais na superfície dos patógenos, os Padrões Moleculares Associados a Patógenos (PAMPs) (Brutscher et al. 2015). A sinalização desencadeada leva a ativação da resposta imune celular mediada por hemócitos, incluindo fagocitose, formação de nódulos e encapsulação da patógenos invasores, o início da cascata de fenoloxidase (PO) que regula a coagulação ou a melanização da hemolinfa, ou a síntese de AMPs (Casteels-Josson et al. 1994; Vizioli e Salzet 2002; Evans et al. 2006).

Algumas das vias da sinalização que controlam a expressão de AMPs e outros fatores antimicrobianos são Imd (*Immune Deficiency*), Jak/STAT (*Janus kinase/Signal Transducer and Activator of Transcription*) e Toll. Imd é uma via específica de resposta antimicrobiana que induz a produção de AMPs e outros genes envolvidos na defesa antimicrobiana através do fator de transcrição NF- κ B Relish. A via de sinalização JAK-STAT contribui também para o sistema imune inato induzindo transdutores de sinal e ativadores de transcrição a regular efetores antimicrobianos como TEP7 (*Thioester-containing protein 7*), TEPA, TEPB e o inibidor SOCS (*Suppressor of Cytokine Signaling*). Já a ativação do complexo Toll leva a degradação do inibidor de NF- κ B Cactus e então a translocação nuclear do fator de transcrição NF- κ B Dorsal que por sua vez aumenta a expressão de AMPs (Royet et al. 2005; Evans et al. 2006; Brutscher et al. 2015). Estas vias desempenham um papel importante para a saúde da abelhas e a desestabilização contribui para o colapso de colônias. Um exemplo vem do parasitismo pelo o ácaro *V. destructor*, que desestabiliza a resposta imune da abelha através da supressão de NF- κ B (Toll) possibilitando uma infecção mais virulenta pelo DWV (Nazzi et al. 2012).

Embora insetos não possuam anticorpos, que carregam a memória imunológica em vertebrados, eles possuem o que é chamado de imune *priming*, uma forma de imunidade transgeracional (Sadd et al. 2005; Freitak et al. 2014). Por exemplo, a prole de *A. mellifera* infectada experimentalmente por *P. larvae* tem maior resistência a uma nova infecção pelo patógeno (Hernández López et al. 2014). Posteriormente foi mostrado que a memória da infecção, que gerou resistência à prole, se dá através do transporte de fragmentos da parede celular do patógeno, contendo elicitores imunológicos, pela proteína vitelogenina (*Vg*) presente nos ovos (Salmela et al. 2015). A *Vg* também desempenha importante papel no controle do polietismo etário (Hartfelder et al. 2006; Dallacqua et al. 2007; Rodriguez Messan et al. 2018), agindo contra estresse oxidativo (Zhang et al. 2017; Park et al. 2018) e na resposta a patógenos (Alaux et al. 2011; Salmela et al. 2015; Steinmann et al. 2015). Uma menor expressão de *Vg* está associada à maturação comportamental acelerada e atividade de forrageamento em abelhas operárias, e a indução do forrageamento precoce pode também estar relacionada a uma resposta adaptativa contra transmissão de patógenos na colônia (Marco Antonio et al. 2008; Natsopoulou et al. 2016). As abelhas também possuem um sistema metabólico sofisticado que media a conversão de xenobióticos nocivos, como agroquímicos, em formas menos tóxicas. Uma das principais superfamílias enzimáticas responsáveis por esse mecanismo de desintoxicação são as monooxigenases do citocromo p450 (p450s), pertencentes à subfamília CYP9Q (Manjon et al. 2018). Já foi mostrado que p450s protegem as abelhas contra os efeitos tóxicos dos próprios inseticidas utilizados no controle de ácaros parasitas como *Varroa* (Mao et al. 2011). A expressão de p450s têm sido inclusive usada como um possível biomarcador em resposta a desafios por xenobióticos (Berenbaum e Johnson 2015; Manjon et al. 2018).

1.3.3 Microbioma de abelhas

As abelhas possuem relações com diversos simbioses bacterianos, os quais desempenham um papel importante na saúde e homeostase do indivíduo, sendo mantidos nas populações por transmissão horizontal e vertical. A comunidade bacteriana melhor caracterizada até então é a de *A. mellifera*, que é composta por cinco grupos de bactérias: dois grupos de Proteobactérias (*Gilliamella* e *Snodgrassella*), dois grupos de Firmicutes (*Lactobacillus* Firm-4 e *Lactobacillus* Firm-5) e um de Actinobacteria (*Bifidobacterium asteroides*) (Kwong e Moran 2016). Estes grupos são também predominantes em *Bombus* e nas

poucas abelhas sem ferrão já caracterizadas, sugerindo que esses *taxa* compreendem o microbioma intestinal padrão de abelhas corbiculadas (Kwong et al. 2017). Outras bactérias em menores quantidades e com nichos específicos no intestino da abelha melífera também compõem o microbioma, como *Frischella perrara*, *Bartonella apis*, *Parasaccharibacter apium* e uma bactéria relacionada à *Gluconobacter*. Enquanto *B. apis* e *F. perrana* são filotipos específicos de abelhas melíferas, *Acetobacter*-like parece ser um filotipo específico de abelhas sem ferrão (Kwong et al. 2017).

A riqueza e a composição da microbiota padrão influencia diretamente na saúde da abelha. Estudos experimentais mostraram que a suscetibilidade de *Bombus terrestris* ao parasita *Crithidia bombi* é predominantemente determinada pela composição da microbiota e apenas secundariamente pelo genoma do hospedeiro (Koch e Schmid-Hempel 2012). O metagenoma de *A. mellifera* sugere que as bactérias como *Snodgrassella* e *Gilliamella* auxiliam na produção de biofilmes e na comunicação celular da abelha, o que poderia contribuir para a proteção contra patógenos. Bactérias dos grupos Gamaproteobacteria, Firmicutes e Bifidobacteria estão provavelmente envolvidas com o transporte e quebra de carboidratos (Engel et al. 2012). O microbioma core também é importante pois, com a presença dessas bactérias intestinais controladas, as abelhas regulam positivamente a expressão gênica de AMPs como apidaecina e himenoptaecina, o que por sua vez estimula o sistema imunológico contra futuras infecções patogênicas (Kwong et al. 2017). A disbiose, caracterizada por uma alteração na composição da microbiota padrão, pode ser causada por diversos fatores de estresse bióticos e abióticos (Hamdi et al. 2011). Pesticidas, por exemplo, podem alterar a abundância relativa de *taxa* microbianos no intestino das abelhas (Motta et al. 2018; Rouzé et al. 2019). A exposição de abelhas ao agroquímico Glifosato levou a uma diminuição na abundância relativa e absoluta de espécies dominantes da microbiota intestinal, como a bactéria *S. alvi*, e também aumentou a taxa de mortalidade de abelhas infectadas pela bactéria oportunista *S. marcescens* (Motta et al. 2018).

1.4 Objetivo

Investigar as causas da síndrome anual das mandaiaias (*Melipona quadrifasciata*) com um olhar para diferentes níveis de organização biológica da colônia e o impacto de estressores ambientais.

1.4.1 Objetivos específicos

- Caracterizar a microbiota intestinal de mandaçaias;
- Verificar a ocorrência de disbiose ou presença de bactérias patogênicas associadas a mandaçaias afetadas pela síndrome;
- Caracterizar o viroma de mandaçaias;
- Avaliar se existe uma relação entre a presença de vírus eucarióticos e a manifestação da síndrome;
- Investigar se mandaçaias adquiriram vírus da abelha exótica *A. mellifera*;
- Determinar a contribuição da genética das colônias e do ambiente para a ocorrência da síndrome;
- Mensurar a resposta imune e comportamental de mandaçaias, em nível de indivíduo e colônia, através de abordagem temporal;
- Investigar o papel de fatores ambientais no desencadeamento da síndrome anual.

CAPÍTULO 2

Report on the microbiota of *Melipona quadrifasciata* affected by a recurrent disease.

Este capítulo apresenta o seguinte artigo publicado:

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Short Communication

Report on the microbiota of *Melipona quadrifasciata* affected by a recurrent disease

Sebastián Díaz^a, Sarah de Souza Urbano^b, Lílian Caesar^a, Betina Blochtein^c, Aroni Sattler^d, Valmir Zuge^e, Karen Luisa Haag^{a,b,*}

^a Programa de Pós-Graduação em Genética e Biologia Molecular, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, CEP 91501-970 Porto Alegre, RS, Brazil

^b Departamento de Genética, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, CEP 91501-970 Porto Alegre, RS, Brazil

^c Departamento de Biodiversidade e Ecologia, Faculdade de Biociências, Pontifícia Universidade Católica do RS, Av. Ipiranga 6681, CEP 90619-900 Porto Alegre, RS, Brazil

^d Laboratório de Apicultura, Departamento de Fitossanidade, Faculdade de Agronomia, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 7712, CEP 91540-000 Porto Alegre, RS, Brazil

^e Associação dos Meliponicultores do Vale do Taquari, Av. Casca 227, CEP 95920-000 Boqueirão do Leão, RS, Brazil

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ABSTRACT

Melipona quadrifasciata is an eusocial stingless bee traditionally used for honey production in Brazil. In the last decades, the species disappeared from the wild in Southern Brazil, being kept exclusively in managed colonies for commercial and recreational purposes. Stingless beekeepers from this region report annual losses of their colonies due to a syndrome of yet unknown causes. We investigate whether it is associated to pathogenic microorganisms already known to cause disease in bees. These results provide a starting point for future studies aimed at clarifying the relationship between the microbial community of stingless bees and their colony collapses.

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1. Introduction

Stingless bees (Apidae, Meliponini) are the only highly social bees other than the true honeybees. In Brazil and other parts of South America stingless bees are by far the most abundant bee species, suggesting that they have a prominent role as pollinators in this region (Giannini et al., 2015; Heard, 1999). Before the introduction of honey bees in the 19th century, colonies of stingless bees and wasps were the only sources of honey used in Brazil (Nogueira-Neto, 1997), and stingless bee culture represents an old aboriginal tradition that helps to increase agricultural production by maintaining ecological interactions (Garibaldi et al., 2016). *Melipona quadrifasciata* is one of the most popular stingless bees cultivated in Brazil (Jaffé et al., 2015), where it is called “man daçaia”, which in the indigenous language means “beautiful vigilant”, referring to the guard that permanently protects the nest entrance. Two *M. quadrifasciata* subspecies that show significant

genetic divergence are recognized by their different abdomen coloration patterns, i.e., *M. q. anthidioides*, found in the southeast and northern Brazil, and *M. q. quadrifasciata*, which occurs in the south (Batalha-Filho et al., 2010; Tavares et al., 2013).

In the southernmost state of Brazil, Rio Grande do Sul, which corresponds to the southern limit of *M. quadrifasciata*'s geographic distribution, wild populations disappeared since more than 50 years, and the species is now regarded as endangered (Blochtein and Marques, 2003; Fundação Zoobotânica, 2014). Furthermore, numerous beekeepers from Rio Grande do Sul have been reporting annual losses of their *M. quadrifasciata* colonies. At the end of summertime, between February and April, workers become unable to fly and crawl with their proboscis everted, leading to massive deaths that ultimately end with the colony collapse. Although such collapses happen synchronously in many different localities, they can't be connected to a common environmental factor, such as a potentially toxic flower or pesticides. Deaths occur in colonies from very dissimilar habitats.

Symbiotic bacteria are known to play an important role in bee health (Hamdi et al., 2011; Vásquez et al., 2012). Pathogens, viruses or other factors may interfere with the normal composition of bacteria associated to the bee gut epithelium (Cariveau et al., 2014;

* Corresponding author at: Programa de Pós-Graduação em Genética e Biologia Molecular, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, CEP 91501-970 Porto Alegre, RS, Brazil.

E-mail address: karen.haag@ufrgs.br (K.L. Haag).

Cox-Foster et al., 2007) and in turn the bacterial colonization interferes with subsequent susceptibility to infections (Koch and Schmid-Hempel, 2012; Schwarz et al., 2016). The aim of the present study is to investigate whether the syndrome that annually leads to *M. quadrifasciata* colony collapses in Southern Brazil is correlated to infection with pathogenic bacteria. We describe, for the first time, the bacterial symbiont communities of this stingless bee species based on high throughput sequencing of 16S rDNA.

2. Materials and methods

2.1. Sampling and DNA extraction

M. quadrifasciata adult individuals manifesting symptoms of disease, i.e., disorientation, flight incapacity or proboscis eversion (unhealthy; $n = 52$) as well as without any detectable symptom (healthy; $n = 24$) were removed from their colonies for DNA extraction using a clean forceps. Stingless bee colonies were sampled in two summers (February/March) of 2014 and 2015 in two localities of Rio Grande do Sul, i.e., Boqueirão do Leão (30°3'9.7"S; 51°11'6.03"W) and Porto Alegre (30°4'30.3"S; 51°8'4.5"W). DNA was extracted using the DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) from individual abdomens, which were separated from bee bodies in aseptic conditions using sterile scalpels.

2.2. Metabarcoding of bacteria, and their possible link to disease

A segment of the bacterial 16S rDNA gene corresponding to the V1-V3 variable region was amplified from the DNA samples with modified barcoded versions of primers 27F (GAGTTTGATCCTGGCT-CAG) (Lane, 1991) and 519R (GTNTTACNGCGGCKGCTG) (Turner et al., 1999) and sequenced using Illumina MiSeq technology. Reads were processed with Mothur v. 1.36.1 (Schloss et al., 2009). After filtering out low quality sequences, chimeras were removed with UCHIME (Edgar et al., 2011), as well non-bacterial sequences, based on a preliminary classification using the SILVA v123 nr database (Quast et al., 2013). Only samples containing at least 500× coverage were retained in subsequent analyses ($n = 33$; see Table S1). Sequences showing $\geq 95\%$ identity were clustered in Operational Taxonomic Units (OTUs). A non-metric multidimensional scaling (NMDS) of Bray-Curtis dissimilarities among bacterial communities was performed in PAST version 3.13 (Hammer et al., 2001). To investigate the dynamics of stingless bee microbiota we also performed a Permutational Multivariate Analysis of Variance (PERMANOVA) of Bray-Curtis pairwise distances, in which the factors “sampling year”, “colony” and “health status”, as well as their interactions, were tested as sources of variation in bacterial community composition. The phylogenetic affinities among principal bacterial OTUs was inferred by maximum likelihood using a dataset of known bee symbiont sequences obtained from GenBank as reference. Alignment was made with MAFFT v. 7.187 (Katoh and Standley, 2013), and phylogenetic analysis was performed with PhyML (Guindon and Gascuel, 2003) using the GTR + G + Inv model ($\alpha = 0.5$), which showed the best AIC score in ModelTest (Darrriba et al., 2012). Local support values were estimated by nonparametric bootstrap based on 500 resamplings.

3. Results and discussion

The 16S rRNA amplicons from 33 *M. quadrifasciata* individuals belonging to 11 colonies (Table S1) yielded a total of 52,545 sequences (mean \pm SD = 1592 \pm 770 per sample) that were binned into 276 OTUs (mean \pm SD = 29 \pm 12 per sample). Rarefaction curves reach OTU saturation, indicating a good sampling (Fig. S1).

The 32 OTUs with ≥ 100 sequences (GenBank accession numbers KX021311-KX021342) that represent 93.8% of the dataset were used for further analyses. The *M. quadrifasciata* bacterial symbiont OTUs were classified in 11 clades (Fig. 1), seven of them belonging to Firmicutes, which correspond to 73.4% of the total sampling.

Overall, the seven clades of Firmicutes and 3 OTUs of Proteobacteria belonging to the family Acetobacteriaceae are the most representative bacteria; Firmicutes Group U, Firmicutes Group Z and Acetobacteraceae correspond respectively to 23%, 23% and 16% of the total sampling. Though OTU frequencies show extensive variation across *M. quadrifasciata* individuals (Fig. 2), the factor that best explains variations in microbiota composition is the colony ($F = 2.752$; $p = 0.0006$); however no significant associations are found between year of sampling ($F = 1.112$; $p = 0.3405$) or stingless bee health status ($F = 0.854$; $p = 0.4915$) and microbiota composition. Interestingly, although main effects of sampling year and health status are not statistically significant, their interaction effect is ($F = 1.146$; $p = 0.0218$), suggesting that the effect of bee health status on microbiota composition is not the same in both years. Overall, there is a crossover effect of sampling year and health status on microbiota composition, which is possibly caused by the higher abundance of Firmicutes group U and Z bacteria in unhealthy bees on 2014, but in healthy bees of 2015 (see Fig. 2). This conclusion is also supported by NMDS, where unhealthy bees of different sampling years fall on opposite sides of coordinate 1 (Fig. S2). Therefore, we tentatively suggest that the syndrome manifested by *M. quadrifasciata* colonies may have a link to its microbiota composition, but we haven't been able to detect it with this preliminary study. Nevertheless, no pathogenic bacteria known for the honeybee, such as *Spiroplasma*, *Melissococcus* and *Paenibacillus* that cause foulbrood disease, and mostly affect honeybee larvae (Bailey and Ball, 1991), were found in our samples.

The main bacterial OTUs identified in our study are phylogenetically related to other known bee symbionts (Fig. 1). Firmicutes group U is related to *Lactobacillus kunkeii*, and belongs to a clade of common symbionts of stingless bee species such as *Tetragonula carbonaria* and *Austroplebeia australis* (Fig. S3; Leonhardt and Kaltenpoth, 2014). Firmicutes group Z clusters with the so-called Firm-5 clade of lactic acid bacteria (Martinson et al., 2011). Different species from this clade were found in *Melipona panamica* (Koch et al., 2013), *Bombus* sp. (Praet et al., 2015) and *Apis mellifera* (Olofsson et al., 2014). The Lactobacillales and the Acetobacteraceae are mostly found in the honeybee stomach and rectum as well as in its hive products (Moran, 2015). Proteobacteria that are dominant in the honeybee ileum, such as *Gilliamella* and *Frischella* (Gammaproteobacteria) or *Snodgrassella* (Betaproteobacteria) are absent in our samples, concordant with previous studies of Meliponini microbiota (Koch et al., 2013). However, a clade of bacteria belonging to the Enterobacteriaceae (Gammaproteobacteria), which are common symbionts of the honeybee ileum, appears in low frequency in our dataset (2% of total sampling), but surprisingly in only four unhealthy individuals (Fig. 2; Table S1). The 16S sequence of this bacterium clusters with another found in the gut of *Eulaema* sp. (Euglossini) from Panama (Fig. 1), and is close to *Yokenella regensburgei* (Koch et al., 2013). Firmicutes group W, which represents 15% of our sampling, is phylogenetically related to *Streptococcus*, a bacterial genus known for causing opportunistic infections in larvae affected by foulbrood disease (Bailey et al., 1973). However, its previously reported presence in *M. panamica* (Koch et al., 2013), as well as the occurrence in healthy and unhealthy *M. quadrifasciata* individuals of the present study suggests a non-pathogenic interaction of *Streptococcus* and *Melipona*. Likewise, we haven't been able to detect other well-known eukaryotic bee pathogens (*Nosema* or *Crithidia*) by PCR (data not shown).

The lack of any direct evidence leaves the question of what is killing *M. quadrifasciata* colonies in Southern Brazil still open. Bee-

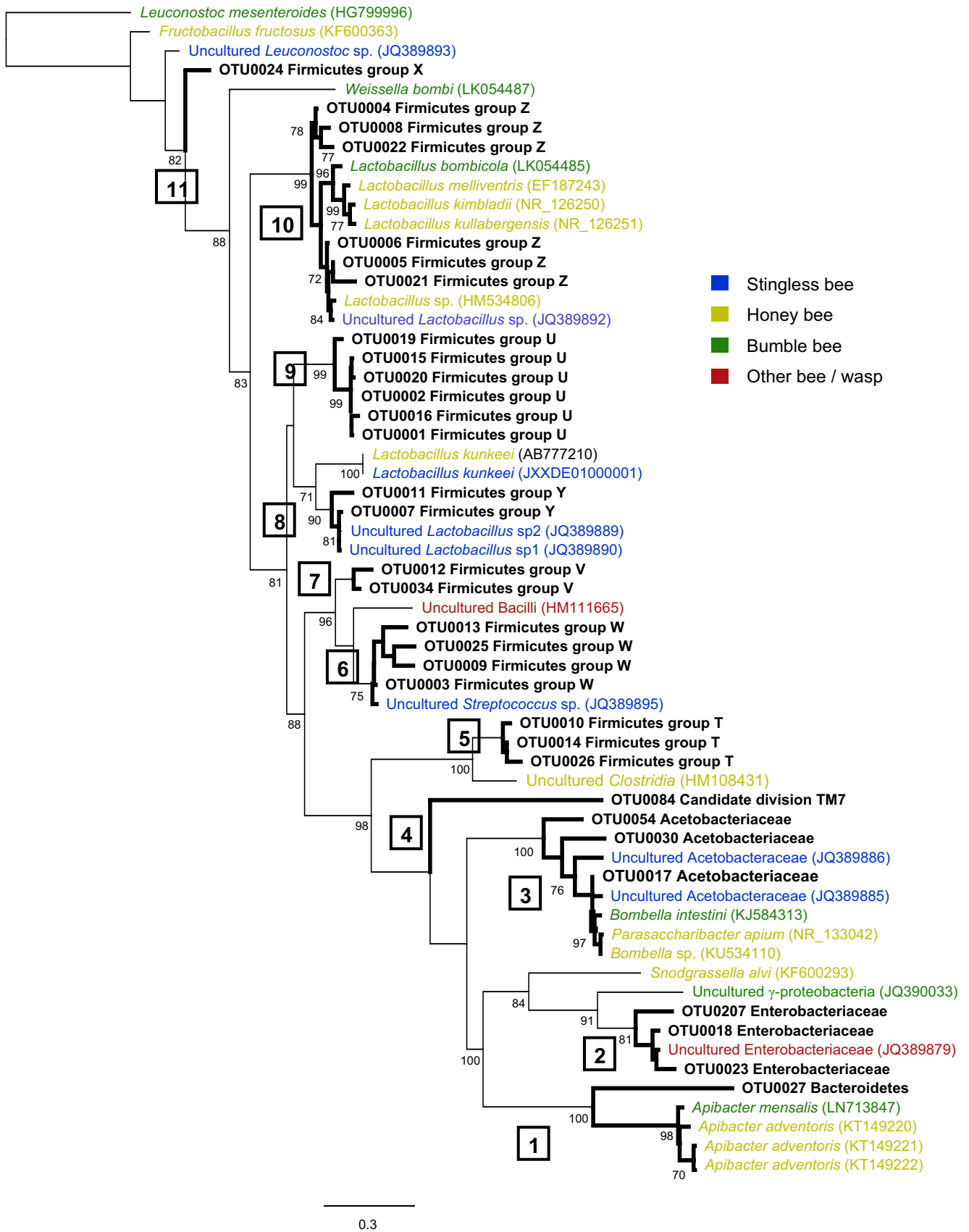


Fig. 1. Phylogenetic reconstruction based on bacterial 16S rRNA sequences. Thirty-two *Melipona quadrifasciata* symbiont OTUs belonging to 11 major clades (shown in bold) are compared to sequences from bacteria previously characterized for other bees, identified by their respective accession numbers. Bootstrap support values larger than 70% are shown at the respective branch nodes.

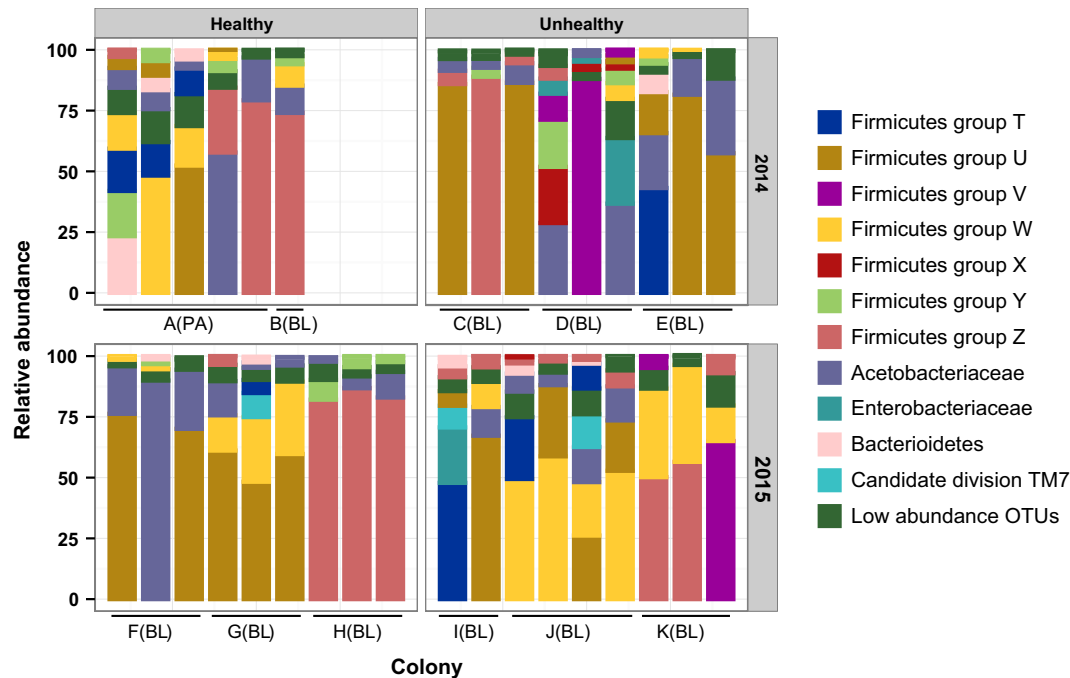


Fig. 2. Relative abundance of the 11 most representative bacterial taxa (clades) of healthy and unhealthy *Melipona quadrifasciata* sampled in two consecutive years. Letters indicate individuals from the same colony; PA and BL refer to the sampling localities, Porto Alegre and Boqueirão do Leão, respectively.

keepers learned that by preventing bees from leaving the colony, or by moving the colony to another locality, it is often possible to avoid the collapse, which makes them suspect that a toxic plant is poisoning their bees, but we observed that the pollen types in the crop of both healthy and unhealthy adults are indistinguishable (data not shown). *M. quadrifasciata* adults seem to forage mostly on *Eucalyptus* spp. – an observation corroborated by other studies on *Melipona* feeding habits in Southern Brazil (Hilgert-Moreira et al., 2014) – and on native Asteraceae, such as *Vernonanthura tweediana*, that bloom in the region in this time of the year. We think that, as already suggested for colony collapses of honeybees (Goulson et al., 2015; Nazzi et al., 2012; VanEngelsdorp et al., 2010), a synergistic effect of multiple factors, such as environmental stresses caused by climatic change, intensive management and the use of pesticides, as well as biological factors that haven't been assessed in the present study, such as viruses or other pathogens, may be at the heart of the problem.

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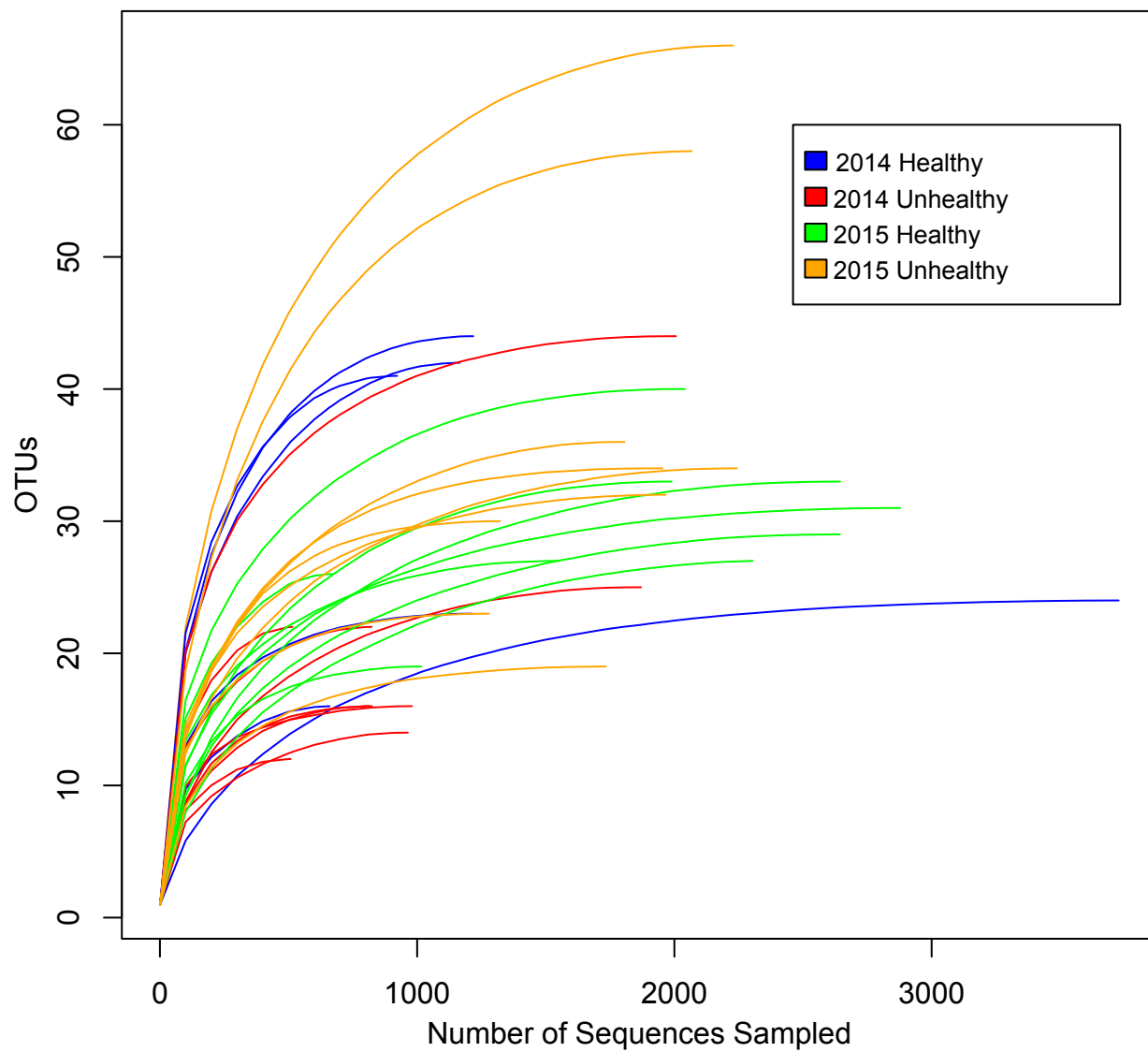
Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.jip.2016.11.012>.

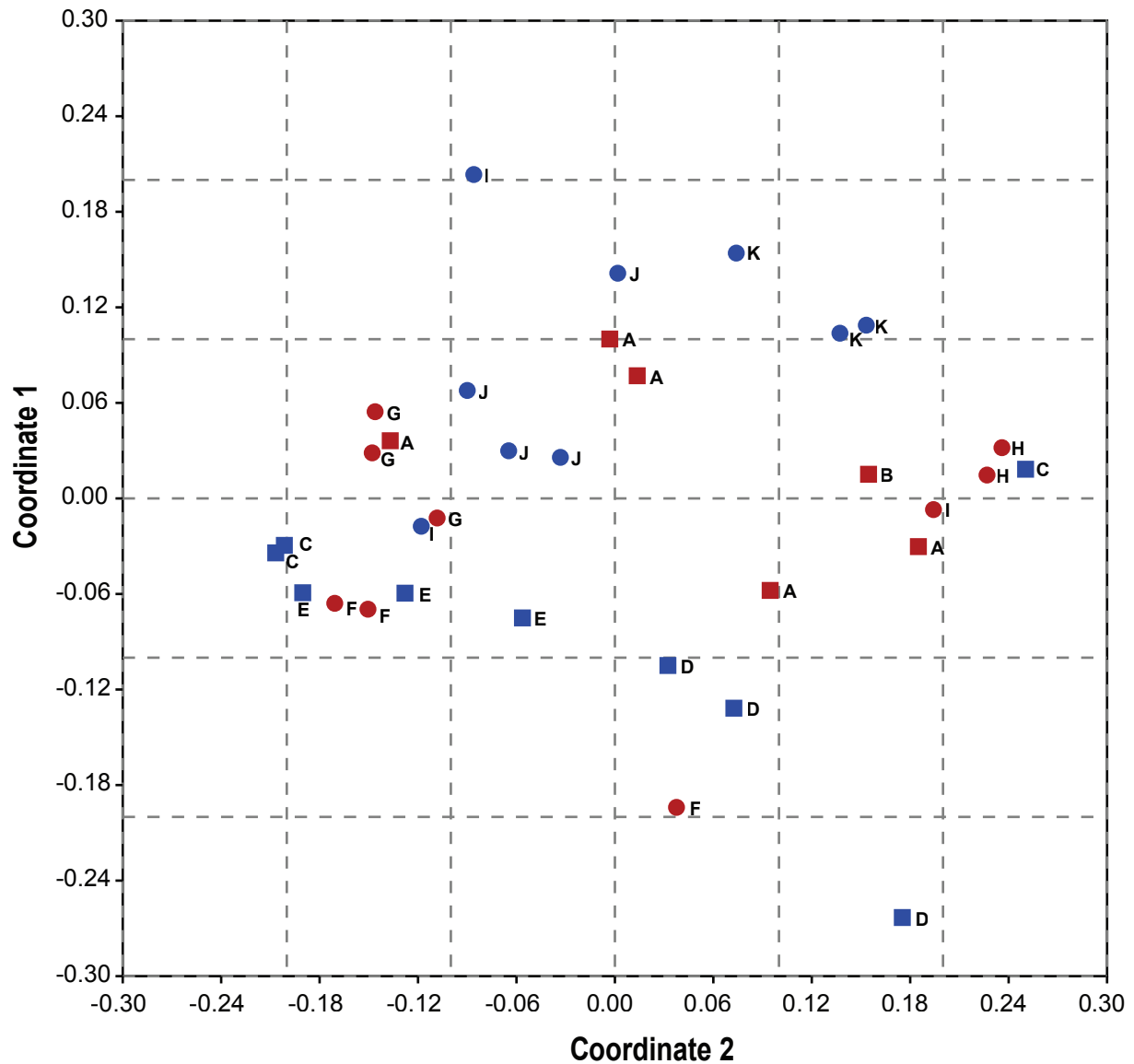
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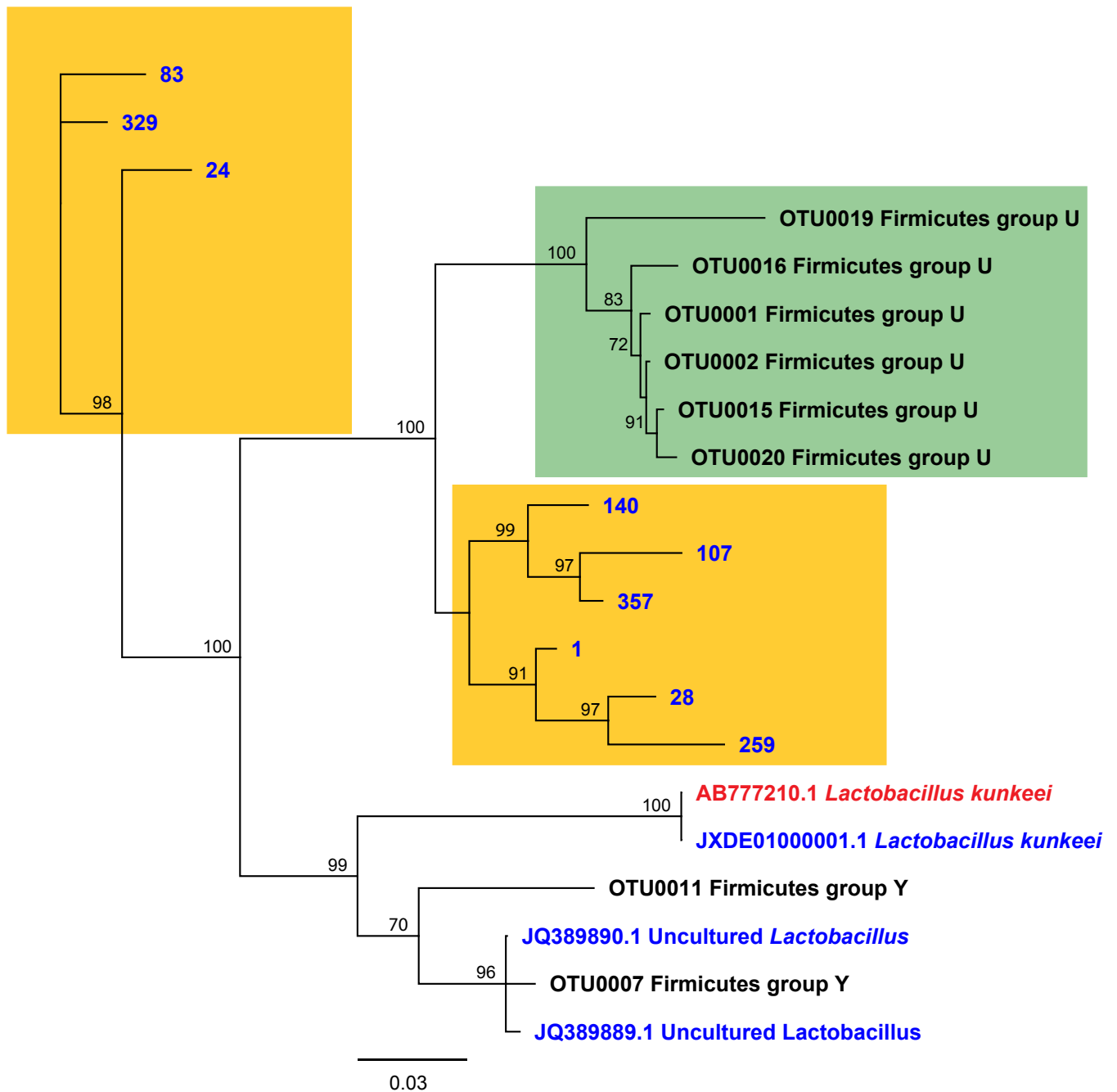
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Supplementary Figure 1. Microbiota rarefaction curves. Each line represents the cumulative fraction of bacterial community represented by the OTUs sampled for each *Melipona quadrifasciata* individual.



Supplementary Figure 2. NMDS ordination plot. Microbial communities are discriminated by Bray-Curtis dissimilarity on two coordinates (stress=0.19). Samples derived from unhealthy and healthy stingless bees are shown in blue and red respectively; squares represent samples from 2014 and circles correspond to samples from 2015. Letters indicate the respective colony of each stingless bee.



Supplementary Figure 3. Phylogenetic relationships of OTUs belonging to Firmicutes group U. Yellow boxes indicate Meliponini-associated OTUs previously identified by Leonhardt and Kaltenpoth (2014) in Australian stingless bees. These bacteria belong to a sister clade of Halictidae-associated Lactobacillales (see Leonhardt and Kaltenpoth for details). Sequences obtained in our study are shown in black, whereas blue and red represent sequences obtained in other studies from stingless bees and honey bees, respectively.

Table S1

Group	Year	Local	Healthy	Colony	# Sequences	# OTUs	Shannon	Chao1	Inverse Simpson	Clade Abundance (%)											
										Firmicutes group T	Firmicutes group U	Firmicutes group V	Firmicutes group W	Firmicutes group X	Firmicutes group Y	Firmicutes group Z	Acetobacteriaceae	Enterobacteriaceae	Bacteroidetes	Candidate division TM7	Low abundance OTUs
Agr10	2014	PA	Yes	A	1166	42	2.61	42.00	8.74	17.41	4.55	0.00	14.67	0.00	18.61	2.92	8.15	0.00	23.33	0.00	10.38
Agr13	2014	PA	Yes	A	922	41	2.37	41.00	4.59	13.77	5.10	0.00	48.26	0.00	4.77	0.76	7.81	0.00	5.97	0.00	13.56
Agr14	2014	PA	Yes	A	1218	44	2.45	44.00	6.54	10.51	52.38	0.00	16.26	0.00	0.49	0.33	3.78	0.00	3.12	0.00	13.14
Agr30	2014	PA	Yes	A	1214	23	1.68	23.00	2.83	0.00	1.57	0.00	2.14	0.00	5.11	26.69	57.74	0.00	0.00	0.00	6.75
Agr33	2014	PA	Yes	A	3727	24	0.76	24.00	1.57	0.00	0.00	0.00	0.13	0.00	0.21	79.23	17.63	0.00	0.00	0.00	2.79
Wal00	2014	PA	Yes	B	659	16	1.85	16.00	5.11	0.00	0.00	0.00	8.80	0.00	3.34	74.05	11.23	0.00	0.00	0.00	2.58
Mq021	2014	BL	No	C	824	16	1.36	16.00	2.75	0.00	85.92	0.00	0.85	0.00	0.00	5.46	4.85	0.00	0.00	0.00	2.91
Mq023	2014	BL	No	C	813	16	1.27	16.00	2.61	0.00	0.25	0.00	0.86	0.00	3.69	88.93	3.69	0.00	0.00	0.00	2.58
Mq024	2014	BL	No	C	508	12	1.32	12.00	2.63	0.00	86.42	0.00	0.59	0.00	0.00	3.54	8.07	0.00	0.00	0.00	1.38
Mq1A1	2014	BL	No	D	515	22	2.26	22.00	7.39	0.00	0.78	10.68	0.97	23.11	19.42	5.24	28.74	6.21	0.00	0.00	4.85
Mq1A3	2014	BL	No	D	1870	25	0.71	25.00	1.31	0.00	0.00	88.02	0.21	3.37	0.16	0.21	1.93	2.35	0.00	0.00	3.74
Mq1A4	2014	BL	No	D	2006	44	2.56	44.00	7.91	0.00	2.34	2.29	6.48	3.09	5.98	0.00	36.69	27.02	0.00	0.00	16.10
Mq1B1	2014	BL	No	E	823	22	2.12	22.00	6.05	43.13	16.89	0.24	2.43	0.00	3.28	0.00	22.60	0.00	8.02	0.00	3.40
Mq1B2	2014	BL	No	E	964	14	1.34	14.00	2.90	0.00	81.54	0.00	1.24	0.00	0.31	0.00	15.56	0.00	0.00	0.00	1.35
Mq1B3	2014	BL	No	E	980	16	1.67	16.00	4.10	0.00	57.45	0.00	0.61	0.00	0.00	0.00	30.71	0.00	0.00	0.00	11.22
MqVD1	2015	BL	Yes	F	2304	27	1.38	27.00	3.01	0.00	76.26	0.00	1.26	0.00	0.00	0.48	19.57	0.00	0.00	0.00	2.43
MqVD2	2015	BL	Yes	F	2644	33	0.73	33.00	1.30	0.00	0.15	0.00	2.12	0.00	1.97	1.17	89.94	0.00	0.00	0.00	4.65
MqVD3	2015	BL	Yes	F	2643	29	1.48	29.00	3.27	0.00	70.07	0.00	0.38	0.00	0.00	0.76	24.33	0.00	0.00	0.00	4.46
MqVF1	2015	BL	Yes	G	669	26	2.17	26.00	5.89	0.00	61.14	0.00	14.50	0.00	0.00	3.59	14.05	0.00	0.00	0.00	6.73
MqVF2	2015	BL	Yes	G	2041	40	2.28	40.00	6.20	5.39	48.31	0.00	26.60	0.00	0.00	0.78	2.20	0.00	1.81	9.90	5.00
MqVF3	2015	BL	Yes	G	1554	27	2.00	27.00	5.04	0.00	59.72	0.00	29.79	0.00	0.00	1.03	2.83	0.00	0.00	0.00	6.63
MqVG1	2015	BL	Yes	H	2878	31	1.55	31.00	2.78	0.00	0.00	0.07	0.45	0.00	8.13	82.07	1.70	0.00	0.00	0.07	7.51
MqVG2	2015	BL	Yes	H	1989	33	1.50	33.00	2.48	0.00	0.50	0.00	0.35	0.00	3.67	86.78	4.88	0.00	0.00	0.00	3.82
MqVG3	2015	BL	Yes	H	1016	19	1.54	19.00	3.00	0.00	0.00	0.00	0.79	0.00	1.67	82.97	10.53	0.00	0.00	0.00	4.04
MqVB4	2015	BL	No	I	1806	36	2.04	36.00	4.75	47.84	6.04	0.00	0.11	0.00	0.00	4.49	0.39	22.81	3.71	8.91	5.70
MqVB5	2015	BL	No	I	1322	30	1.95	30.00	4.53	0.00	67.25	0.00	10.36	0.00	0.00	4.61	11.80	0.00	0.00	0.00	5.98
MqVE1	2015	BL	No	J	2067	58	2.12	58.00	3.97	25.45	1.02	0.00	49.44	0.00	0.10	1.50	7.40	0.00	4.21	0.39	10.50
MqVE2	2015	BL	No	J	2243	34	1.77	34.00	3.46	0.00	29.29	0.00	58.76	0.00	0.00	2.18	5.17	0.00	0.00	0.00	4.59
MqVE3	2015	BL	No	J	2228	66	2.73	66.00	9.43	10.23	26.17	0.00	21.99	0.00	0.00	1.53	14.45	0.00	1.57	13.46	10.59
MqVE4	2015	BL	No	J	1954	34	1.93	34.00	3.89	0.00	20.73	0.00	52.81	0.00	0.00	6.55	14.02	0.00	0.00	0.00	5.89
MqVH1	2015	BL	No	K	1966	32	1.91	32.00	4.27	0.00	0.20	4.53	36.42	0.00	0.00	50.20	0.10	0.00	0.00	0.00	8.55
MqVH2	2015	BL	No	K	1733	19	1.54	19.00	3.64	0.00	0.29	0.00	39.87	0.00	0.00	56.49	0.12	0.00	0.00	0.00	3.23
MqVH3	2015	BL	No	K	1279	23	1.67	23.00	2.91	0.00	0.00	65.05	14.62	0.00	0.55	6.49	0.00	0.00	0.00	0.00	13.29

CAPÍTULO 3

The virome of an endangered stingless bee suffering from annual mortality in southern Brazil

Este capítulo apresenta o seguinte artigo publicado:

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The virome of an endangered stingless bee suffering from annual mortality in southern Brazil

Lílian Caesar¹, Samuel Paulo Cibulski², Cláudio Wageck Canal², Betina Blochtein³, Aroni Sattler⁴ and Karen Luisa Haag^{1,5,*}

Abstract

Meliponiculture – the management of stingless bee colonies – is an expanding activity in Brazil with economic, social and environmental potential. However, unlike in apiculture, the pathogens that impact on meliponiculture remain largely unknown. In southern Brazil, every year at the end of the summer, managed colonies of the stingless bee *Melipona quadrifasciata* manifest a syndrome that eventually leads to collapse. Here we characterize the *M. quadrifasciata* virome using high-throughput sequencing, with the aim of identifying potentially pathogenic viruses, and test whether they are related to the syndrome outbreaks. Two paired viromes are explored, one from healthy bees and another from unhealthy ones. Each virome is built from metagenomes assembled from sequencing reads derived either from RNA or DNA. A total of 40621 reads map to viral contigs of the unhealthy bees' metagenomes, whereas only 11 reads map to contigs identified as viruses of healthy bees. The viruses showing the largest copy numbers in the virome of unhealthy bees belong to the family *Dicistroviridae* – common pathogenic honeybee viruses – as well as *Parvoviridae* and *Circoviridae*, which have never been reported as being pathogenic in insects. Our analyses indicate that they represent seven novel viruses associated with stingless bees. PCR-based detection of these viruses in individual bees (healthy or unhealthy) from three different localities revealed a statistically significant association between viral infection and symptom manifestation in one meliponary. We conclude that although viral infections may contribute to colony collapses in the annual syndrome in some meliponaries, viruses spread opportunistically during the outbreak, perhaps due to colony weakness.

INTRODUCTION

Stingless bee management in Brazil began with indigenous South Americans, who domesticated the non-aggressive native bees as a source for honey [1]. One of these bees, *Melipona quadrifasciata*, which is distributed from the state of Paraíba in the north of Brazil through to the southernmost state, Rio Grande do Sul [2], is the second most cultivated stingless bee in Brazil [3]. In spite of being widely cultivated, natural

populations of stingless bees in the neotropics have reduced drastically in recent years due to different factors, ranging from habitat fragmentation to the introduction of exotic bees [4] that not only compete for resources, but also bring new pathogens to which native bees might be susceptible. In most of southern Brazil, wild populations of the subspecies *M. q. quadrifasciata* have been disappearing for 50 years. The species is currently mostly maintained through management

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Author affiliations: ¹Programa de Pós-Graduação em Genética e Biologia Molecular, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, CEP 91501-970, Porto Alegre, RS, Brazil; ²Laboratório de Virologia, Faculdade de Veterinária, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9090, CEP 91540-000, Porto Alegre, RS, Brazil; ³Escola de Ciências, Pontifícia Universidade Católica do Rio Grande do Sul, Av. Ipiranga 6681, CEP 90619-900, Porto Alegre, RS, Brazil; ⁴Laboratório de Apicultura, Departamento de Fitossanidade, Faculdade de Agronomia, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 7712, CEP 91540-000, Porto Alegre, RS, Brazil; ⁵Departamento de Genética, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves 9500, CEP 91501-970, Porto Alegre, RS, Brazil.

*Correspondence: Karen Luisa Haag, karen.haag@ufrgs.br

Keywords: *Melipona*; Apidae; virome; colony collapse; bee virus.

Abbreviations: ABPV, *Acute bee paralysis virus*; BLAST, Basic Local Alignment Search Tool; BQCV, *Black queen cell virus*; BU, Barnard's Unconditional test; CCD, Colony collapse disorder; CDS, Coding sequence; CMH, Cochran-Mantel-Haenszel; DWV, *Deformed wing virus*; IAPV, *Israeli acute paralysis virus*; KBV, *Kashmir bee virus*; MqC, *Melipona quadrifasciata cyclovirus*; MqC1, *Melipona quadrifasciata cyclovirus 1*; MqC2, *Melipona quadrifasciata cyclovirus 2*; MqD, *Melipona quadrifasciata densovirus*; MqV2, *Melipona quadrifasciata virus 2*; MqV1a, *Melipona quadrifasciata virus 1a*; MqV1b, *Melipona quadrifasciata virus 1a*; SBPV, *Slow bee paralysis virus*; VDV1, *Varroa destructor virus-1*.

MK190907 (MqC1), MK190906 (MqC2), MH340498 (MqD), MH340499 (MqV1a) and MH34500 (MqV1b), MK190905 (MqV2).

Two supplementary figures and four supplementary tables are available with the online version of this article.

in this region, and is therefore considered to be endangered [5, 6]. Managing stingless bees has been crucial for conservation, but on the other hand, practices that involve hive translocation may also spread pathogens [7]. Despite advances in beekeeping legislation and monitoring, there is no official bee surveillance in Brazil and, consequently, there are no regular records on bee mortality caused by pathogens. Nevertheless, it is a common knowledge among beekeepers from different localities in southern Brazil that every year at the end of the summer – normally during the first week of March – their *M. quadrifasciata* bees begin to manifest an unusual behaviour that may include tremors, crawling with everted proboscis and paralysis [8]. Although the disease symptoms are quite variable among stingless bees from different localities, during this period it is common to find large numbers of dead bees inside or in front of hives. Mortality, and the inability of bees to perform their regular activities, sometimes lead to colony collapse. Our previous studies on the *M. quadrifasciata* syndrome searched the associated microbiota for pathogenic bacteria or imbalances in bacterial community composition that could explain the symptoms [8]. However, no consistent differences in microbiota composition were found between healthy and unhealthy bees. While *Apis mellifera* shows a highly conserved core microbiota [9], *M. quadrifasciata*'s associated bacterial community is highly variable across colonies, independent of their health status. Furthermore, no pathogenic bacteria or other common bee pathogens such as *Nosema* and *Crithidia*, were detected in unhealthy bees.

Several viruses have already been identified in *A. mellifera* in Brazil [10], mainly in samples from areas where abnormal population declines have been observed [11]. These have included *Iflaviridae* such as the *Deformed wing virus* (DWV), and *Dicistroviridae* such as the *Black queen cell virus* (BQCV), *Acute bee paralysis virus* (ABPV) and *Israeli acute paralysis virus* (IAPV) [11, 12]. Characteristic symptoms of DWV infections are the death of pupae, or adult bees with deformed wings, sometimes associated with shortened and bloated abdomens, and miscolouring [13]. However, DWV may persist in covert infections with no apparent symptoms [14, 15], in spite of having strongly deleterious effects on honeybee foraging and survival [16]. Similarly, dicistroviruses may also persist with no obvious symptoms at the individual or colony level [17]. Nevertheless, it has been shown that an increase in BQCV titre kills developing queen larvae, whose necrotic remains result in a pupal cell with a darkened colour [18]. Other viruses of this family, such as ABPV and IAPV, are known to cause paralysis [19, 20]. They are extremely virulent when injected into pupae or adults, causing disease in the honeybee with fewer than 100 viral particles [21]. Honeybees experimentally infected with IAPV develop symptoms such as crawling, disorientation and trembling wings, which progress to paralysis and death within or outside the hive [22, 23]. Furthermore, viruses with RNA genomes such as the *Iflaviridae* and *Dicistroviridae*, which show higher mutation rates, quickly evolve into many variants, allowing them to switch between different bee hosts [24–26]. An example of viral host switching between bee species is the detection

of honeybee virus ABPV in managed colonies of *M. scutellaris* suffering from an unexpected increase in worker bee mortality in Brazil [27].

The main routes of virus transmission between bees are vectors such as mites or pollen resource sharing [28]. The most studied vector in honeybees is *Varroa destructor*, which transmits different lineages of DWV, *Varroa destructor virus-1* (VDV1) and IAPV [29–31]. These and many other viruses are also transmitted within and between species via floral sources [24, 32]. Bee species sharing habitats and resources tend to have similar associated micro-organisms. A study on viral distribution via pollen sources showed that in apiaries with colonies affected by colony collapse disorder (CCD), IAPV virus was associated with *A. mellifera* as well with non-*Apis* hymenopteran pollinators [32]. At the same time, in nearby apiaries not affected by CCD, the virus was present in neither *A. mellifera* nor non-*Apis* hymenopterans. The persistence of BQCV, DWV, ABPV and *Slow bee paralysis virus* (SBPV) in wild bumblebee populations in Europe, often at putatively low levels, may also result from indirect interactions with local *A. mellifera* through the shared use of floral resources [24].

Recent studies using high-throughput sequencing technologies expanded the list of known honeybee viruses, previously restricted to the Picornavirales [33]. Among the recently identified viruses are those from the family *Rhabdoviridae* with –ssRNA genomes, ssDNA viruses belonging to the families *Circoviridae* and *Parvoviridae*, and dsDNA viruses from the family *Nudiviridae* [34–36]. These viruses were identified in honeybees displaying variable health conditions. Hence, the viromes of bees have revealed that, in addition to the complex network of host-associated bacteria [9], a very diverse range of viruses are probably acting on and interacting in the bacterial network. Different bee viruses are frequently detected in healthy and unhealthy hosts [24, 34, 35, 37]. Chronic viral infections may become harmful by increasing their loads in genetically predisposed individuals, depending on the environmental conditions [37–39], or may become symbiotic [40].

Given that the symptoms observed in *M. quadrifasciata* affected by the annual syndrome resemble those of honeybee viral diseases such as IAPV and ABPV, and given that stingless bees probably host yet unidentified viruses, some of which may have been spread by honeybees due to beekeeping practices, we focus our investigation on viruses that might be implicated in the disease. Using high-throughput sequencing to characterize the virome of *M. quadrifasciata*, we identify seven novel stingless bee viruses.

RESULTS

Viromes of healthy and unhealthy *M. quadrifasciata*

In order to find viruses associated with the *M. quadrifasciata* syndrome, worker bees from a single colony showing disease symptoms such as tremor and paralysis (unhealthy bees), as well as workers from another colony where none of the individuals showed such symptoms (healthy bees), were

sampled from the same meliponary (place where stingless bees are reared). Each bee pool was macerated and underwent subsequent centrifugation steps, including an ultracentrifugation with a sucrose cushion for virus enrichment. The nucleic acids were then subjected to high-throughput sequencing, yielding the following number of paired-end reads: 640 953 (DNA sample from unhealthy bees=UDNA), 535 631 (DNA sample from healthy bees=HDNA), 582 603 (RNA sample from unhealthy bees=URNA) and 834 753 (RNA sample from healthy bees=HRNA). After assembly, viral contigs larger than 200 bp were classified based on the best BLASTX hit against the nr database, resulting in a total of 989 viral sequences. From these, only five were recovered from healthy bees (three from DNA and two from RNA), whereas all remaining 984 viral sequences were assembled from unhealthy bees.

From the total of 989 viral sequences (Table S1, available in the online version of this article), 901 were identified as bacteriophages and 17 were identified as viruses of unclassified or unknown hosts, and for the purpose of the present study, we focused on the remaining 71 sequences, which were identified as eukaryotic viruses (Fig. 1). The HRNA sample was left out of Fig. 1, since both viral contigs assembled from the RNA of healthy bees were identified as bacteriophages. Thus, the virome of healthy bees contained only three sequences from eukaryotic viruses that belonged to two different families. The virome of unhealthy bees, on the other hand, contained 38 sequences from viruses belonging to 11 different families, as well as 30 contigs showing similarity to unclassified viruses previously found in eukaryotes (Fig. 1). Using sequencing depth as a proxy for abundance, i.e. the number of copies of viruses within each virome, the most representative viruses in unhealthy bees (50–140 X depth) belonged to the families *Parvoviridae* (ssDNA genome) and *Circoviridae* (ssDNA genome). Viruses identified as *Dicistroviridae* (+ssRNA genome) that included potential honeybee pathogens showed lower sequencing depth, ranging from 8 to 15 X.

Characterization of novel *M. quadrifasciata* viruses

Seven eukaryotic viral sequences with significant length and depth were selected as candidates for further investigation: *Melipona quadrifasciata cyclovirus* (MqC), *Melipona quadrifasciata cyclovirus 1* (MqC1) and *Melipona quadrifasciata cyclovirus 2* (MqC2) from the family *Circoviridae*; *Melipona quadrifasciata densovirus* (MqD) from the family *Parvoviridae*; *Melipona quadrifasciata virus 1a* and *1b* (MqV1a and MqV1b) from the family *Dicistroviridae*; and *Melipona quadrifasciata virus 2* (MqV2), which is unclassified (Table S1). To evaluate whether these sequences represent already known or novel viruses, predicted proteins derived from their coding sequences (CDSs) were used for phylogenetic analyses. None of them showed sufficient similarity to other known viruses to be regarded as the same species.

The most abundant virus found in unhealthy stingless bees belonged to the family *Parvoviridae* (MqD; Table S1). The MqD sequence (4214 nt) probably represents a complete genome, encoding the non-structural (534 aa) and structural

(655 aa) proteins, containing conserved domains Parvo_NS1 (cl24009, e-value $4.57e^{-10}$) and Denso_VP4 (cl03545, e-value $4.83e^{-15}$), respectively. Phylogenetic inference based on their concatenated amino acid sequences groups MqD with other *Parvoviridae* found mainly in insects, within the genus *Densovirus* (Fig. S1), such as the recently described *Bombus cryptarum densovirus* [34].

Two *Circoviridae* sequences from unhealthy bees also contained recognizable CDSs: MqC1 and MqC2 (Table S1). MqC1 (1587 nt) is probably a complete genome as well, from which the non-structural protein (228 aa), with a P-loop_NTPase domain (cl21455, e-value $7.94e^{-18}$), and the structural protein (224 aa) are predicted. MqC2 (673 nt) is a partial virus genome bearing a partial non-structural protein (224 aa) with the P-loop_NTPase domain (e-value $3.34e^{-18}$). These two viruses cluster with viruses from the family *Circoviridae* within the genus *Cyclovirus* (Fig. 2), a sister clade of the genus *Circovirus*, that were found recently in *A. mellifera* (Circo-like 1 and Circo-like 2) [35].

Two other partial viral genomes show similarity to *Dicistroviridae* viruses: MqV1a (5913 nt) and MqV1b (1236 nt) (Table S1). A single protein is predicted from each, i.e. the structural protein (1888 aa), with RNA_dep_RNAP (cd01699, e-value $9.44e^{-83}$) and RNA_helicase (pfam00910, e-value $1.24e^{-31}$) domains, is encoded by MqV1a, whereas the partial non-structural protein (412 aa), with RHV_like (cd00205, e-value $5.94e^{-23}$) and Dicistro_VP4 (cl13011, e-value $4.36e^{-08}$) domains, is predicted from MqV1b. Both proteins group these viruses within *Dicistroviridae* known to infect bees and other arthropods (Fig. 3), such as ABPV and IAPV. However, the amino acid identities between MqV1a or MqV1b proteins and known ABPV and IAPV proteins are within the order of 28–15% and 29–16 %, respectively.

MqV2 (3730 nt) shows an unclassified virus as best hit (Table S1), and encodes a non-structural protein (479 aa), which contains RT_like (cl02808, e-value $8.87e^{-11}$) and RdRP_3 (cl24119, e-value $2.48e^{-05}$) domains. MqV2 is related to other unclassified RNA viruses that are found to be associated with a diversity of hosts, from plants to animals such as birds, molluscs and bees (Fig. S2) [41].

Virus detection in stingless bees and honeybees

Having characterized seven novel eukaryotic viruses found in high abundance in unhealthy stingless bees, we tested whether their presence is associated with the manifestation of disease symptoms (Table S2). We reasoned that if a virus is directly implicated in the annual syndrome, it should be detected more often in unhealthy than in healthy bees of different meliponaries. Virus detection by PCR was performed by testing individual worker bees to determine if the disease symptoms were present in three different meliponaries, using primers designed to amplify fragments of about 300 bp from each virus genome (Table 1). Table 2 summarizes the results of Cochran–Mantel–Haenszel (CMH) tests, which were used to verify the association between the detection of each candidate virus with the manifestation of symptoms, controlled

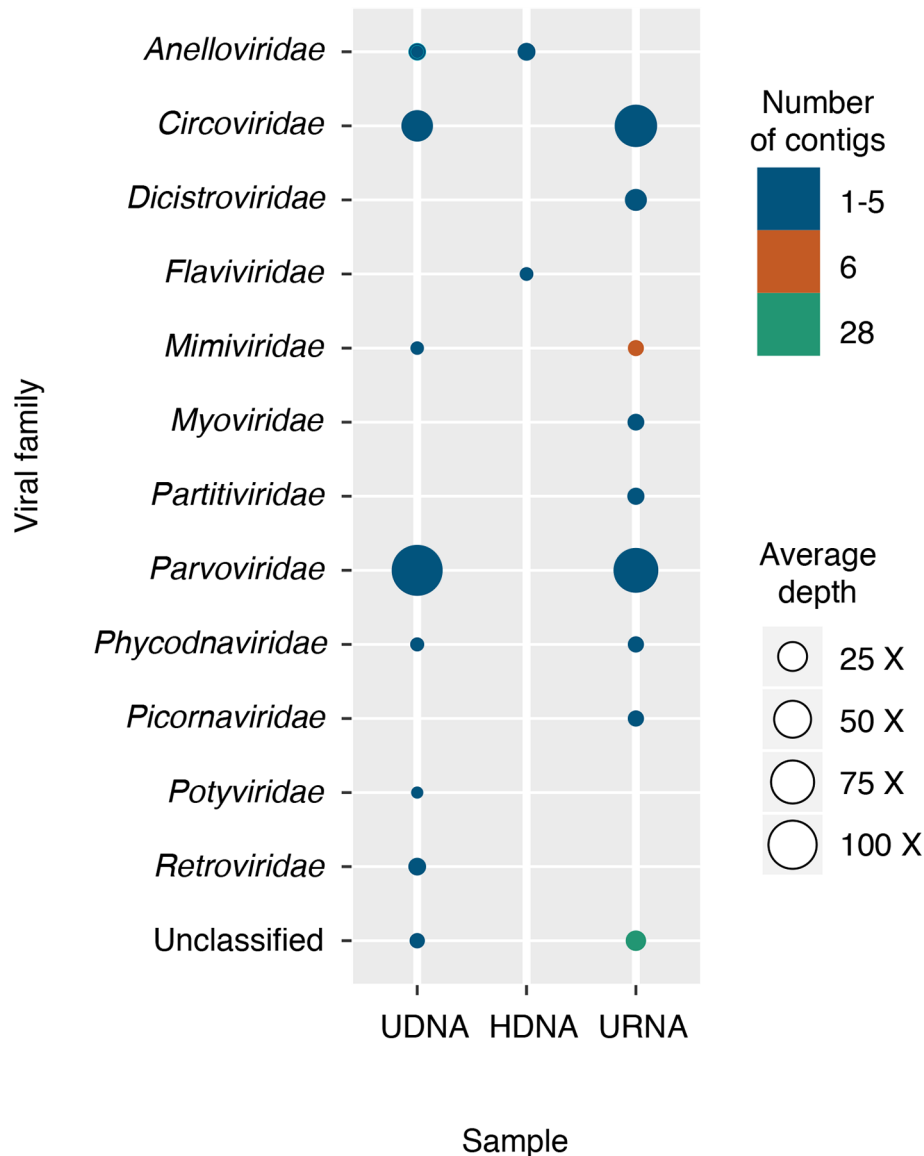
M. quadrifasciata-associated viruses

Fig. 1. Taxonomic distribution of *M. quadrifasciata* viral contigs in metagenomes of healthy (HDNA) and unhealthy bees (UDNA and URNA). Only contigs larger than 200 bp and showing best hits to eukaryotic viruses are considered in this plot. Sequences of viral families showing larger sequencing depth (larger circles) were chosen as candidates in subsequent analyses.

by locality, and the results of Barnard's unconditional (BU) tests applied to individual localities. All viruses were detected in both healthy and unhealthy bees, and only MqV1a was detected in bees from all meliponaries. None of the viruses were found to be significantly more associated with the syndrome manifestation in all localities in view of the CMH test. However, MqC, MqD and MqV1a viruses were more often associated with unhealthy bees in the Boqueirão do Leão (BL) meliponary, where *M. quadrifasciata* was sampled

to build the viromes. Interestingly, the three circoviruses (MqC, MqC1 and MqC2) and the unclassified virus MqV2 were also detected in *A. mellifera* colonies from one of the sampling localities [Bom Princípio (BP)] (see Table 2).

DISCUSSION

Bee populations have been declining for some years, leading to global concern over the plight of plant pollinators [42, 43].

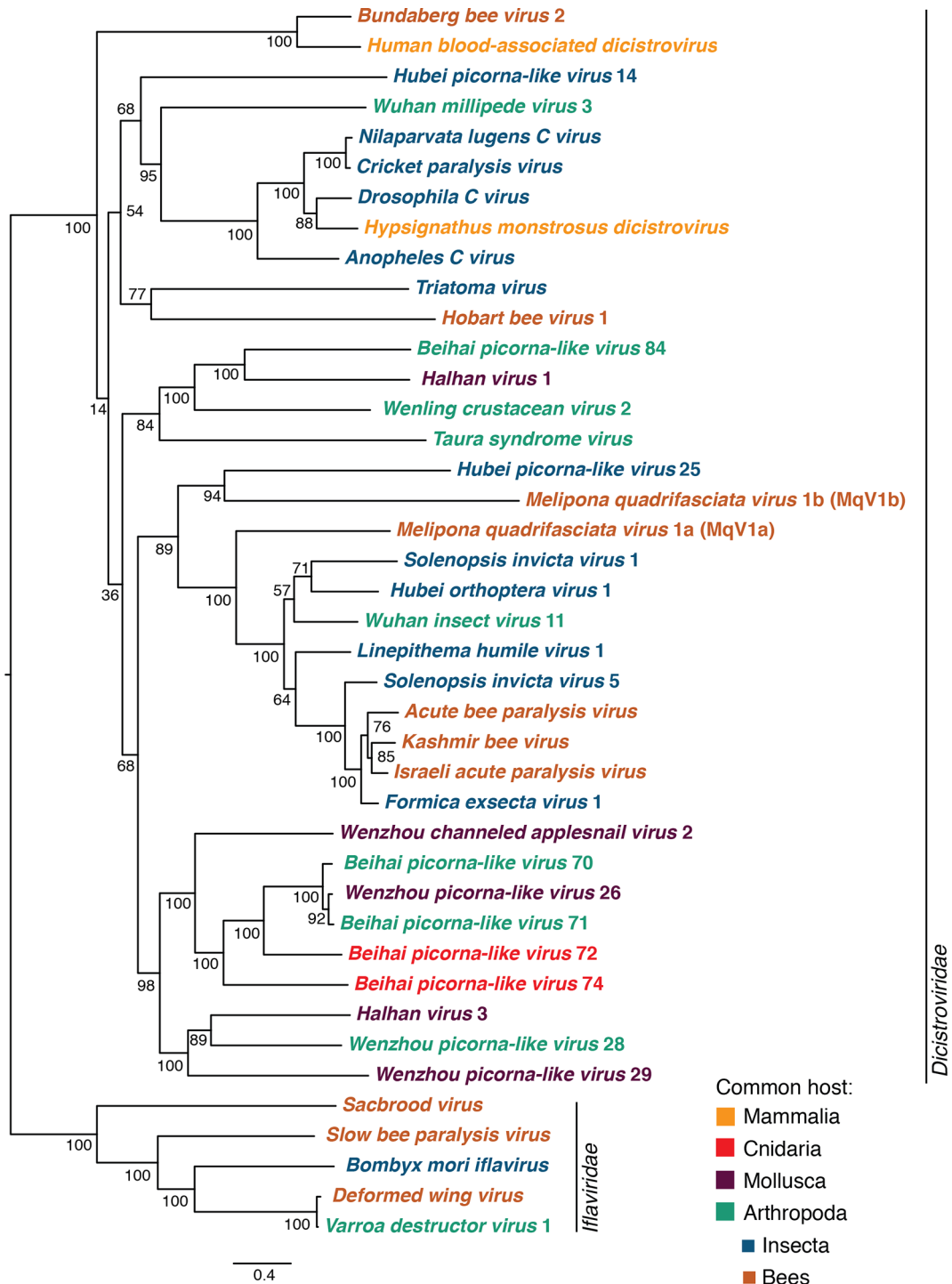


Fig. 2. Phylogenetic inference of MqC1 and MqC2 viruses (*Circoviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 502 aa. The colours of the species names represent the viruses' common hosts (see lower right).

Viruses that are prevalent in weak colonies of honeybees are probably directly implicated in the population decline of different bee species [44–46]. For example, honeybee colonies affected by CCD, a syndrome characterized by the sudden disappearance of honeybees [47], often show higher

prevalence of IAPV, ABPV or *Kashmir bee virus* (KBV) [48, 49]. The apparent spread of CCD in the USA suggests that viruses, among numerous other factors such as pesticides, stress, climate and habitat change, and other natural enemies, could cause honeybee populations to drop so much

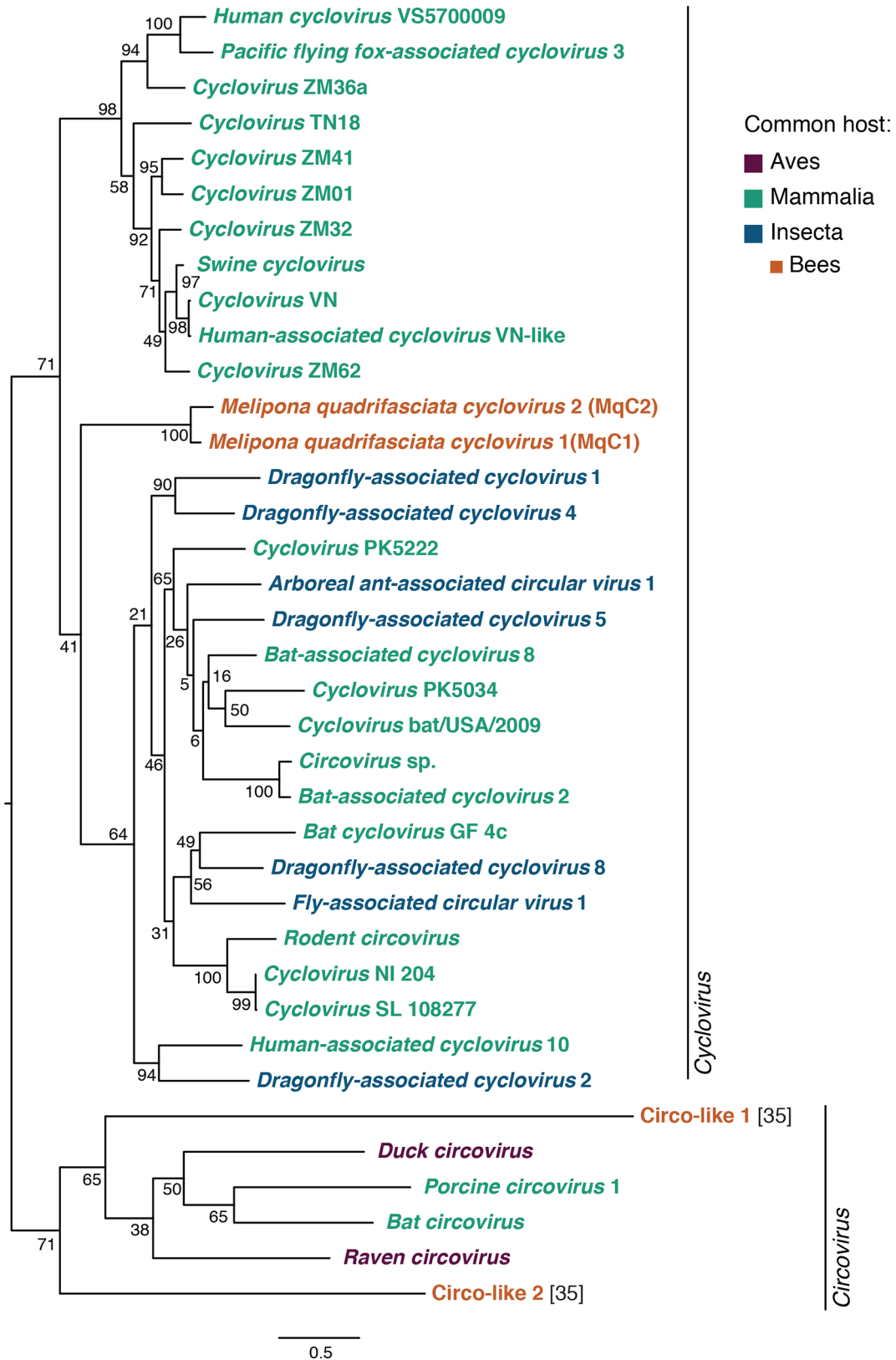


Fig. 3. Phylogenetic inference of MqV1a and MqV1b viruses (*Dicistroviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 2748 aa. The colours of the species names represent the viruses' common hosts (see top right).

Table 1. Primer sequences designed for virus detection

Name	Sequence	Amplicon length (bp)
MqC F	5' ACTTCTGTGCCGTTGGTAGT 3'	300
MqC R	5' TCTCTCAAATTGCTTGCGCC 3'	
MqC1 F	5' GCCACTTCTGTGCCGATAT 3	304
MqC1 R	5' TCCTTCAAAGGTGCCAGCTC 3	
MqC2 F	5' ACTACTGGGAGCACGGAGAT 3	318
MqC2 R	5' ATCCGTCACCACATTCTCT 3	
MqD F	5' TCAAGCAGCGATTCTGGAGA 3'	300
MqD R	5' CCACACAGCGCTACTATTT 3'	
MqV1a F	5' CTCTTTTGCATCGACAAGCT 3'	300
MqV1a R	5' TCAGCCGCAAACCTCTTCGA 3'	
MqV1b F	5' TTAGTCTAAACGGGCCACT 3'	300
MqV1b R	5' TGGACATGCCAACACTACA 3	
MqV2 F	5' GCGCTGTATTGCATCTGGTG 3'	304
MqV2 R	5' CGACGCGCATTTCCTCAAT 3'	

that agricultural pollination will become unsustainable [50]. In spite of being less important with regard to crop pollination than honeybees, stingless bees and other native bees are fundamental to sustain nesting and alternative flower resources for crop pollinators, which are typically unavailable within intensively managed crop fields [51]. Moreover, the disappearance of *M. quadrifasciata* wild nests in southern Brazil is worrying because the management practices that are used to maintain bee populations in this region are not well

regulated, and the trade in stingless bee colonies across the country could potentially spread viruses and other pathogens.

The seven most abundant eukaryotic viruses found in the virome of unhealthy *M. quadrifasciata* are novel viruses. Two partial dicistrovirus genomes were obtained: MqV1a and MqV1b. Although each contains one of the two CDSs of a typical dicistrovirus, our attempts to bridge them by PCR failed (data not shown), suggesting that they may indeed represent related, but different, viruses. Both show low identity to other dicistroviruses causing similar pathological symptoms in honeybees (IAPV and ABPV). Their high divergence from honeybee dicistroviruses and the lack of detection of MqV1a and b sequences in honeybees indicate that the presence of dicistroviruses in *M. quadrifasciata* does not represent a horizontal transmission event from *A. mellifera* to stingless bees, as previously suggested for ABPV infections in *M. scutellaris* [27]. Rather, our phylogenetic analyses indicate that MqV1a and b belong to an evolutionary branch that diverged from the honeybee IAPV long before other dicistroviruses found in unrelated hosts such as ants and crustaceans. Similarly, a recent study on the prevalence of DWV in *Melipona subnitida* and *A. mellifera* colonies from a single island in Brazil showed that DWV strain C, which is typically found in the stingless bee, is virtually absent in the honeybee [52]. Such dissimilar scenarios concerning the simultaneous presence of dicistroviruses in stingless bees and honeybees in Brazil probably represent different stages of the evolutionary divergence process that follows a host-switching event.

Interestingly, the most abundant *M. quadrifasciata* viruses in our study have ssDNA genomes: MqD (genus *Densovirus*, family *Parvoviridae*), MqC, MqC1 and MqC2 (genus *Cyclovirus*, family *Circoviridae*). These viral families have not been

Table 2. Candidate virus detection in *M. quadrifasciata* and *A. mellifera*. The number of *M. quadrifasciata* individuals that were positive for each virus is shown in relation to the total number of tested bees. Differences in the proportion of positive samples between healthy (H) and unhealthy (U) bees were tested for each meliponary (BL, Boqueirão do Leão; BP, Bom Princípio; and RL, Rolante) using Barnard's unconditional (BU) test and for the total number of sampled bees controlled by locality using the Cochran–Mantel–Haenszel (CMH) test. Pools of bees from three colonies of *A. mellifera* from BP were tested for the same viruses

	BL			BP			RL			CMH	<i>A. mellifera</i>		
	H	U	p£	H	U	p£	H	U	p£	p	1	2	3
MqC	8/19	40/57	0.029	0/6	0/3	NT*	1/6	0/3	0.579	0.094	+	+	+
MqC1	13/19	49/57	0.107	2/6	2/3	0.492	0/6	0/3	NT*	0.106	+	-	+
MqC2	5/19	27/57	0.122	0/6	0/3	NT*	0/6	0/3	NT*	NT**	+	+	-
MqD	6/19	6/57	0.031	0/6	0/3	NT*	0/6	0/3	NT*	NT**	-	-	-
MqV1a	0/6	4/6	0.021	8/38	7/27	0.668	0/6	2/37	0.776	0.192	-	-	-
MqV1b	1/6	3/6	0.303	3/38	5/27	0.249	0/6	0/37	NT*	0.165	-	-	-
MqV2	0/6	2/6	0.197	1/38	0/27	0.569	0/6	0/37	NT*	0.919	+	-	+

£, BU test.

*, not tested; virus not detected.

** , not tested; virus detected in a single locality.

found to be associated with other bee species until recently. Using high-throughput sequencing technologies, viruses belonging to the *Nudiviridae* (dsDNA) and *Parvoviridae* (ssDNA) were found in *Bombus* sp. [34], and *Circoviridae* viruses (ssDNA) were identified in *A. mellifera* [35], with no apparent pathological consequences. Densoviruses are known to establish both mutualistic and pathogenic relationships with their arthropod hosts [53–55]. Viruses from the genus *Cyclovirus* are not known to cause pathology in insects, but have been detected in the cerebrospinal fluid of human patients with neurological conditions [56, 57], and in secretions from patients with respiratory disease [58]. Here, the three cycloviruses were detected in honeybees sharing their habitat with *M. quadrifasciata*. It is known that the pollen resources of honeybees and *Melipona* spp. overlap in different regions of Brazil [59–61], and by foraging on the same flowers they may potentially exchange viruses. Inter-species transmission of bee viruses such as DWV, IAPV, SBPV and BQCV through pollen sources is already well documented [32, 62]. It is not possible to confirm that the *M. quadrifasciata* cycloviruses are in fact replicating within the bee body, but the high loads of DNA viruses such as MqD (136 X), MqC (107 X) and MqC1 (83 X) in the metagenome derived from a RNA sample at least suggests that they are active.

Even though no direct association was found between the manifestation of the *M. quadrifasciata* annual syndrome and the detection of the seven candidate viruses in adult stingless bees from all localities, we do not rule out the possibility that these viruses indeed play a role in the outbreaks. Our viromes were built using pools of bees from BL, where they showed the most intense disease symptoms, and three viruses (MqC, MqD and MqV1a) were found significantly more often in unhealthy bees. This indicates that viruses apparently replicate opportunistically on a local basis, and that, given the regular timing of the outbreaks on different meliponaries, the common denominator might be a higher susceptibility of bees at the end of the summer. In the case of honeybee CCD, no single factor explains the manifestation of the disorder; rather, it seems that a combination of several factors may act synergistically [50]. Known examples of synergistic interactions of honeybee viruses with other factors include *Varroa* mites that destabilize DWV–host dynamics via suppression of the honeybee NF- κ B immune response [63] and pesticides that reduce honeybee resistance to viral infections [64]. Bee nutrition, which varies across landscapes and seasons, is also known to affect resistance to viruses and other pathogens [65].

In conclusion, there is no obvious answer to the question of whether or not viruses are implicated in the *M. quadrifasciata* annual syndrome. In spite of having shown a higher diversity and abundance of viruses in the virome of unhealthy bees in one of the studied meliponaries, our study suggests that viruses are not the direct cause of the syndrome, but may influence adult bee symptoms in certain localities. It is worth mentioning that eusocial bees differ from other animals in having an additional higher-level

immunity referred to as social immunity [66, 67]. Because social immunity is negatively correlated with host density [68], it is possible that the annual syndrome actually represents a mechanism of density control in *M. quadrifasciata* populations at the end of the summer. Nevertheless, our study calls attention to the presence of a diversity of as yet unknown bee viruses in stingless bees, and their ability to spread across species boundaries. Given their pathogenic potential, and global concern about the decline of bee populations, viruses must be taken into account when planning management practices and conservation strategies.

METHODS

Worker bee sampling

M. quadrifasciata worker bees were collected from four different meliponaries in southern Brazil: 76 bees were taken from BL (29°18'5.47"S/52°25'57.96"W), 43 bees were taken from Rolante (RL) (29°38'19.78"S/50°26'49.77"W) and 65 bees were taken from BP (29°31'2.30"S/51°17'29.00"W). Sampling was performed in February, March and September (i.e. before, during and after the syndrome outbreak, respectively) in different years. Worker bees with symptoms such as tremors and paralysis (unhealthy) and symptomless bees (healthy) were collected using an entomological pooter, stored temporarily in sample pots and brought alive or in RNAlater (Thermo Fisher Scientific, USA) to the laboratory where they were stored individually at –80 °C until nucleic acid extraction. Healthy individuals were only collected in colonies where none of the bees presented symptoms. During the 2017 syndrome outbreak at BL, an additional 25 healthy and 25 unhealthy worker bees were collected from a colony affected by the syndrome and one not affected by it, respectively, pooled and stored in 5 ml of RNAlater (Thermo Fisher Scientific, USA) at 4 °C until nucleic acid extraction. Additionally, three pools of ~100 *A. mellifera* workers were sampled in September 2018 from different colonies of the BP location and stored as described.

Nucleic acid extraction for metagenome sequencing

Nucleic acids (RNA and DNA) were extracted from samples enriched for viral particles following the protocol of de Sales Lima and collaborators [69]. Briefly, two pools of 25 worker bees (healthy and unhealthy) were individually ground with sterile sand in 3 ml of phosphate-buffered saline (PBS). The homogenate was filtered in a cell strainer to remove bee parts (i.e. wings, legs and cuticles) and then centrifuged at 3000 r.p.m. for 15 min at 4 °C. The supernatant was collected with a syringe and filtered through a 0.45 μ m filter (Sigma-Aldrich, USA) to remove bacteria-sized particles. The filtrate was transferred to a centrifuge tube in an SW-28 Ti rotor (Beckman Coulter, USA) already containing a sucrose cushion (25 % sucrose in Tris-Cl 10 mM, EDTA 1 mM) and ultracentrifuged at 27000 r.p.m. for 4 h at 4 °C. The pellet, enriched for viral particles, was eluted in 200 μ l DEPC-treated water and split into two aliquots of 100 μ l each, one for DNA extraction with the universal phenol-chloroform

protocol [70] and another for RNA extraction with TRIzol (Ambion, USA), following the recommendations of the manufacturers. The yield and quality of nucleic acid purification were assessed with a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA) and a Qubit fluorometer (Invitrogen, USA). Aliquots of the purified RNA were used for cDNA synthesis with the High-Capacity cDNA Reverse Transcription kit (Thermo Fisher Scientific, USA). The cDNA second strand was synthesized using Klenow fragment DNA polymerase (New England Biolabs, USA). Fragment libraries were further prepared with 1 ng of purified DNA or double-stranded cDNA using the Nextera XT DNA Library Preparation kit (Illumina, USA) and paired-end sequenced (2×150 nt) using the MiSeq Reagent kit v2 (Illumina, USA) on a MiSeq instrument (Illumina, USA).

De novo assembly and contig filtering

Paired-end reads from healthy and unhealthy bee DNA and RNA fragment libraries were debarcoded and used for *de novo* assembly. Datasets derived from DNA samples were assembled with SPAdes v3.10.1 [71], whereas RNA-derived reads were assembled with Trinity v2.2.0 [72]. Within SPAdes, reads were assembled with k-mer lengths 21, 33 and 55, without a filtering step before assembly. Within Trinity, a read quality trimming step (*--trimmomatic*) was added with the default settings [73]. Contaminations were removed by building subsets (bins) of the NCBI nucleotide (nt) database with the *blastdb_aliastool* command of BLAST [74]. Contigs with significant hits (e-value cutoff $1e^{-12}$) to bins including sequences from bacteria (taxid: 2), fungi (taxid: 4751) or plants (taxid: 33090) were filtered out. Another bin was used to filter out hits against the *M. quadrifasciata* genome (LIRP00000000.1) using the same parameters.

Virome sequence analysis and candidate virus selection

For taxonomic characterization, the remaining contigs were matched with BLASTX to a viral protein database created from the virus RefSeq database (taxid: 10239). This strategy provided consistent results independently of the BLAST algorithm (BLASTX or BLASTp) or database (nr or RefSeq) used in the analyses (Table S3). Only contigs matching the viral database were retained (e-value cutoff $1e^{-5}$). False positives were then filtered out by comparing the candidate viral dataset with the total protein database (nr) from the NCBI using BLASTX, and removing contigs showing best hits to non-viral sequences. Taxonomic information for retained contigs larger than 200 bp was retrieved with taxdb. Contig depth was estimated with the depth command from Samtools v1.3.1 [75] by mapping the trimmed reads onto the virome with Bowtie 2 v2.3.1 [76], and used as a proxy for abundance. The taxonomic and sequencing depth data were used as inputs for bubble plots drawn with the ggplot2 package [77] in R. Contigs that had a sequencing depth larger than 8 X, were longer than 500 bp and showed best BLASTX hits on eukaryotic viruses were chosen as candidates

for further investigation. Coding sequence prediction and annotation were performed with the prokaryotic genome annotator Prokka v1.12 [78] using the command options *--kingdom* (viruses) and *--metagenome*. To validate annotations with protein-conserved domains, predicted coding sequences were submitted to NCBI's conserved domain database (CDD) with the web application Batch CD-Search (www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi; e-value cutoff $1e^{-3}$).

Phylogenetic inferences

The predicted coding sequences of six candidate viruses (all candidate viruses, except MqC, which does not have predicted protein) were used to search for similar viral sequences in GenBank (e-value cutoff $1e^{-5}$), avoiding species redundancy. These sequences, plus relevant reference sequences (see Table S4), were used for phylogenetic inferences. Sequences were aligned using MAFFT as implemented in Geneious R11 [79], removing columns with more than 60 % gaps. For each alignment, the best-fitted model of amino acid substitution was selected using ProtTest v3.4.2 [80] under corrected Akaike information criteria (AIC). Maximum-likelihood phylogenies with 100 bootstrap resamples of the alignment datasets were generated with RaxML v8.2.9 [81] and then edited and visualized with FigTree v.1.4.2 [82].

Nucleic acid extraction for PCR and RT-PCR

For PCR-based detection of viruses, the extraction of DNA, RNA or simultaneous DNA/RNA from individual bees was performed with the DNeasy Blood and Tissue kit (Qiagen, Germany), TRIzol (Ambion, USA) and the QIAamp Cador Pathogen Mini kit (Qiagen, Germany), respectively, according to the manufacturers' protocols. The nucleic acid extractions tested for the presence of RNA had been treated previously with TURBO DNase (Thermo Fisher Scientific, USA) and were then used for cDNA synthesis with the High-Capacity cDNA Reverse Transcription kit (Thermo Fisher Scientific, USA).

Virus detection by PCR and RT-PCR

Primers for virus detection were designed based on the seven candidate viral contig sequences (Table 1). An aliquot of 100–300 ng of nucleic acids purified from each of the tested samples was used as a template for PCR or RT-PCR, according to the sample type, mixed with 1 U of Platinum *Taq* DNA polymerase (Invitrogen, USA), 1× PCR buffer, 0.2 mM of each dNTP, 1.5 mM MgCl₂ and 0.2 μM of each forward and reverse primer in a final reaction volume of 50 μl. For MqV1a, the temperature cycling protocol used was 94 °C for 5 min, 60 °C for 1 min and 72 °C for 2 min, followed by 20 cycles of 94 °C for 1 min, 55 °C for 1 min and 72 °C for 2 min, with a touchdown of 0.5 °C per cycle, and another 20 cycles of 94 °C for 1 min, 45 °C for 1 min and 72 °C for 2 min, and a final extension step of 72 °C for 10 min. For the remaining six viruses a similar touchdown procedure was used, with primer annealing temperatures

starting at 54 °C and ending at 44 °C. The amplicons were analysed by conventional agarose gel electrophoresis. To test for the association of virus detection in individual bees with the manifestation of disease symptoms we conducted CMH test with Compare2 v.3.85 from WinPep [83] and two-way Barnard's unconditional tests with the Barnard package [84] in R.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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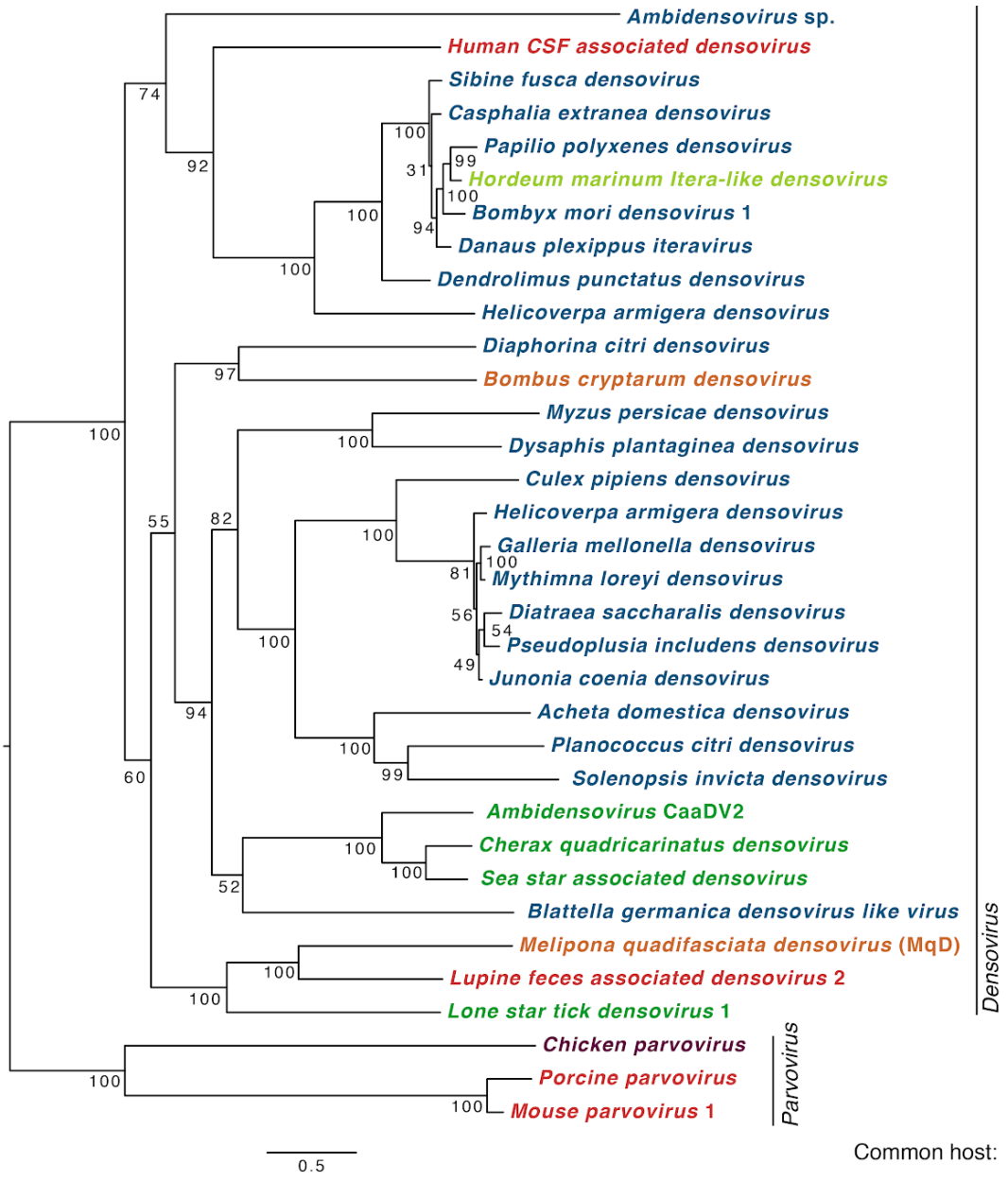
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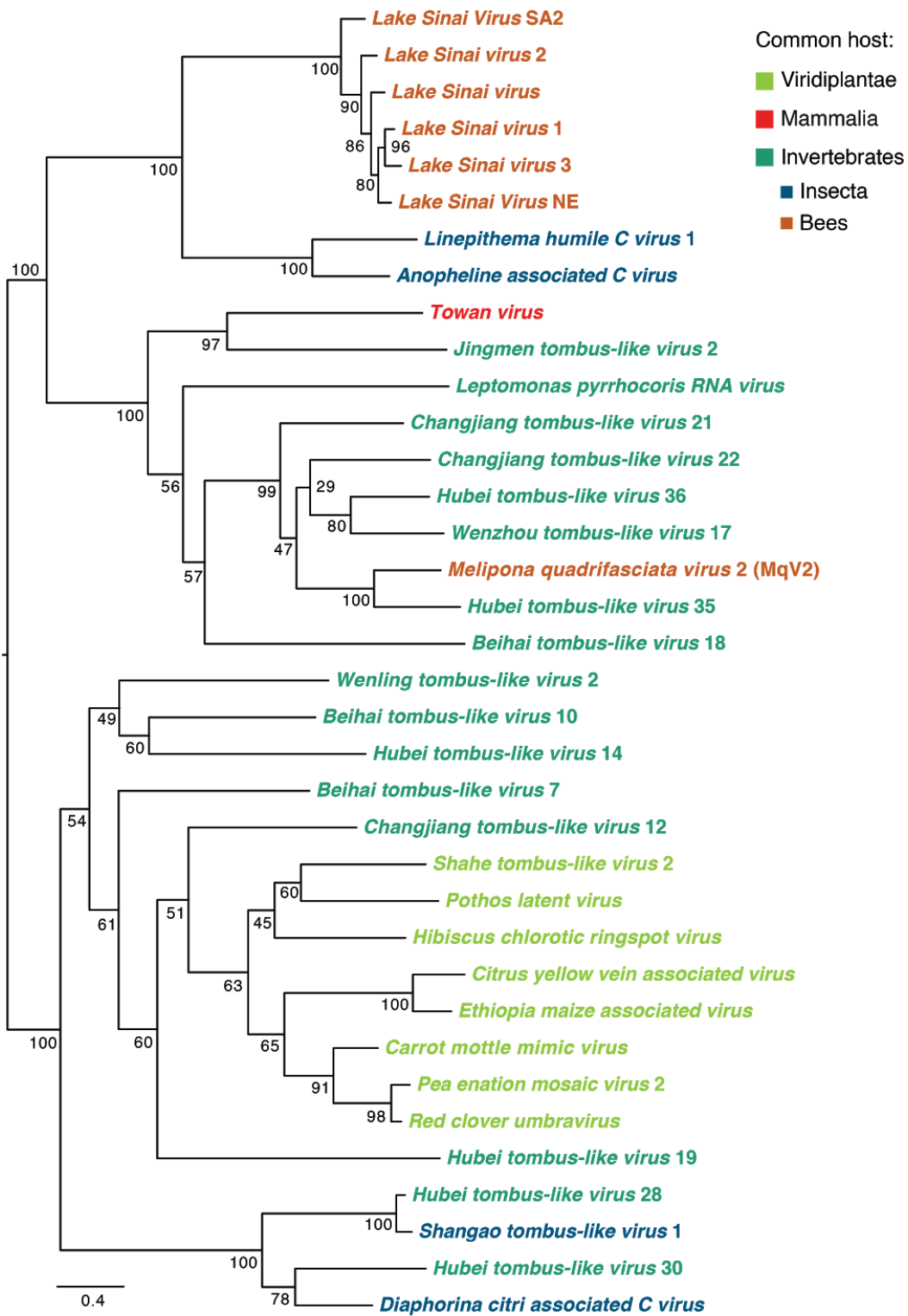
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Supplementary figure 1 - Phylogenetic inference of MqD virus (*Parvoviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 1,310 aa. Species name colours represent the virus common host.

- Common host:
- Viridiplantae
 - Aves
 - Mammalia
 - Invertebrates
 - Bees



Supplementary figure 2 - Phylogenetic inference of MqV2 virus. The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 598 aa. Species name colours represent the virus common host.

Supplementary Table 1 - Virome of unhealthy and healthy *M. quadrifasciata*: taxonomic classification of the best hit of each contig exceeding 200 bp in the four metagenomes (UDNA = DNA from unhealthy bees, HDNA = DNA from healthy bees, URNA = RNA from unhealthy bees, HRNA = RNA from healthy bees). Contigs are ordered according their coverages. Shading color indicates two major host groups bacteria (green) and eukaryotes (purple); highlighted in red are the contigs that were chosen to be investigated for their relation with the annual syndrome.

Name	Query (Contig name)	Length	Mean coverage	Subject	Bitscore	E-value	Staxids	Best hit species	Common host	Common host classification	Viral Order	Viral Family	Virus Molecule type
Unhealthy bees DNA virome													
	NODE 1371 length 261 cov 5101.58	261	5937.31	gi 66395188 ref YP_239478.1	48.9	1.77E-07	320832	<i>Staphylococcus aureus</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 3218 length 202 cov 2485.69	202	4616.9	gi 658607919 ref YP_009044904.1	103	2.02E-28	1262519	<i>Leuconostoc phage phiLN34</i>	<i>Leuconostoc mesenteroides</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 6718 length 1399 cov 2196.09	1399	4396.57	gi 070100089 ref YP_009283993.1	179	1.45E-50	1543206	<i>Staphylococcus phage BP39</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 142 length 837 cov 2004.61	837	3448.91	gi 966201261 ref YP_009191338.1	112	4.28E-27	1747288	<i>Enterococcus phage vIME195</i>	<i>Enterococcus faecium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 82 length 523 cov 1532.21	523	2954.47	gi 107009252 ref YP_009278511.1	158	1.24E-38	182328	<i>Staphylococcus phage SLPV</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 504 length 370 cov 1301.35	370	2793.61	gi 130720151 ref NP_852013.1	109	4.16E-28	230871	<i>Streptococcus phage CI</i>	<i>Streptococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 257 length 556 cov 1608.69	556	2771.15	gi 29565740 ref NP_817314.1	180	8.89E-55	204086	<i>Staphylococcus phage 4AHLID</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 38 length 2005 cov 1102.3	2005	2141.64	gi 66395192 ref YP_239479.1	141	1.52E-35	320832	<i>Staphylococcus phage 66</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 59 length 1601 cov 1305.56	1601	1969.64	gi 71291622 ref YP_009103964.1	55.8	2.64E-07	1161939	<i>Enterococcus phage vB_Efae230P-4</i>	<i>Enterococcus faecium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 390 length 422 cov 1051.65	422	1902.38	gi 71291621 ref YP_009103960.1	101	6.56E-26	1161939	<i>Enterococcus phage vB_Efae230P-4</i>	<i>Enterococcus faecium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 2661 length 219 cov 9609.49	219	1055.29	gi 327197601 ref YP_004301292.1	47.4	3.47E-07	764561	<i>Brochothrix phage NF5</i>	<i>Brochothrix thermosphacta</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 1039 length 277 cov 6070.11	277	798.448	gi 327197601 ref YP_004301292.1	80.1	2.31E-18	764561	<i>Brochothrix phage NF5</i>	<i>Brochothrix thermosphacta</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
MaD	NODE 6 length 4214 cov 47.7802	4214	104.516	gi 5669740 ref YP_164339.1	173	2.00E-43	292208	<i>Dendrolimus punctatus densovirus</i>	<i>Dendrolimus punctatus</i>	Arthropoda; Metazoa; Eukaryota	unclassified	Parvoviridae	ssDNA
MaC2	NODE 181 length 673 cov 27.6828	673	59.263	gi 663089940 ref YP_009047065.1	260	7.66E-87	1348500	<i>Cyclovirus FN</i>	<i>Homo sapiens</i>	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
	NODE 1 length 14405 cov 25.8403	14405	55.6807	gi 151266296 ref YP_001333659.1	206	9.52E-55	338473	<i>Actinomyces phage Av-1</i>	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 482 length 379 cov 9.5957	379	60784059 ref YP_009021845.1	64.3	2.14E-12	1234882	<i>Dragonfly cyclovirus A3</i>	<i>Stomatochloa meridionalis</i>	Arthropoda; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA	
	NODE 47 length 1772 cov 19.8427	1772	38.7472	gi 683110065 ref YP_009042257.1	227	2.90E-64	1327934	<i>Cronobacter phage CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 12 length 2190 cov 15.8786	2190	32.3681	gi 966203645 ref YP_009188960.1	125	9.81E-31	1684115	<i>Cronobacter phage PBES 02</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 75 length 1310 cov 14.4797	1310	32.313	gi 363539710 ref YP_004893995.1	77	4.94E-17	889338	<i>Salmonella phage PVP-SE1</i>	<i>Salmonella enterica subsp. enterica serovar Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 23 length 2531 cov 15.0521	2531	31.1972	gi 593777390 ref YP_009015235.1	253	3.61E-73	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 16 length 2705 cov 15.2894	2705	28.9919	gi 730985156 ref YP_009111241.1	164	9.69E-45	1527519	<i>Escherichia phage As-05</i>	<i>Escherichia coli O157:H7</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 208 length 612 cov 13.7487	612	27.1373	gi 410492669 ref YP_006908871.1	48.9	2.55E-06	1604355	<i>Escherichia phage ECBP2</i>	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 33 length 2212 cov 12.5535	2212	25.9118	gi 966203781 ref YP_009188906.1	60.5	6.08E-11	1684115	<i>Cronobacter phage PBES 02</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 27 length 2374 cov 11.8995	2374	22.9356	gi 363539688 ref YP_004893973.1	183	1.16E-50	889338	<i>Salmonella phage PVP-SE1</i>	<i>Salmonella enterica subsp. enterica serovar Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 19 length 2673 cov 11.95	2673	22.7565	gi 658310257 ref YP_009042449.1	374	2.27E-123	1327934	<i>Cronobacter phage CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 7 length 3822 cov 11.8471	3822	22.5903	gi 658310123 ref YP_009042315.1	394	2.74E-121	1327934	<i>Cronobacter phage CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 14 length 2710 cov 9.11455	2710	21.4587	gi 389059870 ref YP_006383023.1	410	2.03E-126	1162295	<i>Cronobacter phage CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 91 length 1174 cov 9.15155	1174	19.7308	gi 389059880 ref YP_006383033.1	195	1.22E-60	1162295	<i>Cronobacter phage CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 95 length 135 cov 9.35	1135	18.3885	gi 593777139 ref YP_009014984.1	296	5.56E-98	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 36 length 2088 cov 9.15199	2088	17.8252	gi 389059955 ref YP_006383108.1	95.1	4.75E-22	1162295	<i>Cronobacter phage CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 70 length 1325 cov 7.26457	1325	17.6581	gi 388570790 ref YP_006383773.1	51.2	6.96E-08	1187128	<i>Acinetobacter bacteriophage AP22</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 9 length 2927 cov 9.01358	2927	17.6194	gi 658310137 ref YP_009042329.1	208	2.21E-61	1327934	<i>Cronobacter phage CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 110 length 998 cov 6.41569	998	17.5882	gi 682123183 ref YP_009055504.1	254	5.19E-81	1505225	<i>Acinetobacter phage YMC-13-01-C62</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 76 length 1310 cov 9.00717	1310	17.3725	gi 389060084 ref YP_006383237.1	207	3.80E-64	1162295	<i>Cronobacter phage CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 34 length 2102 cov 8.80606	2102	17.0324	gi 593777352 ref YP_009015197.1	410	3.75E-138	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 44 length 1847 cov 8.88895	1847	16.7823	gi 593777363 ref YP_009015208.1	368	2.75E-122	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 3 length 5385 cov 8.33527	5385	16.5744	gi 448244744 ref YP_007392464.1	147	5.62E-37	1116482	<i>Pectobacterium phage phiTE</i>	<i>Pectobacterium atrosepticum SCRI1043</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 86 length 1202 cov 8.1578	1202	16.3378	gi 389059887 ref YP_006383040.1	238	3.03E-77	1162295	<i>Cronobacter phage CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 5 length 4317 cov 8.25059	4317	16.0644	gi 593777283 ref YP_009015128.1	88.6	1.29E-19	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 8 length 3348 cov 7.53325	3348	15.425	gi 563397615 ref YP_008857379.1	202	8.18E-57	1391428	<i>Enterobacteria phage 4MG</i>	<i>Escherichia coli K-12</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 24 length 2521 cov 8.03406	2521	15.386	gi 448246249 ref YP_007348345.1	53.9	5.33E-08	1264737	<i>Cronobacter phage vB_Cskp_GAP27</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 132 length 891 cov 6.60646	891	15.0236	gi 593777268 ref YP_009015113.1	124	3.89E-35	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 98 length 1104 cov 7.55005	1104	15.4616	gi 563397555 ref YP_008857319.1	158	7.26E-45	1391428	<i>Enterobacteria phage 4MG</i>	<i>Escherichia coli K-12</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 607 length 347 cov 7.86301	347	14.5504	gi 593777353 ref YP_009015198.1	61.2	3.75E-13	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 22 length 2568 cov 7.01074	2568	14.1347	gi 966203769 ref YP_009189084.1	68.9	2.43E-13	1684115	<i>Cronobacter phage PBES 02</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 488 length 376 cov 4.82866	376	14.0133	gi 388570783 ref YP_006383766.1	201	1.51E-63	1187128	<i>Acinetobacter bacteriophage AP22</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 163 length 751 cov 8.03679	751	13.7617	gi 563397604 ref YP_008857362.1	63.5	2.51E-12	1391428	<i>Enterobacteria phage 4MG</i>	<i>Escherichia coli K-12</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1590 length 252 cov 9.17766	252	13.6667	gi 966203376 ref YP_009187688.1	134	3.27E-38	1791940	<i>Klebsiella phage vB_KpnM_KB57</i>	<i>Klebsiella pneumoniae</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 236 length 578 cov 7.26195	578	13.4931	gi 363539705 ref YP_004893990.1	49.7	9.71E-08	889338	<i>Salmonella phage PVP-SE1</i>	<i>Salmonella enterica subsp. enterica serovar Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 79 length 1265 cov 6.71157	1265	13.4324	gi 401723087 ref YP_006589997.1	84	3.02E-16	1136535	<i>Burkholderia phage DC1</i>	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 28 length 2286 cov 6.76109	2286	13.0009	gi 563397519 ref YP_008857283.1	124	3.25E-28	1391428	<i>Enterobacteria phage 4MG</i>	<i>Escherichia coli K-12</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 315 length 496 cov 6.16327	496	12.8306	gi 448244797 ref YP_007392517.1	56.6	4.07E-09	1116482	<i>Pectobacterium phage phiTE</i>	<i>Pectobacterium atrosepticum SCRI1043</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 2 length 543 cov 6.22714	543	12.8097	gi 389059922 ref YP_006383076.1	52.8	4.31E-163	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 21 length 2596 cov 5.8717	2596	12.3617	gi 448244800 ref YP_007392520.1	51.4	2.06E-175	1116482	<i>Pectobacterium phage phiTE</i>	<i>Pectobacterium atrosepticum SCRI1043</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 652 length 334 cov 5.73835	334	12.1048	gi 593777273 ref YP_009015118.1	63.9	8.15E-14	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 747 length 315 cov 5.04231	315	11.8286	gi 593777390 ref YP_009015235.1	86.7	1.85E-20	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 26 length 2424 cov 5.68763	2424	11.1993	gi 966203664 ref YP_009188979.1	84.3	3.17E-16	1684115	<i>Cronobacter phage PBES 02</i>	<i>Cronobacter sp.</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 54 length 1661 cov 6.05168	1661	11.0319	gi 563397558 ref YP_008857322.1	155	3.51E-44	1391428	<i>Enterobacteria phage 4MG</i>	<i>Escherichia coli K-12</i>	Proteobacteria; Bacteria	Caudovirales		

NODE 415	length 413	cov 2.89106	413	5.54479	gi 448244935 ref YP_007392655.1	126	1.16E-35	1116482	<i>Pectobacterium</i> phase <i>phiTE</i>	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1907	length 241	cov 3.22043	241	5.53112	gi 070106045 ref YP_009291896.1	71.2	1.18E-15	1792222	<i>Acinetobacter</i> phase <i>LZ35</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 703	length 323	cov 2.89179	323	5.45511	gi 91745247 ref YP_009199435.1	51.2	2.41E-08	1718606	<i>Escherichia</i> phase <i>phiUSP1</i>	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 530	length 365	cov 2.57742	365	5.44411	gi 157235017 ref YP_001468443.1	47.8	4.51E-07	40522	<i>Listeria</i> phase <i>phi500</i>	<i>Listeria monocytogenes</i> WSLC1042	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1759	length 246	cov 3.24607	246	5.26016	gi 414086874 ref YP_006987062.1	85.5	1.20E-20	1141135	<i>Cronobacter</i> phase <i>vB_CsaM_GAP31</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 514	length 368	cov 2.86262	368	5.18207	gi 327198375 ref YP_004306949.1	62	1.56E-11	59241	<i>Streptococcus</i> phase <i>Dp-1</i>	<i>Streptococcus pneumoniae</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1513	length 255	cov 3.845	255	5.14118	gi 448244960 ref YP_007392680.1	144	5.78E-45	1116482	<i>Pectobacterium</i> phase <i>phiTE</i>	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 301	length 514	cov 3.05229	514	5.11673	gi 389060077 ref YP_006383230.1	273	7.32E-92	1162295	<i>Cronobacter</i> phase <i>CR3</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1492	length 256	cov 2.34328	256	5.00781	gi 571798161 ref YP_008770540.1	80.5	1.31E-19	1406786	<i>Bacillus</i> phase <i>Page</i>	<i>Bacillus megaterium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1516	length 255	cov 2.6	255	5.00392	gi 514361130 ref YP_008130364.1	46.6	1.03E-06	1345637	<i>Human</i> phase <i>phiV55700009</i>	<i>Human sapiens</i>	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
NODE 2341	length 227	cov 3.35465	227	5	gi 593777119 ref YP_009014964.1	129	1.49E-36	1162290	<i>Cronobacter</i> phase <i>CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2208	length 231	cov 2.15909	231	4.98701	gi 682123139 ref YP_009055460.1	90.9	6.03E-24	1505225	<i>Acinetobacter</i> phase <i>YMC-13-01-C62</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 431	length 404	cov 1.60458	404	4.82673	gi 472340490 ref YP_007674015.1	142	4.55E-40	754049	<i>Vibrio</i> phase <i>vYD21-A</i>	<i>Vibrio</i> sp. YD21	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1471	length 257	cov 2.9505	257	4.79377	gi 448244955 ref YP_007392675.1	124	2.27E-35	1116482	<i>Pectobacterium</i> phase <i>phiTE</i>	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 400	length 418	cov 2.00926	418	4.73684	gi 070106029 ref YP_009291880.1	66.2	7.89E-13	1792222	<i>Acinetobacter</i> phase <i>LZ35</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 608	length 347	cov 2.82534	347	4.68388	gi 939556927 ref YP_009168411.1	127	3.44E-36	1622234	<i>Citrobacter</i> phase <i>CI722</i>	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1453	length 258	cov 2.12315	258	4.65504	gi 937456469 ref YP_009168394.1	123	1.24E-33	1622234	<i>Citrobacter</i> phase <i>CI722</i>	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 278	length 534	cov 2.40292	534	4.64794	gi 937456502 ref YP_009168428.1	54.7	5.62E-09	1622234	<i>Citrobacter</i> phase <i>CI722</i>	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 542	length 361	cov 2.5817	361	4.46814	gi 9626704 ref NP_040974.1	128	3.95E-37	11673	<i>Feline</i> phase <i>phiIMMDEFICIENCY virus</i>	<i>Felidae</i>	Chordata; Metazoa; Eukaryota	unclassified	Retroviridae	ssRNA RT
NODE 664	length 332	cov 2.11913	332	4.46386	gi 593777132 ref YP_009014977.1	132	3.70E-37	1162290	<i>Cronobacter</i> phase <i>CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1337	length 263	cov 3.02404	263	4.34221	gi 62327110 ref YP_0223898.1	137	2.02E-38	235201	<i>Lactobacillus</i> phase <i>phiJL-1</i>	<i>Lactobacillus plantarum</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 249	length 562	cov 2.46351	562	4.30071	gi 93007440 ref YP_579204.1	123	1.30E-32	370623	<i>Streptomyces</i> phase <i>mul/6</i>	<i>Kitasatospora aureofaciens</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1142	length 272	cov 3.20737	272	4.28676	gi 388570790 ref YP_006383773.1	42	7.15E-06	1187128	<i>Acinetobacter</i> phase <i>AP22</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 374	length 433	cov 2.1746	433	4.27252	gi 658310265 ref YP_009042457.1	211	1.30E-64	1327934	<i>Cronobacter</i> phase <i>CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 366	length 441	cov 2.41451	441	4.26757	gi 1068511077 ref YP_009274031.1	44.3	9.87E-06	1838072	<i>Gordonia</i> phase <i>McGonagall</i>	<i>Gordonia neofelaei</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 466	length 386	cov 1.84229	386	4.24611	gi 658310061 ref YP_009042253.1	152	1.47E-44	1327934	<i>Cronobacter</i> phase <i>CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 611	length 345	cov 2.55172	345	4.23188	gi 448244889 ref YP_007392618.1	153	5.62E-47	1116482	<i>Pectobacterium</i> phase <i>phiTE</i>	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 412	length 415	cov 1.42222	412	4.15181	gi 971763827 ref YP_009216825.1	125	3.77E-36	1229760	<i>Acinetobacter</i> phase <i>phiAC-1</i>	<i>Acinetobacter soli</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 654	length 334	cov 2.48746	334	4.13772	gi 418489115 ref YP_007002969.1	120	1.64E-40	37105	<i>Lactobacillus</i> phase <i>JCL1032</i>	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 245	length 564	cov 2.41625	564	4.13121	gi 151266305 ref YP_001333668.1	112	3.90E-29	338473	<i>Actinomyces</i> phase <i>Av-1</i>	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 371	length 434	cov 2.53298	434	4.1129	gi 971748496 ref YP_009202413.1	62	3.23E-11	1698711	<i>Mycobacterium</i> phase <i>Loh/9</i>	<i>Mycobacterium smegmatis</i> str. <i>MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3036	length 210	cov 2.52903	210	3.9619	gi 151266296 ref YP_001333659.1	57.4	8.65E-11	338473	<i>Actinomyces</i> phase <i>Av-1</i>	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 874	length 295	cov 2.9125	295	3.95254	gi 971747642 ref YP_009201507.1	57.4	3.43E-10	1739609	<i>Lactobacillus</i> phase <i>Ia2</i>	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 971	length 281	cov 2.73894	281	3.92171	gi 985757728 ref YP_009223104.1	128	6.05E-36	1567453	<i>Lactobacillus</i> phase <i>LefSau</i>	<i>Lactobacillus fermentum</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 261	length 553	cov 2.07229	553	3.91139	gi 966203686 ref YP_009189001.1	86.7	2.90E-19	1684115	<i>Cronobacter</i> phase <i>PBES 02</i>	<i>Cronobacter</i> sp.	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3162	length 207	cov 2.63816	207	3.89855	gi 448244802 ref YP_007392522.1	88.6	8.57E-22	1116482	<i>Pectobacterium</i> phase <i>phiTE</i>	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2491	length 223	cov 2.02381	223	3.88341	gi 070067156 ref YP_009289259.1	42.7	8.33E-06	1868596	<i>Pseudomonas</i> phase <i>MD8</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 230	length 582	cov 2.26755	582	3.86254	gi 593777381 ref YP_009015226.1	325	8.25E-111	1162290	<i>Cronobacter</i> phase <i>CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 547	length 359	cov 2.11118	359	3.7883	gi 682123168 ref YP_009055489.1	115	2.51E-31	1505225	<i>Acinetobacter</i> phase <i>YMC-13-01-C62</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 314	length 380	cov 2.93007	380	3.78885	gi 102617795 ref YP_009321856.1	115	3.29E-07	1566993	<i>Streptococcus</i> phase <i>phiARI0746</i>	<i>Streptococcus pneumoniae</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 192	length 651	cov 2.01174	651	3.76651	gi 593777136 ref YP_009014981.1	191	1.65E-55	1162290	<i>Cronobacter</i> phase <i>CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 762	length 312	cov 2.31128	312	3.76603	gi 658310132 ref YP_009042324.1	147	3.21E-43	1327934	<i>Cronobacter</i> phase <i>CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 302	length 514	cov 1.49455	514	3.76265	gi 971746169 ref YP_009200249.1	142	1.55E-39	1636200	<i>Pseudalteromonas</i> phase <i>HI03</i>	<i>Pseudalteromonas marina</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA viruses
NODE 701	length 324	cov 2.21933	324	3.75	gi 658310273 ref YP_009042465.1	175	1.13E-54	1327934	<i>Cronobacter</i> phase <i>CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1004	length 279	cov 2.26786	279	3.65591	gi 937456472 ref YP_009168397.1	102	3.38E-26	1622234	<i>Citrobacter</i> phase <i>CI722</i>	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1145	length 272	cov 2.17051	272	3.63971	gi 318069475 ref YP_004152328.1	66.2	5.33E-14	942033	<i>Cyclovirus</i> PKaoa21/PAK/2009	<i>Capra hircus</i>	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
NODE 2826	length 215	cov 2.78125	215	3.60465	gi 971752673 ref YP_009206702.1	90.9	3.72E-23	1739607	<i>Lactobacillus</i> phase <i>CL1</i>	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2832	length 215	cov 1.99375	215	3.56279	gi 149408208 ref YP_001294642.1	87.4	2.51E-21	347327	<i>Pseudomonas</i> phase <i>PA11</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA viruses
NODE 620	length 342	cov 2.31359	342	3.54971	gi 418489114 ref YP_007002968.1	179	4.48E-54	37105	<i>Lactobacillus</i> phase <i>JCL1032</i>	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 550	length 358	cov 1.72277	358	3.54749	gi 095666753 ref NP_818317.1	82.8	6.19E-19	205879	<i>Mycobacterium</i> phase <i>Omega</i>	<i>Mycobacterium</i> sp.	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 204	length 622	cov 2.00829	622	3.54502	gi 070106079 ref YP_009291948.1	355	3.14E-122	1792222	<i>Acinetobacter</i> phase <i>LZ35</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 645	length 336	cov 1.70107	336	3.54167	gi 764161625 ref YP_009126057.1	57.8	3.29E-09	1566993	<i>Streptococcus</i> phase <i>phiARI-1</i>	<i>Streptococcus pneumoniae</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 643	length 336	cov 1.88612	336	3.54167	gi 571797869 ref YP_008772035.1	145	3.88E-42	1399941	<i>Lactobacillus</i> phase <i>phiJB</i>	<i>Lactobacillus delbrueckii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 838	length 300	cov 2.43265	300	3.53667	gi 971751675 ref YP_009205624.1	97.1	3.92E-24	1175662	<i>Pseudomonas</i> phase <i>PAms42</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 440	length 400	cov 2.02319	400	3.5325	gi 203454733 ref YP_00225049.1	62.4	1.52E-11	546805	<i>Mycobacterium</i> phase <i>Myrna</i>	<i>Mycobacterium smegmatis</i> str. <i>MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2919	length 213	cov 2.67089	213	3.53052	gi 937456472 ref YP_009168397.1	63.5	7.39E-13	1622234	<i>Citrobacter</i> phase <i>CI722</i>	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2115	length 234	cov 1.97027	234	3.52991	gi 658310162 ref YP_009042354.1	111	9.13E-30	1327934	<i>Cronobacter</i> phase <i>CR8</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2827	length 215	cov 2.475	215	3.52558	gi 160700666 ref YP_001552346.1	48.9	8.60E-08	480808	<i>Mycobacterium</i> phase <i>Giles</i>	<i>Mycobacterium smegmatis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1205	length 269	cov 1.70561	269	3.51301	gi 509142291 ref YP_008061153.1	98.2	5.99E-25	1007869	<i>Rhodococcus</i> phase <i>E3</i>	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 307	length 511	cov 1.53289	511	3.45205	gi 410491660 ref YP_006906882.1	58.2	1.22E-09	1150869	<i>Escherichia</i> phase <i>P13374</i>	<i>Escherichia coli</i> O104:H4 str. <i>CB13374</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2957	length 212	cov 1.84713	212	3.43868	gi 530545073 ref YP_008408677.1	67	3.86E-14	1340826	<i>Mycobacterium</</i>					

NODE 317 length 496 cov 1.39229	496	2.69758	gi 203460615 ref YP_002224349.1	98.6	1.32E-24	546808	<i>Mycobacterium phage Spud</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 502 length 371 cov 1.63924	371	2.69003	gi 514051708 ref YP_008126134.1	46.6	4.52E-06	1262532	<i>Mycobacterium phage BTU-1</i>	<i>Mycobacterium smegmatis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1019 length 278 cov 1.86547	278	2.68345	gi 593777132 ref YP_009014977.1	132	1.84E-37	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2238 length 230 cov 2.06571	230	2.66957	gi 68698201 ref YP_009058944.1	73.2	3.46E-16	154219	<i>Torque teno Tadarida brasiliensis virus AT22</i>	<i>Tadarida brasiliensis</i>	Chordata; Metazoa; Eukaryota	unclassified	dsDNA	unclassified
NODE 284 length 531 cov 1.58193	531	2.60264	gi 388570812 ref YP_006383795.1	95.1	5.86E-24	181728	<i>Actinobacter bacteriophage Av-1</i>	<i>Actinobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 812 length 304 cov 1.62499	304	2.59539	gi 151266296 ref YP_001333659.1	110	5.97E-29	338473	<i>Actinomyces phage Av-1</i>	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2350 length 227 cov 1.51163	227	2.57269	gi 971757155 ref YP_009210688.1	44.7	3.84E-06	1701853	<i>Mycobacterium phage Serenity</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 418 length 411 cov 1.70506	411	2.54745	gi 372449476 ref YP_005086972.1	58.9	2.96E-10	1109716	<i>Rhodococcus phage RGL3</i>	<i>Rhodococcus globularius</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 358 length 449 cov 1.63959	449	2.53229	gi 971763799 ref YP_009216797.1	164	2.39E-48	1229760	<i>Acinetobacter phage phiAC-1</i>	<i>Acinetobacter soli</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1962 length 239 cov 2.07065	239	2.51464	gi 985757333 ref YP_009222296.1	50.8	2.63E-08	1567484	<i>Lactobacillus phage LeflnJ</i>	<i>Lactobacillus fermentum</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2788 length 216 cov 1.97516	216	2.49074	gi 1070103328 ref YP_009287971.1	83.6	6.68E-20	1891703	<i>Mycobacterium phage Tonelli</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1730 length 247 cov 1.94792	247	2.44534	gi 371496158 ref YP_004957306.1	58.5	4.18E-11	994601	<i>Plankothrix phage PaV-LD</i>	<i>Plankothrix aqardhii</i> HAB637	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3088 length 209 cov 1.35065	209	2.43062	gi 589895959 ref YP_009004942.1	48.9	9.62E-08	1429768	<i>Erwinia phage Ea35-7</i>	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 702 length 324 cov 1.64312	324	2.42901	gi 215401206 ref YP_002332511.1	162	6.65E-49	575608	<i>Staphylococcus phage phiSauS-IPLA88</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3169 length 207 cov 1.59211	207	2.40997	gi 682123182 ref YP_009055503.1	74.7	6.31E-17	1505225	<i>Acinetobacter phage YMC-13-01-C62</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 391 length 422 cov 2.06571	422	2.37915	gi 937456479 ref YP_009168397.1	156	2.14E-44	1622234	<i>Citrobacter phage CT22</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2275 length 229 cov 1.68966	229	2.34934	gi 937456479 ref YP_009168394.1	115	6.40E-31	1622234	<i>Citrobacter phage CT122</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1494 length 256 cov 1.83085	256	2.34766	gi 1070621526 ref YP_009302998.1	82.8	1.56E-19	1821562	<i>Gordonia phage SoilAssassin</i>	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 409 length 416 cov 1.45706	416	2.33654	gi 593777123 ref YP_009014968.1	176	1.01E-54	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1859 length 243 cov 1.83511	243	2.3251	gi 966203364 ref YP_009186765.1	133	5.86E-41	1719140	<i>Klebsiella phage vB_KpnM_KB57</i>	<i>Klebsiella pneumoniae</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3043 length 210 cov 1.47742	210	2.30476	gi 937424920 ref YP_009165756.1	66.6	5.47E-14	1100043	<i>Apis mellifera filamentum virus</i>	<i>Apis mellifera</i>	Arthropoda; Metazoa; Eukaryota	unclassified	dsDNA	unclassified
NODE 355 length 451 cov 1.2601	451	2.28603	gi 593777121 ref YP_009014966.1	103	3.39E-26	1162290	<i>Cronobacter phage CR9</i>	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1190 length 270 cov 1.7814	270	2.23333	gi 509142181 ref YP_008061043.1	110	4.10E-29	1007869	<i>Rhodococcus hoagii</i>	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 600 length 349 cov 1.10884	349	2.2235	gi 472340491 ref YP_007640161.1	52	3.46E-08	754049	<i>Vibrio phage vYD21-A</i>	<i>Vibrio sp. YD21</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1098 length 274 cov 2.02283	274	2.20438	gi 72142304 ref YP_009104701.1	86.3	1.47E-20	1527515	<i>Idiomarinaeae bacterium M2-2</i>	<i>Idiomarinaeae bacterium M2-2</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1169 length 271 cov 1.73148	271	2.19188	gi 937456498 ref YP_009168424.1	61.6	7.37E-12	1622234	<i>Citrobacter phage CTY22</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 705 length 323 cov 1.21642	323	2.16718	gi 29566640 ref NP_818206.1	78.6	1.31E-17	205277	<i>Mycobacterium phage Bzr1</i>	<i>Mycobacterium sp.</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1006 length 279 cov 1.70982	279	2.16129	gi 1070103030 ref YP_009287678.1	64.7	5.52E-13	1838137	<i>Prionocystis bacterium pseudoreichii</i>	<i>Prionocystis pseudoreichii</i>	Actinobacteria; Bacteria	unclassified	dsDNA	unclassified
NODE 881 length 295 cov 1.23333	295	2.14237	gi 1068511191 ref YP_009274208.1	57	1.47E-11	1838071	<i>Gordonia phage Kvovis</i>	<i>Gordonia vitreum</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 980 length 281 cov 1.16372	281	2.14235	gi 326784531 ref YP_004324978.1	58.9	2.58E-11	445688	<i>Prochlorococcus phage P-SSM7</i>	<i>Prochlorococcus marinus</i> str. NATLLA	Cyanobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2414 length 225 cov 1.51765	225	2.12444	gi 564292915 ref YP_008873609.1	52.8	7.26E-10	1007127	<i>Staphylococcus phage Sb-1</i>	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 954 length 284 cov 1.67249	284	2.12324	gi 593775732 ref YP_009013592.1	76.6	4.44E-17	1089121	<i>Mycobacterium phage Dori</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1620 length 251 cov 1.58163	251	2.11155	gi 937456504 ref YP_009168430.1	114	1.72E-30	1622234	<i>Citrobacter phage CT22</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 943 length 286 cov 1.40226	286	2.10839	gi 388684798 ref YP_006382678.1	65.5	3.70E-13	1161927	<i>Pseudomonas phage Lu11</i>	<i>Pseudomonas putida</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1460 length 258 cov 1.18227	258	2.10078	gi 589287688 ref YP_009010292.1	57.4	2.00E-10	1401669	<i>Erwinia phage PhiEa1</i>	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2243 length 230 cov 1.42286	230	2.1	gi 1070096285 ref YP_009277923.1	112	5.52E-31	1887651	<i>Gordonia phage NvcaH1</i>	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 929 length 289 cov 0.884615	289	2.0692	gi 9626704 ref NP_040974.1	61.2	5.57E-12	11673	<i>Feline immunodeficiency virus</i>	<i>Feline immunodeficiency virus</i>	Chordata; Metazoa; Eukaryota	unclassified	Retroviridae	ssRNA RT
NODE 1801 length 245 cov 1.49474	245	2.05714	gi 440876105 ref YP_006987800.1	49.7	8.18E-08	1141139	<i>Enterobacteria phage vB_EcoP_ACG-C91</i>	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2113 length 234 cov 2.27374	234	2.05128	gi 203454570 ref YP_002225066.1	79	2.56E-18	546805	<i>Mycobacterium phage Myria</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2056 length 247 cov 1.102	247	2.05128	gi 406811846 ref YP_009275124.1	62.4	2.36E-12	1831554	<i>Gordonia phage Etorob</i>	<i>Gordonia vitreum</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 846 length 299 cov 1.32377	299	2.01672	gi 939177065 ref YP_009172504.1	79.3	5.88E-18	1663280	<i>Ostreococcus lucimarinus virus 2</i>	<i>Ostreococcus lucimarinus'</i>	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
NODE 755 length 314 cov 1.40541	314	2.00637	gi 460042347 ref YP_007517785.1	68.2	5.74E-14	1283078	<i>Pelagibacter phage HTCC011P</i>	<i>Candidatus Pelagibacter ubique</i> HTCC01062	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1080 length 275 cov 1.37272	275	2	gi 1173244297 ref YP_009352305.1	60.1	2.32E-11	1220717	<i>Rhizobium phage RHEph10</i>	<i>Rhizobium etli</i> CFN 42	Proteobacteria; Bacteria	Caudovirales	unclassified	unclassified
NODE 2211 length 231 cov 1.63636	231	1.96104	gi 937456465 ref YP_009168390.1	139	1.71E-41	1622234	<i>Citrobacter phage CT22</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1499 length 256 cov 1.22388	256	1.95312	gi 56693176 ref YP_164763.1	79.3	5.45E-19	298338	<i>Lactobacillus phage LP65</i>	<i>Lactobacillus plantarum</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 359 length 449 cov 1.02792	449	1.83964	gi 971748544 ref YP_009202464.1	47.4	3.88E-07	1698711	<i>Mycobacterium phage Lohly9</i>	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 995 length 280 cov 1.25778	280	1.79643	gi 1070096446 ref YP_009278373.1	52	1.72E-08	1883372	<i>Erwinia phage vB_EamM_Ear/PhillipIV</i>	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2679 length 219 cov 1.16463	219	1.78539	gi 849250932 ref YP_009147766.1	85.9	1.16E-20	1560313	<i>Lactococcus phage WRP3</i>	<i>Lactococcus lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1340 length 263 cov 1.36058	263	1.70342	gi 682123292 ref YP_009056237.1	48.9	1.73E-07	1529058	<i>Vibrio phage ICP2_2013_A Haiti</i>	<i>Vibrio cholerae</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 574 length 354 cov 1.08027	354	1.70056	gi 682123169 ref YP_009055490.1	68.2	9.78E-15	1505225	<i>Acinetobacter phage YMC-13-01-C62</i>	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1480 length 257 cov 1.66931	257	1.6965	gi 107006678 ref YP_009283992.1	74.3	1.77E-16	1815509	<i>Bacillus subtilis subsp. subtilis</i> str. 168	<i>Bacillus subtilis subsp. subtilis</i> str. 168	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1736 length 247 cov 1.56625	247	1.6558	gi 1070103030 ref YP_009283947.1	75.1	5.03E-07	184477	<i>Pseudomonas phage NP1</i>	<i>Pseudomonas putida</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1152 length 272 cov 1.02765	272	1.62688	gi 481019400 ref YP_007877754.1	48.1	3.29E-07	356444	<i>Cyanophage P-RSM1</i>	<i>Prochlorococcus marinus</i> str. MIT 9303	Cyanobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1106 length 274 cov 0.940639	274	1.62774	gi 291334961 ref NP_803591.1	53.1	6.63E-09	196683	<i>Pseudomonas phage phiX</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 493 length 374 cov 1.1348	374	1.6123	gi 514361054 ref YP_008130293.1	86.3	5.27E-20	1282995	<i>Serratia phage Etq</i>	<i>Serratia marcescens</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1370 length 262 cov 0.859903	262	1.60305	gi 526120194 ref YP_008320473.1	65.9	1.83E-13	1325731	<i>Flavobacterium phage phiH</i>	<i>Flavobacterium psychrophilum</i>	Bacteroidetes; Bacteria	unclassified	dsDNA	unclassified
NODE 481 length 381 cov 1.17791	381	1.5853	gi 363539900 ref YP_004894381.1	49.7	3.73E-07	1094892	<i>Megavirus chilensis</i>	<i>Acanthamoeba</i>	Longamoebia; Eukaryota	unclassified	Mimiviridae	dsDNA
NODE 1128 length 273 cov 0.958716	273	1.57143	gi 509142296 ref YP_008061158.1	89	1.89E-21	1007869	<i>Rhodococcus hoagii</i>	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 727 length 320 cov 0.977358	320	1.49687	gi 971753194 ref YP_0090207149.1	98.2	2.13E-24	1690425	<i>Streptomyces phase Caliburn</i>	<i>Streptomyces eriseus</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 822 length 303 cov 1.39516	303	1.49175	gi 509142319 ref YP_008061181.1	102	3.41E-26	1007869	<i>Rhodococcus hoagii</i>	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3176 length 207 cov 1.26316	207	1.45894	gi 151266296 ref YP_001333659.1	51.6	8.90E-09	338473	<i>Actinomyces phage Av-1</i>	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3203 length 207 cov 1.19079	207	1.45894	gi 34610177 ref NP_919002.1	90.5	2.18E-22	242861	<i>Burkholderia phage BcepNazgul</i>	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 774 length 311 cov 1.07422	311	1.45659	gi 937456473 ref YP_009168398.1	102	3.42E-26	1622234	<i>Citrobacter phage CT22</i>	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 334 length 208 cov 1.54922	208	1.45659	gi 571198922 ref YP_001468919.1	44.3	3.82E-19	1007869	<i>Caulobacter phage P1201</i>	<i>Caulobacter glutamicum</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3212 length 207 cov 0.842105	207	1.44928	gi 327198317 ref YP_004306893.1	43.1	8.29E-06	59241	<i>Streptococcus phage Dp-1</i>	<i>Streptococcus pneumoniae</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3153 length 208 cov 1.24837	208	1.44712	gi 563398140 ref YP_008									

Table with columns for accession number, length, coverage, and various taxonomic levels (Kingdom, Phylum, Class, Order, Family, Genus, Species) for numerous bacterial and viral sequences.

Healthy bees DNA virome

Summary table for 'Healthy bees DNA virome' showing total counts, seed sizes, lengths, and taxonomic classifications.

Unhealthy bees RNA virome

Large summary table for 'Unhealthy bees RNA virome' with columns for accession number, length, coverage, and taxonomic details for a wide range of viral sequences.

a146107.7 total counts: 6223 Seed: 2 K: 25 length: 980	980	6.25816	gii448244974ref YP_007392694.1	275	8.43E-92	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR1/043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87678.6 total counts: 5258 Seed: 9 K: 25 length: 941	941	6.19497	gii1068358199ref YP_009273940.1	86.7	4.83E-18	1838080	Gordonia phage Vendetta	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a65757.2 total counts: 600 Seed: 2 K: 25 length: 257	257	6.16445	gii593536927ref YP_009168411.2	101	7.99E-27	1622234	Citrobacter phage CVT122	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a88229.6 total counts: 5692 Seed: 2 K: 25 length: 1024	1024	6.16309	gii593771257ref YP_009014970.1	250	1.66E-74	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58559.6 total counts: 3379 Seed: 5 K: 25 length: 610	610	6.14754	gii593777283ref YP_009015128.1	88.6	7.29E-22	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a30198.7 total counts: 3618 Seed: 2 K: 25 length: 524	524	6.12977	gii113232007ref YP_009337788.1	58.2	1.62E-09	1923151	<i>Hubei picorna-like virus 68</i>	<i>Diplodopa</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148940.7 total counts: 2435 Seed: 12 K: 25 length: 372	372	6.12097	gii937456198ref YP_009167808.1	77.8	1.65E-17	438780	Lactobacillus phage phiPYB5	<i>Lactobacillus fermentum</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116141.5 total counts: 2380 Seed: 2 K: 25 length: 475	475	6.05895	gii440789461ref YP_007349171.1	56.6	6.21E-10	1262513	Serratia phage phiMAM1	<i>Serratia</i> sp.	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a147164.6 total counts: 5790 Seed: 8 K: 25 length: 1028	1028	6.04767	gii682123153ref YP_009055474.1	112	9.36E-29	1505225	Acinetobacter phage YMC-13-01-C62	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87623.6 total counts: 2023 Seed: 3 K: 25 length: 385	385	5.99481	gii448244891ref YP_007392611.1	72.4	6.67E-17	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR1/043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a116386.7 total counts: 5103 Seed: 11 K: 25 length: 785	785	5.9172	gii563397698ref YP_008857462.1	65.9	2.20E-13	1391428	Enterobacter phage 4MG	<i>Escherichia coli</i> K-12	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88401.5 total counts: 4397 Seed: 4 K: 25 length: 967	967	5.88004	gii363539710ref YP_004893995.1	77	2.17E-17	889338	Salmonella phage PVP-SE1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a61329.2 total counts: 582 Seed: 2 K: 25 length: 263	263	5.86699	gii764162033ref YP_009126429.1	123	2.71E-35	1561065	Paracoccus phage vB PmaS IMPEP1	<i>Paracoccus marcusii</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87760.5 total counts: 3323 Seed: 8 K: 25 length: 633	633	5.85624	gii113232007ref YP_009337788.1	120	9.32E-31	1923151	<i>Hubei picorna-like virus 68</i>	<i>Diplodopa</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a59531.6 total counts: 9726 Seed: 8 K: 25 length: 1704	1704	5.82453	gii658310294ref YP_009042486.1	377	2.64E-123	1327934	Cronobacter phage CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a117633.5 total counts: 2738 Seed: 6 K: 25 length: 1024	1024	5.82323	gii134598010ref YP_009342255.1	105	9.30E-26	192362	<i>Wuhan arthropod virus 3</i>	<i>Hexapoda</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a116667.5 total counts: 5007 Seed: 5 K: 25 length: 1025	1025	5.71512	gii563397489ref YP_008857253.1	95.5	2.97E-21	1391428	Enterobacter phage 4MG	<i>Escherichia coli</i> K-12	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87688.7 total counts: 2137 Seed: 3 K: 25 length: 333	333	5.68769	gii422937549ref YP_007007754.1	57.4	4.70E-10	1127514	Aeromonas phage vB AsaM-56	<i>Aeromonas salmonicida</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62989.8 total counts: 1709 Seed: 2 K: 25 length: 233	233	5.67811	gii593777355ref YP_009015200.1	82.8	1.63E-20	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a120694.7 total counts: 1942 Seed: 6 K: 25 length: 286	286	5.66667	gii764162223ref YP_009126593.1	133	3.49E-37	1538804	Vibrio phage VpKKS	<i>Vibrio parahaemolyticus</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116247.6 total counts: 3553 Seed: 2 K: 25 length: 661	661	5.66263	gii1070106098ref YP_009291949.1	180	1.62E-53	1792222	Acinetobacter phage LZ35	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146679.6 total counts: 2317 Seed: 4 K: 25 length: 440	440	5.64773	gii1070099784ref YP_009283489.1	44.7	2.08E-06	1647411	Salmonella phage NR01	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1808.3 total counts: 2394 Seed: 2 K: 25 length: 818	818	5.59889	gii971765014ref YP_009218007.1	105	9.57E-25	1755682	Streptomyces phage phiSAJ51	<i>Streptomyces avermitilis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119732.5 total counts: 1999 Seed: 10 K: 25 length: 391	391	5.58568	gii127298679ref YP_00933576.1	72.4	5.33E-15	1922550	<i>Beihai picorna-like virus 121</i>	<i>Lizia exotica</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a60775.5 total counts: 3496 Seed: 3 K: 25 length: 673	673	5.58247	gii971763828ref YP_009216826.1	168	4.65E-51	1229760	Acinetobacter phage phiAC-1	<i>Acinetobacter soli</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a123068.6 total counts: 1164 Seed: 3 K: 25 length: 226	226	5.5708	gii172915520ref YP_009103259.1	55.1	3.92E-10	1481187	Acinetobacter phage vB AbAp Acibel007	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147161.2 total counts: 758 Seed: 4 K: 25 length: 357	357	5.54862	gii712912873ref YP_009099732.1	62.8	4.50E-12	1555208	Ruegeria phage DSS3-P1	<i>Ruegeria pomeroyi</i> DSS-3	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a8802.6 total counts: 2129 Seed: 2 K: 25 length: 384	384	5.53224	gii1070101651ref YP_009285831.1	49.3	5.18E-07	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a157036.2 total counts: 541 Seed: 3 K: 25 length: 258	258	5.52753	gii1068511062ref YP_009274016.1	50.8	3.25E-08	1838072	Gordonia phage McGonagall	<i>Gordonia neofluacis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150472.5 total counts: 1663 Seed: 2 K: 25 length: 344	344	5.50872	gii113232029ref YP_009336506.1	137	4.39E-38	1923011	<i>Hubei orthoherpes virus 3</i>	<i>Orthoherpes</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148545.5 total counts: 4407 Seed: 4 K: 25 length: 906	906	5.4713	gii593777136ref YP_009014981.1	230	8.18E-69	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a17010.8 total counts: 10651 Seed: 7 K: 25 length: 1313	1313	5.46473	gii472342361ref YP_007675869.1	181	8.37E-54	754058	Vibrio phage PWH13a-P1	<i>Vibrio natriegens</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
a91422.5 total counts: 7244 Seed: 6 K: 25 length: 1453	1453	5.46387	gii593777149ref YP_009014994.1	116	7.15E-27	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a12310.3 total counts: 671 Seed: 5 K: 25 length: 285	285	5.44271	gii1070101678ref YP_009285858.1	65.9	4.20E-14	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147994.5 total counts: 2716 Seed: 2 K: 25 length: 623	623	5.40931	gii730985057ref YP_009111142.1	86.3	4.28E-19	1527519	<i>Escherichia</i> phage Av-05	<i>Escherichia coli</i> O157:H7	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a89524.5 total counts: 5704 Seed: 5 K: 25 length: 1090	1090	5.40367	gii593777381ref YP_009015226.1	268	2.17E-85	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a148424.6 total counts: 2706 Seed: 2 K: 25 length: 480	480	5.35113	gii1070101665ref YP_009285845.1	68.2	2.26E-13	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a1179.5 total counts: 4904 Seed: 10 K: 25 length: 928	928	5.34914	gii389059974ref YP_006383127.1	358	2.43E-122	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a10598.3 total counts: 614 Seed: 3 K: 25 length: 239	239	5.33197	gii1070099007ref YP_009281736.1	83.6	9.35E-20	1874002	Bacillus phage Stinch	<i>Bacillus</i> sp.	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a399.5 total counts: 3222 Seed: 2 K: 25 length: 661	661	5.32220	gii1070101651ref YP_009285831.1	49.3	5.18E-07	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146560.3 total counts: 818 Seed: 2 K: 25 length: 311	311	5.31379	gii1068357956ref YP_009273286.1	65.1	4.55E-13	1647470	Gordonia phage GMA1	<i>Gordonia makuake</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87786.4 total counts: 3868 Seed: 4 K: 25 length: 908	908	5.29846	gii363539684ref YP_004893969.1	127	1.86E-35	889338	Salmonella phage PVP-SE1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147329.4 total counts: 4586 Seed: 2 K: 25 length: 1094	1094	5.29616	gii971763920ref YP_009216905.1	56.6	2.14E-08	1522092	Clostridium phage phiCDHM19	<i>Clostridium</i> sp.	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a58707.5 total counts: 7658 Seed: 3 K: 25 length: 1538	1538	5.28088	gii389060077ref YP_006383230.1	47.1	5.19E-164	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29755.9 total counts: 7610 Seed: 2 K: 25 length: 902	902	5.26718	gii1132370509ref YP_009336655.1	81.6	3.01E-16	1923160	<i>Hubei picorna-like virus 76</i>	<i>Mvriapoda</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148214.5 total counts: 1378 Seed: 5 K: 25 length: 322	322	5.26618	gii9633052ref INP_051061.1	48.1	8.03E-07	12417	Lactobacillus phage phiADT	<i>Lactobacillus gasseri</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61287.2 total counts: 413 Seed: 2 K: 25 length: 214	214	5.25413	gii472339880ref YP_007673409.1	46.6	5.33E-07	756282	Cellulophaga phage phiS8	<i>Cellulophaga</i> sp. MM#3	Bacteroidetes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87573.5 total counts: 8642 Seed: 3 K: 25 length: 1816	1816	5.25275	gii730985094ref YP_009111179.1	192	9.27E-53	1527519	<i>Escherichia</i> phage Av-05	<i>Escherichia coli</i> O157:H9	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146137.6 total counts: 2577 Seed: 8 K: 25 length: 483	483	5.21325	gii658310154ref YP_009042486.1	68.2	7.59E-15	1327934	Cronobacter phage CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a60893.5 total counts: 1556 Seed: 5 K: 25 length: 353	353	5.20963	gii593777377ref YP_009015242.1	50.1	3.61E-08	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a11555.7 total counts: 2384 Seed: 2 K: 25 length: 494	494	5.19433	gii966203777ref YP_009189092.1	214	4.67E-67	1684115	Cronobacter phage PBES 02	<i>Cronobacter</i> sp.	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a12003.2 total counts: 666 Seed: 2 K: 25 length: 353	353	5.18405	gii151266302ref YP_001333669.1	58.5	5.24E-07	1162290	Acinetobacter phage CR9	<i>Acinetobacter naeelandii</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a150305.6 total counts: 1803 Seed: 2 K: 25 length: 351	351	5.1453	gii389059922ref YP_006383075.1	86.7	3.30E-20	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147855.5 total counts: 1519 Seed: 6 K: 25 length: 339	339	5.06204	gii571797869ref YP_008772035.1	77.8	2.56E-17	1399941	Lactobacillus phage phiJB	<i>Lactobacillus delbrueckii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58916.5 total counts: 4273 Seed: 4 K: 25 length: 899	899	5.05451	gii971762804ref YP_009215890.1	53.1	6.32E-07	1296655	Bacillus phage JL	<i>Bacillus cereus</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a58466.5 total counts: 1329 Seed: 2 K: 25 length: 293	293	5	gii389060116ref YP_006383269.1	87.8	3.44E-23	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150749.4 total counts: 1179 Seed: 6 K: 25 length: 342	342	4.99457	gii472340162ref YP_007673409.1	45.4	5.94E-06	754067	Salicola phage CGh29	<i>Salicola</i> sp.	Proteobacteria; Bacteria	unclassified	unclassified	RNA
a29359.5 total counts: 3883 Seed: 8 K: 25 length: 780	780	4.95897	gii1132371092ref YP_009337064.1	54.3	1.91E-07	1923150	<i>Hubei picorna-like virus 67</i>	<i>Mvriapoda</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a4746.5 total counts: 1034 Seed: 2 K: 25 length: 230	230	4.8913	gii966203360ref YP_009187671.1	80.5	3.67E-19	1791940	Klebsiella phage vB KpnM KB57	<i>Klebsiella pneumoniae</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a124153.2 total counts: 683 Seed: 2 K: 25 length: 315	315	4.88333	gii374531230ref YP_005098014.1	47.4	3.01E-07	1125653	Salmonella phage SPN15	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a87707.4 total counts: 1477 Seed: 2 K: 25 length: 437	437	4.86041	gii113232007ref YP_009337788.1	48.9	1.33E-06	1923151	<i>Hubei picorna-like virus 68</i>	<i>Diplodopa</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a87941.3 total counts: 2356 Seed: 2 K: 25 length: 744	744	4.84901	gii985760384ref YP_009225904.1	107	9.57E-26	1556290	Streptomyces phage JayZ16	<i>Streptomyces lividans</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149502.4 total counts: 1712 Seed: 5 K: 25 length: 448	448	4.80357	gii593777201ref YP_00915046.1	131	1.61E-35	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88735.5 total counts: 7917 Seed: 7 K: 25 length: 971												

a122019.3 total counts: 1194 Seed: 3 K: 25 length: 366	366	4.31842	gii1070620945freflYYP_009301454.1	64.7	7.17E-13	1821552	Gordonia phage Emalyn	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149361.5 total counts: 1571 Seed: 9 K: 25 length: 310	310	4.3	gii9171763831freflYYP_009216829.1	76.6	5.48E-19	1229760	Acinetobacter phage phiAC-1	<i>Acinetobacter soli</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147715.2 total counts: 378 Seed: 2 K: 25 length: 221	221	4.28602	gii157168388freflYYP_001456745.1	65.9	1.24E-13	28358	Corynebacterium phage BFK20	<i>Brevibacterium flavum</i>	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a48405.4 total counts: 1813 Seed: 7 K: 25 length: 464	464	4.28017	gii593777392freflYYP_009015237.1	45.4	2.37E-06	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a15893.4 total counts: 1127 Seed: 6 K: 25 length: 436	436	4.27509	gii48697198freflYYP_0234928.1	177	5.81E-55	279280	Burkholderia phage BcepC6B	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a30965.4 total counts: 1194 Seed: 2 K: 25 length: 325	325	4.21231	gii848469552freflYYP_009145928.1	70.9	4.86E-15	1220714	Rhizobium phage RHPEf8	<i>Rhizobium etli</i> GR56	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a375.4 total counts: 1247 Seed: 4 K: 25 length: 347	347	4.1902	gii966203437freflYYP_009187754.1	120	3.60E-35	1791440	Klebsiella phage vB_KpnM_KB57	<i>Klebsiella pneumoniae</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a121594.4 total counts: 629 Seed: 6 K: 25 length: 201	201	4.15423	gii593777201freflYYP_009015046.1	115	1.83E-31	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a97527.5 total counts: 2221 Seed: 2 K: 25 length: 436	436	4.15228	gii971762140freflYYP_009215331.1	119	5.01E-32	1636183	Streptomyces phage YDN12	<i>Streptomyces griseus</i> subsp. <i>griseus</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62460.5 total counts: 972 Seed: 5 K: 25 length: 206	206	4.14563	gii389059866freflYYP_006383019.1	54.3	1.05E-09	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a148337.4 total counts: 1892 Seed: 2 K: 25 length: 460	460	4.12609	gii226377831freflYYP_002790879.1	59.7	2.93E-10	631345	<i>Solenopsis invicta</i> virus 3	<i>Solenopsis invicta</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a2658.5 total counts: 1125 Seed: 4 K: 25 length: 262	262	4.11832	gii472342218freflYYP_007675729.1	55.5	5.44E-10	756280	Cellulophaga phage phiSM	<i>Cellulophaga</i> sp. MM#3	Bacteroidetes; Bacteria	Caudovirales	Myoviridae	dsDNA
a147066.5 total counts: 1636 Seed: 3 K: 25 length: 324	324	4.11404	gii410491332freflYYP_0069060554.1	122	5.20E-33	1229786	Propionibacterium phage P101A	<i>Cuitubacterium acnes</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146197.4 total counts: 3045 Seed: 2 K: 25 length: 808	808	4.10877	gii91751687freflYYP_009205612.1	80.9	1.74E-16	1175662	Pseudomonas phage PaMx42	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146950.3 total counts: 532 Seed: 4 K: 25 length: 207	207	4.06557	gii1070620973freflYYP_009301483.1	49.7	5.50E-08	1821552	Gordonia phage Emalyn	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a153042.2 total counts: 381 Seed: 3 K: 25 length: 239	239	4.06298	gii41179371freflYYP_0095679.1	62.5	1.24E-12	194929	Bordetella phage BP1	<i>Bordetella bronchiseptica</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a30547.1 total counts: 6700 Seed: 21 K: 25 length: 552	552	4.02958	gii472449802freflYYP_005087026.1	221	2.13E-70	1109717	Rhodococcus phage RRH1	<i>Rhodococcus rhodocens</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119232.3 total counts: 334 Seed: 2 K: 25 length: 221	221	4.01386	gii971762626freflYYP_009215748.1	93.6	2.37E-23	1718273	Pseudomonas phage PAE1	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64277.5 total counts: 1172 Seed: 5 K: 25 length: 281	281	4.01068	gii448244878freflYYP_007920598.1	96.7	2.72E-24	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR11043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29235.5 total counts: 2308 Seed: 2 K: 25 length: 522	522	4.00766	gii563397465freflYYP_008857229.1	188	5.09E-55	1391428	Enterobacteria phage 4MG	<i>Escherichia coli</i> K-12	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a93068.2 total counts: 738 Seed: 3 K: 25 length: 357	357	4	gii151266305freflYYP_001333668.1	131	8.16E-38	338473	Actinomyces phage Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a4907.4 total counts: 1091 Seed: 5 K: 25 length: 303	303	3.9967	gii971765803freflYYP_009218802.1	119	2.35E-32	1655645	Parabacteroides phage YZ-2015b	<i>na</i>	unclassified	Microviridae	ssDNA +	
a115738.6 total counts: 2739 Seed: 8 K: 25 length: 448	448	3.97768	gii1132371030freflYYP_009337019.1	93.6	4.29E-22	1923158	<i>Hubei picorna-like virus</i> 74	<i>Myriapoda</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a2021.4 total counts: 1002 Seed: 5 K: 25 length: 266	266	3.97744	gii593777354freflYYP_009015199.1	100	2.88E-27	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2748.4 total counts: 2112 Seed: 5 K: 25 length: 600	600	3.96667	gii389059910freflYYP_006383063.1	81.3	8.25E-20	1162295	Cronobacter phage CR3	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150241.4 total counts: 1761 Seed: 6 K: 25 length: 519	519	3.95568	gii448244744freflYYP_007392464.1	55.5	1.25E-08	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR11043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150393.3 total counts: 506 Seed: 4 K: 25 length: 202	202	3.94022	gii146529913freflYYP_001210221.1	46.6	4.79E-07	437329	Burkholderia phage BcepGomr	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a159158.4 total counts: 862 Seed: 6 K: 25 length: 226	226	3.93424	gii2963553freflYYP_059624.1	121	1.03E-35	10754	Enterobacteria phage P22	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147402.3 total counts: 683 Seed: 2 K: 25 length: 224	224	3.92994	gii937456460freflYYP_009168385.1	80.9	2.30E-20	1622234	Citrobacter phage CVT22	<i>Citrobacter</i> sp. TMI552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a150827.3 total counts: 478 Seed: 2 K: 25 length: 211	211	3.89151	gii41179223freflYYP_058561.1	65.9	6.96E-15	139870	Lactobacillus prophage L965	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148796.4 total counts: 1311 Seed: 2 K: 25 length: 335	335	3.88955	gii388570811freflYYP_006383794.1	136	8.44E-38	1187128	Acinetobacter bacteriophage AP22	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146808.5 total counts: 2402 Seed: 2 K: 25 length: 488	488	3.87955	gii490606585freflYYP_009152819.1	52	1.86E-07	1540093	Bacillus phage Pookie	<i>Bacillus megaterium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a29954.4 total counts: 4678 Seed: 6 K: 25 length: 1159	1159	3.86885	gii448244802freflYYP_007392522.1	179	1.16E-50	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR11043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149052.3 total counts: 1216 Seed: 3 K: 25 length: 415	415	3.86024	gii593777266freflYYP_009015111.1	69.7	5.24E-16	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a59372.3 total counts: 1154 Seed: 3 K: 25 length: 355	355	3.84598	gii422935909freflYYP_007005806.1	84.3	1.90E-20	1051675	Erwinia phage vB_Eamp-S6	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149416.3 total counts: 822 Seed: 3 K: 25 length: 265	265	3.80755	gii410492122freflYYP_006907308.1	65.5	2.73E-13	57477	Bacillus phage Bastille	<i>Bacillus cereus</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a35779.4 total counts: 1247 Seed: 6 K: 25 length: 343	343	3.80466	gii363539688freflYYP_004893973.1	99	3.52E-25	889338	<i>Salmonella</i> phage PVP-SE1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147425.5 total counts: 2771 Seed: 5 K: 25 length: 661	661	3.79425	gii563397553freflYYP_008885713.1	121	1.46E-34	1391428	Enterobacteria phage 4MG	<i>Escherichia coli</i> K-12	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1848.3 total counts: 514 Seed: 4 K: 25 length: 200	200	3.785	gii448260870freflYYP_007349227.1	49.7	4.35E-08	1204533	Bacillus phage phiGATE	<i>Bacillus pumilus</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a1847149.9 total counts: 1293 Seed: 4 K: 25 length: 1868	1868	3.78067	gii418484281freflYYP_007003216.1	67	1.48E-14	9070032	Lactobacillus phage phiL1	<i>Lactobacillus</i> sp. M107	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35212.4 total counts: 971 Seed: 8 K: 25 length: 259	259	3.76062	gii593777120freflYYP_009014965.1	134	1.25E-40	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a117265.3 total counts: 661 Seed: 2 K: 25 length: 242	242	3.73554	gii906476396freflYYP_009160400.1	76.3	1.50E-17	1655659	<i>Gakushovirinae</i> Fen7875_21	<i>na</i>	unclassified	Microviridae	ssDNA	
a146821.5 total counts: 2458 Seed: 2 K: 25 length: 524	524	3.71545	gii589893779freflYYP_009010488.1	74.3	4.05E-15	1458842	Geobacillus phage GBK21	<i>Geobacillus kaustophilus</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146506.4 total counts: 3410 Seed: 3 K: 25 length: 814	814	3.71007	gii593777392freflYYP_009015237.1	49.3	3.60E-07	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a158898.2 total counts: 344 Seed: 2 K: 25 length: 206	206	3.68644	gii1070099269freflYYP_009282381.1	47	4.56E-07	1815511	Lactobacillus phage PLE2	<i>Lactobacillus casei</i> BL23	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a65.6 total counts: 4013 Seed: 2 K: 25 length: 656	656	3.65753	gii62327110freflYYP_223898.1	151	2.25E-41	235201	Lactobacillus phage phiJL-1	<i>Lactobacillus plantarum</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150391.2 total counts: 603 Seed: 3 K: 25 length: 285	285	3.63158	gii580177873freflYYP_008050946.1	55.5	1.09E-09	1325953	Mycobacterium phage PcgL-6	<i>Mycobacterium smegmatis</i> str. <i>MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31857.4 total counts: 705 Seed: 2 K: 25 length: 224	224	3.62054	gii90592627freflYYP_529887.1	47.4	1.23E-07	363555	Lactobacillus phage KC5a	<i>Lactobacillus gasseri</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a152065.4 total counts: 2093 Seed: 6 K: 25 length: 561	561	3.61151	gii107096343freflYYP_009277980.1	125	4.45E-33	1654872	Propionibacterium phage QueenBev	<i>Cuitubacterium acnes</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a125574.4 total counts: 3571 Seed: 3 K: 25 length: 1017	1017	3.59095	gii65831013freflYYP_009044224.1	380	4.58E-130	1327934	Cronobacter phage CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a156327.4 total counts: 1421 Seed: 2 K: 25 length: 394	394	3.59073	gii410491739freflYYP_006906961.1	60.5	7.27E-11	1204525	Streptomyces phage SV1	<i>Streptomyces venezuelae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118987.6 total counts: 1591 Seed: 4 K: 25 length: 287	287	3.57491	gii132370375freflYYP_009336558.1	57.4	1.92E-09	1923009	<i>Hubei orbivirus</i> 74	<i>Orbivirus</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a149082.2 total counts: 673 Seed: 5 K: 25 length: 316	316	3.56835	gii12913802freflYYP_009100909.1	69.7	1.41E-14	1536592	Idiomarinaeae bacterium IN2-2	<i>Idiomarinaeae bacterium</i> IN2-2	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a7871.5 total counts: 1965 Seed: 6 K: 25 length: 443	443	3.56659	gii966203781freflYYP_009189096.1	58.9	5.91E-12	1684115	Cronobacter phage PBES 02	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1705.3 total counts: 715 Seed: 3 K: 25 length: 280	280	3.56429	gii448244951freflYYP_007392671.1	137	3.21E-39	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCR11043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a30141.3 total counts: 903 Seed: 9 K: 25 length: 311	311	3.54019	gii593777348freflYYP_009015193.1	166	1.35E-48	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62682.5 total counts: 1539 Seed: 2 K: 25 length: 321	321	3.51325	gii1068512754freflYYP_009276541.1	75.5	6.83E-17	1838064	Gordonia phage BritBrat	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a36095.3 total counts: 1669 Seed: 5 K: 25 length: 594	594	3.4899	gii593777396freflYYP_009015241.1	79.3	1.69E-18	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31951.4 total counts: 1233 Seed: 2 K: 25 length: 360	360	3.48611	gii971848926freflYYP_009035505.1	101	1.28E-25	1416334	Lactobacillus phage phi Jlb1	<i>Lactobacillus gasseri</i> ADH	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146623.4 total counts: 2347 Seed: 5 K: 25 length: 639	639	3.46009	gii1070638430freflYYP_009302456.1	48.5	4.07E-06	1792032	Bacillus phage SP-15	<i>Bacillus paralicheniformis</i> ATCC 9945A	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a15378.3 total counts: 1073 Seed: 9 K: 25 length: 385	385	3.45974	gii593777334freflYYP_009015179.1	127	2.03E-35	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a94066.2 total counts: 399 Seed: 3 K: 25 length: 218	218	3.45525	gii151266296freflYYP_001333659.1	70.5	2.78E-15	338473	Actinomyces phage Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a17374.7 total counts: 1522 Seed: 2 K: 25 length: 431	431	3.45373	gii479336296freflYYP_007869931.1	100	4.6E-25	1305710	Mycobacterium phage vB_MapS_FF47	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155313.4 total counts: 452 Seed: 3 K: 25 length: 217	217	3.4505	gii363553freflYYP_059624.1	121	1.03E-35	10754	Enterobacteria phage P22	<i>Escherichia coli</i> ArS-ArV2	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a5979.2 total counts: 500 Seed: 4 K												

a1509764 total counts: 893 Seed: 3 K: 25 length: 229	229	3.11146	gii219563209 ref YP_002455801.1	55.5	5.84E-10	578234	Lactobacillus phage Lv-1	<i>Lactobacillus jensenii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1494174 total counts: 691 Seed: 4 K: 25 length: 200	200	3.1	gi937456524 ref YP_009168450.1	62.4	1.31E-12	1622234	Citrobacter phage CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a958733 total counts: 1072 Seed: 4 K: 25 length: 418	418	3.09569	gi593777349 ref YP_009015194.1	75.9	2.34E-18	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a528212 total counts: 663 Seed: 2 K: 25 length: 372	372	3.091153	gi107010309 ref YP_009287678.1	105	8.36E-27	1838137	Phycomonobacterium phage PPR1	<i>Phycomonobacterium freudenreichii</i>	Actinobacteria; Bacteria	Caudovirales	unclassified	dsDNA	
a55544 total counts: 1833 Seed: 2 K: 25 length: 435	435	3.08389	gi122935909 ref YP_007005806.1	132	1.05E-38	1051675	Erwinia phage vB_EamP-S6	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a315453 total counts: 713 Seed: 6 K: 25 length: 228	228	3.07895	gi15809314 ref YP_001504127.1	67.4	2.32E-14	442493	Enterococcus phage phiEF24C	<i>Enterococcus faecalis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1547462 total counts: 656 Seed: 4 K: 25 length: 435	435	3.06872	gi1070639841 ref YP_009304190.1	63.9	8.03E-13	1821553	Gordonia phage Guacamole	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1505293 total counts: 678 Seed: 2 K: 25 length: 265	265	3.06415	gi593777538 ref YP_009015381.1	111	9.90E-30	1084719	Bacillus phage G	<i>Bacillus sp.; Geobacillus sp.</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1549172 total counts: 285 Seed: 3 K: 25 length: 207	207	3.06093	gi1102621404 ref YP_009322238.1	52.8	6.69E-10	1813769	Salmonella phage 64795_sal3	<i>Salmonella enterica</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	unclassified	
a641922 total counts: 467 Seed: 2 K: 25 length: 263	263	3.05703	gi1070106096 ref YP_009291947.1	93.6	2.66E-25	1792222	Acinetobacter phage LZ35	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a874334 total counts: 1294 Seed: 2 K: 25 length: 343	343	3.05248	gi682123168 ref YP_009055489.1	82.8	2.68E-19	1505225	Acinetobacter phage YMC-13-01-C62	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1481324 total counts: 936 Seed: 4 K: 25 length: 269	269	3.04516	gi148487735 ref YP_007002058.1	80.9	1.24E-18	1133292	Bruceella phage Tb	<i>Bruceella abortus 544</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a1489592 total counts: 508 Seed: 2 K: 25 length: 249	249	3.03571	gi937456502 ref YP_009168428.1	43.5	7.66E-06	1622234	Citrobacter phage CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a1621052 total counts: 849 Seed: 2 K: 25 length: 395	395	3.03139	gi149408242 ref YP_001294521.1	131	3.54E-36	347328	Pseudomonas phage M6	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a534773 total counts: 1262 Seed: 4 K: 25 length: 401	401	3.02993	gi422937532 ref YP_007007737.1	86.7	1.01E-20	1127514	Aeromonas phage vB_Asam-56	<i>Aeromonas salmonicida</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1496884 total counts: 1078 Seed: 2 K: 25 length: 265	265	3.02199	gi129235852 ref YP_007895923.1	104	3.69E-27	1205510	Mycobacterium phage QanP	<i>Mycobacterium avium subsp. paratuberculosis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a301802 total counts: 792 Seed: 2 K: 25 length: 351	351	3	gi1132370297 ref YP_009336506.1	139	2.85E-28	1923011	<i>Hubei orhotrixa virus 3</i>	<i>Hubei orhotrixa virus 3</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA	
a601663 total counts: 965 Seed: 4 K: 25 length: 366	366	2.9871	gi1543171058 ref YP_008531119.1	75.1	3.68E-17	1354514	Mycobacterium phage M6	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a586553 total counts: 818 Seed: 4 K: 25 length: 302	302	2.98344	gi906476384 ref YP_009169392.1	103	5.69E-28	1655658	<i>Microrividae Fen786 21</i>	<i>na</i>	Actinobacteria; Bacteria	Caudovirales	unclassified	Microviridae	ssDNA
a593676 total counts: 4260 Seed: 3 K: 25 length: 784	784	2.98333	gi764162043 ref YP_009126439.1	59.3	8.04E-10	1561065	Paracoccus phage vB_PmaS IMPEI	<i>Paracoccus caruscii</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1197992 total counts: 1055 Seed: 6 K: 25 length: 453	453	2.97778	gi1068359406 ref YP_009276409.1	248	9.59E-84	1647471	Gordonia phage GMA4	<i>Gordonia makuake</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1476782 total counts: 645 Seed: 2 K: 25 length: 315	315	2.97143	gi971848934 ref YP_009035513.1	82	4.63E-19	1416334	Lactobacillus phage phiJ1b1	<i>Lactobacillus saessleri ADH</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1242683 total counts: 568 Seed: 5 K: 25 length: 216	216	2.96928	gi151266299 ref YP_001133662.1	56.6	1.95E-10	338473	Actinomyces phage Av-1	<i>Actinomyces naesslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a628753 total counts: 1490 Seed: 3 K: 25 length: 454	454	2.96696	gi1003725486 ref YP_009237509.1	73.9	1.69E-15	1685785	<i>Lake Sarah-associated circular virus-8</i>	<i>na</i>	unclassified	unclassified	unclassified		
a668362 total counts: 431 Seed: 3 K: 25 length: 201	201	2.96517	gi209967989 ref YP_002296164.1	53.1	2.54E-09	181082	<i>Emilitania huxleyi virus 8</i>	<i>Emilitania huxleyi</i>	Napthophyta; Chromalveolata; Eukaryota	unclassified	Phycodnaviridae	dsDNA	
a340952 total counts: 691 Seed: 2 K: 25 length: 327	327	2.94792	gi1068511239 ref YP_009274344.1	164	4.47E-49	1647474	Tsakamurella phage TPA4	<i>Tsakamurella paurometabola</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a684302 total counts: 500 Seed: 2 K: 25 length: 247	247	2.93027	gi446730230 ref YP_007173600.1	49.7	8.89E-08	1206110	Lactobacillus phage phiQA113	<i>Lactobacillus helveticus</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a39562 total counts: 423 Seed: 2 K: 25 length: 210	210	2.93006	gi151266299 ref YP_001133662.1	54.3	1.32E-09	338473	Actinomyces phage Av-1	<i>Actinomyces naesslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a1497383 total counts: 735 Seed: 3 K: 25 length: 268	268	2.9291	gi1070620004 ref YP_009304800.1	59.7	1.14E-11	1605379	Acinetobacter phage vB_AbaM phiAbaA1	<i>Acinetobacter baumannii</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1499503 total counts: 649 Seed: 4 K: 25 length: 212	212	2.92777	gi117921818 ref NP_958556.1	72	6.88E-16	139870	Lactobacillus prophage LJr65	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1201982 total counts: 774 Seed: 4 K: 25 length: 343	343	2.92711	gi363540839 ref YP_004894409.1	51.6	6.09E-08	1094892	<i>Megavirus chilensis</i>	<i>Acanthamoeba</i>	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA	
a1280232 total counts: 427 Seed: 3 K: 25 length: 214	214	2.92203	gi149408253 ref YP_001294532.1	57.4	3.20E-11	347328	Pseudomonas phage M6	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a101753 total counts: 723 Seed: 3 K: 25 length: 281	281	2.92171	gi363539649 ref YP_004893934.1	179	6.22E-57	889338	Salmonella phage PVP-SE3	<i>Salmonella enterica subsp. enterica serovar Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1519356 total counts: 4135 Seed: 4 K: 25 length: 711	711	2.91603	gi418489116 ref YP_007002970.1	157	4.63E-47	37105	Lactobacillus phage LJC1032	<i>Lactobacillus delbrueckii subsp. lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1207324 total counts: 839 Seed: 6 K: 25 length: 244	244	2.89855	gi1070101675 ref YP_009285855.1	65.5	2.38E-13	1844477	Pseudomonas phage Np1	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a607762 total counts: 837 Seed: 3 K: 25 length: 364	364	2.88736	gi966203396 ref YP_009187713.1	120	1.49E-34	1791940	Klebsiella phage vB_KpnM KB57	<i>Klebsiella pneumoniae</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1493223 total counts: 1310 Seed: 4 K: 25 length: 469	469	2.8742	gi226377764 ref YP_002790813.1	103	1.70E-25	632112	Lactobacillus phage Lb338-1	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a586723 total counts: 2088 Seed: 3 K: 25 length: 747	747	2.87015	gi4482444883 ref YP_007392603.1	123	5.97E-33	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atropisicum SCR11043</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a296289 total counts: 864 Seed: 2 K: 25 length: 947	947	2.86546	gi971746169 ref YP_009200249.1	149	6.97E-40	1636200	Pseudotolerothomas phage H103	<i>Pseudotolerothomas marina</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA	
a342701 total counts: 865 Seed: 3 K: 25 length: 323	323	2.86538	gi109822826 ref YP_065524099.1	105	2.61E-09	1226169	Acinetobacter phage PBI1	<i>Acinetobacter sp.</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a16753 total counts: 844 Seed: 4 K: 25 length: 302	302	2.86387	gi1068512776 ref YP_009276563.1	73.6	5.16E-36	1838062	Gordonia phage BriffB	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a727102 total counts: 497 Seed: 3 K: 25 length: 327	327	2.85321	gi1070638959 ref YP_009303093.1	54.7	3.34E-09	1796994	Arthrobacter phage Bartel.emon	<i>Arthrobacter sp. ATCC 21022</i>	Actinobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a46325 total counts: 919 Seed: 4 K: 25 length: 220	220	2.85	gi947835102 ref YP_009177523.1	73.2	1.47E-16	1720495	Escherichia phage slur16	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a5936820 total counts: 48740 Seed: 7 K: 25 length: 2470	2470	2.83945	gi401723087 ref YP_006589997.1	100	2.06E-20	1136535	Burkholderia phage DC1	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a1163403 total counts: 783 Seed: 7 K: 25 length: 265	265	2.83774	gi593777364 ref YP_009015209.1	101	1.21E-28	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1465414 total counts: 1219 Seed: 2 K: 25 length: 343	343	2.83544	gi985757694 ref YP_009222820.1	196	2.17E-61	1573458	Pseudomonas phage PS-1	<i>Pseudomonas sp. 1-1-lb</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1474443 total counts: 542 Seed: 2 K: 25 length: 212	212	2.82075	gi110492609 ref YP_006907795.1	47	4.56E-07	1136731	Bacillus phage BPS13	<i>Bacillus cereus</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a360382 total counts: 482 Seed: 5 K: 25 length: 245	245	2.81522	gi609217172 ref YP_008772005.1	50.4	2.50E-08	1406790	Bacillus phage Slash	<i>Bacillus megaterium</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1477452 total counts: 436 Seed: 2 K: 25 length: 222	222	2.81013	gi16271799 ref NP_438136.1	43.9	3.67E-06	173707	Temperate phage phiNH11.1	<i>Streptococcus pyogenes</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a10214 total counts: 2717 Seed: 2 K: 25 length: 670	670	2.80909	gi130546184 ref YP_008409778.1	55.1	4.47E-18	1304825	Mycobacterium phage Trouble	<i>Mycobacterium sp.</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1493572 total counts: 3008 Seed: 2 K: 25 length: 416	416	2.80529	gi117324420 ref YP_009352247.1	70.5	3.55E-14	2098828	<i>Diabrotica virgifera virgifera virus 2</i>	<i>Diabrotica virgifera virgifera</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified	
a90773 total counts: 312 Seed: 3 K: 25 length: 312	312	2.80509	gi103454733 ref YP_002225049.1	105	6.33E-27	1205510	Mycobacterium phage QanP	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1540283 total counts: 851 Seed: 2 K: 25 length: 308	308	2.79221	gi448244788 ref YP_007392508.1	55.1	1.57E-10	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atropisicum SCR11043</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a295082 total counts: 488 Seed: 3 K: 25 length: 290	290	2.76543	gi971821357 ref YP_009208706.1	75.5	1.57E-16	1664247	Achromobacter phage phiAxp-3	<i>Achromobacter xylosoxidans</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a2444 total counts: 3220 Seed: 9 K: 25 length: 772	772	2.75926	gi1068512872 ref YP_009276644.1	72.8	1.03E-13	1838062	Gordonia phage Blueberry	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a122312 total counts: 723 Seed: 2 K: 25 length: 368	368	2.74728	gi966203619 ref YP_009188934.1	191	2.98E-60	1684115	Cronobacter phage PBES 02	<i>Cronobacter sp.</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a21663 total counts: 570 Seed: 4 K: 25 length: 243	243	2.7426	gi206599597 ref YP_002242036.1	44.3	2.24E-06	561996	Mycobacterium phage Bruitia	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1488602 total counts: 904 Seed: 2 K: 25 length: 419	419	2.74107	gi971757354 ref YP_009210861.1	47	4.26E-06	1647301	Mycobacterium phage Vincenzo	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1465093 total counts: 878 Seed: 3 K: 25 length: 312	312	2.73944	gi9632906 ref NP_049935.1	49.3	2.65E-07	72638	Streptococcus phage Sfi19	<i>Streptococcus thermophilus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a60342 total counts: 325 Seed: 3 K: 25 length: 229	229	2.73684	gi643654753 ref YP_009035933.1	62	2.75E-12	1458711	Mycobacterium phage HawkEye	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1462135 total counts: 919 Seed: 2 K: 25 length: 215	215	2.72093	gi682123142 ref YP_009055463.1	76.3	2.21E-18	1505225	Acinetobacter phage YMC-13-01-C62	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a657532 total counts: 359 Seed: 2 K: 25 length: 216	216	2.71698	gi1068357916 ref YP_009273246.1	53.9	1.39E-09	1647474	Gordonia phage GMA1	<i>Gordonia makuake</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA	
a1178002 total counts: 538 Seed: 4 K: 25 length: 250	250	2.716	gi15809316 ref YP_001504129.1	77.8	1.27E-18	442493	Enterococcus phage phiEF24C	<i>Enterococcus faecalis</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA	
a1004222 total counts: 381 Seed: 2 K: 25 length: 298	298	2.71233	gi1360789 ref YP_003305689.1	84.1	2.67E-18	1093817	Citrobacter phage CVT21	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA	
a384393 total counts: 588 Seed: 3 K: 25 length: 259	259												

a150732.2	total counts: 730 Seed: 4 K: 25 length: 327	327	2.45051	gi 966198655 ref YP_009188488.1	61.6	1.29E-11	1589270	Streptococcus phase Str-PAP-1	<i>Streptococcus parauberis</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a30131.2	total counts: 500 Seed: 3 K: 25 length: 300	300	2.44	gi 14087049 ref YP_006987236.1	47.4	8.74E-07	1141136	Cronobacter phase vB_CsaM GAP32	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a59248.2	total counts: 493 Seed: 4 K: 25 length: 248	248	2.43145	gi 313768216 ref YP_004681896.1	105	2.68E-27	880161	<i>Micromonas sp. RCV119 virus Mp11</i>	<i>Micromonas pusilla</i>	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a7992.2	total counts: 506 Seed: 2 K: 25 length: 248	248	2.42742	gi 2088931 ref FNP_624351.1	95.1	4.89E-24	1511847	<i>Fixastrum solani virus 1</i>	<i>Fixastrum solani</i>	Ascomycota; Fungi; Eukaryota	unclassified	Partitiviridae	dsDNA
a147754.4	total counts: 1356 Seed: 5 K: 25 length: 347	347	2.42604	gi 1068358200 ref YP_009273941.1	63.9	2.15E-12	1838080	Gordonia phase Yenetta	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a94533.4	total counts: 673 Seed: 7 K: 25 length: 200	200	2.42568	gi 937456498 ref YP_009168424.1	79.7	1.27E-18	1622234	Citrobacter phase CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a89575.3	total counts: 1059 Seed: 2 K: 25 length: 328	328	2.42378	gi 282599097 ref YP_003359014.1	48.5	1.36E-07	665032	Deflia phase pHW-14	<i>Deflia acidovorans</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	ssRNA
a95022.2	total counts: 512 Seed: 2 K: 25 length: 312	312	2.42308	gi 1043372878 ref YP_009259743.1	64.7	6.18E-13	1676182	<i>Chimpanzee faeces associated microphage 2 na</i>	na	na	unclassified	Microviridae	dsDNA
a31208.2	total counts: 431 Seed: 3 K: 25 length: 225	225	2.42222	gi 971848665 ref YP_009042132.1	47	6.13E-07	1465639	<i>Podovirus Lau218</i>	na	na	Caudovirales	Podoviridae	dsDNA
a87520.2	total counts: 530 Seed: 3 K: 25 length: 263	263	2.40928	gi 971748533 ref YP_009202450.1	52.8	1.39E-09	1698711	Mycobacterium phase Lolly9	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a32291.2	total counts: 651 Seed: 2 K: 25 length: 291	291	2.39437	gi 338826843 ref YP_004678757.1	125	4.69E-34	1041524	Enterobacteria phase K30	<i>Escherichia sp.</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a35855.2	total counts: 537 Seed: 4 K: 25 length: 252	252	2.39286	gi 509142181 ref YP_008061043.1	54.7	1.69E-09	1007869	Rhodococcus phase E3	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a906.7	total counts: 14133 Seed: 6 K: 25 length: 1980	1980	2.3758	gi 589893782 ref YP_009010491.1	59.7	3.12E-08	1488842	Geobacillus phase GBK2	<i>Geobacillus kaustophilus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62006.4	total counts: 686 Seed: 2 K: 25 length: 214	214	2.37383	gi 282598836 ref YP_003359159.1	49.7	6.76E-09	686439	Clavibacter phase CPM1	<i>Clavibacter michiganensis subsp. michiganensis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87978.3	total counts: 685 Seed: 5 K: 25 length: 251	251	2.36255	gi 29135075 ref FNP_803705.1	48.1	2.75E-07	169683	<i>Pseudomonas phase pHZK</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a122566.2	total counts: 607 Seed: 3 K: 25 length: 320	320	2.35925	gi 109492549 ref YP_009207616.1	46.2	3.52E-06	167978	<i>Multivirus ribesiae</i>	<i>Acinobambos castellanii</i>	Longamoebia; Amoebozoa; Eukaryota	unclassified	unclassified	unclassified
a87947.2	total counts: 443 Seed: 3 K: 25 length: 230	230	2.33918	gi 937456514 ref YP_009168440.1	47.8	1.93E-07	1622234	Citrobacter phase CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a67842.3	total counts: 594 Seed: 4 K: 25 length: 251	251	2.32407	gi 1102618170 ref YP_009321910.1	73.2	3.93E-16	1792274	Flavobacterium phase Fvp20	<i>Flavobacterium psychrophilum</i>	Bacteroidetes; Bacteria	unclassified	unclassified	unclassified
a151216.3	total counts: 567 Seed: 2 K: 25 length: 243	243	2.32099	gi 203454799 ref YP_002225115.1	60.5	6.17E-12	546805	Mycobacterium phase Myrma	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a117809.3	total counts: 563 Seed: 2 K: 25 length: 225	225	2.31556	gi 658310061 ref YP_009042253.1	102	1.71E-26	1327934	Cronobacter phase CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a88403.2	total counts: 486 Seed: 2 K: 25 length: 290	290	2.31529	gi 937456498 ref YP_009168424.1	112	1.79E-29	1622234	Citrobacter phase CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a58070.3	total counts: 2596 Seed: 4 K: 25 length: 848	848	2.31486	gi 448244948 ref YP_007392668.1	216	5.42E-71	1116482	Pectobacterium phase phiTE	<i>Pectobacterium atropiscenum SCR1043 [Brevibacterium] flavum</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a146862.3	total counts: 1436 Seed: 3 K: 25 length: 465	465	2.31111	gi 157168378 ref YP_001456735.1	144	8.02E-42	28358	Corynebacterium phase BFK20	<i>Corynebacterium phase BFK20</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35231.3	total counts: 562 Seed: 4 K: 25 length: 248	248	2.28629	gi 448244878 ref YP_007392598.1	71.6	1.49E-15	1116482	Pectobacterium phase phiTE	<i>Pectobacterium atropiscenum SCR1043</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a91292.2	total counts: 562 Seed: 2 K: 25 length: 301	301	2.28571	gi 593777139 ref YP_009014984.1	104	7.99E-28	1162290	Cronobacter phase pHKZ	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a35475.2	total counts: 405 Seed: 2 K: 25 length: 230	230	2.28261	gi 29135232 ref FNP_803862.1	63.9	7.48E-14	169683	<i>Pseudomonas phase pHZK</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a58842.3	total counts: 703 Seed: 2 K: 25 length: 227	227	2.28194	gi 147800662 ref YP_009349663.1	59.7	2.18E-11	1925010	<i>Enterovirus AN12</i>	<i>Bos taurus</i>	Chordata; Metazoa; Eukaryota	unclassified	Microviridae	ssRNA + dsDNA
a63607.2	total counts: 825 Seed: 2 K: 25 length: 394	394	2.27919	gi 985760870 ref YP_009226385.1	49.7	1.01E-07	129659	Paenibacillus phase Jimmer1	<i>Paenibacillus phase Jimmer1</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146574.4	total counts: 2199 Seed: 2 K: 25 length: 626	626	2.27473	gi 148750838 ref YP_001285880.1	150	2.25E-42	12348	Lactobacillus phase LL-H	<i>Lactobacillus delbrueckii subsp. lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a90322.3	total counts: 622 Seed: 4 K: 25 length: 229	229	2.26894	gi 966198576 ref YP_009188410.1	44.3	2.00E-06	164774	Gordonia phase GT16	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147979.2	total counts: 377 Seed: 4 K: 25 length: 204	204	2.2598	gi 310831534 ref YP_003970177.1	53.9	1.42E-09	693272	<i>Cafeteria roenbergensis virus BV-PW1</i>	<i>Cafeteria roenbergensis</i>	Bicosocida; Eukaryota	unclassified	Mimiviridae	dsDNA
a148421.2	total counts: 718 Seed: 4 K: 25 length: 409	409	2.25428	gi 593777612 ref YP_009015458.1	81.6	3.33E-18	1084719	Bacillus phase G	<i>Bacillus sp.; Geobacillus sp.</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA
a87756.2	total counts: 535 Seed: 2 K: 25 length: 294	294	2.2487	gi 372449823 ref YP_005087046.1	155	1.15E-45	1109713	Rhodococcus phase REO2	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120792.3	total counts: 859 Seed: 3 K: 25 length: 338	338	2.2426	gi 658310047 ref YP_009042239.1	157	3.09E-46	1327934	Cronobacter phase CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a90837.2	total counts: 749 Seed: 2 K: 25 length: 402	402	2.24129	gi 589898964 ref YP_009005029.1	45.1	4.97E-06	1429768	Erwinia phase Ea35-7	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a5407.2	total counts: 487 Seed: 3 K: 25 length: 261	261	2.23372	gi 203454799 ref YP_002225113.1	62.4	3.40E-13	546805	Mycobacterium phase Myrma	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a73295.2	total counts: 394 Seed: 2 K: 25 length: 218	218	2.22936	gi 589898919 ref YP_009004802.1	53.9	1.79E-09	1429768	Erwinia phase Ea35-7	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a97454.2	total counts: 421 Seed: 2 K: 25 length: 232	232	2.22845	gi 985757311 ref YP_009222774.1	46.2	9.92E-07	1567484	Lactobacillus phase L1efn1	<i>Lactobacillus fermentum</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA
a155665.2	total counts: 740 Seed: 2 K: 25 length: 417	417	2.21343	gi 906476413 ref YP_009160408.1	140	2.11E-41	1655661	<i>Agrobacterium delbrueckii Fcn719 21</i>	na	na	unclassified	Microviridae	dsDNA
a21517.2	total counts: 365 Seed: 4 K: 25 length: 307	307	2.21556	gi 72915791 ref YP_009103574.1	201	1.01E-07	194699	Paenibacillus phase vB_AbaM Acibel004	<i>Paenibacillus baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a90635.3	total counts: 848 Seed: 5 K: 25 length: 312	312	2.20502	gi 1179374 ref FNP_958682.1	87.8	6.96E-21	194699	Bordetella phase BPP-1	<i>Bordetella bronchiseptica</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a15758.3	total counts: 526 Seed: 3 K: 25 length: 229	229	2.17419	gi 1068512709 ref YP_009276510.1	63.5	8.02E-13	1838066	Gordonia phase Cozz	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a630.5	total counts: 1097 Seed: 5 K: 25 length: 264	264	2.17045	gi 428782719 ref YP_007112472.1	58.5	2.16E-11	1147158	Enterobacterial phase mEP390	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147453.6	total counts: 4131 Seed: 4 K: 25 length: 675	675	2.16846	gi 971741645 ref YP_009196166.1	244	1.01E-78	1632621	Paenibacillus phase Veas	<i>Paenibacillus larvae</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149767.2	total counts: 429 Seed: 2 K: 25 length: 260	260	2.16154	gi 363540041 ref YP_004894551.1	107	3.90E-28	1094892	<i>Megavirus chilensis</i>	<i>Acinobambos</i>	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a147905.2	total counts: 452 Seed: 2 K: 25 length: 280	280	2.15714	gi 46401632 ref YP_006476.1	59.7	3.82E-11	10678	Enterobacteria phase P1	<i>Escherichia coli</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a89668.2	total counts: 489 Seed: 2 K: 25 length: 273	273	2.14286	gi 29134961 ref FNP_803591.1	66.6	1.39E-13	169683	<i>Pseudomonas phase pHZK</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a1231.2	total counts: 571 Seed: 2 K: 25 length: 341	341	2.13818	gi 1068357955 ref YP_009273285.1	47	1.66E-06	1647740	Gordonia phase GMA1	<i>Gordonia mалаquae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a4768.2	total counts: 352 Seed: 3 K: 25 length: 243	243	2.12346	gi 906476306 ref YP_009160347.1	99	2.84E-25	1655649	<i>Gokushovirinae GbM5712 52</i>	na	na	unclassified	Microviridae	ssDNA
a99443.2	total counts: 420 Seed: 2 K: 25 length: 256	256	2.12109	gi 363540687 ref YP_004894539.1	56.6	2.74E-10	1094892	<i>Megavirus chilensis</i>	<i>Acinobambos</i>	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a33766.2	total counts: 736 Seed: 4 K: 25 length: 404	404	2.11881	gi 65831013 ref YP_009042329.1	174	3.70E-56	1327934	Cronobacter phase CR8	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a3153.3	total counts: 602 Seed: 2 K: 25 length: 311	311	2.11622	gi 1070160646 ref YP_009219977.1	44.3	9.81E-06	192922	Citrobacter phase LZ35	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a94289.3	total counts: 739 Seed: 2 K: 25 length: 257	257	2.10644	gi 151266296 ref YP_001333659.1	62.8	2.05E-12	338473	Actinomyces phase Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a151167.2	total counts: 478 Seed: 3 K: 25 length: 273	273	2.10256	gi 607840598 ref YP_009021847.1	61.6	6.34E-12	1234881	<i>Dragonfly cyclovirus 3</i>	<i>Erythema simplicicollis</i>	Arthropoda; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
a2130.2	total counts: 374 Seed: 2 K: 25 length: 217	217	2.09924	gi 593774692 ref YP_009012312.1	90.5	4.54E-23	1074309	Mycobacterium phase BioEz	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151570.2	total counts: 914 Seed: 7 K: 25 length: 393	393	2.07143	gi 589287448 ref YP_009010939.1	48.5	9.21E-07	1465618	Salmoneilla phase vB_Sen-Ent2	<i>Salmonella enterica subsp. enterica serovar Enteritidis</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116535.3	total counts: 1708 Seed: 2 K: 25 length: 582	582	2.06701	gi 448244963 ref YP_007392683.1	145	5.42E-43	1116482	Pectobacterium phase phiTE	<i>Pectobacterium atropiscenum SCR1043</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a157881.2	total counts: 336 Seed: 3 K: 25 length: 209	209	2.06699	gi 363540510 ref YP_004894822.1	57.8	6.12E-11	1094892	<i>Megavirus chilensis</i>	<i>Acinobambos</i>	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a59635.4	total counts: 790 Seed: 2 K: 25 length: 231	231	2.06494	gi 226377831 ref YP_002790879.1	58.5	4.65E-11	631345	<i>Solenopsis invicta virus 3</i>	<i>Solenopsis invicta</i>	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a88597.2	total counts: 485 Seed: 2 K: 25 length: 294	294	2.04422	gi 971764182 ref YP_009217184.1	62.4	4.52E-12	998086	<i>Pseudomonas phase PhiPA3</i>	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Mycoviridae	dsDNA
a87844.4	total counts: 778 Seed: 2 K: 25 length: 224	224	2.04151	gi 971757354 ref YP_009210861.1	111	1.00E-29	1647301	Mycobacterium phase VinC10	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a159521.2	total counts: 405 Seed: 2 K: 25 length: 210	210	2.0381	gi 446730260 ref YP_007173630.1	57	1.42E-10	1260110	Lactobacillus phase pHAc1133	<i>Lactobacillus helveticus</i>	Firmicutes; Bacteria	Caudovirales	Mycoviridae	dsDNA
a67732.2	total counts: 346 Seed: 3 K: 25 length: 200	200	2.03382	gi 937456478 ref YP_0091									

a150626.4 total counts: 2102 Seed: 2 K: 25 length: 586	586	2	gii971748726ref YF_009202615.1	88.6	6.66E-20	1698356	Mycobacterium phage Phatniss	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30887.3 total counts: 2539 Seed: 2 K: 25 length: 774	774	2	gii58989373ref YF_009010023.1	89.4	2.32E-19	1458846	Mycobacterium phage RhvO	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146282.4 total counts: 5091 Seed: 2 K: 25 length: 1297	1297	2	gii764160062ref YF_009124741.1	274	1.24E-86	567475	Mycobacterium phage ShyB	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a139119.3 total counts: 778 Seed: 4 K: 25 length: 286	286	2	gii97936632ref YF_007869980.1	60.8	1.35E-11	1205710	Mycobacterium phage VB ManS FF47	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151831.3 total counts: 578 Seed: 2 K: 25 length: 228	228	2	gii530546937ref YF_008410526.1	61.6	1.79E-12	1340713	Mycobacterium phage Wanda	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87667.2 total counts: 336 Seed: 2 K: 25 length: 219	219	2	gii5091410533ref YF_008059937.1	44.7	2.96E-06	1327036	Mycobacterium phage WIVsmall	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31358.5 total counts: 1878 Seed: 2 K: 25 length: 404	404	2	gii985760367ref YF_009225887.1	76.6	8.27E-17	1556290	Streptomyces phage Jay2Jay	<i>Streptomyces lividans</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146790.4 total counts: 3112 Seed: 6 K: 25 length: 754	754	2	gii9717650116ref YF_009218009.1	63.9	8.38E-11	1755682	Streptomyces phage phiSAJ51	<i>Streptomyces avermitilis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a152986.2 total counts: 486 Seed: 2 K: 25 length: 304	304	2	gii326425096ref YF_004286319.1	7.9	7.87E-20	981330	Tsukamurella phage TPA2	<i>Tsukamurella paurometabola</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116252.1 total counts: 45454 Seed: 6 K: 25 length: 4300	4300	2	gii22296541ref NP_680501.1	62	4.31E-09	51369	Lactobacillus phage A2	<i>Lactobacillus paracetaboli</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29349.2 total counts: 802 Seed: 4 K: 25 length: 384	384	2	gii418489408ref YF_007003225.1	47.4	2.32E-06	947980	Lactobacillus phase LF1	<i>Lactobacillus</i> sp.	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147077.5 total counts: 4358 Seed: 2 K: 25 length: 855	855	2	gii195661221ref YF_002117689.1	47.8	8.41E-06	496874	Lactobacillus phage LRm	<i>Lactobacillus rhamnosus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146940.5 total counts: 1211 Seed: 3 K: 25 length: 274	274	2	gii571797865ref YF_008772031.1	68.9	1.83E-14	1399941	Lactobacillus phage phiB	<i>Lactobacillus delbrueckii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a154177.3 total counts: 506 Seed: 3 K: 25 length: 226	226	2	gii557307973ref YF_008767295.1	78.2	5.30E-20	39103	Lactobacillus phage PL-1	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87642.7 total counts: 5502 Seed: 2 K: 25 length: 856	856	2	gii557307959ref YF_008767281.1	123	2.69E-33	39103	Lactobacillus phage PL-1	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149756.3 total counts: 714 Seed: 4 K: 25 length: 245	245	2	gii30949662ref YF_007869980.1	60.8	1.35E-11	1205710	Mycobacterium phage VB ManS FF47	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a127697.2 total counts: 395 Seed: 4 K: 25 length: 226	226	2	gii526244864ref YF_008320190.1	42.3	8.01E-06	1229751	Lactococcus phage BM13	<i>Lactococcus lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a89897.3 total counts: 1259 Seed: 2 K: 25 length: 396	396	2	gii66395809ref YF_2401178.1	46.6	5.02E-06	320841	Staphylococcus phage EM	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30153.7 total counts: 2236 Seed: 7 K: 25 length: 362	362	2	gii971766715ref YF_009219657.1	100	2.28E-26	1610872	Staphylococcus phage IWE-SA4	<i>Staphylococcus aureolyticus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a153673.2 total counts: 398 Seed: 4 K: 25 length: 203	203	2	gii66394700ref YF_240855.1	42.4	8.81E-06	320850	Staphylococcus phage X2	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151174.4 total counts: 983 Seed: 4 K: 25 length: 267	267	2	gii9632896ref NP_049925.1	68.2	3.27E-15	72638	Streptococcus phage Sfi19	<i>Streptococcus thermophilus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155772.2 total counts: 737 Seed: 2 K: 25 length: 368	368	2	gii32469465ref NP_862873.1	63.9	2.80E-12	157924	Streptococcus phage SM1	<i>Streptococcus mitis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146417.4 total counts: 1476 Seed: 2 K: 25 length: 408	408	2	gii764162029ref YF_009126425.1	108	7.12E-28	1561065	Paracoccus phage vB PmaS IMPE1	<i>Paracoccus marcusii</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116451.5 total counts: 4758 Seed: 5 K: 25 length: 1031	1031	2	gii1070101634ref YF_009285814.1	92	2.14E-21	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a145642.3 total counts: 725 Seed: 2 K: 25 length: 263	263	2	gii1070101664ref YF_009285844.1	80.1	7.76E-19	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30328.3 total counts: 1021 Seed: 4 K: 25 length: 408	408	2	gii1070101679ref YF_009285859.1	118	4.27E-33	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a7418.5 total counts: 4292 Seed: 8 K: 25 length: 853	853	2	gii1070101667ref YF_009285847.1	262	2.14E-86	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118866.3 total counts: 1884 Seed: 4 K: 25 length: 577	577	2	gii171762591ref YF_009215714.1	87.4	2.35E-19	1718273	Pseudomonas phage PAE1	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a122622.3 total counts: 1093 Seed: 5 K: 25 length: 344	344	2	gii374531258ref YF_005098041.1	56.6	6.11E-10	1129145	Pseudomonas phage phi297	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a67923.2 total counts: 681 Seed: 4 K: 25 length: 318	318	2	gii162135148ref YF_001595889.1	63.9	1.73E-12	462590	Pseudomonas phage YUa	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29473.2 total counts: 964 Seed: 2 K: 25 length: 471	471	2	gii1621351088ref YF_001595829.1	62.4	3.14E-11	462590	Pseudomonas phage YUa	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a145784.8 total counts: 4517 Seed: 6 K: 25 length: 590	590	2	gii472340490ref YF_00764015.1	133	1.06E-35	754049	Vibrio phage pYD21-A	<i>Vibrio</i> sp. YD21	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58882.3 total counts: 799 Seed: 4 K: 25 length: 306	306	2	gii764162223ref YF_009126593.1	96.3	7.07E-24	1538804	Vibrio phage VnKKS	<i>Vibrio parahaemolyticus</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a20767.2 total counts: 277 Seed: 2 K: 25 length: 205	205	2	gii102619166ref YF_009323093.1	58.2	2.92E-11	1883368	Synechococcus phage S-CAM7	<i>Synechococcus</i> sp.	Cyanobacteria; Bacteria	unclassified	unclassified	dsDNA
a70564.3 total counts: 651 Seed: 2 K: 25 length: 228	228	2	gii509140424ref YF_008059305.1	50.4	3.02E-08	1273749	Halovirus HTGV-1	<i>Halovirus</i> sp. SSS-1	Eurarchaeota; Archaea	unclassified	unclassified	dsDNA
a147494.5 total counts: 2823 Seed: 4 K: 25 length: 627	627	2	gii1068513125ref YF_009276859.1	116	2.32E-30	1567487	Bacillus phage BaIMu-1	<i>Bacillus alcalophilus</i> ATCC 27647 = CGMCC 1.3604	Firmicutes; Bacteria	unclassified	unclassified	dsDNA
a146566.4 total counts: 819 Seed: 6 K: 25 length: 210	210	2	gii163932187ref YF_001642377.1	55.1	9.19E-11	139871	Lactobacillus johnsonii prophage L1771	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a9208.3 total counts: 823 Seed: 3 K: 25 length: 295	295	2	gii163932195ref YF_001642385.1	45.8	3.69E-06	139871	Lactobacillus johnsonii prophage L1771	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a151847.2 total counts: 406 Seed: 2 K: 25 length: 216	216	2	gii1070639738ref YF_009304106.1	120	2.78E-33	1718278	Bruceella phage BiPB01	<i>Bruceella inopinata</i>	Proteobacteria; Bacteria	unclassified	unclassified	unclassified
a41174 total counts: 1746 Seed: 4 K: 25 length: 498	498	2	gii174646469ref YF_009204499.1	185	2.58E-55	1632600	<i>Pseudomonas marina</i>	<i>Pseudomonas marina</i>	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a119264.6 total counts: 4099 Seed: 5 K: 25 length: 723	723	2	gii481018921ref YF_007872778.1	53.5	2.50E-08	371373	Vibrio phage helene 12B3	<i>Vibrio splendidus</i>	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a89109.5 total counts: 2537 Seed: 4 K: 25 length: 541	541	1.99333	gii93007440ref YF_579204.1	103	2.09E-25	370623	Streptomyces phage mu11	<i>Kitatospora aureofaciens</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61764.3 total counts: 1169 Seed: 2 K: 25 length: 378	378	1.98684	gii149882819ref YF_001294798.1	107	2.50E-28	446529	Microbacterium phage MinI	<i>Microbacterium nematophilum</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116831.4 total counts: 1468 Seed: 5 K: 25 length: 420	420	1.98305	gii3292972735ref YF_006488695.1	47.4	2.63E-06	1118063	Staphylococcus phage SpaA1	<i>Staphylococcus pasteuri</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a34480.2 total counts: 589 Seed: 2 K: 25 length: 356	356	1.97753	gii448244966ref YF_007392686.1	89.4	4.71E-23	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150691.2 total counts: 408 Seed: 3 K: 25 length: 228	228	1.96789	gii151266296ref YF_001333659.1	49.7	6.78E-08	338473	Actinomyces phage Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a87571.2 total counts: 502 Seed: 2 K: 25 length: 232	232	1.96552	gii906476306ref YF_009160347.1	116	1.68E-31	1655649	<i>Gokushovirinae</i> Bogs712_52	na	unclassified	Microviridae	ssDNA	
a159187.2 total counts: 584 Seed: 4 K: 25 length: 366	366	1.96104	gii298103488ref YF_003714730.1	71.6	6.13E-15	747763	Streptomyces phage phiSASD1	<i>Streptomyces avermitilis</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149541.4 total counts: 2097 Seed: 4 K: 25 length: 524	524	1.96026	gii971762571ref YF_009215694.1	80.1	3.04E-18	1718273	Pseudomonas phage PAE1	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116854.3 total counts: 570 Seed: 3 K: 25 length: 201	201	1.9602	gii422957534ref YF_007007739.1	65.9	1.02E-13	1127514	Aeromonas phage vB AAS-56	<i>Aeromonas salmonicida</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29426.4 total counts: 3393 Seed: 5 K: 25 length: 879	879	1.96	gii172449802ref YF_005087076.1	117	4.48E-29	1199717	Rhodococcus phage RRH1	<i>Rhodococcus rhodochrous</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148540.2 total counts: 364 Seed: 2 K: 25 length: 265	265	1.94717	gii2493981192ref YF_009052394.1	56.2	4.90E-10	1474887	<i>Autococcus anophageferens</i>	<i>Autococcus anophageferens</i>	Actinobacteria; Bacteria	unclassified	Phycodiviridae	dsDNA
a88247.2 total counts: 457 Seed: 3 K: 25 length: 264	264	1.94156	gii966198557ref YF_009188391.1	72	3.92E-16	1647744	Gordonia phage GTE	<i>Gordonia</i> sp.	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a32896.3 total counts: 834 Seed: 6 K: 25 length: 310	310	1.93793	gii192824184ref YF_001994825.1	53.9	6.00E-09	540068	Mycobacterium phage Pukovnik	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a95332.2 total counts: 393 Seed: 3 K: 25 length: 216	216	1.93716	gii971745058ref YF_009199262.1	44.3	3.95E-06	1690817	Streptomyces phage Sfi1	<i>Streptomyces lividans</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147319.5 total counts: 4372 Seed: 2 K: 25 length: 958	958	1.93293	gii9633052ref NP_050160.1	129	2.57E-32	12417	Lactobacillus phage phiAD	<i>Lactobacillus gasseri</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58114.4 total counts: 1409 Seed: 5 K: 25 length: 385	385	1.92949	gii764159561ref YF_009124300.1	46.2	5.09E-06	1536603	Mycobacterium phage Estavel	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148590.2 total counts: 421 Seed: 2 K: 25 length: 216	216	1.92949	gii1621351088ref YF_001595849.1	125	1.04E-34	462590	Pseudomonas phage YUa	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a125126.3 total counts: 637 Seed: 3 K: 25 length: 218	218	1.92202	gii985757280ref YF_009222243.1	66.2	8.18E-14	1567484	Lactobacillus phage Lfelnf	<i>Lactobacillus fermentum</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a120378.2 total counts: 408 Seed: 3 K: 25 length: 232	232	1.91139	gii937456462ref YF_009168387.1	105	9.21E-28	1622234	Citrobacter phage CVT22	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a7292.3 total counts: 998 Seed: 5 K: 25 length: 352	352	1.91083	gii1070098399ref YF_009281132.1	62.8	6.93E-12	1887647	Gordonia phage					

a147032.4 total counts: 2138 Seed: 3 K: 25 length: 573	573	1.75194	gi 1068359285 ref YP_009275707.1	87	9.94E-20	1622193	Gordonia phage Gspu1	<i>Gordonia sputi</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a115875.2 total counts: 873 Seed: 2 K: 25 length: 442	442	1.175	gi 1498828405 ref YP_011294819.1	51.2	3.65E-08	465259	Microbacterium phage Min1	<i>Microbacterium nematophilum</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88076.5 total counts: 2208 Seed: 6 K: 25 length: 460	460	1.75	gi 29566753 ref NP_818317.1	162	5.40E-48	205879	Mycobacterium phage Omega	<i>Mycobacterium sp.</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88739.6 total counts: 2738 Seed: 12 K: 25 length: 457	457	1.175	gi 22258026 ref NP_690786.1	59.7	2.91E-11	10717	Bacillus phage phi105	<i>Bacillus subtilis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118768.3 total counts: 1047 Seed: 7 K: 25 length: 347	347	1.74419	gi 206600214 ref YP_002241820.1	90.9	3.44E-23	56132	Mycobacterium phage Ramsey	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119050.10 total counts: 6075 Seed: 15 K: 25 length: 629	629	1.74419	gi 59378368 ref YP_00916208.1	84	5.17E-18	691963	Rhodococcus phage ReaPiNe5	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61291.3 total counts: 674 Seed: 2 K: 25 length: 236	236	1.74153	gi 388570814 ref YP_006383797.1	45.4	2.00E-06	118128	Acinetobacter bacteriophage AP22	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29416.1 total counts: 128119 Seed: 2 K: 25 length: 6724	6724	1.73988	gi 1068512423 ref YP_009276106.1	271	1.43E-78	1647473	Gordonia phage GRU3	<i>Gordonia makuaje</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29962.5 total counts: 3288 Seed: 7 K: 25 length: 648	648	1.73563	gi 563398140 ref YP_008857900.1	77.4	6.86E-16	1414742	Arthrobacter phage vB ArS-ArV2	<i>Arthrobacter</i> sp.	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150174.3 total counts: 1110 Seed: 2 K: 25 length: 426	426	1.73563	gi 9635029 ref NP_056694.1	80.5	1.15E-17	78541	Streptococcus phage Sfi11	<i>Streptococcus</i> sp.	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116838.3 total counts: 618 Seed: 2 K: 25 length: 262	262	1.72519	gi 448244890 ref YP_007392610.1	45.1	1.73E-06	1116482	Pectobacterium phage phiTE	<i>Pectobacterium atrosepticum</i> SCRI1043	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88657.2 total counts: 472 Seed: 2 K: 25 length: 273	273	1.71759	gi 1068357954 ref YP_009273284.1	79.3	4.24E-18	1647470	Gordonia phage GMA1	<i>Gordonia makuaje</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146554.3 total counts: 1817 Seed: 3 K: 25 length: 623	623	1.71591	gi 11792888 ref NP_958506.1	85.1	1.20E-18	139872	Lactobacillus prophage Ia928	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a73400.2 total counts: 365 Seed: 2 K: 25 length: 206	206	1.71341	gi 971748040 ref NP_009201826.1	77	1.00E-19	1739608	Lactobacillus phage CL2	<i>Lactobacillus paracasei</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116936.2 total counts: 396 Seed: 2 K: 25 length: 244	244	1.71311	gi 158079460 ref YP_001504273.1	51.8	8.20E-09	442495	Enterococcus phage phiEFT24C	<i>Enterococcus faecalis</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a149390.2 total counts: 192 Seed: 2 K: 25 length: 210	210	1.70913	gi 107015036 ref YP_009100193.1	57.6	2.85E-24	183786	Weissella phage W1	<i>Weissella sp.</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a124699.3 total counts: 522 Seed: 3 K: 25 length: 220	220	1.70455	gi 74589249 ref YP_009035508.1	51.6	8.20E-11	1416334	Lactobacillus phage phi jh1	<i>Lactobacillus gasseri</i> ADH	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a15593.2 total counts: 633 Seed: 4 K: 25 length: 307	307	1.68404	gi 643217946 ref YP_009036156.1	98.2	9.92E-25	1486659	Bacillus phage Hakuna	<i>Bacillus thuringiensis</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a8778.2 total counts: 444 Seed: 2 K: 25 length: 266	266	1.67039	gi 589287594 ref YP_009010198.1	62	5.37E-12	1401669	Erwinia phage PhiEaH1	<i>Erwinia amylovora</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118240.2 total counts: 479 Seed: 2 K: 25 length: 272	272	1.66544	gi 313768160 ref YP_004061597.1	45.1	5.39E-06	880159	<i>Bathyococcus</i> sp. RCC1105 virus Bp17	<i>Bathyococcus prasinos</i> RCC1105	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a88367.5 total counts: 3217 Seed: 4 K: 25 length: 612	612	1.66013	gi 764162223 ref YP_009126593.1	200	5.15E-60	1538804	Vibrio phage VpKks5	<i>Vibrio parahaemolyticus</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87757.8 total counts: 9851 Seed: 3 K: 25 length: 1279	1279	1.65934	gi 970580046 ref YP_009193590.1	118	6.89E-31	1572743	Mannheimia phage vB MhS_535AP2	<i>Mannheimia haemolytica</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a3464.2 total counts: 448 Seed: 4 K: 25 length: 321	321	1.65421	gi 993777360 ref YP_009015205.1	60.8	1.17E-11	1162290	Cronobacter phage CR9	<i>Cronobacter sakazakii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2900.3 total counts: 631 Seed: 2 K: 25 length: 257	257	1.65027	gi 151266300 ref YP_001333663.1	77.4	1.62E-17	338473	Actinomyces phage Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a119791.7 total counts: 4210 Seed: 2 K: 25 length: 595	595	1.64964	gi 157325017 ref YP_001468443.1	100	1.16E-26	40522	Listeria phage AS00	<i>Listeria monocytogenes</i> WSLC1042	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31868.3 total counts: 2017 Seed: 5 K: 25 length: 703	703	1.64835	gi 1070619841 ref YP_009304275.1	74.7	1.34E-14	1821557	Gordonia phage LuckV10	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64513.3 total counts: 687 Seed: 2 K: 25 length: 237	237	1.64481	gi 971748533 ref YP_009202450.1	48.1	5.41E-08	1698711	Mycobacterium phage LolyV9	<i>Mycobacterium smegmatis</i> str. MC2 155	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149411.3 total counts: 766 Seed: 2 K: 25 length: 252	252	1.64286	gi 414090422 ref YP_006909535.1	44.3	5.88E-06	204534	Clostridium phage phiMMPQ2	<i>Clostridium difficile</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a66453.4 total counts: 996 Seed: 5 K: 25 length: 285	285	1.63243	gi 971751675 ref YP_009205624.1	93.6	4.30E-23	1175662	Pseudomonas phage PAmX42	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155141.2 total counts: 477 Seed: 2 K: 25 length: 306	306	1.63072	gi 909592623 ref YP_529883.1	160	1.56E-46	363555	Lactobacillus phage KCS5a	<i>Lactobacillus gasseri</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146813.3 total counts: 3069 Seed: 9 K: 25 length: 926	926	1.62703	gi 526177379 ref YP_008241215.1	185	1.04E-52	327983	Cellulophaga phage phi18.3	<i>Cellulophaga batlica</i>	Bacteroidetes; Bacteria	Caudovirales	Podoviridae	dsDNA
a96090.3 total counts: 507 Seed: 2 K: 25 length: 213	213	1.62385	gi 151266296 ref YP_001333659.1	64.3	3.94E-13	338473	Actinomyces phage Av-1	<i>Actinomyces naeslundii</i>	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a148252.4 total counts: 837 Seed: 3 K: 25 length: 245	245	1.61983	gi 1070096285 ref YP_009277923.1	59.7	2.12E-11	1887651	Gordonia phage Nvevrae	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119564.3 total counts: 930 Seed: 3 K: 25 length: 345	345	1.60963	gi 1070101647 ref YP_009285827.1	151	4.09E-44	1844477	Pseudomonas phage NP1	<i>Pseudomonas</i> sp.	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a10171.2 total counts: 387 Seed: 2 K: 25 length: 213	213	1.60932	gi 338826838 ref YP_004678752.1	110	2.04E-29	1041524	Enterobacteria phage K30	<i>Escherichia</i> sp.	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a14779.2 total counts: 342 Seed: 3 K: 25 length: 221	221	1.60633	gi 971763757 ref YP_009216768.1	45.4	1.56E-06	1701405	Gokushovirinae GNX3R	na	unclassified	Microviridae	ssDNA	
a1742.2 total counts: 564 Seed: 4 K: 25 length: 292	292	1.59788	gi 593779801 ref YP_009017628.1	119	4.07E-32	691965	Rhodococcus phage ReaPiPev6	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146533.5 total counts: 4704 Seed: 2 K: 25 length: 977	977	1.59259	gi 372449804 ref YP_005087028.1	180	4.15E-53	1109717	Rhodococcus phage RRH1	<i>Rhodococcus rhodochrous</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a14624.4 total counts: 3208 Seed: 5 K: 25 length: 758	758	1.58421	gi 849250882 ref YP_009147716.1	125	4.80E-33	560313	Lactococcus phage WRP2	<i>Lactococcus lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35573.3 total counts: 829 Seed: 3 K: 25 length: 295	295	1.58182	gi 107013030 ref YP_009287878.1	94.7	1.07E-30	283817	Protonibacterium phage PFR1	<i>Protonibacterium Freudenbergii</i>	Firmicutes; Bacteria	Caudovirales	unclassified	unclassified
a150131.2 total counts: 402 Seed: 2 K: 25 length: 220	220	1.57592	gi 163932515 ref YP_001462345.1	47.9	9.66E-08	139871	Lactobacillus johnsonii prophage Lj771	<i>Lactobacillus johnsonii</i>	Firmicutes; Bacteria	Caudovirales	unclassified	unclassified
a59363.5 total counts: 3352 Seed: 10 K: 25 length: 636	636	1.57447	gi 1068358199 ref YP_009273940.1	151	2.89E-42	1838080	Gordonia phage Vendetta	<i>Gordonia terrae</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a839.6 total counts: 1702 Seed: 2 K: 25 length: 318	318	1.55862	gi 48697428 ref YP_024813.1	72.4	2.26E-15	279303	Actinoplanes phage phiAsp2	<i>Actinoplanes</i> sp. SN223/29	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a89492.2 total counts: 518 Seed: 4 K: 25 length: 241	241	1.54772	gi 563397579 ref YP_008857343.1	81.3	4.79E-20	1391428	Enterobacteria phage 4MG	<i>Escherichia coli</i> K-12	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88549.2 total counts: 594 Seed: 2 K: 25 length: 296	296	1.54138	gi 939536933 ref YP_009168408.1	61.2	1.82E-13	1622234	Citrobacter phage CVT22	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a98953.2 total counts: 444 Seed: 2 K: 25 length: 292	292	1.53082	gi 971752893 ref YP_009206906.1	48.5	3.81E-07	1690456	Bacillus phage TsrBomba	<i>Bacillus</i> sp.	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a122345.2 total counts: 557 Seed: 3 K: 25 length: 260	260	1.53017	gi 937456522 ref YP_009168448.1	73.2	1.07E-16	1622234	Citrobacter phage CVT22	<i>Citrobacter</i> sp. TM1552	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a146785.2 total counts: 434 Seed: 2 K: 25 length: 234	234	1.52632	gi 418489112 ref YP_007002966.1	62.8	2.80E-13	37105	Lactobacillus phage JCL1032	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a23069 total counts: 35374508 Seed: 6 K: 25 length: 11549	11549	1.52282	gi 712916232 ref YP_009103975.1	271	2.98E-75	1161939	Enterococcus phage vB EfaE30F-4	<i>Enterococcus faecium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a159472.2 total counts: 356 Seed: 2 K: 25 length: 215	215	1.51256	gi 1068511238 ref YP_009273434.1	76.3	2.43E-17	1647276	Tsukamurella phage TP44	<i>Tsukamurella paurometabola</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a100116.2 total counts: 419 Seed: 2 K: 25 length: 241	241	1.46829	gi 588590800 ref YP_009003341.1	44.3	5.98E-06	192321	Streptococcus phage T06A17	<i>Streptococcus thermophilus</i> DSM 20617	Firmicutes; Bacteria	Caudovirales	unclassified	unclassified
a117786.2 total counts: 734 Seed: 3 K: 25 length: 328	328	1.46629	gi 20566753 ref NP_818317.1	115	1.02E-30	205879	Mycobacterium phage Omega	<i>Mycobacterium sp.</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64062.2 total counts: 761 Seed: 2 K: 25 length: 345	345	1.43478	gi 1070106098 ref YP_009291949.1	97.8	2.93E-24	1792222	Acinetobacter phage LZ35	<i>Acinetobacter baumannii</i>	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58823.3 total counts: 507 Seed: 3 K: 25 length: 211	211	1.43128	gi 56693176 ref YP_164763.1	90.9	1.10E-23	298338	Lactobacillus phage LP65	<i>Lactobacillus plantarum</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a150645.4 total counts: 1468 Seed: 2 K: 25 length: 368	368	1.42587	gi 589286930 ref YP_009007125.1	47	1.62E-06	1449337	Pseudomonas phage vB PaeP Tr60 AB31	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
a30269.2 total counts: 378 Seed: 2 K: 25 length: 201	201	1.41294	gi 56693142 ref YP_164729.1	64.7	2.48E-13	298338	Lactobacillus phage LP65	<i>Lactobacillus plantarum</i>	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a132959.2 total counts: 344 Seed: 3 K: 25 length: 214	214	1.41121	gi 363540839 ref YP_004894409.1	51.2	1.65E-08	1094892	Megavirus chilensis	<i>Megavirus chilensis</i>	Lonamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a100241.2 total counts: 326 Seed: 2 K: 25 length: 200	200	1.41	gi 906476402 ref YP_009164042.1	49.7	4.41E-08	1655660	Microviridae Fen7895_21	na	unclassified	Microviridae	ssDNA	
a152403.3 total counts: 578 Seed: 3 K: 25 length: 214	214	1.40476	gi 238801907 ref YP_009225110.1	60.1	1.35E-11	646413	Streptococcus phage S093	<i>Streptococcus thermophilus</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149773.2 total counts: 397 Seed: 2 K: 25 length: 215	215	1.40465	gi 848469534 ref YP_009145910.1	101	4.31E-							

a58124:1283 total counts: 2159833 Seed: 5 K: 25 length: 1707	1707	1	gi 66395192 ref YP_239479.1	160	1.08E-42	320832	Staphylococcus phage 66	<i>Staphylococcus aureus</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a5806:2 total counts: 572 Seed: 3 K: 25 length: 293	293	1	gi 966198655 ref YP_009188488.1	57.4	3.10E-10	1589270	Streptococcus phage Str-PAP-1	<i>Streptococcus parauberis</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a145743:2 total counts: 471 Seed: 2 K: 25 length: 262	262	1	gi 937456458 ref YP_009168383.1	63.2	4.86E-13	1622234	Citrobacter phage CVT22	<i>Citrobacter sp. TM1552</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a154779:3 total counts: 942 Seed: 3 K: 25 length: 323	323	1	gi 41057303 ref NP_958202.1	62.8	7.36E-13	10761	Shiella phage Sif6	<i>Shiella fleisneri</i>	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a62341:3 total counts: 1220 Seed: 4 K: 25 length: 422	422	1	gi 338826904 ref YP_004678817.1	50.1	4.09E-07	981323	Gordonia phage GTE2	<i>Nocardia; Rhodococcus; Gordonia</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147877:3 total counts: 1313 Seed: 4 K: 25 length: 440	440	1	gi 530546920 ref YP_008410509.1	63.2	1.22E-12	1052673	Mycobacterium phage Thibault	<i>Mycobacterium smegmatis str. MC2 155</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119828:3 total counts: 1364 Seed: 5 K: 25 length: 451	451	1	gi 372449813 ref YP_005087037.1	134	4.40E-37	1109717	Rhodococcus phage RRH1	<i>Rhodococcus rhodochrous</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a63661:2 total counts: 479 Seed: 2 K: 25 length: 301	301	1	gi 764162114 ref YP_009126495.1	62	1.20E-12	1552735	Lactobacillus phage Ldl1	<i>Lactobacillus delbrueckii subsp. lactis</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151973:2 total counts: 631 Seed: 5 K: 25 length: 306	306	1	gi 327198366 ref YP_004306940.1	67.8	7.10E-14	59241	Streptococcus phage Dp-1	<i>Streptococcus pneumoniae</i>	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146202:6 total counts: 3699 Seed: 5 K: 25 length: 635	635	1	gi 146329916 ref YP_001210224.1	240	2.19E-76	437329	Burkholderia phage BcepGomr	<i>Burkholderia cepacia</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62462:5 total counts: 1641 Seed: 3 K: 25 length: 339	339	1	gi 399528722 ref YP_006560759.1	92.8	1.33E-22	1132026	Burkholderia phage KL1	<i>Burkholderia cenocepacia</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147376:5 total counts: 1753 Seed: 7 K: 25 length: 376	376	1	gi 62362234 ref YP_224159.1	118	2.71E-31	101570	Enterobacteria phage ES18	<i>Salmonella enterica subsp. enterica serovar Typhimurium</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29643:2 total counts: 737 Seed: 2 K: 25 length: 321	321	1	gi 1070106097 ref YP_009291948.1	144	6.53E-42	1792222	Pseudomonas phage NP1	<i>Pseudomonas sp.</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a11418:2 total counts: 484 Seed: 3 K: 25 length: 227	227	1	gi 162135148 ref YP_001595889.1	114	5.43E-31	462590	Pseudomonas phage YuA	<i>Pseudomonas aeruginosa</i>	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a117147:6 total counts: 3442 Seed: 3 K: 25 length: 595	595	1	gi 372450021 ref YP_005087242.1	168	1.12E-48	1109714	Rhodococcus phage REO3	<i>Rhodococcus hoagii</i>	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
Healthy bees RNA virome												
a332225:2 total counts: 397 Seed: 2 K: 25 length: 219	219	2.38813	gi 1068512422 ref YP_009276105.1	70.1	3.92E-15	1647473	<i>Gordonia phage GRU3</i>	<i>Gordonia rubripertincta</i>	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a18498:2 total counts: 429 Seed: 2 K: 25 length: 236	236	2	gi 712916216 ref YP_009103959.1	58.9	3.34E-11	1161939	<i>Enterococcus phage vB_Efae230P-4</i>	<i>Enterococcus faecium</i>	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA

Supplementary Table 2 - Detection of *M. quadrifasciata* viruses in stingless bee samples: samples of healthy (H) and unhealthy bees (U) of four different meliponaries in Southern of Brazil (BL = Boqueirão do Leão, BP = Bom Principio and RL = Rolante) were tested for virus presence/absence via PCR/RT-PCR. The + symbol means positive samples for the detection of the respective virus. Viruses with DNA genomes were only tested for detection in samples from which the DNA was extracted, the same for RNA viruses in samples from which the RNA was extracted (cells in gray were not tested).

Locality	Year	Syndrome period	Health	Sample type	MqC	MqC1	MqC2	MqD	MqV1a	MqV1b	MqV2
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+	+				
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body	+						
BL	2014	During	U	DNA whole body	+	+	+				
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body							
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+		+			
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	H	DNA whole body	+	+					
BL	2015	During	H	DNA whole body			+				
BL	2015	During	H	DNA whole body	+	+	+				
BL	2015	During	H	DNA whole body		+	+				
BL	2015	During	H	DNA whole body	+						
BL	2015	During	H	DNA whole body	+	+					
BL	2015	During	H	DNA whole body	+						
BL	2015	During	H	DNA whole body		+	+				
BL	2015	During	H	DNA whole body	+	+	+				
BL	2015	During	H	DNA whole body	+	+	+				

Supplementary Table 3 - Tests for the choice of BLAST type to be used for the retrieval and taxonomy of contigs. A sub-sample of contigs (49 contigs of unhealthy bees RNA viroma) was used in the blastP (tab 1) and blastX tests (tab 2), both against the nr database and against the viral RefSeq. In red are highlighted the candidate viral contigs used in the study.

BlastP against nr										BlastP against RefSeq									
Translated contig (amino acids)		subject acc.ver	name	% identity	alignment length	evaluate	bit score	subject acc.ver	name	% identity	alignment length	evaluate	bit score	subject acc.ver	name	% identity	alignment length	evaluate	bit score
115738_6	total_counts: 2739	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	3.64E-19	93.6	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	4.19E-22	93.6	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	4.19E-22	93.6
115755_8	total_counts: 8948	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	6.73E-43	170	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	7.76E-46	170	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	7.76E-46	170
115910_13	total_counts: 77920	AGP76667.1	hypothetical protein 1 [Wuhan insect virus 11]	45.7	870	0.00E+00	731	YP_009342327.1	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	728	YP_009342327.1	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	728
117633_5	total_counts: 2738	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	37.9	190	9.68E-24	108	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	37.9	190	1.12E-26	108	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	37.9	190	1.12E-26	108
118987_6	total_counts: 1591	YP_009336558.1	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	4.70E-07	56.6	YP_009336558.1	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	5.42E-10	56.6	YP_009336558.1	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	5.42E-10	56.6
119065_2	total_counts: 518	BAW18990.1	hypothetical protein [Ralstonia phage RP12]	38.9	90	7.70E-16	79.7	YP_00207816.1	hypothetical protein [Ralstonia phage RSF1]	30.5	82	1.85E-06	46.2	YP_00207816.1	hypothetical protein [Ralstonia phage RSF1]	30.5	82	1.85E-06	46.2
119732_5	total_counts: 1999	YP_00233576.1	hypothetical protein 1 [Beihai picorna-like virus 121]	38.8	116	1.08E-15	82.8	YP_00933376.1	hypothetical protein 1 [Beihai picorna-like virus 121]	38.8	116	1.25E-18	82.8	YP_00933376.1	hypothetical protein 1 [Beihai picorna-like virus 121]	38.8	116	1.25E-18	82.8
121873_2	total_counts: 283	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.12E-05	51.2	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.29E-08	51.2	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.29E-08	51.2
145875_124	total_counts: 517623	ASM93489.1	NS1 [Lupine feces-associated densovirus 2]	37.1	510	2.32E-94	323	YP_00925621.1	putative nonstructural protein NS1 [Diaphorina citri densovirus]	31.8	453	1.66E-49	190	YP_00925621.1	putative nonstructural protein NS1 [Diaphorina citri densovirus]	31.8	453	1.66E-49	190
145875_124	total_counts: 517623	ASM93488.1	VP1 [Lupine feces-associated densovirus 2]	34.5	348	7.41E-44	180	YP_00925621.2	putative structural protein [Diaphorina citri densovirus]	26.6	173	5.49E-06	53.1	YP_00925621.2	putative structural protein [Diaphorina citri densovirus]	26.6	173	5.49E-06	53.1
147897_7	total_counts: 2386	SCDD_C	Chain C, Structural Polyprotein, Vp2 [ABPV]	36.2	105	9.07E-24	100	NP_066242.1	capsid protein [Acute bee paralysis virus]	39.0	105	9.84E-26	102	NP_066242.1	capsid protein [Acute bee paralysis virus]	39.0	105	9.84E-26	102
149357_2	total_counts: 908	YP_009352233.1	polyprotein [Diabroica virgifera virgifera virus 2]	29.3	133	3.93E-16	84.3	YP_009352233.1	polyprotein [Diabroica virgifera virgifera virus 2]	29.3	133	4.53E-19	84.3	YP_009352233.1	polyprotein [Diabroica virgifera virgifera virus 2]	29.3	133	4.53E-19	84.3
149871_4	total_counts: 1261	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	7.15E-06	53.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	8.24E-09	53.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	8.24E-09	53.9
150472_5	total_counts: 1663	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	2.89E-35	137	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	3.33E-38	137	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	3.33E-38	137
151167_2	total_counts: 478	ADFR80789.1	replication-association protein, partial [Cyclovirus PKbee25]	43.8	64	1.23E-09	60.5	YP_009021847.1	replication-associated protein [Dragonfly associated cyclovirus 3]	41.3	75	1.59E-11	60.5	YP_009021847.1	replication-associated protein [Dragonfly associated cyclovirus 3]	41.3	75	1.59E-11	60.5
23_106	total_counts: 85879	AEL28798.1	replication-associated protein [Bat circovirus ZS/Yunnan-China/2009]	61.2	49	1.31E-10	71.2	YP_009506302.1	replication-associated protein [Pacific flying fox associated cyclovirus-3]	56.3	48	5.42E-13	69.7	YP_009506302.1	replication-associated protein [Pacific flying fox associated cyclovirus-3]	56.3	48	5.42E-13	69.7
29359_5	total_counts: 3883	YP_009337064.1	hypothetical protein 1 [Hubei picorna-like virus 67]	29.9	131	9.52E-05	55.1	YP_009337064.1	hypothetical protein 1 [Hubei picorna-like virus 67]	29.9	131	1.10E-10	55.1	YP_009337064.1	hypothetical protein 1 [Hubei picorna-like virus 67]	29.9	131	1.10E-10	55.1
29755_9	total_counts: 7610	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.55E-13	81.6	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.94E-16	81.6	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.94E-16	81.6
30180_2	total_counts: 792	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	8.88E-36	139	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	1.02E-38	139	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	1.02E-38	139
30198_7	total_counts: 3618	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	32.6	129	2.01E-06	57.8	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	32.6	129	2.32E-09	57.8	YP_009337788.1	hypothetical protein 1 [Hubei picorna-like virus 68]	32.6	129	2.32E-09	57.8
30839_3	total_counts: 767	AXA52568.1	putative RdRp [LinpetHEMA humile polytipovirus 1]	42.7	75	1.02E-07	57.8	NP_00407943.1	RNA-dependent RNA polymerase, partial [Lasius niger virus 1]	36.6	71	7.04E-09	52.8	NP_00407943.1	RNA-dependent RNA polymerase, partial [Lasius niger virus 1]	36.6	71	7.04E-09	52.8
356_26	total_counts: 96963	APG76480.1	hypothetical protein 2, partial [Hubei tombs-like virus 35]	51.3	517	7.89E-169	521	YP_009337674.1	hypothetical protein 2 [Changjiang tombs-like virus 22]	39.8	487	1.40E-103	339	YP_009337674.1	hypothetical protein 2 [Changjiang tombs-like virus 22]	39.8	487	1.40E-103	339
3942_5	total_counts: 1878	AZB48781.1	VP1, partial [Norovirus GII]	26.6	124	1.66E-05	52.4	YP_009237901.1	VP1 [Norovirus GII]	30.9	81	4.50E-06	47	YP_009237901.1	VP1 [Norovirus GII]	30.9	81	4.50E-06	47
58152_5	total_counts: 2250	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	9.85E-48	176	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	1.14E-50	176	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	1.14E-50	176
58401_11	total_counts: 3538	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	9.52E-15	79.3	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	1.10E-17	79.3	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	1.10E-17	79.3
58842_3	total_counts: 703	AEK82102.1	polyprotein [Human parechovirus 2]	43.5	69	3.19E-09	61.6	YP_009508969.1	hypothetical protein 2C [Dromedary camel enterovirus 19CC]	37.1	70	5.19E-12	61.2	YP_009508969.1	hypothetical protein 2C [Dromedary camel enterovirus 19CC]	37.1	70	5.19E-12	61.2
59635_4	total_counts: 790	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	9.04E-10	63.2	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	1.04E-12	63.2	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	1.04E-12	63.2
60807_6	total_counts: 1537	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	7.09E-08	58.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	8.17E-11	58.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	8.17E-11	58.9
61026_4	total_counts: 679	YP_00933392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.49E-05	50.8	YP_00933392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.71E-08	50.8	YP_00933392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.71E-08	50.8
61384_15	total_counts: 5882	ASM93488.1	VP1 [Lupine feces-associated densovirus 2]	37.8	119	1.80E-19	93.6	NP_694830.1	structural protein VP4 [Galleria mellonella densovirus]	34.2	79	2.00E-06	48.1	NP_694830.1	structural protein VP4 [Galleria mellonella densovirus]	34.2	79	2.00E-06	48.1
62223_3	total_counts: 1272	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	2.67E-52	179	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	3.08E-55	179	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	3.08E-55	179
6453_2	total_counts: 487	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	2.82E-13	73.2	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	3.25E-16	73.2	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	3.25E-16	73.2
7992_2	total_counts: 506	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.14E-21	95.1	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.78E-24	95.1	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.78E-24	95.1
87654_83	total_counts: 129393	YP_004152328.1	Cap protein [Cyclovirus PKgoat21/PAK/2009]	37.5	168	6.00E-22	104	YP_004152328.1	Cap protein [Cyclovirus PKgoat21/PAK/2009]	37.5	168	6.92E-25	104	YP_004152328.1	Cap protein [Cyclovirus PKgoat21/PAK/2009]	37.5	168	6.92E-25	104
87654_83	total_counts: 129393	YP_008130363.1	replication association protein [Human cyclovirus VSS700009]	57.1	226	6.48E-88	281	YP_008130363.1	replication association protein [Human cyclovirus VSS700009]	57.1	226	7.47E-91	281	YP_008130363.1	replication association protein [Human cyclovirus VSS700009]	57.1	226	7.47E-91	281
87760_5	total_counts: 3323	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	7.90E-28	120	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	9.11E-31	120	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	9.11E-31	120
87907_9	total_counts: 11161	AA919088.1	structural polyprotein, partial [Kashmir bee virus]	32.2	404	3.35E-44	174	NP_851404.2	structural polyprotein, partial [Kashmir bee virus]	31.4	408	2.26E-46	172	NP_851404.2	structural polyprotein, partial [Kashmir bee virus]	31.4	408	2.26E-46	172
87919_8	total_counts: 5141	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	4.19E-39	154	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	4.83E-42	154	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	4.83E-42	154

BLASTX against nr										BLASTX against RefSeq									
Contig (nucleotide)		subject acc.ver	name	% identity	alignment length	evaluate	bit score	frame	name	% identity	alignment length	evaluate	bit score	frame	name	% identity	alignment length	evaluate	bit score
115738_6	total_counts: 2739	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	4.04E-19	93.6	-3/0	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	1.10E-23	93.6	-3/0	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	1.10E-23	93.6
115755_8	total_counts: 8948	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	9.48E-43	170	1/0	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	2.58E-47	170	1/0	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	2.58E-47	170
115910_13	total_counts: 77920	AGP76667.1	hypothetical protein 1 [Wuhan insect virus 11]	45.7	870	0.00E+00	726	2/0	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	723	2/0	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	723
117633_5	total_counts: 2738	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	1.08E-23	108	2/0	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	2.93E-28	108	2/0	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	2.93E-28	108
118987_6	total_counts: 1591	ATOS9710.1	structural polyprotein [Solenopsis invicta virus 5]	33.8	74	2.65E-07	57.4												

Supplementary Table 4 - Accession number (ID) of the sequences used in phylogenetic inferences.

IDs	Species
MqV2 phylogeny	
YP_009388491.1	<i>Lake Sinai Virus SA2</i>
ASS83296.1_	<i>Lake Sinai virus 2</i>
AJR19138.1	<i>Lake Sinai virus</i>
ASS83254.1	<i>Lake Sinai virus 1</i>
AYP65068.1	<i>Lake Sinai virus 3</i>
YP_009388495.1	<i>Lake Sinai Virus NE</i>
AXA52557.1	<i>Linepithema humile C virus 1</i>
YP_009011225.1	<i>Anopheline-associated C virus</i>
AOG30801.1	<i>Towan virus</i>
YP_009344965.1	<i>Jingmen tombus-like virus 2</i>
ASN64759.1	<i>Leptomonas pyrrhocoris RNA virus</i>
YP_009337040.1	<i>Changjiang tombus-like virus 21</i>
YP_009337674.1	<i>Changjiang tombus-like virus 22</i>
YP_009337712.1	<i>Hubei tombus-like virus 36</i>
YP_009342273.1	<i>Wenzhou tombus-like virus 17</i>
APG76480.1	<i>Hubei tombus-like virus 35</i>
YP_009336952.1	<i>Beihai tombus-like virus 18</i>
YP_009337190.1	<i>Wenling tombus-like virus 2</i>
YP_009336894.1	<i>Beihai tombus-like virus 10</i>
YP_009336965.1	<i>Hubei tombus-like virus 14</i>
YP_009337688.1	<i>Beihai tombus-like virus 7</i>
YP_009337155.1	<i>Changjiang tombus-like virus 12</i>
YP_009336861.1	<i>Shahe tombus-like virus 2</i>
BAU09527.1	<i>Pothos latent virus</i>
NP_619671.1	<i>Hibiscus chlorotic ringspot virus</i>
AGG23390.1	<i>Citrus yellow vein-associated virus</i>
AWS06679.1	<i>Ethiopia maize-associated virus</i>
ACJ03575.1	<i>Carrot mottle mimic virus</i>
NP_620846.3	<i>Pea enation mosaic virus 2</i>
AXN55932.1	<i>Red clover umbravirus</i>
YP_009336880.1	<i>Hubei tombus-like virus 19</i>
YP_009337113.1	<i>Hubei tombus-like virus 28</i>
APG76298.1	<i>Shangao tombus-like virus 1</i>
YP_009333257.1	<i>Hubei tombus-like virus 30</i>
ALV85423.1	<i>Diaphorina citri-associated C virus</i>
MqC1 and MqC2 phylogeny	
YP_008130364.1/YP_008130363.1	<i>Human cyclovirus VS5700009</i>
AMH87656.1/AMH87655.1	<i>Pacific flying fox-associated cyclovirus 3</i>
YP_009104365.1/YP_009104366.1	<i>Cyclovirus ZM36a</i>
ADD62479.1/ADD62480.1	<i>Cyclovirus TN18</i>
BAP81876.1/BAP81877.1	<i>Cyclovirus ZM41</i>
BAP81871.1/BAP81870.1	<i>Cyclovirus ZM01</i>
BAP81869.1/BAP81868.1	<i>Cyclovirus ZM32</i>
AIZ46815.1/AIZ46816.1	<i>Swine cyclovirus</i>
AGO59220.1/AGO59219.1	<i>Cyclovirus VN</i>
AIZ46821.1/AIZ46822.1	<i>Human cyclovirus VN-like</i>
BAP81882.1/BAP81883.1	<i>Cyclovirus ZM62</i>

ADY17984.1/ADY17985.1	<i>Dragonfly-associated cyclovirus 1</i>
YP_009513184.1/YP_009513183.1	<i>Dragonfly-associated cyclovirus 4</i>
YP_009506320.1/YP_009506319.1	<i>Cyclovirus PK5222</i>
AXL65887.1/AXL65888.1	<i>Arboreal ant-associated circular virus 1</i>
AFS65280.1/AFS65281.1	<i>Dragonfly-associated cyclovirus 5</i>
YP_009506293.1	<i>Bat-associated cyclovirus 8</i>
YP_009506324.1/YP_009506323.1	<i>Cyclovirus PK5034</i>
YP_004152332.1/YP_004152331.1	<i>Cyclovirus bat/USA/2009</i>
ARO38287.1/ARO38286.1	<i>Circovirus sp</i>
YP_009506285.1/YP_009506286.1	<i>Bat-associated cyclovirus 2</i>
YP_009362253.1/YP_009362252.1	<i>Bat cyclovirus GF 4c</i>
YP_009506313.1/YP_009506314.1	<i>Dragonfly-associated cyclovirus 8</i>
AXL65889.1/AXL65890.1	<i>Fly-associated circular virus 1</i>
ATP66708.1	<i>Rodent circovirus</i>
AKE49354.1/AKE49355.1	<i>Cyclovirus NI 204</i>
YP_009506329.1/YP_009506330.1	<i>Cyclovirus SL 108277</i>
YP_009021871.2/YP_009021870.2	<i>Human-associated cyclovirus 10</i>
AFS65290.1/AFS65289.1	<i>Dragonfly-associated cyclovirus 2</i>
Ref [35]	<i>Circo-like 1</i>
YP_271918.1/YP_271921.1	<i>Duck circovirus</i>
NP_065678.1/NP_065679	<i>Porcine circovirus</i>
YP_009423856.1/YP_009423857.1	<i>Bat circovirus</i>
YP_764455.1/YP_764456.1	<i>Raven circovirus</i>
Ref [35]	<i>Circo-like 2</i>

MqV1a and MqV1b phylogeny

AWK77852.1/AWK77853.1	<i>Bundaberg bee virus 2</i>
AWK23470.1/AWK23471.1	<i>Human blood-associated dicistrovirus</i>
YP_009337313.1/YP_009337314.1	<i>Hubei picorna-like virus 14</i>
YP_009345054.1/YP_009345055.1	<i>Wuhan millipede virus 3</i>
AIY53985.1/AIY53986.1	<i>Nilaparvata lugens C virus</i>
AKA63263.1/AKA63264.1	<i>Cricket paralysis virus</i>
NP_044945.1/NP_044946.1	<i>Drosophila C virus</i>
AZR39355.1/AZR39356.1	<i>Hypsignathus monstrosus dicistrovirus</i>
YP_009252204.1/YP_009252205.1	<i>Anopheles C virus</i>
NP_620562.1/NP_620563.1	<i>Triatoma virus</i>
AWK77884.1/AWK77885.1	<i>Hobart bee virus 1</i>
YP_009333496.1/YP_009333497.1	<i>Beihai picorna-like virus 84</i>
AYN75548.1/AYN75549.1	<i>Halhan virus 1</i>
YP_009336690.1/YP_009336691.1	<i>Wenling crustacean virus 2</i>
AFO53688.1/AFO53689.1	<i>Taura syndrome virus</i>
YP_009337654.1/YP_009337655.1	<i>Hubei picorna-like virus 25</i>
YP.164440.1/YP.164441.1	<i>Solenopsis invicta virus 1</i>
YP_009336557.1/YP_009336558.1	<i>Hubei orthoptera virus 1</i>
APG76667.1/APG76668.1	<i>Wuhan insect virus 11</i>
AXA52579.1/AXA52580.1	<i>Linepithema humile virus 1</i>
ATO59709.1/ATO59710.1	<i>Solenopsis invicta virus 5</i>
NP_066241.1/NP_066242.1	<i>Acute bee paralysis virus</i>
AHL83499.1/AHL83500.1	<i>Kashmir bee virus</i>
ABY57949.1/ABY57950.1	<i>Israeli acute paralysis virus</i>
YP_008888535.1/YP_008888536.1	<i>Formica exsecta virus 1</i>
YP_009336777.1/YP_009336778.1	<i>Wenzhou channeled applesnail virus 2</i>

APG76699.1/APG76700.1	<i>Beihai picorna-like virus 70</i>
YP_009337682.1/YP_009337683.1	<i>Wenzhou picorna-like virus 26</i>
YP_009333456.1/YP_009333457.1	<i>Beihai picorna-like virus 71</i>
APG76793.1/APG76794.1	<i>Beihai picorna-like virus 72</i>
APG78016.1/APG78017.1	<i>Beihai picorna-like virus 74</i>
AYN75554.1/AYN75555.1	<i>Halhan virus 3</i>
YP_009336994.1/YP_009336995.1	<i>Wenzhou picorna-like virus 28</i>
APG78539.1/APG78540.1	<i>Wenzhou picorna-like virus 29</i>
NP_049374.1	<i>Sacbrood virus</i>
YP_003622540.1	<i>Slow bee paralysis virus</i>
YP_009162630.1	<i>Bombyx mori iflavivirus</i>
NP_853560.2	<i>Deformed wing virus</i>
YP.145791.1/	<i>Varroa destructor virus 1</i>

MqD phylogeny

AWV66973.1/AWV66974.1	<i>Ambidensovirus sp.</i>
ANG55951.1/ANG55948.1	<i>Human CSF-associated densovirus</i>
YP_006576512.1/YP_006576514.1	<i>Sibine fusca densovirus</i>
NP_694838.1/NP_694840.1	<i>Casphalia extranea densovirus</i>
YP_006589928.1/YP_006589930.1	<i>Papilio polyxenes densovirus</i>
AIT71975.1/AIT71974	<i>Hordeum marinum Itera-like densovirus</i>
NP_542609.1/NP_542611.1	<i>Bombyx mori densovirus 1</i>
YP_009021036.1/YP_009021038.1	<i>Danaus plexippus plexippus iteravirus</i>
YP.164339.1/YP.164341.1	<i>Dendrolimus punctatus densovirus</i>
YP_004678720.1/YP_004678721.1	<i>Helicoverpa armigera densovirus</i>
YP_009256211.1/YP_009256212.1	<i>Diaphorina citri densovirus</i>
AVH76852.1/AVH76854.1	<i>Bombus cryptarum densovirus</i>
NP_874376.1/NP_874377.1	<i>Myzus persicae densovirus</i>
YP_009362129.1/YP_009362131.1	<i>Dysaphis plantaginea densovirus</i>
YP_002887625.1/YP_002887627.1	<i>Culex pipiens densovirus</i>
AFK91980.1/AFK91983.1	<i>Helicoverpa armigera densovirus</i>
NP_899650.1/NP_694830.1	<i>Galleria mellonella densovirus</i>
NP_958099.1/NP_958101.1	<i>Mythimna loreyi densovirus</i>
NP_046813.1/NP_046815.1	<i>Diatraea saccharalis densovirus</i>
YP_007003823.1/YP_007003825.1	<i>Pseudoplusia includens densovirus</i>
NP_694824.1/NP_694823.1	<i>Junonia coenia densovirus</i>
AGO32210.1/AGO32212.1	<i>Acheta domestica densovirus</i>
NP_694843.1/NP_694842.1	<i>Planococcus citri densovirus</i>
YP_008766862.1/YP_008766863.1	<i>Solenopsis invicta densovirus</i>
ARI46485.1/ARI46488.1	<i>Ambidensovirus CaaDV2</i>
YP_009134732.1/YP_009134734.1	<i>Cherax quadricarinatus densovirus</i>
YP_009507340.1/YP_009507339.1	<i>Sea star-associated densovirus</i>
AFC75858.1/AFC75860.1	<i>Blattella germanica densovirus-like virus</i>
ASM93489.1/ASM93488.1	<i>Lupine feces-associated densovirus 2</i>
ASU47551.1/ASU47552.1	<i>Lone star tick densovirus 1</i>
AYG77882.1/AYG77881.1/AYG77880.1	<i>Chicken parvovirus</i>
NP_757371.1/NP_757369.1	<i>Porcine parvovirus</i>
AAA61405.1/AAA61406.1	<i>Mouse parvovirus 1</i>

CAPÍTULO 4

Delayed effects of low gene expression, and behavioral changes associated with a stingless bee annual syndrome

Este capítulo apresenta o seguinte artigo em preparação para publicação:

Caesar L, Lopes AMC, Konzen ER, Radaeski JN, Bauermann SG, Sattler A, Pombert JF, Termignoni C, Blochtein B, Carvalho AT, Haag KL. Delayed effects of low gene expression, and behavioral changes associated with a stingless bee annual syndrome. *Em preparação*.

CAPÍTULO 5

Recomendações para o manejo da mandaçaia no RS

Este capítulo apresenta um folder de divulgação científica direcionado, principalmente, aos meliponicultores.

CAPÍTULO 6

Discussão e conclusão

6. Discussão e conclusão

Doenças de abelhas e o colapso de suas colônias tem desafiado pesquisadores na busca dos fatores causais. Embora a CCD explique apenas uma parte do colapso de colônias nos EUA, ela ficou conhecida pelo grande esforço feito por parte de diversos laboratórios para encontrar a causa da desordem (Williams et al. 2010). Os estudos foram primeiramente conduzidos com o intuito de buscar um agente causador único, mas o que foi encontrado até o momento é que múltiplos fatores podem estar envolvidos no colapso, como patógenos, desnutrição e agroquímicos (Cox-Foster et al. 2007; vanEngelsdorp et al. 2009; VanEngelsdorp et al. 2010). Efeitos subletais destes diversos fatores, agindo ou não de forma sinérgica, passaram a explicar grande parte do colapso de colônias pelo mundo (Bryden et al. 2013; Goulson et al. 2015). O que aumenta ainda mais o desafio do estudo do colapso de colônias é também a complexidade inerente às abelhas sociais, pois as respostas de como estes fatores agem podem estar no nível do indivíduo, da colônia ou mesmo da população (López-Urbe et al. 2020).

O estudo sobre a mortalidade anual de mandaiaias no RS se mostrou também bastante desafiador. Ao longo de nossas observações e amostragens percebemos que a síndrome, apesar de sazonal, ocorre em meliponários com distintos contextos ambientais e mostram uma variedade de sintomas com diferentes intensidades. Também não são todas as colônias de mandaiaias que são afetadas. A dificuldade de observarmos um fator em comum em todos locais e colônias afetadas indicava a possibilidade da ação de múltiplos fatores para o desfecho da síndrome. Investigando aspectos chave da saúde das mandaiaias, em nível de indivíduo e de colônia, identificamos alguns fatores relacionados à ocorrência da síndrome.

Primeiramente investigamos o papel do microbioma bacteriano das abelhas na ocorrência da síndrome (Díaz et al. 2017; Capítulo 2). Nosso estudo foi o primeiro a caracterizar a microbiota de uma abelha nativa do Brasil, a qual se mostrou bastante diversa e composta principalmente por bactérias do grupo Firmicutes (como diferentes tipos de *Lactobacillus*), assim como em *A. mellifera*. Entretanto, diferentemente da abelha melífera, que possui alta conservação nos grupos de bactérias associadas ao intestino (Martinson et al. 2011), *M. quadrifasciata* apresenta grande variação na composição da microbiota entre

abelhas de diferentes colônias (Díaz et al. 2017). É possível que tais padrões tenham relação com o processo de domesticação que a *A. mellifera* já sofre há mais tempo e mais intensamente (Zheng et al. 2018). Concluímos com esta investigação que a síndrome anual não é causada por alguma bactéria patogênica e também não parece estar relacionada à disbiose. Ou seja, não há diferença na composição geral da microbiota comparando abelhas doentes e saudáveis, apesar dos resultados sugerirem que a composição da microbiota nos diferentes *status* de saúde é dependente do ano. No entanto, não podemos descartar que a falta de algum padrão claro esteja relacionado a grande variação na microbiota. Um estudo acompanhando flutuações na composição da microbiota temporalmente poderia complementar os achados deste trabalho e faz parte das perspectivas desta tese. Já temos o DNA abdominal de 120 amostras de mandaçaia (ANEXO I), coletadas entre 2018-2019 para o estudo do Capítulo 4 (5 operárias/colônia/localidade/mês, utilizadas para pesagem e quantificação da atividade de GOX), a serem submetidas à amplificação de fragmentos de 16S (bactérias) e ITS (fungos) por PCR, sequenciamento e análises comparativas.

A partir da observação dos sintomas de mandaçaia afetadas pela síndrome, direcionamos as investigações para a possibilidade de uma infecção viral (Caesar et al. 2019; Capítulo 3). Tremores, paralisia e incapacidade de voar são alguns dos sintomas que podem ser observados em operárias de colônias afetadas. Tais sintomas assemelham-se aos observados em infecções por dicistrovírus em *Apis* spp. (McMenamin e Genersch 2015), mas nenhum destes vírus (ex: ABPV, IAPV, KBV) foi detectado nas mandaçaia. Porém, novos vírus da família *Dicistroviridae* (MqV1a e MqV1b) foram descritos, assim como da família *Circoviridae* (MqC, MqC1 e MqC2) e *Densoviridae* (MqD). Nenhum deles foi consistentemente relacionado à ocorrência da síndrome, mas alguns destes novos vírus foram mais detectados em um meliponário onde os sintomas observados durante a síndrome foram mais intensos (Caesar et al. 2019). Uma investigação envolvendo a quantificação da densidade da infecção viral poderia contribuir para entender a sua relação com os sintomas observados e faz parte das perspectivas desta tese. Amostras de colônias do meliponário onde observam-se sintomas mais intensos nas forrageiras afetadas foram coletadas durante a síndrome de 2019 e armazenadas a -80 °C (ANEXO II) para futura extração de DNA ou RNA, síntese de cDNA e quantificação absoluta dos vírus por qPCR.

Outro achado interessante desta etapa do estudo foi a detecção de vírus da manduca também em *A. mellifera*. Embora não possamos confirmar a direção da transmissão dos vírus, este dado chama atenção para a ocorrência de troca de patógenos entre abelhas exóticas e nativas.

A ausência de algum patógeno consistentemente associado às abelhas de colônias que sofreram mortalidade nos levou então a uma investigação integrativa sobre o *status* de saúde das colônias no período que engloba a síndrome. Avaliamos diversas características das manducaias tanto em nível de indivíduo quanto de colônia (Caesar et al. *em preparação*; Capítulo 4). Planejamos este estudo de forma a discriminar a contribuição genética da colônia bem como do ambiente para o desfecho da síndrome. As características em nível de colônia foram as que mais explicaram o *status* de saúde, como a perda do controle da umidade e temperatura, principalmente em colônias afetadas pela síndrome. Tais traços, no entanto, são consequência de diversos processos biológicos que ocorrem em nível individual. Nós verificamos que forrageiras das colônias que adoeceram tiveram uma menor expressão de genes relacionados, na abelha modelo *A. mellifera*, à capacidade de detoxificação de agroquímicos (*p450*) e resposta imune (*Vg* e *PO*). Assim como observado em outros eventos de colapso de colônias, sugerimos com este estudo que o efeito subletal de estressores como agroquímicos, competição por recursos e exposição a patógenos possam estar na raiz desta síndrome.

Todos estes achados foram usados como base para a elaboração de um manual de recomendações aos meliponicultores (Capítulo 5), os quais trouxeram aos pesquisadores o problema da síndrome anual das manducaias. A meliponicultura é uma atividade que tem tomado proporções cada vez maiores no Brasil, sendo que até 2015 estimava-se que haviam mais de 5.000 meliponicultores (Jaffé et al. 2015). A criação e manejo de abelhas sem ferrão pode ajudar comunidades como uma forma de renda adicional através da venda de produtos das colônias, e também incentiva a proteção de habitats naturais como fontes de alimento e locais de nidificação para as abelhas, assim como contribui na prestação de serviços de polinização da flora selvagem e de cultivares agrícolas (Slaa et al. 2006; Jaffé et al. 2015). A legislação atual, em nível nacional, impõe algumas regras aos meliponicultores, como o registro daqueles que possuem mais de 50 colônias, a

comercialização de colônias e produtos derivados apenas mediante autorização e restringe a translocação de colônias entre regiões (CONAMA, 2004). No entanto, além destas normas não serem suficientes para a preservação das espécies nativas, elas também não são estritamente seguidas, principalmente pela burocracia envolvida, como relatam os meliponicultores (Jaffé et al. 2015).

A translocação de colônias, por exemplo, é uma prática comum e um dos fatores que mais influencia nos padrões de diversidade genética entre espécies de abelhas sem ferrão das Américas (Jaffé et al. 2016). Alguns meliponicultores costumam comprar colônias de outras regiões do Brasil com o objetivo de fortalecer as colônias. No entanto, esta prática pode levar à homogeneização do perfil genético das populações e perda de adaptações locais importantes para a sobrevivência da espécie, como uma maior resistência a baixas temperaturas ou a agroquímicos (Jaffé et al. 2016). Nós observamos que a síndrome anual das mandaaias tem um componente genético, ou seja, há colônias mais suscetíveis aos efeitos subletais de estressores ambientais e também mais resistentes. A homogeneização do perfil genético das populações pode levar à perda do perfil genético destas colônias que respondem melhor aos fatores que contribuem para a ocorrência da síndrome. Por outro lado, certos genótipos também estão sendo grandemente expandidos através da comercialização de colméias obtidas por divisão, uma prática comum para obtenção de novas colônias (Jaffé et al. 2015). A mistura de genótipos através da translocação de colônias, combinada com a sua expansão pela divisão, altera completamente a estrutura genética das populações de abelhas sem ferrão. Esta prática pode ter afetado mais intensamente a mandaia, que é uma das espécies mais manejada historicamente (Jaffé et al. 2015). Isto, associado ao fato de que não há mais ninhos silvestres, com indivíduos capazes de fornecer genes às colônias manejadas, sugere que a questão genética é um fator importante para a ocorrência da síndrome.

Outro impacto resultante da translocação de colônias é a introdução de patógenos. Estudos realizados em diferentes estados do Brasil detectaram recentemente a presença de microsporídios, bactérias e vírus potencialmente patogênicos em abelhas sem ferrão (de Souza et al. 2019; Guimarães-Cestaro et al. 2020; Teixeira et al. 2020). Embora nem todas as colônias nas quais estes patógenos foram detectados apresentavam sintomas típicos de

cada infecção, em outros contextos a infecção por eles pode levar a diferentes desfechos. Sabe-se, por exemplo, que o DWV é mais virulento no inverno, levando ao colapso de inúmeras colônias de *A. mellifera* na Europa (Natsopoulou et al. 2017). Desta forma, caso este vírus seja trazido para o sul do Brasil, onde o inverno é mais rigoroso, ele poderia ser mais virulento e causar sintomas observáveis e danosos a diversas colônias. Além disso, há evidências de troca de patógenos entre abelhas sem ferrão e *A. mellifera*, inclusive em nosso estudo, sugerindo que ambas possam ser afetadas com a introdução de novos patógenos (Caesar et al. 2019; de Souza et al. 2019; Guimarães-Cestaro et al. 2020).

Outra prática bastante usada na meliponicultura é a suplementação alimentar de colônias, principalmente em períodos de maior escassez de recursos. Nós constatamos que a perda de peso das abelhas, possivelmente relacionada a competição por recursos, é um fator implicado na ocorrência da síndrome das mandaias. Porém, ao mesmo tempo que fornecer alimento às abelhas pode fortalecer as colônias para o período da síndrome, a suplementação alimentar também irá mascarar colônias geneticamente suscetíveis à mortalidade anual. Além disso, a dieta natural das abelhas é bastante equilibrada, enquanto o néctar fornece a principal fonte de carboidratos, o pólen fornece proteínas, lipídios e outros micronutrientes (Vaudo et al. 2015). Em *A. mellifera* e *B. terrestris* já foi mostrado que a atividade de forrageio é altamente regulada de acordo com as necessidades das colônias (Paoli et al. 2014; Stabler et al. 2015). Portanto, o uso de xarope e pólen apícola como suplementação alimentar deve ser evitado, e se for feito, é de extrema importância que o meliponicultor tome medidas sanitárias adequadas. Um estudo recente, que diagnosticou pela primeira vez a bactéria *M. plutonius* e os sintomas da doença conhecida como cria pútrida européia em *Melipona* spp., mostrou a presença do patógeno no pólen apícola oferecido às colônias que se infectaram (Teixeira et al. 2020).

A melhor forma de garantir a qualidade nutricional das colônias é promover pasto apícola diverso nos arredores do meliponário, proporcional à quantidade de colônias manejadas, como através da preservação de matas nativas (Vaudo et al. 2015). Com isso também será possível amenizar os efeitos da competição por recursos. Um estudo conduzido em região de Mata Atlântica mostrou que *M. quadrifasciata* e *A. mellifera* competem pelos recursos das mesmas flores, e o pico de coleta da abelha sem ferrão

ocorreu quando a abelha melífera não estava competindo pelo mesmo recurso (Wilms e Wiechers 1997). Com uma menor sobreposição dessas duas espécies também haverá uma diminuição no risco da troca de patógenos.

Outro fator de risco às mandaçaias, e mesmo a outras abelhas sem ferrão, é o uso de agroquímicos. Nossos resultados indicam diferenças entre colônias na capacidade de detoxificação destes compostos, o que por sua vez influencia no desfecho da síndrome. Por mais que os agroquímicos sejam ministrados de forma correta e nenhuma letalidade seja observada no período de aplicação, efeitos subletais podem afetar a saúde das colônias, e apenas tardiamente serem observados os efeitos. Em *B. terrestris* expostas à neonicotinóides durante qualquer um dos estágios do desenvolvimento há uma redução no desenvolvimento de partes do cérebro das abelhas que, apenas semanas depois, quando adultas, apresentaram uma resposta menor ao oferecimento de açúcar e dificuldade na aprendizagem (Smith et al. 2020). Portanto, é importante evitar o uso de agroquímicos nas proximidades do meliponário ou áreas de forrageio.

Por fim, concluímos que a síndrome anual das mandaçaias é resultado da combinação de efeitos subletais de múltiplos fatores, como a genética da colônia, competição por recursos, exposição a patógenos e agroquímicos. Nós acreditamos que há formas de amenizar os efeitos da mortalidade anual das mandaçaias, e que preservando a espécie *M. quadrifasciata* estaremos também contribuindo para a manutenção de outras abelhas sem ferrão que possam estar sofrendo pela ação dos mesmos fatores.

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ANEXO I

ID amostra	Status de saúde	Colônia	Amostra da colônia	Mês	DNA ng/ul	260/280
41	saudável	PA1	1	Jan	63,8	2,13
42	saudável	PA1	2	Jan	65	2,19
43	saudável	PA1	3	Jan	120,2	2,13
44	saudável	PA1	4	Jan	75,3	2,1
45	saudável	PA1	5	Jan	106,7	2,17
51	doente	PA2	1	Jan	71,5	2,15
52	doente	PA2	2	Jan	107,3	2,18
53	doente	PA2	3	Jan	128,4	2,15
54	doente	PA2	4	Jan	116,1	2,15
55	doente	PA2	5	Jan	139,1	2,12
56	doente	PA3	1	Jan	178,4	2,19
57	doente	PA3	2	Jan	199,7	2,21
58	doente	PA3	3	Jan	261,2	2,18
59	doente	PA3	4	Jan	278,7	2,13
60	doente	PA3	5	Jan	274,4	2,17
61	doente	BP3	1	Jan	245,5	2,16
62	doente	BP3	2	Jan	213,1	2,16
63	doente	BP3	3	Jan	267,2	2,14
64	doente	BP3	4	Jan	303,4	2,16
65	doente	BP3	5	Jan	226,7	2,21
66	doente	BP2	1	Jan	126,3	2,08
67	doente	BP2	2	Jan	118,1	2,12
68	doente	BP2	3	Jan	146,7	2,19
69	doente	BP2	4	Jan	84,3	2,19
70	doente	BP2	5	Jan	114,4	2,06
76	saudável	BP1	1	Jan	74,7	2,17
77	saudável	BP1	2	Jan	115	2,17
78	saudável	BP1	3	Jan	111,3	2,13
79	saudável	BP1	4	Jan	106,2	2,17
80	saudável	BP1	5	Jan	66,2	2,2
81	saudável	PA1	1	Fev	76,6	2,09
82	saudável	PA1	2	Fev	36,6	1,94
83	saudável	PA1	3	Fev	61,5	2,1
84	saudável	PA1	4	Fev	119,4	2,04
85	saudável	PA1	5	Fev	37,3	1,83
91	doente	PA2	1	Fev	59	2,15
92	doente	PA2	2	Fev	78,2	2,17
93	doente	PA2	3	Fev	74,1	2,28
94	doente	PA2	4	Fev	64,6	2,29
95	doente	PA2	5	Fev	70,3	2,24
96	doente	PA3	1	Fev	98,6	2,24
97	doente	PA3	2	Fev	158,5	2,17
98	doente	PA3	3	Fev	179,4	2,2
99	doente	PA3	4	Fev	152,9	2,21
100	doente	PA3	5	Fev	191	2,18
101	saudável	BP1	1	Fev	156,5	2,18
102	saudável	BP1	2	Fev	113,5	2,19
103	saudável	BP1	3	Fev	115,8	2,15
104	saudável	BP1	4	Fev	123,4	1,92
105	saudável	BP1	5	Fev	179,8	2,19
111	doente	BP2	1	Fev	106,3	2,19
112	doente	BP2	2	Fev	108,7	2,13
113	doente	BP2	3	Fev	61,8	1,98
114	doente	BP2	4	Fev	155,3	2,14
115	doente	BP2	5	Fev	111,8	2,14

116	saudável	BP1	1	Fev	102,6	2,12
117	saudável	BP1	2	Fev	71,5	2,18
118	saudável	BP1	3	Fev	111	2,15
119	saudável	BP1	4	Fev	77,9	2,04
120	saudável	BP1	5	Fev	58,3	1,97
121	saudável	PA1	1	Mar	100	2,25
122	saudável	PA1	2	Mar	100,8	2,24
123	saudável	PA1	3	Mar	132,2	2,25
124	saudável	PA1	4	Mar	160,6	2,23
125	saudável	PA1	5	Mar	152,8	2,14
131	doente	PA2	1	Mar	275,5	2,22
132	doente	PA2	2	Mar	153,3	2,25
133	doente	PA2	3	Mar	129,7	2,22
134	doente	PA2	4	Mar	141,3	2,25
135	doente	PA2	5	Mar	339,7	2,21
136	doente	PA3	1	Mar	148,8	2,13
137	doente	PA3	2	Mar	151,7	2,31
138	doente	PA3	3	Mar	150,8	2,27
139	doente	PA3	4	Mar	87,4	2,22
140	doente	PA3	5	Mar	113,6	2,25
141	doente	BP3	1	Abr	149,6	2,09
142	doente	BP3	2	Abr	118,8	2,25
143	doente	BP3	3	Abr	125,8	2,23
144	doente	BP3	4	Abr	149	2,3
145	doente	BP3	5	Abr	106,1	2,26
146	doente	BP2	1	Abr	115,5	2,24
147	doente	BP2	2	Abr	141,7	2,25
148	doente	BP2	3	Abr	102,6	2,3
149	doente	BP2	4	Abr	84,6	2,33
150	doente	BP2	5	Abr	73,7	2,36
156	saudável	BP1	1	Abr	90,9	2,36
157	saudável	BP1	2	Abr	146,9	2,27
158	saudável	BP1	3	Abr	118,2	2,32
159	saudável	BP1	4	Abr	48,6	2,29
160	saudável	BP1	5	Abr	138,6	2,34
161	saudável	PA1	1	Abr	54,4	2,12
162	saudável	PA1	2	Abr	42,6	2,33
163	saudável	PA1	3	Abr	59,5	2,16
164	saudável	PA1	4	Abr	100,3	2,27
165	saudável	PA1	5	Abr	40,6	2,29
171	doente	PA2	1	Abr	38,5	2,17
172	doente	PA2	2	Abr	80	2,38
173	doente	PA2	3	Abr	60,6	2,21
174	doente	PA2	4	Abr	35,3	2,21
175	doente	PA2	5	Abr	59,8	2,24
176	doente	PA3	1	Abr	60,6	2,14
177	doente	PA3	2	Abr	54,7	2,17
178	doente	PA3	3	Abr	64,6	2,24
179	doente	PA3	4	Abr	60,3	2,16
180	doente	PA3	5	Abr	78,2	2,36
181	saudável	BP1	1	Mar	176,7	2,26
182	saudável	BP1	2	Mar	149	2,31
183	saudável	BP1	3	Mar	127,6	2,23
184	saudável	BP1	4	Mar	137,6	2,28
185	saudável	BP1	5	Mar	135,3	2,28
191	doente	BP2	1	Mar	79,2	2,2
192	doente	BP2	2	Mar	80,7	2,3

193	doente	BP2	3	Mar	99,1	2,28
194	doente	BP2	4	Mar	165,3	2,28
195	doente	BP2	5	Mar	105,5	2,38
196	doente	BP3	1	Mar	133,7	2,29
197	doente	BP3	2	Mar	89,8	2,29
198	doente	BP3	3	Mar	82,8	2,23
199	doente	BP3	4	Mar	140,8	2,3
200	doente	BP3	5	Mar	62,1	2,33

ANEXO II

Colônia	Espécie	Status de saúde	Operárias	Larvas	Pupas	Ovos	Rainhas	Ácaros	Formigas	Fezes	Mel	Pólen
BLA	<i>M. quadrifasciata</i>	Doentes	5		10			x		x	x	
BLB	<i>M. quadrifasciata</i>	Doentes	5		10			x	x	x	x	x
BLC	<i>M. quadrifasciata</i>	Doentes - com carvão ativado	5		10			x			x	x
BLD	<i>M. bicolor</i>	Doentes	5		5				x		x	x
BLE	<i>M. scutellaris</i>	Doentes	5		6			x	x		x	x
BLF	<i>M. seminigra</i>	Saudáveis	5							x	x	x
BLG	<i>M. seminigra</i>	Doentes	5		10			x		x	x	x
BLH	<i>M. scutellaris</i>	Doentes - com carvão ativado	5		4					x	x	x
BLI	<i>S. postica</i>	Doentes	5		5						x	x
BLJ	<i>M. quadrifasciata</i>	Saudáveis – no cativeiro	5		10			x			x	
BLK	<i>M. quadrifasciata</i>	Saudáveis – no cativeiro	5	10				x			x	
BLL	<i>M. scutellaris</i>	Saudáveis – no cativeiro	5									
BLM	<i>M. seminigra</i>	Saudáveis – no cativeiro	5					x			x	
BLN	<i>A. melifera</i>	Saudáveis	5									x
BLO	<i>A. melifera</i>	Saudáveis	5									x
BLP	<i>A. melifera</i>	Saudáveis	5									x
BLQ	<i>M. quadrifasciata</i>	Doentes	5	10	10	10	1				x	x
BLR	<i>M. quadrifasciata</i>	Doentes	5	10	10	10	1				x	x