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МЕТАГЕНОМНАЯ МОДЕЛЬ ДИНАМИКИ МИКРОБИОТЫ КЛАРИЕВОГО СОМА *CLARIAS GARIEPINUS* (BURCHELL, 1822) (CLARIIDAE) В ПЕРВЫЕ МЕСЯЦЫ ЖИЗНИ

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Аннотация. Представлено метагеномное исследование динамики микробиоты кишечника африканского клариевого сома *Clarias gariepinus* в первые 60 дней жизни. Цель исследования – построение модели смены микробного сообщества при переходе с живого корма на стартовый комбикорм. Метагеномный анализ показал, что личиночный этап характеризуется доминированием *Proteobacteria* (*Cetobacterium*, *Pseudoalteromonas*). При переходе на сухой корм (8 сутки) наблюдается резкий рост *Firmicutes* (*Clostridium*) и всплеск численности условно-патогенных *Serratia* (до 14,8 %). К 60 суткам формируется стабильное сообщество с восстановлением доли *Cetobacterium*. На основе кластерного и регрессионного анализа построена трехкомпонентная модель (ранние протеобактерии, продуценты короткоцепочечных жирных кислот, стабилизаторы), позволяющая прогнозировать состав микробиоты в разные моменты времени. Выявлено функциональное «ядро» (*Clostridium* + *Cetobacterium*), характерное для всеядных рыб. Результаты обосновывают необходимость применения пробиотиков в период смены корма (5–14 сутки).

Ключевые слова: клариевый сом, *Clarias gariepinus*, микробиота, метагеном, аквакультура, пробиотики.

A METAGENOMIC MODEL OF MICROBIOTA DYNAMICS OF THE AFRICAN SHARPTOOTH CATFISH *CLARIAS GARIEPINUS* (BURCHELL, 1822) (CLARIIDAE) DURING THE FIRST MONTHS OF LIFE

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Abstract. The study presents a metagenomic analysis of intestinal microbiota dynamics in the African sharptooth catfish *Clarias gariepinus* during the first 60 days of life, aiming to model microbial community succession during the transition from live to formulated feed. The larval stage was dominated by *Proteobacteria* (*Cetobacterium*, *Pseudoalteromonas*), whereas switching to dry feed (day 8) triggered a rapid increase in *Firmicutes* (*Clostridium*) and an increase in conditionally pathogenic *Serratia* (up to 14.8%). By day 60, a stable community developed with recovered *Cetobacterium* abundance. Cluster and regression analyses yielded a three-component model (early *Proteobacteria* – SCFA-producing *Firmicutes* – stabilizer taxa) that predicts microbiota composition throughout development. Network analysis identified a functional “core” comprising *Clostridium* and *Cetobacterium*, characteristic of omnivorous fishes. These findings support the strategic use of probiotics during the critical feed transition window (days 5–14).

Keywords: African sharptooth catfish, *Clarias gariepinus*, microbiota, metagenome, aquaculture, probiotics.

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